



HAL
open science

A stage-dependent seed defense response to explain efficient seed transmission of *Xanthomonas citri* pv. *fuscans* to common bean

Armelle Darrasse, Łukasz Pawel Tarkowski, Martial Briand, David Lalanne, Nicolas Chen, Matthieu Barret, Jerome Verdier

► To cite this version:

Armelle Darrasse, Łukasz Pawel Tarkowski, Martial Briand, David Lalanne, Nicolas Chen, et al.. A stage-dependent seed defense response to explain efficient seed transmission of *Xanthomonas citri* pv. *fuscans* to common bean. *Plant, Cell and Environment*, 2024, 10.1111/pce.15037 . hal-04665509

HAL Id: hal-04665509

<https://hal.inrae.fr/hal-04665509v1>

Submitted on 31 Jul 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License



A “ceasefire” model to explain efficient seed transmission of *Xanthomonas citri* pv. *fuscans* to common bean.

| | |
|-------------------------------|---|
| Journal: | <i>Plant, Cell & Environment</i> |
| Manuscript ID | PCE-23-1399 |
| Wiley - Manuscript type: | Original Article |
| Date Submitted by the Author: | 05-Dec-2023 |
| Complete List of Authors: | Verdier, Jerome; Institut de Recherche en Horticulture et Semences Darrasse, Armelle; Institut de Recherche en Horticulture et Semences Tarkowski, Łukasz Paweł; Institut de Recherche en Horticulture et Semences Briand, Martial; Institut de Recherche en Horticulture et Semences Lalanne, David; Institut de Recherche en Horticulture et Semences Chen, Nicolas W.G.; Institut de Recherche en Horticulture et Semences barret, matthieu; Institut de Recherche en Horticulture et Semences |
| Suggested Editor: | Corne Pieterse |
| Environment Keywords: | pathogens |
| Physiology Keywords: | development |
| Other Keywords: | Seed, <i>Xanthomonas</i> , transmission, <i>Phaseolus vulgaris</i> |
| Abstract: | <p>Although seed represents an important means of plant pathogen dispersion, the seed-pathogen dialogue remains largely unexplored. A multi-omic approach (<i>i.e.</i> dual RNAseq, plant small RNAs and methylome) was performed at different seed developmental stages of common bean (<i>Phaseolus vulgaris</i> L.) during asymptomatic colonization by <i>Xanthomonas citri</i> pv. <i>fuscans</i> (<i>Xcf</i>). In this condition, <i>Xcf</i> did not produce disease symptoms, neither affect seed development. Although, an intense molecular dialogue, via important transcriptional changes, was observed at the early seed developmental stages with down-regulation of plant defense signal transduction, via action of plant miR, and upregulation of the bacterial Type 3 Secretion System. At later seed maturation stages, molecular dialogue between host and pathogen was reduced to few transcriptome changes, but marked by changes in DNA methylation of plant defense and germination genes, in response to <i>Xcf</i> colonization, potentially acting as defense priming to prepare the host for the post-germination battle . This distinct response of infected seeds during maturation, with a more active role at early stages refutes the widely diffused assumption considering seeds as passive carriers of microbes. Finally, our data support a novel plant-pathogen interaction model, specific to the seed tissues, which differs from others by the existence of distinct phases during seed-pathogen interaction with seeds first actively interacting with colonizing pathogens, then both belligerents switch to more passive mode at later stages. We contextualized this</p> |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | |
|---|--|
| | observed scenario in a novel hypothetical model that we called "ceasefire", where both the pathogen and the host benefit from temporarily laying down their weapons until the moment of germination. |
| | |
| Note: The following files were submitted by the author for peer review, but cannot be converted to PDF. You must view these files (e.g. movies) online. | |
| Supplementary Data S1.xlsx Supplementary Data S3.xlsx | |



1
2
3 1 **A “ceasefire” model to explain efficient seed transmission of *Xanthomonas citri* pv.**
4 ***fuscans* to common bean.**

5 2
6 3
7 4 Armelle Darrasse, Łukasz Paweł Tarkowski, Martial Briand, David Lalanne, Nicolas W.G.
8 Chen, Matthieu Barret, Jerome Verdier

9 5
10 6
11 7 Univ Angers, Institut Agro, INRAE, IRHS, SFR QUASAV, F-49000 Angers, France

12 8
13 9 Author for correspondence: Jerome Verdier

14 10 jerome.verdier@inrae.fr

15 11
16 12 **ORCID**s

17 13 Armelle Darrasse: 0000-0002-9334-5862

18 14 Łukasz Paweł Tarkowski: 0000-0002-5419-6606

19 15 Nicolas W.G. Chen: 0000-0002-7528-4656

20 16 Matthieu Barret: 0000-0002-7633-8476

21 17 Jerome Verdier: 0000-0003-3039-2159

22 18
23 19 *Indicate the number of words (Full papers <6,500 words): 6,425*

24 20 *Indicate the number of figures: 4 figures (all in color), 2 tables, 4 supplementary data*

25 21
26 22 **Summary**

- 27 23
- 28 • Although seed represents an important means of plant pathogen dispersion, the seed-pathogen dialogue remains largely unexplored.
 - 29 • A multi-omic approach (*i.e.* dual RNAseq, plant small RNAs and methylome) was performed at different seed developmental stages of common bean (*Phaseolus vulgaris* L.) during asymptomatic colonization by *Xanthomonas citri* pv. *fuscans* (*Xcf*).
 - 30 • In this condition, *Xcf* did not produce disease symptoms, neither affect seed development. Although, an intense molecular dialogue, via important transcriptional changes, was observed at the early seed developmental stages with down-regulation of plant defense signal transduction, via action of plant miR, and upregulation of the bacterial Type 3 Secretion System. At later seed maturation stages, molecular dialogue between host and pathogen was reduced to few transcriptome changes, but marked by changes in DNA methylation of plant defense and germination genes, in response to *Xcf* colonization, potentially acting as defense priming to prepare the host for the post-germination battle. This distinct response of infected seeds during
- 31
32
33
34
35
36

1
2
3 37 maturation, with a more active role at early stages refutes the widely diffused
4 38 assumption considering seeds as passive carriers of microbes.

- 5 39
- 6 39 • Finally, our data support a novel plant-pathogen interaction model, specific to the seed
7 40 tissues, which differs from others by the existence of distinct phases during seed-
8 41 pathogen interaction with seeds first actively interacting with colonizing pathogens,
9 42 then both belligerents switch to more passive mode at later stages. We contextualized
10 43 this observed scenario in a novel hypothetical model that we called “ceasefire”, where
11 44 both the pathogen and the host benefit from temporarily laying down their weapons
12 45 until the moment of germination.
13 46

14 47 **Key words:** Seed, *Xanthomonas*, transmission, dialogue, epigenome, *Phaseolus*
15 48 *vulgaris*, dual transcriptomics.
16 49

17 50 Introduction

18 51 Legumes provide a sustainable source of proteins for human and livestock diet,
19 52 moreover their symbiotic nitrogen fixation capacity contributes to soil preservation and reduces
20 53 the need for chemical fertilizers (Stagnari et al., 2017; Ferreira et al., 2021). An important
21 54 factor limiting legume utilization is their relatively high yield variability, greatly due to their
22 55 susceptibility to environmental factors such as biotic and abiotic stresses (Cernay et al., 2015;
23 56 Martins et al., 2020). While legumes are expected to better perform under changing climatic
24 57 conditions in relation to other crops thanks to higher biomass accumulation under increased
25 58 atmospheric CO₂ levels and higher photosynthetic efficiency under increased irradiation
26 59 levels, other traits are predicted to be negatively affected, such as seed quality and resistance
27 60 to pathogens (Myers et al., 2014).

28 61 Pathogens are responsible for 35-70% yield losses on grain legumes (Martins et al.,
29 62 2020). An important determinant of disease outbreak is pathogen dispersal through infected
30 63 seeds (Denancé and Grimault, 2022). The mode of transmission of pathogens to the seed can
31 64 be schematically summarized in three non-exclusive pathways: internal (*via* the host xylem),
32 65 floral (*via* the pistil) and external as a consequence of contact of the seed with symptomatic
33 66 fruit tissues or with threshing residues (Maude, 1996). For instance, *Xanthomonas citri* pv.
34 67 *fuscans* (*Xcf*), causal agent of common bacterial blight of bean (CBB), can use these three
35 68 pathways for its transmission to common bean seeds (Darsonval et al., 2008; Darrasse et al.,
36 69 2018). Contaminated seeds can be symptomatic or asymptomatic, and are generally
37 70 associated with high or moderate bacterial population sizes, respectively, moreover
38 71 symptomatic seeds often fail to germinate (Darrasse et al. 2018; Chen et al., 2021a) and no
39 72 viable pathogen control method to counteract bacterial seed infections exists.

Decades of research led to a comprehensive overview of the genetic (for review Dodds and Rathjen, 2010; Wirthmueller et al., 2013) and epigenetic (for review Hannan Parker et al., 2022) mechanisms involved in plant-pathogen interactions during vegetative growth. However, the molecular dialogue that takes place between seeds and pathogens was overlooked to date. On the plant side, in the event of an incompatible interaction between *Medicago truncatula* and *X. campestris* pv. *campestris* (*Xcc*), seed transcriptome exhibited an activation of defense response and a repression of seed maturation pathways (Terrasson et al., 2015). From the bacterial side, some specific genetic determinants such as the type 3 secretion system (T3SS, Darsonval et al., 2008) and adhesins (Darsonval et al., 2009) were shown to be involved in the transmission of *Xcf* to common bean seeds. Involvement of the T3SS in seed transmission was also documented for *Acidovorax citrulli* in watermelon (Dutta et al., 2014). However, a global view of bacterial transcriptomic changes occurring during seed transmission is currently missing. This lack of knowledge is partly due to the difficulties of collecting enough bacterial RNA from the seeds. Indeed seed-associated bacterial population sizes are usually very low (from 10 to 1,000 CFU per bean seed; Chesneau et al., 2022) and follow a Poisson distribution, which complicates the sampling of contaminated seeds and prevent molecular analysis of seed-pathogens interactions (Gitaitis and Walcott, 2007).

Since knowledge regarding molecular interactions occurring during bacterial seed infections is currently lacking, the objective of this work was to decipher the molecular dialogue between the common bean (*Phaseolus vulgaris* L.) seed and a seed pathogen at several stages of seed development in order to identify major molecular factors involved in seed infection establishment and pathogen transmission to the seedling. A dual RNAseq approach to identify both the host seed and the *Xcf* pathogen transcriptomes was performed at three stages of seed development during seed filling, seed maturation and seed maturity. The technical limitation of low bacterial population within seeds was successfully bypassed using bacterial transcript enrichment. This transcriptomic analysis was complemented by the analysis of small RNAs and DNA methylation changes in infected seeds to reveal the role of these mechanisms in the seed-pathogen interaction, which allowed us to propose a novel model in plant-pathogen interactions specific to seed developmental stage and explaining the efficiency of pathogen seed transmission.

Materials and Methods

Bacterial strain and inoculum preparation

The *Xcf* bacterial strain 7767R (Rif^R, Darrasse et al., 2018) was grown for 24h at 28°C in Tryptic Soy Agar at 10% (1.7 g.L⁻¹ tryptone, 0.3 g.L⁻¹ soybean peptone, 0.25 g.L⁻¹ glucose, 0.5 g.L⁻¹ NaCl, 0.5 g.L⁻¹ K₂HPO₄ and 15 g.L⁻¹ agar) supplemented with 50 mg.L⁻¹ rifamycin.

1
2
3 109 Bacterial cells were suspended in sterile distilled water, calibrated at 10^8 CFU.mL⁻¹ (OD₆₀₀ =
4 110 0.1) and adjusted to 10^6 CFU.mL⁻¹ for spray-inoculation.

5
6 111

8 112 **Plant materials and production of contaminated seeds**

9 113 Experiments were performed with *Phaseolus vulgaris* L. cv. Flavert, a cultivar
10 114 susceptible to CBB (Darrasse et al., 2007). Seeds were sown in one liter of Tray substrate
11 115 (NF U 44–551, Klasmann- Deilmann GmbL, Rippert France). Plants were grown in a controlled
12 116 growth chamber with 16h of light at 23°C and 8h of dark at 20°C and a relative humidity (RH)
13 117 of 70%. Plants were watered twice a week during the first three weeks, then with a nutrient
14 118 solution (N/P/K=15/10/30). Plants were staked and pinched after the third leaf.

15 119 Plants were spray-inoculated at the flower bud stage (R5, Michael 1994) with either
16 120 *Xcf* bacterial suspension (10^6 CFU.mL⁻¹) or water as control. The day prior to inoculation,
17 121 temperature (day 25°C/night 23°C) and RH (95%) were increased. Inoculation was performed
18 122 using a two-step protocol. First, small green flower buds were sprayed. Three days later,
19 123 flower buds at the pollination stage were tagged. Then, a second inoculation was performed
20 124 at one day after pollination (DAP) when tagged organs turned into open flowers. Then
21 125 afterward, RH was reduced to 70% to limit pathogen symptom development and seed
22 126 abortion. Three independent replicates of five plants ($n=15$) were inoculated. Tagged pods
23 127 were harvested at 24, 35 and 42 DAP. Seeds were collected aseptically from pods to avoid
24 128 contamination by external bacterial populations (Darsonval et al., 2008).

25 129

26 130 **Monitoring of bacterial population sizes**

27 131 For each sample, *Xcf* population sizes were determined from ten individual seeds and from
28 132 five pools of three seeds. Seeds were soaked in 0.5 mL of sterile water per seed overnight at
29 133 4°C under shaking (150 rpm). Then, 50 µL of serial dilutions were plated on 10% TSA.
30 134 Colonies were monitored five days after incubation at 28°C. The contamination rate of a
31 135 sample (p) was calculated from the analysis of N sub-samples according to the formula $p = 1 -$
32 136 $(Y/N)^{1/n}$ (Maury et al., 1985), where n is the number of seeds in each group and Y the number
33 137 of healthy groups.

34 138

35 139 **Seed physiological analyses**

36 140 Three sub-samples of ten seeds were used to determine dry weight and water content. Each
37 141 sub-sample was weighed before and after incubation (3 days) in a 96°C incubator (Mettler).

38 142

39 143 **Plant and bacterial RNA extraction and RNA sequencing**

40 144 Seed samples harvested at 24, 35 and 42 DAP were flash-frozen in liquid nitrogen.
41 145 Samples were ground in liquid nitrogen using a mechanical grinder (Retsch MM300

1
2
3 146 TissueLyser) during 1 min at 30 Hertz. Total RNAs were extracted using the NucleoSpin® RNA
4 147 Plant and Fungi Kit (Macherey-Nagel, Düren, Germany), according to the manufacturer
5 148 instructions. RNA quantity and integrity were assessed respectively using a NanoDrop
6 149 ND-1000 (NanoDrop Technologies, Wilmington, DE, USA) and a 2100 Bioanalyzer (Agilent
7 150 Technologies, Santa Clara, CA, USA). Library constructions and single-end sequencing
8 151 (SE50, 20M) were outsourced to the Beijing Genomics Institute (BGI, <https://www.bgi.com>)
9 152 using the Illumina Hiseq 2500 technology. Raw reads are available at GSE226918.
10 153

11 154 Using the same seed lots as for plant RNAs, bacterial macerates were collected after
12 155 soaking contaminated seeds (2 mL per gram of seed) overnight in KPO₄ buffer, (50 mM, pH
13 156 6.8), supplemented with 20% of blocking agent (RNAlater, ThermoFisher scientific, Carlsbad,
14 157 CA, United States). After centrifugation (15 min at 15,000 g) and removal of the supernatant,
15 158 total RNAs were extracted as previously described (Darsonval et al., 2009). Concentration
16 159 and integrity of RNAs were assessed with Qubit (Invitrogen, Carlsbad, CA, USA) and a 2100
17 160 Bioanalyzer (Agilent Technologies, Santa Clara, CA, USA), respectively. As total RNA
18 161 extracted from bacterial macerates corresponded mainly to plant transcripts (not shown), we
19 162 designed a procedure of bacterial transcript enrichment. Bacterial mRNAs were captured
20 163 using the SureSelectXT RNA Direct technology (Agilent, Santa Clara, CA, USA). A total of
21 164 54,548 probes of 120-nts length were designed based on the predicted mRNAs of *Xcf7767R*
22 165 genome sequence (GCA_900234465; Chen et al., 2018). Quality and quantity of sequencing
23 166 libraries were evaluated and quantified using Bioanalyzer and KAPA Library Quantification
24 167 assay (Roche, Basel Switzerland). Paired-end sequencing (2 × 75 bp) was performed with a
25 168 NextSeq 550 System High OutPut kit (Illumina, San Diego, CA, USA). Raw reads are available
26 169 at GSE227386.

27 170 After quality control, high-quality reads were mapped either on *Xcf7767R* transcriptome
28 171 (Briand et al., 2021) (<https://bbric-pipelines.toulouse.inra.fr/myGenomeBrowser?browse=1&portalname=Xcf7767Rpb&owner=armelle.darrasse@inrae.fr&key=TwzQ08DA>) or on *P. vulgaris* transcriptome version 2.1
29 172 (https://phytozome-next.jgi.doe.gov/info/Pvulgaris_v2_1) using quasi-mapping alignment and
30 173 quantification methods of Salmon algorithm v.1.2 (Patro et al., 2017). RNA-Seq data were
31 174 normalized as transcripts per million (TPM). Differentially expressed genes (DEGs) were
32 175 determined using DESeq2 v1.22.2 (Love et al., 2014), using an adjusted p-value <5%. *Xcf*
33 176 DEGs were analyzed between sampling dates. *P. vulgaris* DEGs were obtained by comparing
34 177 *Xcf*- versus H₂O-inoculated seeds at each developmental stage. Gene annotations were
35 178 provided with the *P. vulgaris* version 2.1 genome and Mapman functional categories v.4 were
36 179 determined using Mercator tool from the predicted protein sequences (Schwacke et al., 2019).
37 180 Bacterial Type III effectors were predicted using the automated machine-learning based web
38 181
39 182

1
2
3 183 server Effectidor (Wagner et al., 2022). Over representation analyses of MapMan or COG
4 184 terms were performed, respectively for plant and bacteria DEGs, using Clusterprofiler (Yu et
5 185 al., 2012) package in R by applying an adjusted p -value cut-off <0.05 obtained after the
6 186 Bonferroni-Hochberg procedure.

7
8
9 187 Differentially expressed genes during seed germination were identified using the data
10 188 generated by Narsai et al. (2017) available in the SRA database (accession GSE94457). Raw
11 189 reads were downloaded and mapped against the Arabidopsis transcriptome using Salmon
12 190 algorithm and DEGs during germination kinetic were determined using ImpulseDE2 algorithm
13 191 (Fischer et al., 2018) following an adjusted p -value $<1\%$.

14 192 To determine genes involved in post-germination defense, we inoculated healthy
15 193 seeds with 10^7 of *Xcf* CFU.mL⁻¹ or H₂O during 25 min followed by 3 min of vacuum infiltration
16 194 before seed drying at room temperature. Inoculated dried seeds displaying between 10^4 and
17 195 10^5 CFU.seed⁻¹ of *Xcf* were used for germination assay on Whatman paper in 16h-light growth
18 196 chamber at 25°C. *Xcf*- and H₂O-inoculated seeds were collected at 3 and 7 Days After
19 197 Imbibition (DAI) and dissected as separated cotyledons and radicles for real-time qRT-PCR
20 198 experiments. RNA were extracted at different germination timepoints and in different tissues
21 199 using the NucleoSpin® RNA Plant and Fungi Kit (Macherey-Nagel, Düren, Germany) as
22 200 described above but including a DNase treatment (Macherey-Nagel, rDNase set, Düren,
23 201 Germany). RNA were quantified using a using a NanoDrop ND-1000 (NanoDrop
24 202 Technologies, Wilmington, DE, USA) and cDNA was synthesized from 1 µg of total RNA using
25 203 the Reverse Transcription system (iScript™ cDNA synthesis kit, Bio-Rad). Quantitative Real
26 204 time PCR was performed using Sybr Green Master Mix (SYBR Green master mix, Bio-Rad)
27 205 on a CFX96 real-time detection system (Bio-Rad Laboratories). *EF1* and *UBI* genes were used
28 206 as housekeeping genes as described in Darrasse et al. (2010). Primers used for Real-time
29 207 PCR are listed in Supplementary Table S4.

30 208

31 209 **small RNA extraction and analysis (sRNA-seq)**

32 210 Using the same frozen powders obtained from *Xcf*- and H₂O-inoculated seeds from 24
33 211 DAP and 42 DAP, we extracted small RNA using the NucleoSpin® miRNA Kit
34 212 (Macherey-Nagel, Düren, Germany), according to the manufacturer's instructions. Small RNA
35 213 enrichment was validated using Bioanalyzer small RNA analysis. Small RNAs were
36 214 sequenced using DNBseq sequencing technology (SE50 40M, BGI) and Unique Sequence
37 215 identifiers (UMI) to correctly quantify unique reads. Reads of 20 to 24 nucleotides were
38 216 extracted and mapped on the reference mature miRNA database available in miRBase version
39 217 22 (Kozomara et al., 2019) using bowtie (Langmead et al., 2009) and quantified using
40 218 SAMtools (Li et al., 2009). Differentially expressed small RNA between *Xcf*-inoculated versus
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3 219 H₂O-inoculated seeds at 24 and 42 DAP were determined using DESeq2 following a *p*-value
4 220 threshold < 5% from the SARTools R package (Varet et al., 2016). Known and putative novel
5 221 small RNAs were mapped to the *P. vulgaris* genome sequence using ShortStack4 algorithm
6 222 (Johnson et al., 2016) and displayed in the dedicated Jbrowse
7 223 https://iris.angers.inrae.fr/pvulgaris_v2 in the 'small RNA tracks' section. Transcripts
8 224 potentially targeted by miRNAs were predicted via analyzing complementary matching
9 225 between sRNA and target and evaluating target site accessibility using psRNATarget tool (Dai
10 226 and Zhao, 2011; Dai et al., 2018) and a threshold of expectation below 5 was set to consider
11 227 transcripts as putative miRNA targets. Raw reads are publicly available at GSE226920.
12
13
14
15
16
17
18

219 **Plant DNA extraction and Bisulfite sequencing experiments (BS-seq)**

20 230 From the same frozen seed powders used for RNA extractions, we performed DNA
21 231 extraction, on the three biological replicates of *Xcf*- and H₂O-inoculated seeds at 42 DAP,
22 232 using the NucleoSpin® DNA Food Kit (Macherey-Nagel, Düren, Germany), according to the
23 233 manufacturer's instructions. DNA samples were sent to the BGI Genomics (Hong Kong) for
24 234 bisulfite treatment using a ZYMO EZ DNA Methylation-Gold kit, library construction and
25 235 paired-end sequencing using BGISEQ-500 sequencing technology (PE100 45M). FastQC
26 236 was used to check sequencing quality and clean reads were mapped to the *P. vulgaris*
27 237 genome version 2.1 using Bismark software (Krueger and Andrews, 2011). After mapping,
28 238 deduplication of sequences and quantification of cytosine methylation were performed using
29 239 Bismark_deduplicate and Bismark_methylation_extractor. Each context of methylation was
30 240 considered independently: CG, CHG, or CHH and corresponding bigwig files were generated
31 241 using bismark_to_bigwig python script and displayed in the dedicated Jbrowse:
32 242 https://iris.angers.inrae.fr/pvulgaris_v2. Putative differentially methylated regions (DMRs)
33 243 were identified in each independent methylation context using DMRCaller algorithm available
34 244 in R (Catoni et al., 2018). Raw reads are publicly available at
35 245 <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE226919>.
36
37
38
39
40
41
42
43
44
45
46
47
48

246

247 **Results**

248 ***Seed transmission of moderate Xcf population sizes does not impact seed*** 249 ***development***

250 Seed transmission of *Xcf* 7767R was investigated following spray-inoculation of *P.*
251 *vulgaris* L. cv Flavert. Three stages of seed development were targeted: (i) 24 DAP (seed
252 filling), (ii) 35 DAP (seed maturation) and 42 DAP (seed maturity). Seed water content (Fig.
253 1A) and dry seed weight (Fig. 1B) were not significantly impacted by *Xcf*-inoculation. As

1
2
3 254 described in Darsonval et al. (2008), we used 10^6 CFU.mL⁻¹ for *Xcf* spray-inoculation at
4 255 flowering time to allow seed bacterial transmission without apparition of symptoms during seed
5 256 development. Otherwise, higher concentration could generate symptomatic seed bacterial
6 257 transmission leading to defect in germination of infected seeds. Following this mild treatment,
7 258 about 80% of seeds were contaminated with *Xcf* with an average population size of 10^5 CFU.g⁻¹
8 259 of seeds at 24 DAP (Fig. 1C). Over the course of seed development, the frequency of
9 260 detection of *Xcf* decreased from 80% to 50%. This was accompanied by a significant decrease
10 261 in *Xcf* population size from 35 to 42 DAP, down to an average of 10^3 CFU.g⁻¹ of seeds at
11 262 maturity (Fig. 1C).

18 263 ***Changes in the Xcf bacterial transcriptome during seed development***

21 264 To explore the genetic determinants involved in *Xcf* seed transmission, dual (host and
22 265 pathogen) transcriptome sequencing was performed at 24, 35 and 42 DAP. An essential step
23 266 to obtain sufficient bacterial transcript data was to enrich RNA-Seq libraries for *Xcf* transcripts
24 267 using 54,656 capture-probes. Among a total of 27.7 to 61.3 M sequenced reads that were
25 268 obtained for each sample, 4.7 to 55.1 M mapped on the predicted transcriptome of *Xcf* strain
26 269 7767R (Supplementary Table S1). A total of 4,372 mRNA were detected in at least one sample
27 270 (count ≥ 10), which corresponded to >96% of the 4,537 predicted mRNA, thus validating our
28 271 *Xcf* transcriptome enrichment strategy. Extensive changes in *Xcf* transcriptome were
29 272 observed between seed filling (24 DAP) and the two other seed maturation stages (35 and 42
30 273 DAP). Indeed, 865 and 1,674 DEGs were detected between 24 and 35 DAP and 24 and 42
31 274 DAP, respectively, (Fig. 2A). On the other hand, only 17 DEGs were detected between 35 and
32 275 42 DAP, indicating that transcriptomic levels stabilized between seed maturation and maturity
33 276 stages. In line with this result, over-representation analyses of COG terms associated to
34 277 bacterial DEGs were performed and revealed that intracellular trafficking and secretion terms
35 278 were enriched at 24 DAP and post-translational modification at 35 and 42 DAP (Fig. 2B). The
36 279 other enriched categories were translation and repair, both enriched at 42 DAP,
37 280 and extracellular structure and cell motility, both enriched at 24 DAP (Fig. 2B).

38 281 A focus on the COG related to secretion processes revealed that all T3SS encoding
39 282 genes and several *xps* genes involved in the T2SS were up-regulated at the seed filling stage,
40 283 but not later during seed maturation (Supplementary Table S1). This was consistent with the
41 284 observed up-regulation of the master regulator *hrpG* that is known to control many genes
42 285 involved in the interaction with the host plant (Teper et al., 2021) such as the T3SS
43 286 transcriptional activator *hrpX* and cognate effectors (T3Es) but also the *xps* genes involved in
44 287 the secretion of cell wall degrading enzymes (Szczyzny et al., 2010). In line with this result,
45 288 26/40 (65%) of T3E-encoding genes and several genes encoding pectin lyase (1), pectate
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3 289 lyases (2), glycoside hydrolases (34) and proteases (40) were only up-regulated at early stage
4 290 (Supplementary Table S1). As demonstrated in Darsonval et al. (2008), T3SS encoding
5 291 genes, including hrpG and hrpX are essential genes for efficient bacterial seed transmission.
6
7 292 Together, these results suggested that bacteria were actively interacting with the host plant
8
9 293 only at early seed maturation stages, but not later.

12 294 **Transcriptomic analysis of bean seeds in response to pathogen colonization**

14
15 295 Changes in *P. vulgaris* transcriptome were assessed using the same seed lots as for
16 296 the *Xcf* transcriptome analyses described above. All results from this RNA-Seq analysis are
17 297 displayed in the dedicated Jbrowse (https://iris.angers.inrae.fr/pvulgaris_v2) and in
18 298 Supplementary Table S1. Similar to what was observed in *Xcf* transcriptome changes, RNA-
19 299 Seq analysis revealed that the plant response to the bacteria was higher at early than later
20 300 stages of seed maturation, with 1,826 DEGs at 24 DAP, 1,351 at 35 DAP and only 105 at 42
21 301 DAP (Fig. 2C). Only 137 DEGs (7.5% of 24 DAP DEGs) were shared between 24 and 35 DAP,
22 302 indicating that the plant's response was different between these stages, ending up with almost
23 303 no response in mature seeds. Only one DEG, encoding a CHAPERONE PROTEIN DNAJ-
24 304 LIKE PROTEIN, was found to be in common between all the three stages
25 305 (*Phvul.001G262000*) and could reflect a cellular stress in seeds inoculated with *Xcf*. This low
26 306 overlap in DEGs across different seed developmental stages was also reflected at the level of
27 307 functional category enrichments, which were different between 24, 35 and 42 DAP (Fig. 2D).
28 308 The 24 DAP timepoint displayed the most complex response, with six up-regulated and nine
29 309 down-regulated Mapman functional categories detected through functional enrichment
30 310 analysis of DEGs. Some categories had well characterized roles in the plant-microbe
31 311 molecular dialogue, such as Leucine Rich Repeat protein kinases (LRRs), which were up-
32 312 regulated in *Xcf*-inoculated seeds (*i.e.* up-regulation of 15 annotated LRR related proteins),
33 313 whereas the Mitogen-Activated Protein Kinases (MAPKs) and transcription factors (TF) of the
34 314 bZIP, TIFY and AP2/ERF classes were down-regulated. At 24 DAP, in parallel to the down-
35 315 regulation of MAPKs known to be involved in defense signal transduction such as MAPKKK3,
36 316 MAPK3 or MAPK4, we also identified down-regulation of defense related genes such as two
37 317 encoding thaumatin pathogenesis-related (PR) proteins, five JAZ and one JAR genes involved
38 318 in the jasmonic acid pathway, but also *PAD4*, a central regulator of the salicylic acid pathway
39 319 (Supplementary Table S1). At 35 DAP, functional ontology enrichment detected four up-
40 320 regulated categories related to peptidase/protease activities and transfer of carbon skeletons.
41 321 At 42 DAP, only two up-regulated categories (chromatin regulation and calcium-permeable
42 322 channel) were detected.

59 323 **Small RNAs associated with *Xcf* seed colonization**

1
2
3 324 To further characterize the molecular dialogue between the colonized seeds and *Xcf*
4 and the changes in plant transcript expression we focused our analysis on small RNA changes
5 325 between colonized and healthy seeds at two contrasted stages, at 24 DAP to decipher if
6 326 transcriptome changes due to plant response to pathogen could be mediated by small RNAs
7 327 and at 42 DAP to reveal if specific small RNA could be stored at seed maturity to mediate
8 328 defense response at post-germinative stage. Following sequencing and mapping against the
9 329 mature miRNA database (miRBase release 22), we observed a total of 255 and 112 mature
10 330 miRNAs differentially expressed ($p < 0.05$) between *Xcf*-colonized and healthy seeds at 24 and
11 331 42 DAP, respectively. At 24 DAP, mature miRNA up-regulated in *Xcf*-colonized seeds
12 332 belonged to six miRNA families (miR162, miR172, miR396, miR482, miR6478 and miR8175),
13 333 while four miRNA families showed down-regulation (let7, miR21, miR2111 and miR482)
14 334 (Supplementary Table S2, Table 1). Similarly, at 42 DAP, we observed up-regulation of only
15 335 one miRNA family (miR31) and down-regulation of two miRNA families (miR164 and miR451)
16 336 (Supplementary Table S2, table 1). These data further confirmed that the molecular dialogue
17 337 was more intense at early stages compared to later stages. Moreover, several miRNA families
18 338 differentially regulated in *Xcf*-inoculated seeds were known to be involved in plant defense
19 339 response such as miR482 (Shivaprasad et al., 2012), miR396 (Soto-Suárez et al., 2017) and
20 340 miR172 (Holt et al., 2015). Known and unknown identified small RNAs were mapped to the
21 341 genome using ShortStack version 4 and are available in the dedicated *P. vulgaris* Jbrowse
22 342 (https://iris.angers.inrae.fr/pvulgaris_v2).
23 343

24
25
26
27 344 To reveal the potential response mediated by these miRNAs, we identified putative
28 345 transcript targets using (i) psRNATarget predictive tool (Dai et al. 2018) combined with (ii) our
29 346 generated transcriptomic data at these two stages (Supplementary Table S2). To clarify, a
30 347 transcript was considered as putative miRNA target if (i) its expectation (E) score from
31 348 PsRNATarget was below 5 and if (ii) its expression was down-regulated when miRNA was up-
32 349 regulated or inversely. Following these criteria, we identified between one to 11 putative
33 350 miRNA target transcripts depending on miRNA families (Table 1). Among miRNAs up-
34 351 regulated at 24 DAP in *Xcf*-inoculated, there were target transcripts related to defense such
35 352 as miR8175 that could down-regulate key defense genes such as *PAD4-LIKE* involved in the
36 353 defense pathway mediated by salicylic acid or more generic ones potentially involved in
37 354 defense signaling such as a calcium-dependent-lipid-binding domain gene (CalB) or
38 355 phospholipase A1 (Table 1). At the opposite, in the *Xcf*-inoculated seeds, we observed down-
39 356 regulation of miRNA families such as let7, miR21, miR2111 and miR482 that potentially
40 357 enhanced expression of developmental/growth genes such as TOR-LIKE, MED15, MED13,
41 358 NOC1/SWA2. At 42 DAP, only three miR families, miR31, miR451 and miR164, showed
42 359 significant expression changes between *Xcf*-infected and healthy seeds. An unique putative

1
2
3 360 transcript target was identified associated with miR451, which encodes a UBP26-LIKE protein
4 361 potentially involved in the heterochromatin silencing at the end of the seed maturation (Luo et
5 362 al., 2008). In conclusion, these results suggested that miRNA did mediate seed growth by
6 363 silencing defense response at 24 DAP during early seed development. On the other hand at
7 364 maturity, even if miR164 up-regulation was already shown to be involved in plant defense
8 365 against fungi in cotton (*Gossypium hirsutum*) and *Populus tomentosa* (Hu et al., 2020; Chen
9 366 et al., 2021b), in our susceptible host this miR was down-regulated at 42 DAP, which did not
10 367 support the hypothesis that specific miRNA were accumulated in *Xcf*-inoculated seeds to
11 368 prepare plant defense during germination. Interestingly, at 24 and 42 DAP, we observed that
12 369 plant miRNA could support seed defense silencing probably due to the bacteria infection
13 370 arsenal such as its T3Es activated early during seed development.

371 ***Seed methylome dynamics associated with Xanthomonas seed colonization***

372 To better understand the plant defense response and the impact of the bacterial
373 colonization during seed development, we analyzed the changes in the seed methylomes of
374 healthy and *Xcf*-colonized bean seeds at seed maturity (42 DAP). Indeed, DNA methylation
375 was already described as a relevant mechanism in defense priming and plant immunity (for
376 review see Deleris et al., 2016; Espinas et al., 2016). By focusing on the mature stage, we
377 intended to capture the cumulative impact on DNA methylation of the bacterial colonization
378 throughout seed development. The comparison of *Xcf*-colonized **versus healthy seeds**
379 **samples** revealed 954 Differentially Methylated Regions (DMRs), of which 61.95% were
380 hypomethylated (loss of methylation due to bacterial colonization) and 38.05%
381 hypermethylated (gain of methylation due to bacterial colonization) (Supplementary Table S3).
382 Not surprisingly, DMRs were predominantly localized on sequences containing transposable
383 elements or repeats (74.1% of total DMRs), while 7.9% and 4.5% were located within gene
384 and promoter sequences, respectively (Fig. 3A). Regarding the methylation context, we mainly
385 observed DMRs in the CHH (*i.e.* 481 DMRs) and CHG (*i.e.* 394 DMRs) contexts, while only
386 79 were related to the CG context. The complete list of the differentially methylated genes can
387 be found in Supplementary Table S3 and in the dedicated Jbrowse
388 (https://iris.angers.inrae.fr/pvulgaris_v2).

389 We identified a total of 102 DMRs located within either coding (n=66) or promoter
390 regions (n=36) of annotated genes, affecting 99 unique genes. Among coding sequences, 33
391 genes resulted in hypomethylation and 33 hypermethylation, while among promoter regions
392 27 genes were hypomethylated and 9 hypermethylated (Fig. 3B). To understand the role of
393 genes differentially methylated in promoter and coding sequences at seed maturity, we
394 compared with their changes in expression and did not observe any overlap with the DEGs

1
2
3 395 between *Xcf*-colonized and non-colonized mature seeds, suggesting that differentially
4 396 methylated regions did not regulate gene expression during seed development. To understand
5 397 the potential role of these DMRs in the host-pathogen interaction, we looked at genes involved
6 398 both in the germination and defense processes. First, from the dataset generated from Narsai
7 399 et al. (2017) during ten early stages of *A. thaliana* seed germination, we identified 21,015
8 400 genes showing a differential expression (adjusted *p*value <1% using ImpulseDE2) during
9 401 germination process, therefore potentially involved in germination. By mapping *P. vulgaris*
10 402 transcripts on Arabidopsis transcripts, we identified potential homologous transcripts in these
11 403 two species and revealed a statistically significant enrichment (Fig. 3B, Fisher's Exact test *p*-
12 404 value < 2.2e-16) of *P. vulgaris* genes displaying DMRs following pathogen colonization with
13 405 those differentially expressed during germination. Indeed, out of the 90 homologous genes
14 406 identified in *A. thaliana* and displaying DMR, 78 were genes differentially expressed during
15 407 germination (Fig. 3C). Second, by analyzing the list of 99 unique genes displaying changes in
16 408 methylation levels following bacterial colonization, we compiled a list of genes with putative
17 409 roles in defense. We identified 17 genes, 10 hypomethylated and 7 hypermethylated following
18 410 bacterial infection (Table 2). As example, we observed five LRR-related protein kinases, two
19 411 PR proteins, and some genes identified as involved in immune response such as *PUB13-*
20 412 *LIKE*, *CES11-LIKE* or *WRKY72* (complete list in Supplementary Table S3). As it is known that
21 413 changes in the methylation state of transposable regions can also spread to adjacent regions
22 414 and regulate nearby gene expression (Ahmed et al., 2011), we extended our search to coding
23 415 sequences that are 5kb nearby DMRs located in transposable regions. This analysis detected
24 416 additional 280 genes potentially associated with DMRs located in transposable regions (61.4%
25 417 with hypomethylated regions and 38.6% with hypermethylated regions). Among these genes,
26 418 we observed a subgroup coding for disease resistance proteins, with 5 additional putative TIR-
27 419 NB-LRR proteins (*Phvul.004G105600*, *Phvul.004G100300*, *Phvul.010G026400*,
28 420 *Phvul.010G027900*, *Phvul.010G028000*), 3 putative NB-ARC proteins (*Phvul.002G130300*,
29 421 *Phvul.002G130400*, *Phvul.004G076100*) and 4 putative LRR kinases (*Phvul.008G164500*,
30 422 *Phvul.008G164600*, *Phvul.005G162100*, *Phvul.005G162000*) (Table 2, Supplementary Table
31 423 S3 and in the dedicated Jbrowse). In total, we listed 17 DMRs nearby genes associated with
32 424 defense processes (Table 2). A comparison between these two lists revealed that 5 genes
33 425 encoding three *LRR related proteins* (*Phvul.008G164600*, *Phvul.005G162000* and
34 426 *Phvul.005G163000*), one *TIR NBS LRR protein* (*Phvul.010G026400*) and *WRKY72 TF*
35 427 (*Phvul.003G068700*), displayed DMRs both within their gene sequences and in transposable
36 428 elements located in proximal genomic regions. To define if these DMRs present in defense
37 429 genes could be associated to a mechanism of defense priming induced by the presence of
38 430 the pathogen during seed development, we selected the most differentially methylated, the
39 431 *WRKY72* gene, and validated its implication in *Xcf* response during germination. By qRT-PCR,

1
2
3 432 we analyzed the expression profile of *WRKY72* during germination in healthy seeds that
4 433 germinated in presence of water versus *Xcf*. We clearly observed an over-expression of
5 434 *WRKY72* at 7 days after imbibition in radicle of germinated seeds in presence of *Xcf*, showing
6 435 the role of this gene in the defense response to *Xcf* infection during germination (Fig. 3D).

7
8
9
10 436 Together, these results suggested that DMRs due to the presence of *Xcf* were mainly
11 437 located in genes that could serve during the germination process and/or to the plant immune
12 438 response to *Xcf*. In other word, pathogen-specific DNA methylations occurring during seed
13 439 development could serve as defense priming to regulate gene expressions during the
14 440 germination process, including a resumption of the molecular dialogue with the pathogen.

15
16
17
18
19 441

20 442 Discussion

21
22
23 443 Seeds are essential components of plants fitness and represent an important means
24 444 of pathogen dispersion. To date, seed-pathogen interactions have been understudied at the
25 445 molecular level, with, to our knowledge, only one plant-orientated study describing the
26 446 transcriptomic response of *Medicago truncatula* seeds to bacterial pathogens of the
27 447 Xanthomonadaceae family (Terrasson et al., 2015). We thus attempted to mitigate this
28 448 knowledge gap by describing the molecular dialogue between common bean seeds and *Xcf*
29 449 in conditions that seed bacterial transmission was asymptomatic. A first central result
30 450 regarding this interaction is that *Xcf* was able to colonize seeds without major impact on seed
31 451 physiology parameters, which was reflected by similar dry weights and water contents in
32 452 healthy- and infected-seeds (Fig. 1). Consequently, we could not observe any obvious
33 453 morphological changes in *Xcf*-colonized seeds compared to mock treated samples. Such
34 454 findings indicate that asymptomatic *Xcf* colonization does not impact seed development or
35 455 alter seed growth. This is consistent with previous report in *M. truncatula* during compatible
36 456 interaction with *X. euvesicatoria* pv. *alfalfae*, while incompatible interaction with *X. campestris*
37 457 pv. *campestris* resulted in developmental defects alongside a strong activation of defense
38 458 pathways (Terrasson et al., 2015).

39
40
41
42
43 459 To look into molecular dialogue, transcriptomic changes were assessed using dual
44 460 RNAseq, which implies that we profiled both bacterial and plant transcripts during seed
45 461 development generating the first dual transcriptomic analysis of a seed-pathogen interaction
46 462 ever made. Profiling of bacterial transcripts represented the main challenge we faced due to
47 463 the low concentration of bacterial cells within seeds. In this study, we successfully achieved
48 464 this technological breakthrough by an enrichment step of bacterial transcripts using an RNA
49 465 capture technology provided by Agilent. Our study revealed that *Xcf* and common bean seeds
50
51
52
53
54
55
56
57
58
59
60

1
2
3 466 establish an intense molecular dialogue at the early stages of seed development that appears
4
5 467 to become less intense as seed maturity approaches (Fig. 2).

6 468 On the pathogen side, the up-regulation of the T3SS genes and cognate effectors
7
8 469 observed in the early stages in comparison with 42 DAP suggests they could play a role in the
9
10 470 host defense silencing during the early step of seed colonization (Buttner, 2016). Indeed,
11 471 **Xanthomonads** T3SS and T3Es are known to play two crucial roles in allowing efficient
12
13 472 bacterial seed transmission (Darsonval et al., 2008) and in suppressing plant innate immunity
14
15 473 and modulate plant pathways for the benefits of the bacteria (Büttner, 2016). Interestingly,
16 474 down-regulated categories at early stages include basic biological processes such as
17
18 475 translation, protein turnover and DNA replication. This might suggest that *Xcf* multiplication is
19 476 hampered, consistently with the observation that number of *Xcf* cells in seeds does not
20
21 477 increase significantly throughout seed developmental stages (Fig. 1C). Fewer functional
22 478 categories were enriched at 35 DAP (Fig. 2D). The up-regulated ones (4 out of 5) included
23
24 479 peptidases, glycosylases and methyl transferases. Such functions can be associated with both
25
26 480 suppression of defense (peptidases, Figaj et al., 2019) and cell wall remodeling, which could
27
28 481 help bacterial colonization of seed tissues, with no detectable impact on the seed physiology
29 482 and morphology, although more subtle microscopical effects cannot be excluded (Fig. 1).

30 483 On the host side, we also observed intense gene expression changes at early seed
31
32 484 developmental stage (24 DAP) in comparison to later ones, concomitantly with the intense
33
34 485 bacterial secretion activity. We observed an enrichment of up-regulated Leucine Rich Repeat
35 486 (LRR) protein kinases (2 categories out of 6, LRR class VIII and class Xb), which are known
36 487 to have prominent roles in microbe perception and defense activation **in non-seed tissues**
37
38 488 (Chakraborty et al., 2019), suggesting that the host may be able to recognize the pathogen.
39
40 489 On the other hand, RNA-Seq data highlighted a down-regulation of gene categories with well
41
42 490 characterized roles in the transduction of defense signaling pathways, including Mitogen-
43
44 491 Activated Protein Kinases (MAPKs such as MAPKKK3, MAPK3 or MAPK4) and transcription
45
46 492 factors of the bZIP (basic leucine ZIPper), TIFY, and AP2/ERF (APETALA 2/ Ethylene
47
48 493 Responsive Factor) families (Bethke et al., 2009; Bai et al., 2011; Tintor et al., 2013; Noman
49
50 494 et al., 2017). In line with this, we observed down-regulation of transcription factor families
51
52 495 known to have wider functions in plant stress signaling, such as the TUB or TLP (TUBBY-Like
53
54 496 Proteins) and the HSF (Heat Shock Transcription factor), as well as genes encoding PR
55
56 497 proteins, including *JAZ* and *JAR* genes involved in the jasmonic acid pathway, and *PAD4*
57
58 498 involved in the salicylic acid pathway. Such data suggest that even the transduction
59
60 499 components of the defense pathway are inhibited, potentially due to the bacterial T3E,
500 ultimately avoiding a defense response.

501 Similar to transcriptomic data, changes in expression of small RNA at 24 DAP and 42
502 DAP were consistent with silencing of downstream defense gene response. Indeed, analysis

1
2
3 503 of the differentially expressed miRNA at 24 DAP and their putative target genes suggest a
4 504 growth/defense trade-off mechanism in favor of growth in *Xcf*-inoculated seeds, with down-
5 505 regulation of defense-associated transcripts (e.g. putative ortholog of PAD4
6 506 (*Phvul002G274500*, Phyto Alexin Deficient 4, involved in salicylic acid signaling in *A. thaliana*
7 507 (Pruitt et al., 2021)), a pepsin-type protease (*Phvul001G229200*) and up-regulation of
8 508 development-associated transcripts (e.g. TOR-LIKE (*Phvul011G050300*) and
9 509 MED15 (*Phvul010G157900*, MEDIATOR 15, required for correct embryogenesis in *A. thaliana*
10 510 (Kim et al., 2016)). Interestingly, a heat shock protein (HSP70, *Phvul003G154800*) was
11 511 detected as down-regulated genes at 24 DAP in *Xcf*-inoculated seeds and potential target of
12 512 miR396, which complete the observed downregulation of HSF and smallHSP from our infected
13 513 host transcriptome data (Fig. 2D). Recently it was showed that heat shock proteins are the
14 514 most represented family among the down-regulated DEGs in leaf in a resistant common bean
15 515 genotype towards common bacterial blight (caused by *Xcf* and *Xanthomonas phaseoli* pv.
16 516 *phaseoli*) in comparison to a susceptible one (Foucher et al., 2020). On the other hand, data
17 517 obtained at 42 DAP revealed only down-regulation of one miRNA family miR451, potentially
18 518 regulating the up-regulation of its predicted target gene (*Phvul009G100000*) (Table 1). Its *A.*
19 519 *thaliana* homolog (AT3G49600.1) deubiquitinates the histone H2B and is required for
20 520 heterochromatin silencing during seed development (Luo et al., 2008). It is worth noting that
21 521 chromatin reorganization processes due to histone modifications are among the categories
22 522 enriched at 42 DAP (Fig. 2D), therefore suggesting that epigenetic regulation is a relevant
23 523 component of the seed-pathogen molecular dialogue at this stage, potentially acting as
24 524 priming for post-germination phase. Globally, the transcriptomic response of the susceptible
25 525 host plant suggests that developing seeds are able to perceive the pathogen, and that defense
26 526 responses might be largely inhibited by the bacterial T3SS arsenal. Consistent with
27 527 suppression of the plant defense, up-regulation of photosynthesis and down-regulation of cell
28 528 wall organization enzymes (Fig.2D) were also previously observed in leaves of susceptible
29 529 common bean plants upon infection (Foucher et al., 2020). On the other hand, down-regulation
30 530 of HSP and HSF, and AP2/ERF transcription factors (Fig.2D) were the hallmark of resistant
31 531 plants. This suggests that a balance between susceptibility and resistance exist in *Xcf*-infected
32 532 seeds, which could explain why, despite active bacterial colonization, the seeds were
33 533 asymptomatic and presented no obvious physiological impact.

534

535 In this study, we also revealed that DNA methylation changes in *Xcf*-inoculated seed
536 may also act as defense priming for post-germination phase. Indeed, the seed host methylome
537 analysis at 42 DAP revealed significant changes in methylation status in 826 different genomic
538 regions, affecting a total of 99 different genes, which did not display any change in gene
539 expression during seed maturation. Of these, 17 can be associated to defense processes in

1
2
3 540 a relatively straightforward manner (Table 2). As hypomethylation of defense genes has been
4 541 widely associated with increased resistance to biotic stress (Downen et al., 2012; Annacondia
5 542 et al., 2021), the hypomethylated genes of this list (10 out of 17) can be considered as
6 543 candidates for epigenetic-dependent defense priming. The concept of defense priming
7 544 postulates that plants conserve the memory of previous encounters with pathogens by
8 545 preparing their defense networks to respond more rapidly and strongly to a future aggression
9 546 (Martinez-Medina et al., 2016). Enhanced chromatin access to defense genes through
10 547 hypomethylation is one of the best characterized mechanisms in this sense (Hannan Parker
11 548 et al., 2022). Furthermore, epigenetic defense priming can be transmitted to the next
12 549 generations (Slaughter et al., 2012). This would be consistent with a scenario where *Xcf*
13 550 colonization does not directly induce defense gene activation in common bean seeds, but
14 551 rather triggers a primed state that prepare defense networks for the moment when the
15 552 pathogen will again become virulent (after germination). Hypomethylation of transposable
16 553 elements is another well-characterized mechanism of epigenetic regulation of plant defenses,
17 554 as it can lead to the euchromatisation of wide genomic regions, both proximal and distal (López
18 555 Sánchez et al., 2016; Halter et al., 2021). The five defense genes present in Table 2 are thus
19 556 likely to be good candidates for relevant roles in bean resistance against *Xcf*. They include
20 557 three genes affected by hypomethylation (*Phvul.008G164600*, *Phvul.005G163000*,
21 558 *Phvul.010G026400*), namely two putative LRR kinase receptors and one effector receptor, all
22 559 uncharacterized. The other two genes affected by hypermethylation are another
23 560 uncharacterized LRR kinase receptor (*Phvul.005G162000*) and the putative bean homolog of
24 561 WRKY72 (*Phvul.003G068700*). This transcription factor has the highest methylation gain
25 562 among all the genes detected (fold change of +4,3), suggesting that its methylation status
26 563 might be important in response to *Xcf* infection. Indeed, the role of WRKY72 orthologs is
27 564 contradictory in different species. A positive role on defense responses was showed in *A.*
28 565 *thaliana* and tomato (*Solanum lycopersicum*) against oomycetes and bacteria, respectively
29 566 (Bhattarai et al., 2010), but regarding the interaction between rice (*Oryza sativa*) and
30 567 *Xanthomonas oryzae* pv. *Oryzae*, it was showed to negatively regulate rice defense responses
31 568 by repressing jasmonate biosynthetic genes (Hou et al., 2019). In our study, we validated its
32 569 role as *Xcf*-response genes during germination by highlighting its over-expression at 7 DAI in
33 570 radicles of germinated seeds in presence of *Xcf*. Another consideration regarding our
34 571 methylome data is the high overlap between DMRs-containing genes and germination-DEGs
35 572 (Fig. 3B). This suggests that the DMR-containing genes following bacterial infection detected
36 573 in this study may serve during the germination process through a defense priming mechanism.
37 574 More investigation will be required to define if these methylation changes will have positive or
38 575 negative impacts on defense- and/or germination-related gene expressions and will require
39 576 extensive transcriptomic analyses.

1
2
3 577

4 578 All together, these results indicate that the molecular mechanisms involved in the
5 579 pathogen-seed dialogue change radically across the developmental stages for both the host
6 580 and the pathogen side, potentially suggesting the existence of distinct phases in the
7 581 considered seed-pathogen interaction. It would be interesting to explore whether such **pattern**
8 582 takes place in other seed-pathogen interactions. By summing our physiological and molecular
9 583 observations, with the previous findings of Terrasson et al. (2015), we can propose a model
10 584 where the recognition of a host-specific pathogen at the early stages of seed development
11 585 fails to trigger seed defense activation, as if the presence of the pathogen was “accepted” by
12 586 the host. Even if we cannot define whether this suppression is caused by the pathogen or by
13 587 the host, two *Xanthomonas* studies would support the role of bacterial T3SS in host defense
14 588 silencing. Darsonval et al. (2008) showed the essential role of T3E for an efficient seed
15 589 colonization in the *X. citri* pv. *fuscans*-bean seed interaction and Terrasson et al. (2015)
16 590 showed that *X. euvesicatoria* pv. *Alfalfae* was able to silence some defense genes in a
17 591 compatible interaction, but not in an incompatible one. In any case, the result is a situation
18 592 where the seed develops normally without any obvious fitness costs associated to an eventual
19 593 defense activation, while the host-specific pathogen displays a non-aggressive behavior
20 594 throughout all the seed development and limits its proliferation (Fig. 4). Such “ceasefire”
21 595 scenario might be advantageous for both parts: the seed is able to reach maturity, which would
22 596 potentially be beneficial for the pathogen as well by allowing it to infect the future germinated
23 597 seedling, therefore giving it access to nourishment and facilitating its dispersal. On the other
24 598 hand, data at 42 DAP suggest a relevant role for epigenetic modifications in the host. It is
25 599 tempting to speculate that such modifications contribute to prepare the host to face a novel
30 600 pathogen assault after germination (Fig. 4). Detailed analysis of the transcriptome and
31 601 epigenome of the bean-*Xcf* interaction during the germination process would be a promising
32 602 future research direction in this sense. Recent data from the compatible interaction *Alternaria*
33 603 *brassicicola*-*A. thaliana*, used as seed transmission model, showed that host defense
34 604 pathways are subjected to drastic changes during the germination process (Ortega-Cuadros
35 605 et al., 2022). It would be interesting to explore whether such rearrangements take place in
36 606 other compatible interactions such as *Xcf*-bean and if a link with epigenetic modifications
37 607 exists.

38 608

39 609 To summarize, the present study adds novel elements to the current knowledge gap
40 610 of seed-pathogen interactions. The dual transcriptomic analysis allowed for the first time to
41 611 describe the molecular dialogue from both host and pathogen sides, while methylome and
42 612 sRNAs profiling added further indications on the potential regulatory mechanisms and the
43 613 genes involved. A dedicated Jbrowse containing all these generated data will serve as

614 baseline tool for the scientific communities and will be enriched by future related studies. An
615 important general conclusion that we can draw is that seeds have primarily an active role in
616 this interaction at early seed maturation stage, contrary to the widely diffused assumption
617 considering seeds as passive carriers of microbes (Dutta et al., 2014). As the role of
618 seedborne pathogens in causing yield losses receives relatively little attention, we hope that
619 the present study can stimulate novel research efforts in this sense to shed light on the many
620 obscure points still shrouding seed-pathogen interactions.

621

622 **Supplemental data**

623 Supplementary Data S1: Result tables of RNA-seq data

624 Supplementary Data S2: Result tables of sRNA-seq data

625 Supplementary Data S3: Result tables of BS-seq data

626 Supplementary Data S4: Primers used for qPCR experiments.

627

628 **Acknowledgements**

629 This work was supported by the French National Research Agency in the framework of the
630 SUCSEED project (ANR-20-PCPA-0009) and by the RFI "Objectif Végétal" supported by the
631 French Region Pays de la Loire, Angers Loire Métropole, and the European Regional
632 Development Fund. The authors wish to thank Daniel Sochard (Phenotic platform, SFR
633 Quasav) for crop management, Muriel Bahut (ANAN platform, SFR Quasav) for bacterial RNA
634 sequencing, Sébastien Carrère (LIPME, Toulouse) for the annotation of *Xcf* genome
635 sequences and Sylvain Gaillard for the public release of the *Phaseolus* Jbrowse.

636

637 **Author contributions**

638 AD, MBarret and JV designed the research. AD, MBarret and JV supervised the
639 experiments; AD, LPT, DL, NC, MBriand, MBarret, JV performed and analysed the
640 experiments. AD, LPT, NC, MBarret and JV wrote the manuscript and all co-authors
641 reviewed and edited the manuscript.

642

643 **Data availability**

644 The data that support the findings of this study have been deposited in NCBI Gene Expression
645 Omnibus and are accessible through GEO Super Series accession number GSE227421
646 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE227421>) or individually through
647 GEO accession numbers GSE227386 (bacterial RNA-seq,
648 <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE227386>), GSE226918 (plant

1
2
3 649 RNAseq, <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE226918>), GSE226919
4 650 (plant methylome, <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE226919>) and
5 651 GSE226920 (sRNA-Seq, <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE226920>).

6 652

7 653

10 654 **References**

12 655 **Ahmed I, Sarazin A, Bowler C, Colot V, Quesneville H** (2011) Genome-wide evidence for
14 656 local DNA methylation spreading from small RNA-targeted sequences in Arabidopsis.
15 657 *Nucleic Acids Res* **39**: 6919–6931

17 658 **Annacondia ML, Markovic D, Reig-Valiente JL, Scaltsoyiannes V, Pieterse CMJ,**
18 659 **Ninkovic V, Slotkin RK, Martinez G** (2021) Aphid feeding induces the relaxation of
20 660 epigenetic control and the associated regulation of the defense response in
21 661 Arabidopsis. *New Phytol* **230**: 1185–1200

23 662 **Bai Y, Meng Y, Huang D, Qi Y, Chen M** (2011) Origin and evolutionary analysis of the
24 663 plant-specific TIFY transcription factor family. *Genomics* **98**: 128–136

26 664 **Bethke G, Unthan T, Uhrig JF, Poschl Y, Gust AA, Scheel D, Lee J** (2009) Flg22
28 665 regulates the release of an ethylene response factor substrate from MAP kinase 6 in
29 666 Arabidopsis thaliana via ethylene signaling. *Proc Natl Acad Sci* **106**: 8067–8072

31 667 **Bhattarai KK, Atamian HS, Kaloshian I, Eulgem T** (2010) WRKY72-type transcription
33 668 factors contribute to basal immunity in tomato and Arabidopsis as well as gene-for-gene
34 669 resistance mediated by the tomato R gene Mi-1. *Plant J* **63**: 229–240

36 670 **Brewer PB, Howles PA, Dorian K, Griffith ME, Ishida T, Kaplan-Levy RN, Kilinc A,**
37 671 **Smyth DR** (2004) PETAL LOSS, a trihelix transcription factor gene, regulates perianth
39 672 architecture in the Arabidopsis flower. *Development* **131**: 4035–4045

41 673 **Briand M, Ruh M, Darrasse A, Jacques M-A, Chen NWG** (2021) Complete and
42 674 Circularized Genome Sequences of 17 *Xanthomonas* Strains Responsible for Common
44 675 Bacterial Blight of Bean. *Microbiol Resour Announc* **10**: e00371-21

46 676 **Büttner D** (2016) Behind the lines-actions of bacterial type III effector proteins in plant cells.
47 677 *FEMS Microbiol Rev* **40**: 894–937

49 678 **Catoni M, Tsang JM, Greco AP, Zabet NR** (2018) DMRcaller: a versatile R/Bioconductor
50 679 package for detection and visualization of differentially methylated regions in CpG and
51 680 non-CpG contexts. *Nucleic Acids Res* **46**: e114

53 681 **Cernay C, Ben-Ari T, Pelzer E, Meynard JM, Makowski D** (2015) Estimating variability in
54 682 grain legume yields across Europe and the Americas. *Sci Rep* **5**: 11171

56 683 **Chakraborty S, Nguyen B, Wasti SD, Xu G** (2019) Plant leucine-rich repeat receptor
58 684 kinase (LRR-RK): Structure, ligand perception, and activation mechanism. *Molecules*
59 685 **24**: 3081

- 1
2
3 686 **Chen NWG, Ruh M, Darrasse A, Foucher J, Briand M, Costa J, Studholme DJ, Jacques**
4 **MA** (2021a) Common bacterial blight of bean: a model of seed transmission and
5 687 pathological convergence. *Mol Plant Pathol* **22**: 1464–1480
6 688
7
8 689 **Chen S, Wu J, Zhang Y, Zhao Y, Xu W, Li Y, Xie J** (2021b) Genome-Wide Analysis of
9 690 Coding and Non-coding RNA Reveals a Conserved miR164–NAC–mRNA Regulatory
10 691 Pathway for Disease Defense in Populus. *Front Genet* **12**: 668940
11
12
13 692 **Chesneau G, Laroche B, Prévieux A, Marais C, Briand M, Marolleau B, Simonin M,**
14 **Barret M** (2022) Single Seed Microbiota: Assembly and Transmission from Parent
15 693 Plant to Seedling. *MBio* **13**: e0164822
16 694
17
18 695 **Dai X, Zhao PX** (2011) psRNATarget: a plant small RNA target analysis server. *Nucleic*
19 696 *Acids Res* **39**: W155-9
20
21 697 **Dai X, Zhuang Z, Zhao PX** (2018) psRNATarget: a plant small RNA target analysis server
22 698 (2017 release). *Nucleic Acids Res* **46**: W49–W54
23
24 699 **Darrasse A, Barret M, Cesbron S, Compant S, Jacques M-A** (2018) Niches and routes of
25 700 transmission of *Xanthomonas citri* pv. *fuscans* to bean seeds. *Plant Soil* **422**: 115–128
26
27 701 **Darrasse A, Bureau C, Samson R, Morris CE, Jacques M-A** (2007) Contamination of
28 702 bean seeds by *Xanthomonas axonopodis* pv. *phaseoli* associated with low bacterial
29 703 densities in the phyllosphere under field and greenhouse conditions. *Eur J Plant Pathol*
30 704 **119**: 203–215
31
32
33 705 **Darsonval A, Darrasse A, Durand K, Bureau C, Cesbron S, Jacques MA** (2009)
34 706 Adhesion and fitness in the bean phyllosphere and transmission to seed of
35 707 *xanthomonas fuscans* subsp. *Fuscans*. *Mol Plant-Microbe Interact* **22**: 747–757
36
37
38 708 **Darsonval A, Darrasse A, Meyer D, Demarty M, Durand K, Bureau C, Manceau C,**
39 709 **Jacques MA** (2008) The type III secretion system of *Xanthomonas fuscans* subsp.
40 710 *fuscans* is involved in the phyllosphere colonization process and in transmission to
41 711 seeds of susceptible beans. *Appl Environ Microbiol* **74**: 2669–2678
42
43
44 712 **Deleris A, Halter T, Navarro L** (2016) DNA Methylation and Demethylation in Plant
45 713 Immunity. *Annu Rev Phytopathol* **54**: 579–603
46
47
48 714 **Denancé N, Grimault V** (2022) Seed pathway for pest dissemination: The ISTA Reference
49 715 Pest List, a bibliographic resource in non-vegetable crops. *EPPO Bull* **52**: 434–445
50
51 716 **Dodds PN, Rathjen JP** (2010) Plant immunity: towards an integrated view of plant–
52 717 pathogen interactions. *Nat Rev Genet* **11**: 539–548
53
54 718 **Downen RH, Pelizzola M, Schmitz RJ, Lister R, Downen JM, Nery JR, Dixon JE, Ecker JR**
55 719 (2012) Widespread dynamic DNA methylation in response to biotic stress. *Proc Natl*
56 720 *Acad Sci U S A*. **109**: E2183-91
57
58
59 721 **Dutta B, Gitaitis R, Smith S, Langston D** (2014) Interactions of seedborne bacterial
60 722 pathogens with host and non-host plants in relation to seed infestation and seedling

- 1
2
3 723 transmission. *PLoS One* **9**: e99215
- 4 724 **Espinas NA, Saze H, Saijo Y** (2016) Epigenetic Control of Defense Signaling and Priming
5 725 in Plants. *Front Plant Sci* **7**: 1201
- 6 726 **Ferreira H, Pinto E, Vasconcelos MW** (2021) Legumes as a Cornerstone of the Transition
7 727 Toward More Sustainable Agri-Food Systems and Diets in Europe. *Front Sustain Food*
8 728 *Syst* **5**: 694121
- 9 729 **Figaj D, Ambroziak P, Przepiora T, Skorko-Glonek J** (2019) The Role of Proteases in the
10 730 Virulence of Plant Pathogenic Bacteria. *Int J Mol Sci* **20**: 672
- 11 731 **Fischer DS, Theis FJ, Yosef N** (2018) Impulse model-based differential expression analysis
12 732 of time course sequencing data. *Nucleic Acids Res* **46**: e119–e119
- 13 733 **Foucher J, Ruh M, Prévieux A, Carrère S, Pelletier S, Briand M, Serre R-F, Jacques M-
14 734 A, Chen NWG** (2020) Common bean resistance to *Xanthomonas* is associated with
15 735 upregulation of the salicylic acid pathway and downregulation of photosynthesis. *BMC*
16 736 *Genomics* **21**: 566
- 17 737 **Gitaitis R, Walcott R** (2007) The epidemiology and management of seedborne bacterial
18 738 diseases. *Annu Rev Phytopathol* **45**: 371–397
- 19 739 **Halter T, Wang J, Amesefe D, Lastrucci E, Charvin M, Singla Rastogi M, Navarro L**
20 740 (2021) The Arabidopsis active demethylase ROS1 cis-regulates defence genes by
21 741 erasing DNA methylation at promoter-regulatory regions. *Elife* **10**: e62994
- 22 742 **Hannan Parker A, Wilkinson SW, Ton J** (2022) Epigenetics: a catalyst of plant immunity
23 743 against pathogens. *New Phytol* **233**: 66–83
- 24 744 **Holt DB, Gupta V, Meyer D, Abel NB, Andersen SU, Stougaard J, Markmann K** (2015)
25 745 micro RNA 172 (miR172) signals epidermal infection and is expressed in cells primed
26 746 for bacterial invasion in *Lotus japonicus* roots and nodules. *New Phytol* **208**: 241–256
- 27 747 **Hou Y, Wang Y, Tang L, Tong X, Wang L, Liu L, Huang S, Zhang J** (2019) SAPK10-
28 748 Mediated Phosphorylation on WRKY72 Releases Its Suppression on Jasmonic Acid
29 749 Biosynthesis and Bacterial Blight Resistance. *iScience* **16**: 499–510
- 30 750 **Hu G, Lei Y, Liu J, Hao M, Zhang Z, Tang Y, Chen A, Wu J** (2020) The ghr-miR164 and
31 751 GhNAC100 modulate cotton plant resistance against *Verticillium dahlia*. *Plant Sci* **293**:
32 752 110438
- 33 753 **Johnson NR, Yeoh JM, Coruh C, Axtell MJ** (2016) Improved Placement of Multi-mapping
34 754 Small RNAs. *G3 (Bethesda)* **6**: 2103–2111
- 35 755 **Kim MJ, Jang I-C, Chua N-H** (2016) The Mediator Complex MED15 Subunit Mediates
36 756 Activation of Downstream Lipid-Related Genes by the WRINKLED1 Transcription
37 757 Factor. *Plant Physiol* **171**: 1951–1964
- 38 758 **Kozomara A, Birgaoanu M, Griffiths-Jones S** (2019) miRBase: from microRNA
39 759 sequences to function. *Nucleic Acids Res* **47**: D155–D162

- 1
2
3 760 **Krueger F, Andrews SR** (2011) Bismark: a flexible aligner and methylation caller for
4 761 Bisulfite-Seq applications. *Bioinformatics* **27**: 1571–1572
- 6 762 **Langmead B, Trapnell C, Pop M, Salzberg SL** (2009) Ultrafast and memory-efficient
7 763 alignment of short DNA sequences to the human genome. *Genome Biol* **10**: R25
- 9 764 **Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G,**
11 765 **Durbin R** (2009) The Sequence Alignment/Map format and SAMtools. *Bioinformatics*
12 766 **25**: 2078–2079
- 14 767 **López Sánchez A, Stassen JHM, Furci L, Smith LM, Ton J** (2016) The role of DNA
15 768 (de)methylation in immune responsiveness of Arabidopsis. *Plant J* **88**: 361–374
- 17 769 **Love MI, Huber W, Anders S** (2014) Moderated estimation of fold change and dispersion
18 770 for RNA-seq data with DESeq2. *Genome Biol* **15**: 550
- 20 771 **Luo M, Luo M-Z, Buzas D, Finnegan J, Helliwell C, Dennis ES, Peacock WJ, Chaudhury**
22 772 **A** (2008) UBIQUITIN-SPECIFIC PROTEASE 26 Is Required for Seed Development and
23 773 the Repression of PHERES1 in Arabidopsis. *Genetics* **180**: 229–236
- 25 774 **Martinez-Medina A, Flors V, Heil M, Mauch-Mani B, Pieterse CMJ, Pozo MJ, Ton J, van**
26 775 **Dam NM, Conrath U** (2016) Recognizing Plant Defense Priming. *Trends Plant Sci* **21**:
28 776 818–822
- 30 777 **Martins D, Araújo S de S, Rubiales D, Vaz Patta MC** (2020) Legume Crops and Biotrophic
31 778 Pathogen Interactions: A Continuous Cross-Talk of a Multilayered Array of Defense
32 779 Mechanisms. *Plants (Basel)* **9**: 1460
- 34 780 **Maude RB** (1996) Seedborne Diseases and Their Control: Principles and Practice. CAB
35 781 International
- 37 782 **Maury Y, Duby C, Bossenec J-M, Boudazin G** (1985) Group analysis using ELISA :
38 783 determination of the level of transmission of Soybean Mosaic Virus in soybean seed.
39 784 *Agronomie* **5**: 405–415
- 41 785 **Mozgová I, Wildhaber T, Liu Q, Abou-Mansour E, L'Haridon F, Métraux JP, Gruissem**
42 786 **W, Hofius D, Hennig L** (2015) Chromatin assembly factor CAF-1 represses priming of
43 787 plant defence response genes. *Nat Plants* **1**: 15127
- 45 788 **Myers SS, Zanobetti A, Kloog I, Huybers P, Leakey ADB, Bloom AJ, Carlisle E,**
46 789 **Dietterich LH, Fitzgerald G, Hasegawa T, et al** (2014) Increasing CO₂ threatens
47 790 human nutrition. *Nature* **510**: 139–142
- 49 791 **Narsai R, Gouil Q, Secco D, Srivastava A, Karpievitch Y V, Liew LC, Lister R, Lewsey**
50 792 **MG, Whelan J** (2017) Extensive transcriptomic and epigenomic remodelling occurs
51 793 during Arabidopsis thaliana germination. *Genome Biol* **18**: 172
- 53 794 **Noman A, Liu Z, Aqeel M, Zainab M, Khan MI, Hussain A, Ashraf MF, Li X, Weng Y, He**
54 795 **S** (2017) Basic leucine zipper domain transcription factors: the vanguards in plant
55 796 immunity. *Biotechnol Lett* **39**: 1779–1791

- 1
2
3 797 **Ortega-Cuadros M, De Souza TL, Berruyer R, Aligon S, Pelletier S, Renou JP, Arias T,**
4 **Campion C, Guillemette T, Verdier J, et al** (2022) Seed Transmission of Pathogens:
5 798 Non-Canonical Immune Response in Arabidopsis Germinating Seeds Compared to
6 799 Early Seedlings against the Necrotrophic Fungus *Alternaria brassicicola*. *Plants* (Basel)
7 800 **11**: 1708
8
9
10
11 802 **Patro R, Duggal G, Love MI, Irizarry RA, Kingsford C** (2017) Salmon provides fast and
12 803 bias-aware quantification of transcript expression. *Nat Methods* **14**: 417–419
13
14 804 **Pruitt RN, Locci F, Wanke F, Zhang L, Saile SC, Joe A, Karelina D, Hua C, Fröhlich K,**
15 **Wan WL, et al** (2021) The EDS1–PAD4–ADR1 node mediates Arabidopsis pattern-
16 805 triggered immunity. *Nature* **598**: 495–499
17 806
18
19 807 **Schwacke R, Ponce-Soto GY, Krause K, Bolger AM, Arsova B, Hallab A, Gruden K,**
20 **Stitt M, Bolger ME, Usadel B** (2019) MapMan4: A Refined Protein Classification and
21 808 Annotation Framework Applicable to Multi-Omics Data Analysis. *Mol Plant* **12**: 879–892
22 809
23
24 810 **Shivaprasad P V, Chen H-M, Patel K, Bond DM, Santos BACM, Baulcombe DC** (2012) A
25 811 MicroRNA Superfamily Regulates Nucleotide Binding Site–Leucine-Rich Repeats and
26 812 Other mRNAs . *Plant Cell* **24**: 859–874
27
28 813 **Slaughter A, Daniel X, Flors V, Luna E, Hohn B, Mauch-Mani B** (2012) Descendants of
29 814 Primed Arabidopsis Plants Exhibit Resistance to Biotic Stress. *Plant Physiol* **158**: 835–
30 815 843
31
32
33 816 **Soto-Suárez M, Baldrich P, Weigel D, Rubio-Somoza I, San Segundo B** (2017) The
34 817 Arabidopsis miR396 mediates pathogen-associated molecular pattern-triggered
35 818 immune responses against fungal pathogens. *Sci Rep* **7**: 44898
36
37
38 819 **Stagnari F, Maggio A, Galieni A, Pisante M** (2017) Multiple benefits of legumes for
39 820 agriculture sustainability: an overview. *Chem Biol Technol Agric* **4**: 2
40
41 821 **Teper D, Pandey SS, Wang N** (2021) The HrpG/HrpX Regulon of Xanthomonads-An Insight
42 822 to the Complexity of Regulation of Virulence Traits in Phytopathogenic Bacteria.
43 823 *Microorganisms* **9**: 187
44
45
46 824 **Terrasson E, Darrasse A, Righetti K, Buitink J, Lalanne D, Ly Vu B, Pelletier S,**
47 **Bolingue W, Jacques MA, Leprince O** (2015) Identification of a molecular dialogue
48 825 between developing seeds of *Medicago truncatula* and seedborne xanthomonads. *J*
49 826 *Exp Bot* **66**: 3737–3752
50
51
52 828 **Tintor N, Ross A, Kanehara K, Yamada K, Fan L, Kemmerling B, Nürnberger T, Tsuda**
53 **K, Saijo Y** (2013) Layered pattern receptor signaling via ethylene and endogenous
54 829 elicitor peptides during Arabidopsis immunity to bacterial infection. *Proc Natl Acad Sci U*
55 830 *S A* **110**: 6211–6216
56
57 831
58 832 **Varet H, Brillet-Guéguen L, Coppée J-Y, Dillies M-A** (2016) SARTools: A DESeq2- and
59 833 EdgeR-Based R Pipeline for Comprehensive Differential Analysis of RNA-Seq Data.

1
2
3 834 PLoS One 11: e0157022

4 835 **Wagner N, Avram O, Gold-Binshtok D, Zerah B, Teper D, Pupko T.** (2022). Effectidor: an
5 836 automated machine-learning-based web server for the prediction of type-III secretion
6 837 system effectors. *Bioinformatics* 38, 2341–2343.

7
8 838 **Wirthmueller L, Maqbool A, Banfield MJ** (2013) On the front line: structural insights into
9 839 plant-pathogen interactions. *Nat Rev Microbiol* 11: 761–776

10 840 **Yu C, Song L, Song J, Ouyang B, Guo L, Shang L, Wang T, Li H, Zhang J, Ye Z** (2018)
11 841 ShCIGT, a Trihelix family gene, mediates cold and drought tolerance by interacting with
12 842 SnRK1 in tomato. *Plant Sci* 270: 140–149

13 843 **Yu G, Wang L-G, Han Y, He Q-Y** (2012) clusterProfiler: an R package for comparing
14 844 biological themes among gene clusters. *OMICS* 16: 284–287

15 845

16 846

17 847

18 848 **Legends**

19 849 **Figure 1. Transmission of *Xcf* to bean seeds.** (A) Seed water content (B) Seed dry weight
20 850 (gram) and (C) *Xcf* population size (\log_{10} CFU per gram of seed) at the different sampling
21 851 stages (24DAP, 35DAP and 42DAP). Differences between the sampling stage and the
22 852 treatment (H_2O - or *Xcf*-inoculated) were assessed by Kruskal-Wallis test followed by post-hoc
23 853 Dunn's test. The percentages of observed contaminated seeds at different seed
24 854 developmental stages are indicated (expressed as averages with SD between brackets). P-
25 855 values are indicated as * <5%, ** <1% and *** <0.1%.

26 856

27 857 **Figure 2. Dual transcriptomic analysis of the *Xcf*-*P. vulgaris* seed interaction.** (A) & (C)
28 858 Histograms summarizing the number of differentially expressed genes (DEGs) detected
29 859 comparing datasets from different seed development stages from *Xcf* samples (A) and DEGs
30 860 from different development stages from *P. vulgaris* samples (C). The number of DEGs is
31 861 indicated on the bars. (B) & (D) Dot plots showing category enrichment results obtained
32 862 through gene ontology analysis of DEGs from *Xcf* (B) and *P. vulgaris* (D). Gene ontology
33 863 analysis was performed with the Clusterprofiler package for R.

34 864 **Figure 3. Summary of methylome analysis data generated by comparing *Xcf*-colonized
35 865 and uncolonized seeds at 42 DAP.** (A) Pie chart illustrating the repartition of differentially
36 866 methylated regions (DMRs) following *Xcf* colonization on *P. vulgaris* genome at 42 DAP. (B)
37 867 Venn diagram illustrating the overlap between gene sequences containing DMRs at 42 DAP
38 868 and differentially expressed genes (DEGs) during germination (see details in text).

39 869

40 870

41 871

42 872

43 873

44 874

45 875

1
2
3 869 **Figure 4. Schematic model of the *Xcf*-bean seed dialogue.** Left panel: at early seed
4 870 development stages (24 DAP), *Xcf* is recognized by the host. Despite the bacterial recognition,
5 871 defense transduction pathways based on MAP kinases cascades (MAPKs) and transcription
6 872 factors (TFs) activation are suppressed in seeds, thus failing to induce a defense reaction.
7
8 873 Red dotted lines with flat end indicate hypothetical inhibition. Middle Panel: at 35 DAP, both
9 874 the bacterial pathogen and the host plant are still transcriptionally active. Bacterial populations
10 875 continue to grow, but the T3SS is no longer active, suggesting that the bacteria lowered its
11 876 weapons, keeping the seed alive and healthy. Right panel: at seed maturation (42 DAP), the
12 877 dialogue between *Xcf* and seed is much less detectable in comparison to earlier stages but
13 878 epigenetic mechanisms such as DNA methylation could be active, which was observed at
14 879 seed maturity by the changes in the methylation status of genes identified as involved in both
15 880 defense and germination processes. This change in DNA methylation could prime genes
16 881 involved in defense/germination, ultimately preparing the host for the post-germination battle
17 882 with the virulent *Xcf* (see text for more details).

25 883

26 884

27 885

28 886

29 887

30 888

31 889

32 890

33 891

34 892

35 893

36 894

37 895

38 896

39 897

40 898

41 899

42

43

44

45

1
2
3 900
4
5 901
6
7 902
8
9 903
10
11 904
12
13 905
14
15 906
16
17 907

Tables

Table 1. Summary of differentially accumulated small RNAs (up- or down-regulated) detected at 24 and 42 DAP in *Xcf*-colonized *P. vulgaris* seeds with their putative target genes according to psRNAtarget.

| Seed developmental stages | DEseq2 | | psRNAtarget combined with corresponding significant expression changes from RNAseq data |
|---------------------------|---|------------|---|
| | Up- or down-regulation in <i>Xcf</i> -colonized seeds | mature miR | variants putative targets using psRNAtarget (= miRNA potential target genes) |
| 24DAP | Up | miR162 | a,b Phvul.007G067800 (HSF), Phvul.008G055500 (TGD3), Phvul.006G176000 (trihelix DNA-binding), Phvul.008G114700 (Rab-GDP) |
| | Up | miR172 | a,c,d,e,f,g,h,i,l Phvul.009G014600 (cardiolipin deacylase), Phvul.001G212400 (RING-domain E3 ligase), Phvul.005G068800 (Probable E3 ubiquitin-protein ligase), Phvul.003G053000 (glycosyltransferase) |
| | Up | miR396 | a,b,c,d,e,i Phvul.009G246000 (SNF4-like), Phvul.001G229200 (pepsin-type protease), Phvul.002G026300 integrin-like protein, Phvul.003G154800 (HSP70) |
| | Up | miR482 | 3p, b-3p, d-3p Phvul.011G149100 Transducin/WD40 repeat-like, Phvul.008G055500 (ATPase component TGD3 of TGD), Phvul.003G295800 (ATG2-like), Phvul.011G082700 (P-loop NTPase), Phvul.010G141400 (DOF1-like TF), Phvul.002G261500 (RNA polymerase regulatory protein) |
| | Up | miR6478 | - Phvul.003G155500 (component SR-alpha of SRP) |
| | Up | miR8175 | - Phvul.002G059000 (Phospholipase A1), Phvul.002G274500 (PAD4-like), Phvul.010G082300 (UDP-D-glucuronic acid 4-epimerase), Phvul.005G035400 (mRNA-splicing factor 18), Phvul.001G240600 (CaLB domain) |
| | Down | let7 | a,c,d,f Phvul.001G022700 (REMORIN-LIKE), Phvul.003G119100 (calcium-dependent lipid-binding), Phvul.011G061600 (PTAC16-like), Phvul.003G035400 (XYL1-like), Phvul.004G121666 (subunit of CF1 of ATP synthase), Phvul.008G163350 (cohesin cofactor (PDS5)), Phvul.011G050300 (protein kinase (PIKK) TOR-like), Phvul.003G050600 (catalytic protein (CER2)), Phvul.007G069900, Phvul.011G001200 (SAC1-like), Phvul.002G185150 (sodium:proton antiporter (SOS1)) |
| | Down | miR21 | a Phvul.010G157900 (MED15-like), Phvul.007G191600 (CHR8-like) |
| | Down | miR2111 | a,b,c,d,e,f,g,h,i,j,k,m,n,o Phvul.001G269300 (MED13-like), Phvul.001G179300 (PGP1-like), Phvul.010G125200 (NOC1/SWA2-like), Phvul.007G168500 (Solute transport channels) |
| | Down | miR482 | 5p Phvul.004G170000 (STT3-like), Phvul.010G125200 (NOC1/SWA2-like), Phvul.007G244066, Phvul.002G189700 (UPL1-like) |
| 42DAP | Up | miR31 | - |
| | Down | miR451 | a Phvul.009G100000 (UBP26-like) |
| | Down | miR164 | a,b,c,d,e,f,g,h,i,j,k - |

38 908
39
40 909
41
42 910
43
44 911
45 912
46
47 913
48 914
49
50 915
51 916
52
53 917
54
55 918
56 919
57
58 920
59
60 921

1
2
3 922
4
5 923
6 924
7
8 925
9
10 926
11 927
12
13 928
14 929
15
16 930
17 931
18
19 932
20
21 933
22 934
23
24 935
25 936
26
27 937
28
29 938
30 939

Table 2. List of differentially methylated regions located in defense-associated genes in of *P. vulgaris* seeds following *Xcf* colonization at 42 DAP. DMRs were located in promoter or gene sequences, but also in transposable elements located within 5kb of genic regions. The *P. vulgaris* annotation column was filled according to the *P. vulgaris* genome (v2.1). The location indicates whether the region is localized in a coding region (gene) or in the promoter (1kbprom) or in TE within 5kb of genic regions (within 5kb). The putative ortholog was assigned as best hit based on sequence similarity in the *A. thaliana* genome (v.11). The “gain or loss” column shows whether the differentially methylated region associated with the corresponding *P. vulgaris* gene is hypo- (loss) or hypermethylated (gain) in response to *Xcf* colonization at 42 DAP. FC, fold change of methylation between *Xcf*- versus H₂O-treated seeds. FC ratios are not indicated for DMRs within 5kb of genic regions because they correspond to multiple DMRs.

| <i>P. vulgaris</i> locus ID | Location | <i>P. vulgaris</i> annotation | <i>A. thaliana</i> putative ortholog | <i>A. thaliana</i> symbol | <i>A. thaliana</i> annotation | Methylation FC (Xcf vs H ₂ O) | Gain or loss of methylation in <i>Xcf</i> -treated seeds |
|-----------------------------|------------|--|--------------------------------------|---------------------------|---|--|--|
| Phvul.001G233000 | gene | protein kinase (SD-1) | AT3G16030 | CES101 | lectin protein kinase family protein | 0.52 | loss |
| Phvul.002G125500 | within 5kb | not annotated | AT5G08315 | | Defensin-like (DEFL) family protein | | loss |
| Phvul.002G130300 | within 5kb | not annotated | AT3G14470 | | NB-ARC domain-containing disease resistance protein | | gain |
| Phvul.002G130400 | within 5kb | not annotated | AT3G14470 | | NB-ARC domain-containing disease resistance protein | | gain |
| Phvul.003G021700 | 1kbprom | transferase transferring phosphorus-containing group | AT1G07040 | | Protein kinase superfamily protein | 0.51 | loss |
| Phvul.003G040300 | 1kbprom | 6-deoxocasterone 6-oxidase | AT3G03180 | BR6OX2 | brassinosteroid-6-oxidase 2 | 2.98 | gain |
| Phvul.003G056900 | within 5kb | systemic acquired resistance (SAR) regulator protein (SN1) | AT4G18470 | SN1 | negative regulator of systemic acquired resistance (SN1) | | loss |
| Phvul.003G068700 | gene | transcription factor (WRKY) | AT5G15130 | WRKY72 | WRKY DNA-binding protein 72 | 4.30 | gain |
| Phvul.003G068700 | within 5kb | transcription factor (WRKY) | AT5G15130 | WRKY72 | WRKY DNA-binding protein 72 | | gain |
| Phvul.003G175700 | gene | DRB4-DRB7.1 regulator complex component DRB7 | AT5G20320 | DCL4 | dicer-like 4 | 0.37 | loss |
| Phvul.004G076100 | within 5kb | not annotated | AT3G14470 | | NB-ARC domain-containing disease resistance protein | | loss |
| Phvul.004G105600 | within 5kb | not annotated | AT2G34930 | | disease resistance family protein / LRR family protein | | loss |
| Phvul.005G162000 | 1kbprom | transferase transferring phosphorus-containing group | AT4G29990 | | Leucine-rich repeat transmembrane protein kinase protein | 2.36 | gain |
| Phvul.005G162000 | within 5kb | transferase transferring phosphorus-containing group | AT4G29990 | | Leucine-rich repeat transmembrane protein kinase protein | | gain |
| Phvul.005G162100 | within 5kb | transferase transferring phosphorus-containing group | AT1G51800 | | Leucine-rich repeat protein kinase family protein | | gain |
| Phvul.005G163000 | gene | transferase transferring phosphorus-containing group | AT4G29990 | | Leucine-rich repeat transmembrane protein kinase protein | 0.38 | loss |
| Phvul.005G163000 | within 5kb | transferase transferring phosphorus-containing group | AT4G29990 | | Leucine-rich repeat transmembrane protein kinase protein | | loss |
| Phvul.006G006800 | gene | TKL protein kinase superfamily protein kinase (DUF26) | AT4G05200 | CRK25 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | 0.18 | loss |
| Phvul.006G033200 | gene | not annotated | AT5G38280 | PR5K | PR5-like receptor kinase | 0.52 | loss |
| Phvul.007G187700 | 1kbprom | not annotated | AT3G04720 | PR4 | pathogenesis-related 4 | 0.37 | loss |
| Phvul.007G241200 | gene | transcription factor (MYB-related) | AT5G47390 | | myb-like transcription factor family protein | 3.25 | gain |
| Phvul.007G241200 | within 5kb | transcription factor (MYB-related) | AT5G47390 | | myb-like transcription factor family protein | | gain |
| Phvul.007G241300 | within 5kb | Ser/Thr protein kinase | AT1G50240 | FU | Protein kinase family protein with ARM repeat domain | | gain |
| Phvul.008G164500 | within 5kb | transferase transferring phosphorus-containing group | AT3G21340 | | Leucine-rich repeat protein kinase family protein | | loss |
| Phvul.008G164600 | gene | not annotated | AT1G05700 | | Leucine-rich repeat transmembrane protein kinase protein | 0.45 | loss |
| Phvul.008G164600 | within 5kb | not annotated | AT1G05700 | | Leucine-rich repeat transmembrane protein kinase protein | | loss |
| Phvul.008G228714 | gene | S8-class protease (subtilisin) families protease (SBT4) | AT3G46850 | | Subtilase family protein | 4.29 | gain |
| Phvul.008G229400 | gene | S8-class protease (subtilisin) families protease (SBT4) | AT5G59100 | | Subtilisin-like serine endopeptidase family protein | 0.48 | loss |
| Phvul.010G026400 | 1kbprom | effector receptor (NLR) | AT5G36930 | | Disease resistance protein (TIR-NBS-LRR class) family | 0.35 | loss |
| Phvul.010G026400 | within 5kb | effector receptor (NLR) | AT5G36930 | | Disease resistance protein (TIR-NBS-LRR class) family | | loss |
| Phvul.010G027900 | within 5kb | effector receptor (NLR) | AT5G36930 | | Disease resistance protein (TIR-NBS-LRR class) family | | loss |
| Phvul.010G028000 | within 5kb | effector receptor (NLR) | AT5G36930 | | Disease resistance protein (TIR-NBS-LRR class) family | | loss |
| Phvul.010G062500 | within 5kb | WRKY33-dependent plant immunity transcription factor | AT2G38470 | WRKY33 | WRKY DNA-binding protein 33 | | loss |
| Phvul.011G064700 | gene | U-Box E3 ligase activities E3 ubiquitin ligase (PUB) | AT3G46510 | PUB13 | plant U-box 13 | 4.06 | gain |
| Phvul.011G108300 | gene | transferase transferring phosphorus-containing group | AT1G29730 | | Leucine-rich repeat transmembrane protein kinase | 2.32 | gain |
| Phvul.011G176100 | gene | transferase transferring one-carbon group | AT3G11480 | BSMT1 | S-adenosyl-L-methionine-dependent methyltransferases family protein | 2.56 | gain |

31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51 940
52 941
53
54
55 942
56
57
58
59
60

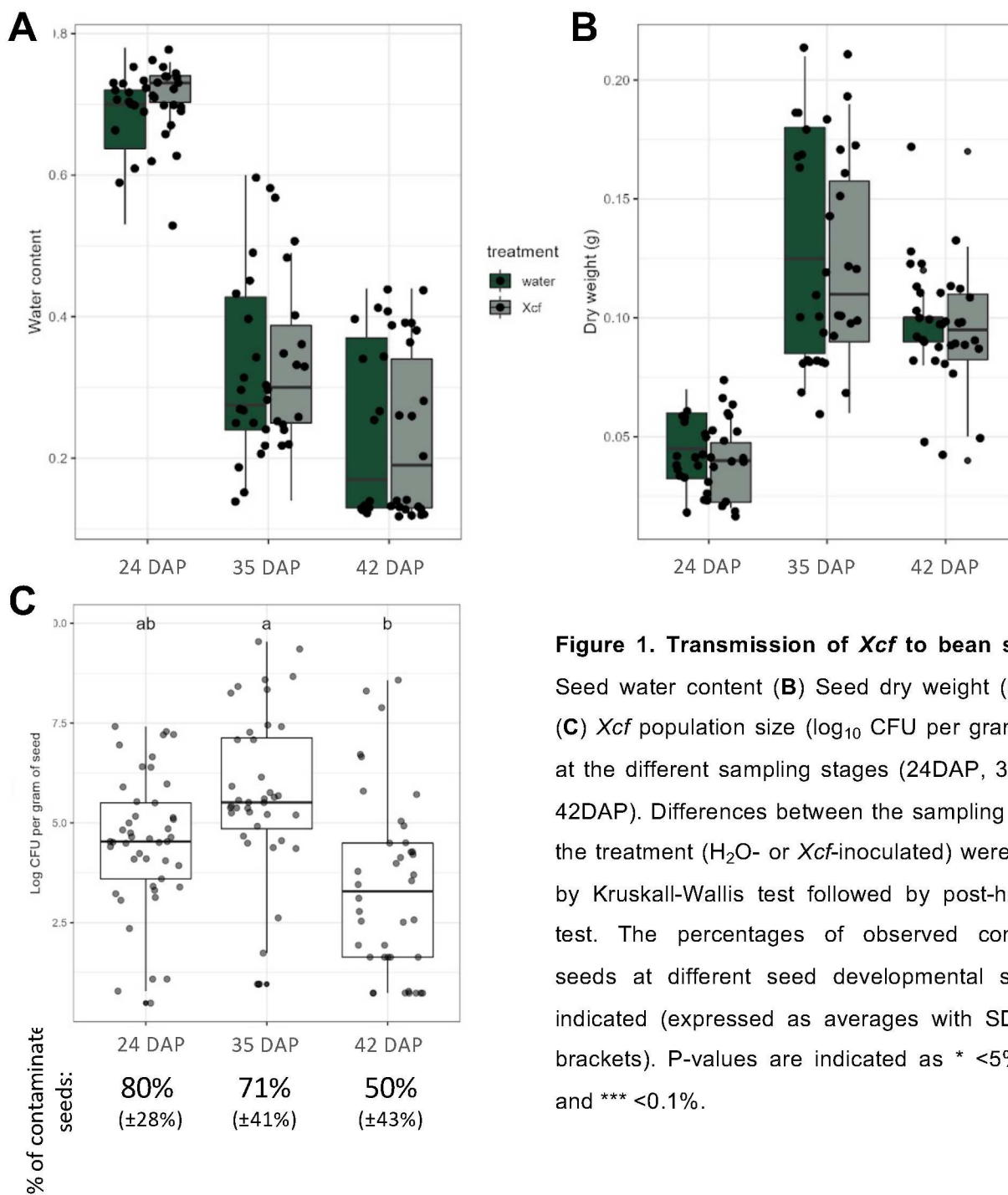


Figure 1. Transmission of Xcf to bean seeds. (A) Seed water content (B) Seed dry weight (gram) and (C) Xcf population size (log₁₀ CFU per gram of seed) at the different sampling stages (24DAP, 35DAP and 42DAP). Differences between the sampling stage and the treatment (H₂O- or Xcf-inoculated) were assessed by Kruskal-Wallis test followed by post-hoc Dunn's test. The percentages of observed contaminated seeds at different seed developmental stages are indicated (expressed as averages with SD between brackets). P-values are indicated as * <5%, ** <1% and *** <0.1%.

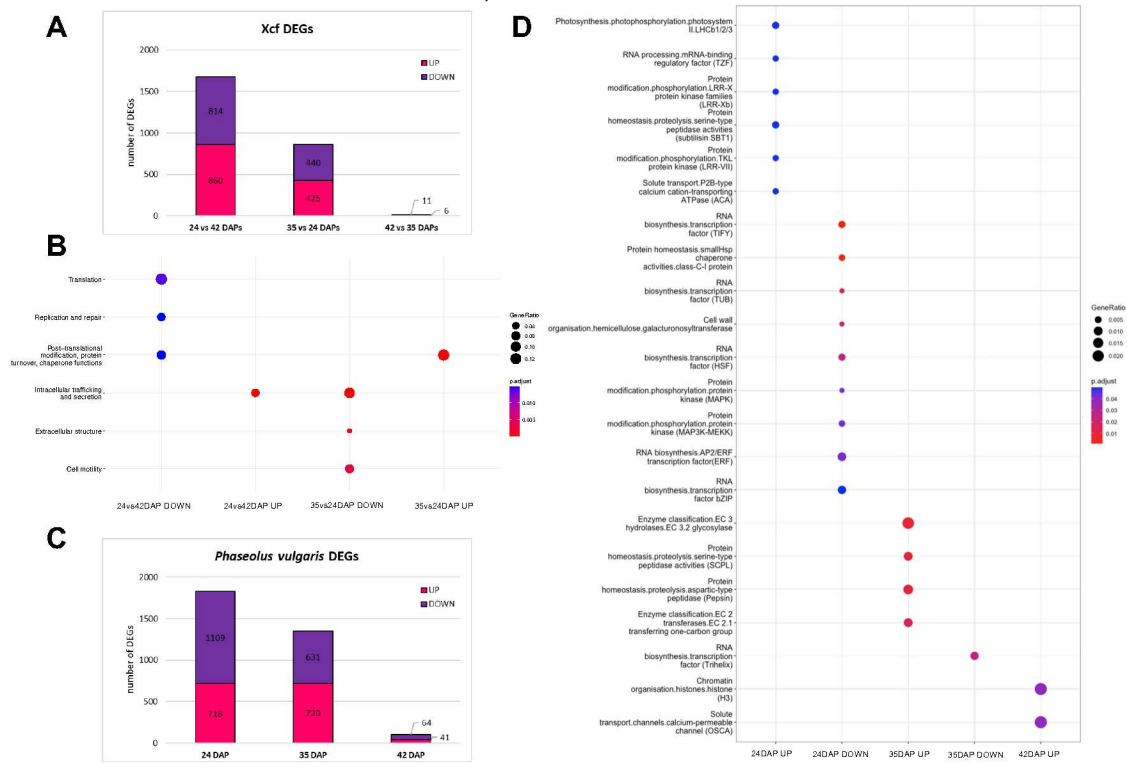


Figure 2. Dual transcriptomic analysis of the *Xcf-P. vulgaris* seed interaction.

(A)(C) Histograms summarizing the number of differentially expressed genes (DEGs) detected comparing datasets from different seed development stages from *Xcf* samples (A) and DEGs from different development stages from *P. vulgaris* samples (C). The number of DEGs is indicated on the bars. (B) (D) Dot plots showing category enrichment results obtained through gene ontology analysis of DEGs from *Xcf* (B) and *P. vulgaris* (D). Gene ontology analysis was performed with the ClusterProfiler package for R.

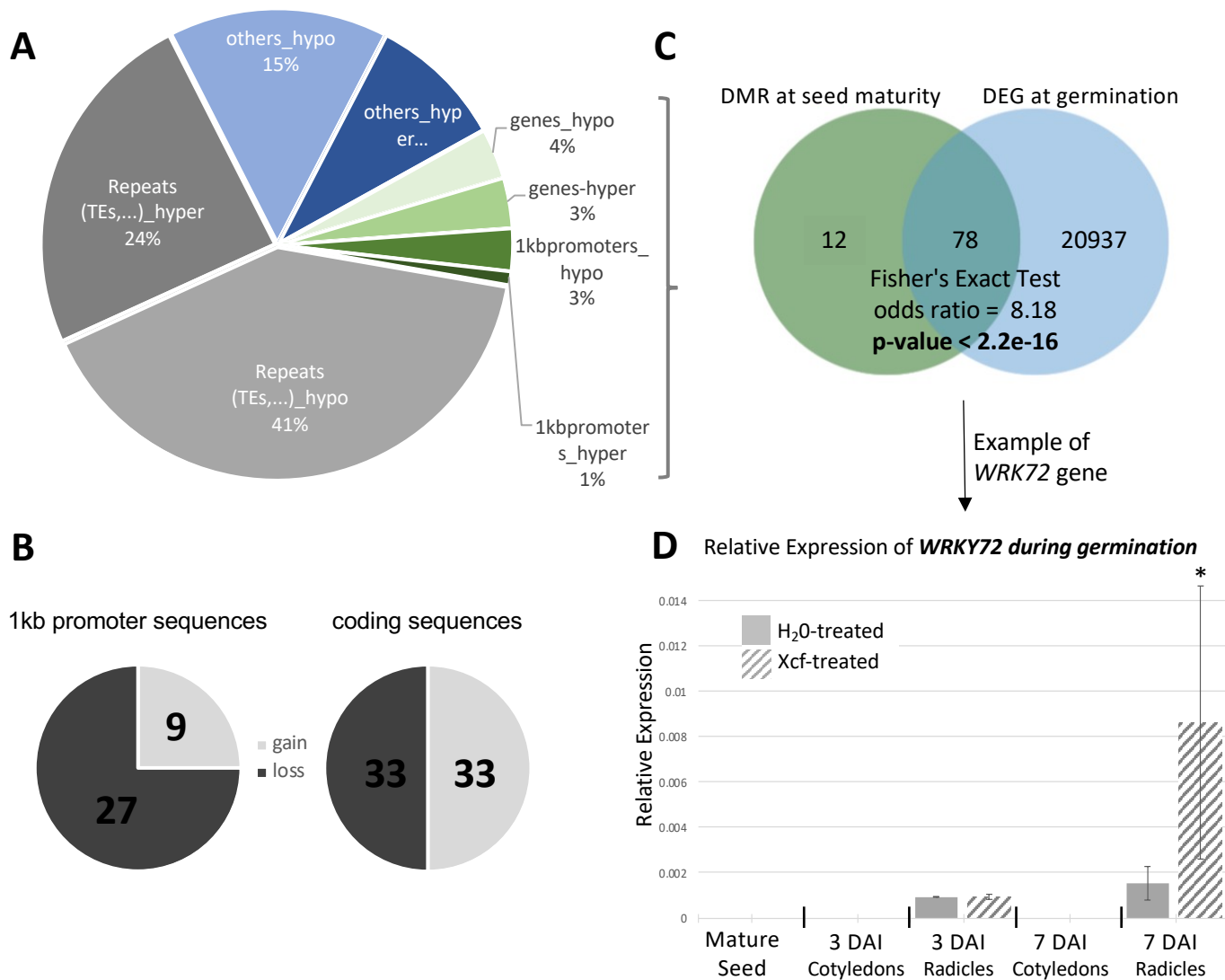


Figure 3. Summary of methylome analysis data generated by comparing *Xcf*-colonized and uncolonized seeds at 42 DAP. (A) Pie chart illustrating the repartition of differentially methylated regions (DMRs) following *Xcf* colonization on *P. vulgaris* genome at 42 DAP. (B) Pie charts illustrating the number of hypo-(loss) and hyper-(gain) methylated DMRs located in annotated genes (1kb promoter or coding sequences). (C) Venn diagram illustrating the overlap between gene sequences containing DMRs at 42 DAP and differentially expressed genes (DEGs) during germination (see details in text). (D) Relative expression of *WRKY72* during germination (at 3 and 7 Days after imbibition, DAI) in H₂O- and *Xcf*-treated seeds.

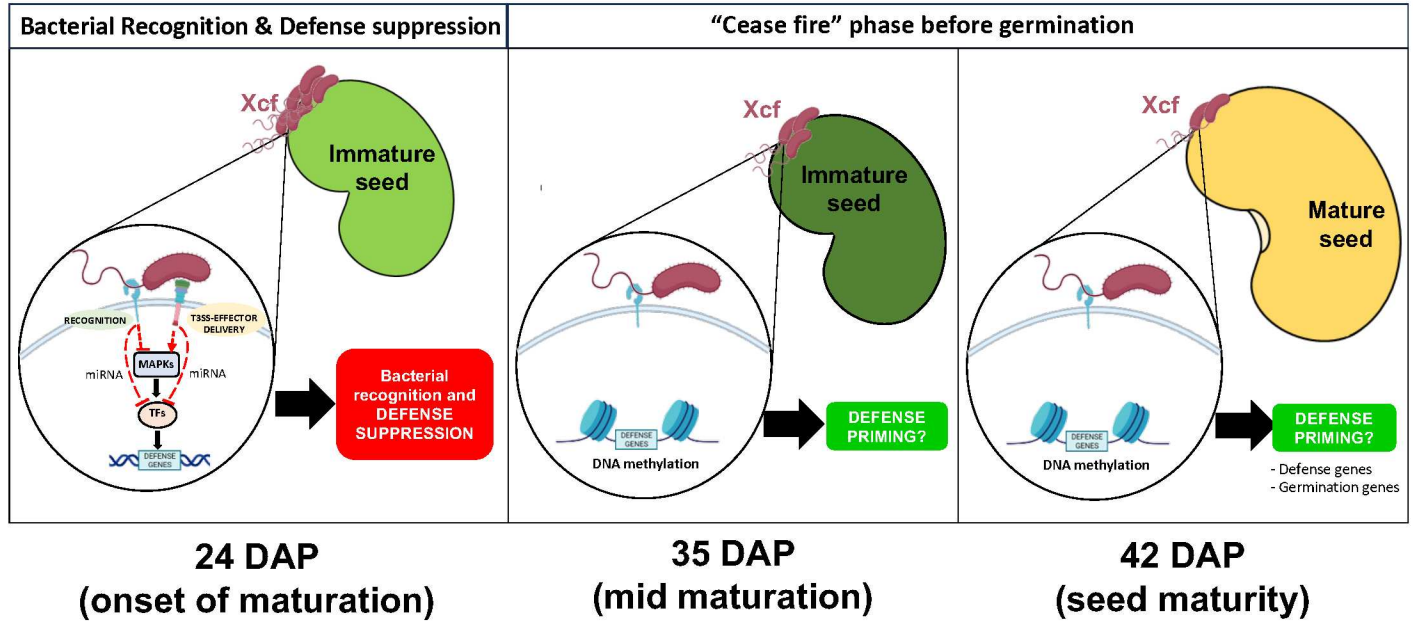


Figure 4. Schematic model of the *Xcf*-bean seed dialogue. Left panel: at early seed development stages (24 DAP), *Xcf* is recognized by the host. Despite the bacterial recognition, defense transduction pathways based on MAP kinases cascades (MAPKs) and transcription factors (TFs) activation are suppressed in seeds, thus failing to induce a defense reaction. Red dotted lines with flat end indicate hypothetical inhibition. Middle Panel: at 35 DAP, both the bacterial pathogen and the host plant are still transcriptionally active. Bacterial populations continue to grow, but the T3SS is no longer active, suggesting that the bacteria lowered its weapons, keeping the seed alive and healthy. Right panel: at seed maturation (42 DAP), the dialogue between *Xcf* and seed is much less detectable in comparison to earlier stages but epigenetic mechanisms such as DNA methylation could be active, which was observed at seed maturity by the changes in the methylation status of genes identified as involved in both defense and germination processes. This change in DNA methylation could prime genes involved in defense/germination, ultimately preparing the host for the post-germination battle with the virulent *Xcf* (see text for more details).

Table 2. List of differentially methylated regions located in defense-associated genes in of *P. vulg*

| <i>P. vulgaris</i> locus ID | Location | <i>P. vulgaris</i> annotation |
|-----------------------------|------------|---|
| Phvul.001G233000 | gene | protein kinase (SD-1) |
| Phvul.002G125500 | within 5kb | not annotated |
| Phvul.002G130300 | within 5kb | not annotated |
| Phvul.002G130400 | within 5kb | not annotated |
| Phvul.003G021700 | 1kbProm | transferase transferring phosphorus-containing group |
| Phvul.003G040300 | 1kbProm | 6-deoxocastasterone 6-oxidase |
| Phvul.003G056900 | within 5kb | systemic acquired resistance (SAR) regulator protein (SNI1) |
| Phvul.003G068700 | gene | transcription factor (WRKY) |
| Phvul.003G068700 | within 5kb | transcription factor (WRKY) |
| Phvul.003G175700 | gene | DRB4-DRB7.1 regulator complex.component DRB7 |
| Phvul.004G076100 | within 5kb | not annotated |
| Phvul.004G105600 | within 5kb | not annotated |
| Phvul.005G162000 | 1kbProm | transferase transferring phosphorus-containing group |
| Phvul.005G162000 | within 5kb | transferase transferring phosphorus-containing group |
| Phvul.005G162100 | within 5kb | transferase transferring phosphorus-containing group |
| Phvul.005G163000 | gene | transferase transferring phosphorus-containing group |
| Phvul.005G163000 | within 5kb | transferase transferring phosphorus-containing group |
| Phvul.006G006800 | gene | TKL protein kinase superfamily.protein kinase (DUF26) |
| Phvul.006G033200 | gene | not annotated |
| Phvul.007G187700 | 1kbProm | not annotated |
| Phvul.007G241200 | gene | transcription factor (MYB-related) |
| Phvul.007G241200 | within 5kb | transcription factor (MYB-related) |
| Phvul.007G241300 | within 5kb | Ser/Thr protein kinase |
| Phvul.008G164500 | within 5kb | transferase transferring phosphorus-containing group |
| Phvul.008G164600 | gene | not annotated |
| Phvul.008G164600 | within 5kb | not annotated |
| Phvul.008G228714 | gene | S8-class protease (subtilisin) families.protease (SBT4) |
| Phvul.008G229400 | gene | S8-class protease (subtilisin) families.protease (SBT4) |
| Phvul.010G026400 | 1kbProm | effector receptor (NLR) |
| Phvul.010G026400 | within 5kb | effector receptor (NLR) |
| Phvul.010G027900 | within 5kb | effector receptor (NLR) |
| Phvul.010G028000 | within 5kb | effector receptor (NLR) |
| Phvul.010G062500 | within 5kb | WRKY33-dependent plant immunity transcription factor |
| Phvul.011G064700 | gene | U-Box E3 ligase activities.E3 ubiquitin ligase (PUB) |
| Phvul.011G108300 | gene | transferase transferring phosphorus-containing group |
| Phvul.011G176100 | gene | transferase transferring one-carbon group |

3aris seeds following Xcf colonization at 42 DAP. DMRs were located in promoter or gene sequences:

| <i>A. thaliana</i> putative ortholog | <i>A. thaliana</i> symbol | <i>A. thaliana</i> annotation |
|--|------------------------------|---|
| AT3G16030 | CES101 | lectin protein kinase family protein |
| AT5G08315 | | Defensin-like (DEFL) family protein |
| AT3G14470 | | NB-ARC domain-containing disease resistance protein |
| AT3G14470 | | NB-ARC domain-containing disease resistance protein |
| AT1G70740 | | Protein kinase superfamily protein |
| AT3G30180 | BR6OX2 | brassinosteroid-6-oxidase 2 |
| AT4G18470 | SNI1 | negative regulator of systemic acquired resistance (SNI1) |
| AT5G15130 | WRKY72 | WRKY DNA-binding protein 72 |
| AT5G15130 | WRKY72 | WRKY DNA-binding protein 72 |
| AT5G20320 | DCL4 | dicer-like 4 |
| AT3G14470 | | NB-ARC domain-containing disease resistance protein |
| AT2G34930 | | disease resistance family protein / LRR family protein |
| AT4G29990 | | Leucine-rich repeat transmembrane protein kinase protein |
| AT4G29990 | | Leucine-rich repeat transmembrane protein kinase protein |
| AT1G51800 | | Leucine-rich repeat protein kinase family protein |
| AT4G29990 | | Leucine-rich repeat transmembrane protein kinase protein |
| AT4G29990 | | Leucine-rich repeat transmembrane protein kinase protein |
| AT4G05200 | CRK25 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 |
| AT5G38280 | PR5K | PR5-like receptor kinase |
| AT3G04720 | PR4 | pathogenesis-related 4 |
| AT5G47390 | | myb-like transcription factor family protein |
| AT5G47390 | | myb-like transcription factor family protein |
| AT1G50240 | FU | Protein kinase family protein with ARM repeat domain |
| AT3G21340 | | Leucine-rich repeat protein kinase family protein |
| AT1G05700 | | Leucine-rich repeat transmembrane protein kinase protein |
| AT1G05700 | | Leucine-rich repeat transmembrane protein kinase protein |
| AT3G46850 | | Subtilase family protein |
| AT5G59100 | | Subtilisin-like serine endopeptidase family protein |
| AT5G36930 | | Disease resistance protein (TIR-NBS-LRR class) family |
| AT5G36930 | | Disease resistance protein (TIR-NBS-LRR class) family |
| AT5G36930 | | Disease resistance protein (TIR-NBS-LRR class) family |
| AT5G36930 | | Disease resistance protein (TIR-NBS-LRR class) family |
| AT2G38470 | WRKY33 | WRKY DNA-binding protein 33 |
| AT3G46510 | PUB13 | plant U-box 13 |
| AT1G29730 | | Leucine-rich repeat transmembrane protein kinase |
| AT3G11480 | BSMT1 | S-adenosyl-L-methionine-dependent methyltransferases family protein |

s, but also in transposable elements located within 5kb of genic regions. The *P. vulgaris* annotation column

| Methylation FC (Xcf vs H2O) | Gain or loss of methylation in Xcf-treated seeds |
|-----------------------------|--|
| 0.52 | loss |
| | loss |
| | gain |
| | gain |
| 0.51 | loss |
| 2.98 | gain |
| | loss |
| 4.30 | gain |
| | gain |
| 0.37 | loss |
| | loss |
| | loss |
| 2.36 | gain |
| | gain |
| | gain |
| 0.38 | loss |
| | loss |
| 0.18 | loss |
| 0.52 | loss |
| 0.37 | loss |
| 3.25 | gain |
| | gain |
| | gain |
| | loss |
| 0.45 | loss |
| | loss |
| 4.29 | gain |
| 0.48 | loss |
| 0.35 | loss |
| | loss |
| | loss |
| | loss |
| | loss |
| 4.06 | gain |
| 2.32 | gain |
| 2.56 | gain |

| | loss | gain |
|------------------------|------|------|
| Protein kinases | 6 | 2 |
| Resistance proteins | 1 | 0 |
| Transcription factors | 0 | 1 |
| Antimicrobial proteins | 2 | 1 |
| | loss | gain |
| Protein kinases | 4 | 3 |
| Resistance proteins | 4 | 2 |
| Transcription factors | 1 | 1 |
| Antimicrobial proteins | 1 | 0 |

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2 in was filled according to the *P. vulgaris* genome (v2.1). The location indicates whether the region is li
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

ocalized in a coding region (gene) or in the promoter (1kbprom) or in TE within 5kb of genic regions (

Do not distribute

1
2 within 5kb). The putative ortholog was assigned as best hit based on sequence similarity in the A. the
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

aliana genome (v.11). The “gain or loss” column shows whether the differentially methylated region is

Do not distribute

1
2 associated with the corresponding *P. vulgaris* gene is hypo- (loss) or hypermethylated (gain) in respor
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

rise to Xcf colonization at 42 DAP. FC, fold change of methylation between Xcf- versus H₂O-treated se

Do not distribute

eds. FC ratios are not indicated for DMRs within 5kb of genic regions because they correspond to m

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Multiple DMR

Do not distribute

| Seed developmental stages | DEseq2 | | |
|---------------------------|---|------------|-----------------------------|
| | Up- or down-regulation in <i>Xcf</i> -colonized seeds | mature miR | variants |
| 24DAP | Up | miR162 | a,b |
| | Up | miR172 | a,c,d,e,f,g,h,i,l |
| | Up | miR396 | a,b,c,d,e,i |
| | Up | miR482 | 3p, b-3p, d-3p |
| | Up | miR6478 | - |
| | Up | miR8175 | - |
| | Down | let7 | a,c,d,f |
| | Down | miR21 | a |
| | Down | miR2111 | a,b,c,d,e,f,g,h,i,j,k,m,n,o |
| | Down | miR482 | 5p |
| 42DAP | Up | miR31 | - |
| | Down | miR451 | a |
| | Down | miR164 | a,b,c,d,e,f,g,h,i,j,k |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| psRNA target combined with corresponding significant expression changes from RNAseq data |
|---|
| putative targets using psRNA target (= miRNA potential target genes) |
| Phvul.007G067800 (HSF), Phvul.008G055500 (TGD3), Phvul.006G176000 (tripleix DNA-binding), Phvul.008G114700 (Rab-GDP) |
| Phvul.009G014600 (cardiolipin deacylase), Phvul.001G212400 (RING-domain E3 ligase), Phvul.005G068800 (Probable E3 ubiquitin-protein ligase), Phvul.003G053000 (glycosyltransferase) |
| Phvul.009G246000 (SNF4-like), Phvul.001G229200 (pepsin-type protease), Phvul.002G026300 integrin-like protein), Phvul.003G154800 (HSP70) |
| Phvul.011G149100 Transducin/WD40 repeat-like), Phvul.008G055500 (ATPase component TGD3 of TGD), Phvul.003G295800 (ATG2-like), Phvul.011G082700 (P-loop NTPase), Phvul.010G141400 (DOF1-like TF), Phvul.002G261500 (RNA polymerase regulatory protein) |
| Phvul.003G155500 (component SR-alpha of SRP) |
| Phvul.002G059000 (Phosphoinpase A1), Phvul.002G274500 (PAD4-like), Phvul.010G082300 (UDP-D-glucuronic acid 4-epimerase), Phvul.005G035400 (mRNA-splicing factor 18), Phvul.001G240600 (Cal B domain) |
| Phvul.001G022700 (REIMORIN-LIKE), Phvul.003G119100 (calcium-dependent lipid-binding), Phvul.011G061600 (PTAC16 -like), Phvul.003G035400 (XYL1-like), Phvul.004G121666 (subunit of CF1 of ATP synthase), Phvul.008G163350 (cohesin cofactor (PDS5)), Phvul.011G050300 (protein kinase (PIKK) TOR-like), Phvul.003G050600 (catalytic protein (CER2)), Phvul.007G069900, Phvul.011G001200 (SAC1-like), Phvul.002G185150 (sodium-proton antiporter (SOS1)) |
| Phvul.010G157900 (MED15-like), Phvul.007G191600 (CHR8-like) |
| Phvul.001G269300 (MED13-like), Phvul.001G179300 (PGP1-like), Phvul.010G125200 (NOC1/SWA2-like), Phvul.007G168500 (Solute transport channels) |
| Phvul.004G170000 (STT3-like), Phvul.010G125200 (NOC1/SWA2-like), Phvul.007G244066, Phvul.002G189700 (LIP1-like) |
| - |
| Phvul.009G100000 (UBP26-like) |
| - |

| | Id | H24_1 | H24_2 | H24_3 | X24_1 | X24_2 |
|----|----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | | | | | | |
| 4 | | | | | | |
| 5 | csi-miR482e-3p | 492 | 0 | 0 | 1 | 0 |
| 6 | ata-miR5168-3p | 314 | 1 | 0 | 2 | 1 |
| 7 | bdi-miR166h-3p | 314 | 1 | 0 | 2 | 1 |
| 8 | osa-miR166k-3p | 314 | 1 | 0 | 2 | 1 |
| 9 | osa-miR166l-3p | 314 | 1 | 0 | 2 | 1 |
| 10 | osa-miR166l-3p | 314 | 1 | 0 | 2 | 1 |
| 11 | sbi-miR166e | 314 | 1 | 0 | 2 | 1 |
| 12 | sbi-miR166g | 314 | 1 | 0 | 2 | 1 |
| 13 | sbi-miR166g | 314 | 1 | 0 | 2 | 1 |
| 14 | zma-miR166j-3p | 314 | 1 | 0 | 2 | 1 |
| 15 | zma-miR166k-3p | 314 | 1 | 0 | 2 | 1 |
| 16 | zma-miR166k-3p | 314 | 1 | 0 | 2 | 1 |
| 17 | zma-miR166n-3p | 314 | 1 | 0 | 2 | 1 |
| 18 | ami-let-7f-5p | 53 | 36 | 153 | 10 | 39 |
| 19 | ggo-let-7f | 53 | 36 | 153 | 10 | 39 |
| 20 | oar-let-7f | 53 | 36 | 153 | 10 | 39 |
| 21 | oar-let-7f | 53 | 36 | 153 | 10 | 39 |
| 22 | efu-let-7c | 106 | 111 | 486 | 62 | 89 |
| 23 | abu-let-7c | 96 | 107 | 463 | 60 | 82 |
| 24 | aca-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 25 | aca-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 26 | ami-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 27 | bta-let-7c | 96 | 107 | 463 | 60 | 82 |
| 28 | cfa-let-7c | 96 | 107 | 463 | 60 | 82 |
| 29 | cfa-let-7c | 96 | 107 | 463 | 60 | 82 |
| 30 | chi-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 31 | cja-let-7c | 96 | 107 | 463 | 60 | 82 |
| 32 | cli-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 33 | cli-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 34 | cpi-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 35 | cpo-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 36 | dma-let-7c | 96 | 107 | 463 | 60 | 82 |
| 37 | dma-let-7c | 96 | 107 | 463 | 60 | 82 |
| 38 | dno-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 39 | dre-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 40 | dre-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 41 | eca-let-7c | 96 | 107 | 463 | 60 | 82 |
| 42 | gga-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 43 | gmo-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 44 | gmo-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 45 | hhi-let-7c | 96 | 107 | 463 | 60 | 82 |
| 46 | hsa-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 47 | ipu-let-7c | 96 | 107 | 463 | 60 | 82 |
| 48 | mml-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 49 | mml-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 50 | mmr-let-7c | 96 | 107 | 463 | 60 | 82 |
| 51 | mmu-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 52 | mze-let-7c | 96 | 107 | 463 | 60 | 82 |
| 53 | mze-let-7c | 96 | 107 | 463 | 60 | 82 |
| 54 | nbr-let-7c | 96 | 107 | 463 | 60 | 82 |
| 55 | nle-let-7c | 96 | 107 | 463 | 60 | 82 |
| 56 | oan-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 57 | oar-let-7c | 96 | 107 | 463 | 60 | 82 |
| 58 | oar-let-7c | 96 | 107 | 463 | 60 | 82 |
| 59 | ocu-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 60 | | | | | | |

| | | | | | | |
|----|---------------|-----|-----|-----|----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | oga-let-7c | 96 | 107 | 463 | 60 | 82 |
| 4 | oha-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 5 | oni-let-7c | 96 | 107 | 463 | 60 | 82 |
| 6 | pal-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 7 | pbv-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 8 | pha-let-7c | 96 | 107 | 463 | 60 | 82 |
| 9 | ppy-let-7c | 96 | 107 | 463 | 60 | 82 |
| 10 | pol-let-7a-5p | 96 | 107 | 463 | 60 | 82 |
| 11 | ppa-let-7c | 96 | 107 | 463 | 60 | 82 |
| 12 | ppy-let-7c | 96 | 107 | 463 | 60 | 82 |
| 13 | ptr-let-7c | 96 | 107 | 463 | 60 | 82 |
| 14 | rno-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 15 | ssa-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 16 | ssc-let-7c | 96 | 107 | 463 | 60 | 82 |
| 17 | tcf-let-7-5p | 96 | 107 | 463 | 60 | 82 |
| 18 | tgu-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 19 | xla-let-7c-5p | 96 | 107 | 463 | 60 | 82 |
| 20 | xtr-let-7c | 96 | 107 | 463 | 60 | 82 |
| 21 | efu-let-7f | 174 | 117 | 380 | 52 | 105 |
| 22 | aca-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 23 | bta-let-7f | 172 | 115 | 379 | 52 | 105 |
| 24 | cfa-let-7f | 172 | 115 | 379 | 52 | 105 |
| 25 | cgr-let-7f | 172 | 115 | 379 | 52 | 105 |
| 26 | chi-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 27 | cja-let-7f | 172 | 115 | 379 | 52 | 105 |
| 28 | cli-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 29 | cpi-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 30 | cpo-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 31 | dma-let-7f | 172 | 115 | 379 | 52 | 105 |
| 32 | dno-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 33 | dre-let-7f | 172 | 115 | 379 | 52 | 105 |
| 34 | eca-let-7f | 172 | 115 | 379 | 52 | 105 |
| 35 | gga-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 36 | gmo-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 37 | hsa-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 38 | ipu-let-7f | 172 | 115 | 379 | 52 | 105 |
| 39 | mdo-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 40 | mml-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 41 | mmr-let-7f | 172 | 115 | 379 | 52 | 105 |
| 42 | mmu-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 43 | nle-let-7f | 172 | 115 | 379 | 52 | 105 |
| 44 | oan-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 45 | ocu-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | oga-let-7f | 172 | 115 | 379 | 52 | 105 |
| 4 | oha-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 5 | oni-let-7f | 172 | 115 | 379 | 52 | 105 |
| 6 | pal-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 7 | pbv-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 8 | pha-let-7f | 172 | 115 | 379 | 52 | 105 |
| 9 | ppa-let-7f | 172 | 115 | 379 | 52 | 105 |
| 10 | ppy-let-7f | 172 | 115 | 379 | 52 | 105 |
| 11 | ptr-let-7f | 172 | 115 | 379 | 52 | 105 |
| 12 | rno-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 13 | sbo-let-7f | 172 | 115 | 379 | 52 | 105 |
| 14 | ssc-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 15 | tch-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 16 | tgu-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 17 | xla-let-7f-5p | 172 | 115 | 379 | 52 | 105 |
| 18 | xtr-let-7f | 172 | 115 | 379 | 52 | 105 |
| 19 | aly-miR2111a-5p | 555 | 707 | 456 | 105 | 264 |
| 20 | aly-miR2111b-5p | 555 | 707 | 456 | 105 | 264 |
| 21 | aly-miR2111c-5p | 555 | 707 | 456 | 105 | 264 |
| 22 | ath-miR2111a-5p | 555 | 707 | 456 | 105 | 264 |
| 23 | ath-miR2111b-5p | 555 | 707 | 456 | 105 | 264 |
| 24 | bna-miR2111a-5p | 555 | 707 | 456 | 105 | 264 |
| 25 | bna-miR2111b-5p | 555 | 707 | 456 | 105 | 264 |
| 26 | bna-miR2111d | 555 | 707 | 456 | 105 | 264 |
| 27 | bra-miR2111a-5p | 555 | 707 | 456 | 105 | 264 |
| 28 | bra-miR2111b-5p | 555 | 707 | 456 | 105 | 264 |
| 29 | cme-miR2111a | 555 | 707 | 456 | 105 | 264 |
| 30 | cme-miR2111b | 555 | 707 | 456 | 105 | 264 |
| 31 | gma-miR2111b | 555 | 707 | 456 | 105 | 264 |
| 32 | gma-miR2111c | 555 | 707 | 456 | 105 | 264 |
| 33 | gma-miR2111e | 555 | 707 | 456 | 105 | 264 |
| 34 | gma-miR2111f | 555 | 707 | 456 | 105 | 264 |
| 35 | lja-miR2111-5p | 555 | 707 | 456 | 105 | 264 |
| 36 | mdm-miR2111a | 555 | 707 | 456 | 105 | 264 |
| 37 | mdm-miR2111b | 555 | 707 | 456 | 105 | 264 |
| 38 | mes-miR2111a | 555 | 707 | 456 | 105 | 264 |
| 39 | mes-miR2111b | 555 | 707 | 456 | 105 | 264 |
| 40 | mtr-miR2111a-5p | 555 | 707 | 456 | 105 | 264 |
| 41 | mtr-miR2111b | 555 | 707 | 456 | 105 | 264 |
| 42 | mtr-miR2111c | 555 | 707 | 456 | 105 | 264 |
| 43 | mtr-miR2111d-5p | 555 | 707 | 456 | 105 | 264 |
| 44 | mtr-miR2111e-5p | 555 | 707 | 456 | 105 | 264 |
| 45 | mtr-miR2111f | 555 | 707 | 456 | 105 | 264 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | mtr-miR2111g-5p | 555 | 707 | 456 | 105 | 264 |
| 4 | mtr-miR2111h | 555 | 707 | 456 | 105 | 264 |
| 5 | mtr-miR2111i | 555 | 707 | 456 | 105 | 264 |
| 6 | mtr-miR2111j | 555 | 707 | 456 | 105 | 264 |
| 7 | mtr-miR2111k | 555 | 707 | 456 | 105 | 264 |
| 8 | mtr-miR2111m-5p | 555 | 707 | 456 | 105 | 264 |
| 9 | mtr-miR2111n | 555 | 707 | 456 | 105 | 264 |
| 10 | mtr-miR2111o | 555 | 707 | 456 | 105 | 264 |
| 11 | ppe-miR2111a | 555 | 707 | 456 | 105 | 264 |
| 12 | ppe-miR2111b | 555 | 707 | 456 | 105 | 264 |
| 13 | ppe-miR2111c | 555 | 707 | 456 | 105 | 264 |
| 14 | ppe-miR2111d | 555 | 707 | 456 | 105 | 264 |
| 15 | tcc-miR2111 | 555 | 707 | 456 | 105 | 264 |
| 16 | csi-miR2111-5p | 509 | 626 | 412 | 92 | 239 |
| 17 | ptc-miR2111a | 509 | 626 | 412 | 92 | 239 |
| 18 | ptc-miR2111b | 509 | 626 | 412 | 92 | 239 |
| 19 | fve-miR2111a | 509 | 626 | 411 | 92 | 239 |
| 20 | fve-miR2111b-5p | 509 | 626 | 411 | 92 | 239 |
| 21 | fve-miR2111c | 509 | 626 | 411 | 92 | 239 |
| 22 | efu-let-7d | 73 | 45 | 170 | 27 | 42 |
| 23 | bta-let-7d | 65 | 44 | 166 | 25 | 42 |
| 24 | cgr-let-7d-5p | 65 | 44 | 166 | 25 | 42 |
| 25 | chi-let-7d-5p | 65 | 44 | 166 | 25 | 42 |
| 26 | cja-let-7d | 65 | 44 | 166 | 25 | 42 |
| 27 | cli-let-7d-5p | 65 | 44 | 166 | 25 | 42 |
| 28 | cpi-let-7d-5p | 65 | 44 | 166 | 25 | 42 |
| 29 | cpo-let-7d-5p | 65 | 44 | 166 | 25 | 42 |
| 30 | dno-let-7d-5p | 65 | 44 | 166 | 25 | 42 |
| 31 | eca-let-7d | 65 | 44 | 166 | 25 | 42 |
| 32 | hsa-let-7d-5p | 65 | 44 | 166 | 25 | 42 |
| 33 | mml-let-7d | 65 | 44 | 166 | 25 | 42 |
| 34 | mmu-let-7d-5p | 65 | 44 | 166 | 25 | 42 |
| 35 | oan-let-7d-5p | 65 | 44 | 166 | 25 | 42 |
| 36 | ocu-let-7d-5p | 65 | 44 | 166 | 25 | 42 |
| 37 | oha-let-7d-5p | 65 | 44 | 166 | 25 | 42 |
| 38 | pbv-let-7d-5p | 65 | 44 | 166 | 25 | 42 |
| 39 | ppy-let-7d | 65 | 44 | 166 | 25 | 42 |
| 40 | ptr-let-7d | 65 | 44 | 166 | 25 | 42 |
| 41 | rno-let-7d-5p | 65 | 44 | 166 | 25 | 42 |
| 42 | ssc-let-7d-5p | 65 | 44 | 166 | 25 | 42 |
| 43 | tgu-let-7d-5p | 65 | 44 | 166 | 25 | 42 |
| 44 | pvu-miR482-5p | 395 | 278 | 197 | 141 | 106 |
| 45 | bta-miR-21-5p | 5527 | 1944 | 4924 | 1486 | 1872 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | cpo-miR-21-5p | 5527 | 1944 | 4924 | 1486 | 1872 |
| 4 | dno-miR-21-5p | 5527 | 1944 | 4924 | 1486 | 1872 |
| 5 | ocu-miR-21-5p | 5527 | 1944 | 4924 | 1486 | 1872 |
| 6 | sha-miR-21 | 5527 | 1944 | 4924 | 1486 | 1872 |
| 7 | ami-miR-21-5p | 5489 | 1934 | 4893 | 1478 | 1859 |
| 8 | chi-miR-21-5p | 5489 | 1934 | 4893 | 1478 | 1859 |
| 9 | dma-miR-21 | 5489 | 1934 | 4893 | 1478 | 1859 |
| 10 | mmr-miR-21 | 5489 | 1934 | 4893 | 1478 | 1859 |
| 11 | nle-miR-21 | 5489 | 1934 | 4893 | 1478 | 1859 |
| 12 | oar-miR-21 | 5489 | 1934 | 4893 | 1478 | 1859 |
| 13 | oga-miR-21 | 5489 | 1934 | 4893 | 1478 | 1859 |
| 14 | pbv-miR-21-5p | 5489 | 1934 | 4893 | 1478 | 1859 |
| 15 | pha-miR-21 | 5489 | 1934 | 4893 | 1478 | 1859 |
| 16 | sbo-miR-21 | 5489 | 1934 | 4893 | 1478 | 1859 |
| 17 | aca-miR-21-5p | 1292 | 407 | 432 | 239 | 354 |
| 18 | age-miR-21 | 1292 | 407 | 432 | 239 | 354 |
| 19 | cfa-miR-21 | 1292 | 407 | 432 | 239 | 354 |
| 20 | cgr-miR-21-5p | 1292 | 407 | 432 | 239 | 354 |
| 21 | cja-miR-21 | 1292 | 407 | 432 | 239 | 354 |
| 22 | cli-miR-21-5p | 1292 | 407 | 432 | 239 | 354 |
| 23 | cpi-miR-21-5p | 1292 | 407 | 432 | 239 | 354 |
| 24 | eca-miR-21 | 1292 | 407 | 432 | 239 | 354 |
| 25 | gga-miR-21-5p | 1292 | 407 | 432 | 239 | 354 |
| 26 | ggo-miR-21 | 1292 | 407 | 432 | 239 | 354 |
| 27 | hsa-miR-21-5p | 1292 | 407 | 432 | 239 | 354 |
| 28 | mdo-miR-21-5p | 1292 | 407 | 432 | 239 | 354 |
| 29 | mml-miR-21-5p | 1292 | 407 | 432 | 239 | 354 |
| 30 | mmu-miR-21a-5p | 1292 | 407 | 432 | 239 | 354 |
| 31 | mne-miR-21 | 1292 | 407 | 432 | 239 | 354 |
| 32 | oan-miR-21-5p | 1292 | 407 | 432 | 239 | 354 |
| 33 | oha-miR-21-5p | 1292 | 407 | 432 | 239 | 354 |
| 34 | pal-miR-21-5p | 1292 | 407 | 432 | 239 | 354 |
| 35 | ppa-miR-21 | 1292 | 407 | 432 | 239 | 354 |
| 36 | ppy-miR-21 | 1292 | 407 | 432 | 239 | 354 |
| 37 | ptr-miR-21 | 1292 | 407 | 432 | 239 | 354 |
| 38 | rno-miR-21-5p | 1292 | 407 | 432 | 239 | 354 |
| 39 | ssc-miR-21-5p | 1292 | 407 | 432 | 239 | 354 |
| 40 | tch-miR-21-5p | 1292 | 407 | 432 | 239 | 354 |
| 41 | tgu-miR-21-5p | 1292 | 407 | 432 | 239 | 354 |
| 42 | efu-miR-34a | 175 | 95 | 221 | 65 | 86 |
| 43 | ami-miR-34a-5p | 174 | 95 | 220 | 65 | 86 |
| 44 | cja-miR-34a | 174 | 95 | 220 | 65 | 86 |
| 45 | gga-miR-34a-5p | 174 | 95 | 220 | 65 | 86 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|----|-----|----|----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | mdo-miR-34a-5p | 174 | 95 | 220 | 65 | 86 |
| 4 | oha-miR-34a-5p | 174 | 95 | 220 | 65 | 86 |
| 5 | tch-miR-34a-5p | 174 | 95 | 220 | 65 | 86 |
| 6 | xtr-miR-34a | 174 | 95 | 220 | 65 | 86 |
| 7 | | | | | | |
| 8 | ame-let-7-5p | 80 | 75 | 204 | 53 | 63 |
| 9 | | | | | | |
| 10 | bdo-let-7 | 80 | 75 | 204 | 53 | 63 |
| 11 | bmo-let-7-5p | 80 | 75 | 204 | 53 | 63 |
| 12 | | | | | | |
| 13 | cte-let-7 | 80 | 75 | 204 | 53 | 63 |
| 14 | dan-let-7 | 80 | 75 | 204 | 53 | 63 |
| 15 | der-let-7 | 80 | 75 | 204 | 53 | 63 |
| 16 | dgr-let-7 | 80 | 75 | 204 | 53 | 63 |
| 17 | | | | | | |
| 18 | dme-let-7-5p | 80 | 75 | 204 | 53 | 63 |
| 19 | dmo-let-7 | 80 | 75 | 204 | 53 | 63 |
| 20 | | | | | | |
| 21 | dpe-let-7 | 80 | 75 | 204 | 53 | 63 |
| 22 | dps-let-7 | 80 | 75 | 204 | 53 | 63 |
| 23 | dqu-let-7-5p | 80 | 75 | 204 | 53 | 63 |
| 24 | dse-let-7 | 80 | 75 | 204 | 53 | 63 |
| 25 | | | | | | |
| 26 | dsi-let-7 | 80 | 75 | 204 | 53 | 63 |
| 27 | dvi-let-7 | 80 | 75 | 204 | 53 | 63 |
| 28 | dwi-let-7 | 80 | 75 | 204 | 53 | 63 |
| 29 | | | | | | |
| 30 | dya-let-7 | 80 | 75 | 204 | 53 | 63 |
| 31 | ggo-let-7a | 80 | 75 | 204 | 53 | 63 |
| 32 | isc-let-7 | 80 | 75 | 204 | 53 | 63 |
| 33 | | | | | | |
| 34 | ngi-let-7 | 80 | 75 | 204 | 53 | 63 |
| 35 | nvi-let-7 | 80 | 75 | 204 | 53 | 63 |
| 36 | ola-let-7a-5p | 80 | 75 | 204 | 53 | 63 |
| 37 | | | | | | |
| 38 | sha-let-7a | 80 | 75 | 204 | 53 | 63 |
| 39 | hme-let-7 | 80 | 75 | 204 | 53 | 64 |
| 40 | pca-let-7-5p | 80 | 75 | 204 | 53 | 64 |
| 41 | | | | | | |
| 42 | abu-miR-34 | 134 | 76 | 189 | 56 | 75 |
| 43 | age-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 44 | bta-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 45 | ccr-miR-34 | 134 | 76 | 189 | 56 | 75 |
| 46 | cfa-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 47 | cgr-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 48 | chi-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 49 | | | | | | |
| 50 | cli-miR-34a-5p | 134 | 76 | 189 | 56 | 75 |
| 51 | cpi-miR-34a-5p | 134 | 76 | 189 | 56 | 75 |
| 52 | cpo-miR-34a-5p | 134 | 76 | 189 | 56 | 75 |
| 53 | dno-miR-34a-5p | 134 | 76 | 189 | 56 | 75 |
| 54 | | | | | | |
| 55 | dre-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 56 | eca-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 57 | ega-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 58 | | | | | | |
| 59 | ggo-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | gmo-miR-34-5p | 134 | 76 | 189 | 56 | 75 |
| 4 | hsa-miR-34a-5p | 134 | 76 | 189 | 56 | 75 |
| 5 | ipu-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 6 | lla-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 7 | lla-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 8 | mml-miR-34a-5p | 134 | 76 | 189 | 56 | 75 |
| 9 | mml-miR-34a-5p | 134 | 76 | 189 | 56 | 75 |
| 10 | mmr-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 11 | mmu-miR-34a-5p | 134 | 76 | 189 | 56 | 75 |
| 12 | mmu-miR-34a-5p | 134 | 76 | 189 | 56 | 75 |
| 13 | mne-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 14 | mze-miR-34 | 134 | 76 | 189 | 56 | 75 |
| 15 | nbr-miR-34 | 134 | 76 | 189 | 56 | 75 |
| 16 | nle-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 17 | nle-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 18 | ocu-miR-34a-5p | 134 | 76 | 189 | 56 | 75 |
| 19 | oga-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 20 | oni-miR-34 | 134 | 76 | 189 | 56 | 75 |
| 21 | oni-miR-34 | 134 | 76 | 189 | 56 | 75 |
| 22 | pal-miR-34a-5p | 134 | 76 | 189 | 56 | 75 |
| 23 | pbv-miR-34a-5p | 134 | 76 | 189 | 56 | 75 |
| 24 | pbv-miR-34a-5p | 134 | 76 | 189 | 56 | 75 |
| 25 | ppy-miR-34 | 134 | 76 | 189 | 56 | 75 |
| 26 | ppa-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 27 | ppy-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 28 | ptr-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 29 | ptr-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 30 | rno-miR-34a-5p | 134 | 76 | 189 | 56 | 75 |
| 31 | sla-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 32 | sla-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 33 | ssc-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 34 | tgu-miR-34a | 134 | 76 | 189 | 56 | 75 |
| 35 | prd-let-7-5p | 283 | 201 | 540 | 169 | 186 |
| 36 | abu-let-7a | 276 | 195 | 528 | 165 | 184 |
| 37 | abu-let-7a | 276 | 195 | 528 | 165 | 184 |
| 38 | aca-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 39 | ami-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 40 | asu-let-7-5p | 276 | 195 | 528 | 165 | 184 |
| 41 | asu-let-7-5p | 276 | 195 | 528 | 165 | 184 |
| 42 | bbe-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 43 | bfl-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 44 | bma-let-7 | 276 | 195 | 528 | 165 | 184 |
| 45 | bta-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 46 | bta-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 47 | cbn-let-7 | 276 | 195 | 528 | 165 | 184 |
| 48 | cbr-let-7 | 276 | 195 | 528 | 165 | 184 |
| 49 | cbr-let-7 | 276 | 195 | 528 | 165 | 184 |
| 50 | ccr-let-7a | 276 | 195 | 528 | 165 | 184 |
| 51 | cel-let-7-5p | 276 | 195 | 528 | 165 | 184 |
| 52 | cfa-let-7a | 276 | 195 | 528 | 165 | 184 |
| 53 | cfa-let-7a | 276 | 195 | 528 | 165 | 184 |
| 54 | cgr-let-7a | 276 | 195 | 528 | 165 | 184 |
| 55 | chi-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 56 | cja-let-7a | 276 | 195 | 528 | 165 | 184 |
| 57 | cja-let-7a | 276 | 195 | 528 | 165 | 184 |
| 58 | cli-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 59 | cpi-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 60 | | | | | | |

| | | | | | | |
|----|---------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | cpo-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 4 | crm-let-7 | 276 | 195 | 528 | 165 | 184 |
| 5 | dma-let-7a | 276 | 195 | 528 | 165 | 184 |
| 6 | dno-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 7 | dre-let-7a | 276 | 195 | 528 | 165 | 184 |
| 8 | eca-let-7a | 276 | 195 | 528 | 165 | 184 |
| 9 | fru-let-7a | 276 | 195 | 528 | 165 | 184 |
| 10 | gga-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 11 | gga-let-7j-5p | 276 | 195 | 528 | 165 | 184 |
| 12 | gmo-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 13 | hpo-let-7-5p | 276 | 195 | 528 | 165 | 184 |
| 14 | hsa-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 15 | ipu-let-7a | 276 | 195 | 528 | 165 | 184 |
| 16 | lgi-let-7 | 276 | 195 | 528 | 165 | 184 |
| 17 | mdo-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 18 | mml-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 19 | mmr-let-7a | 276 | 195 | 528 | 165 | 184 |
| 20 | mmu-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 21 | mze-let-7a | 276 | 195 | 528 | 165 | 184 |
| 22 | nbr-let-7a | 276 | 195 | 528 | 165 | 184 |
| 23 | nle-let-7a | 276 | 195 | 528 | 165 | 184 |
| 24 | oar-let-7a | 276 | 195 | 528 | 165 | 184 |
| 25 | ocu-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 26 | oga-let-7a | 276 | 195 | 528 | 165 | 184 |
| 27 | oha-let-7a | 276 | 195 | 528 | 165 | 184 |
| 28 | oha-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 29 | ola-let-7a | 276 | 195 | 528 | 165 | 184 |
| 30 | oni-let-7a | 276 | 195 | 528 | 165 | 184 |
| 31 | pal-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 32 | pbv-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 33 | pha-let-7a | 276 | 195 | 528 | 165 | 184 |
| 34 | pma-let-7a | 276 | 195 | 528 | 165 | 184 |
| 35 | pny-let-7a | 276 | 195 | 528 | 165 | 184 |
| 36 | ppa-let-7a | 276 | 195 | 528 | 165 | 184 |
| 37 | ppc-let-7 | 276 | 195 | 528 | 165 | 184 |
| 38 | ppy-let-7a | 276 | 195 | 528 | 165 | 184 |
| 39 | pte-let-7-5p | 276 | 195 | 528 | 165 | 184 |
| 40 | ptr-let-7a | 276 | 195 | 528 | 165 | 184 |
| 41 | rno-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 42 | sbo-let-7a | 276 | 195 | 528 | 165 | 184 |
| 43 | sko-let-7 | 276 | 195 | 528 | 165 | 184 |
| 44 | ssa-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 45 | ssc-let-7a | 276 | 195 | 528 | 165 | 184 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|------|------|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | tgu-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 4 | tni-let-7a | 276 | 195 | 528 | 165 | 184 |
| 5 | xla-let-7a-5p | 276 | 195 | 528 | 165 | 184 |
| 6 | xtr-let-7a | 276 | 195 | 528 | 165 | 184 |
| 7 | | | | | | |
| 8 | abu-miR-429b | 9 | 37 | 167 | 23 | 39 |
| 9 | aca-miR-429-3p | 9 | 37 | 167 | 23 | 39 |
| 10 | bta-miR-429 | 9 | 37 | 167 | 23 | 39 |
| 11 | cca-miR-429 | 9 | 37 | 167 | 23 | 39 |
| 12 | ccr-miR-429 | 9 | 37 | 167 | 23 | 39 |
| 13 | cfa-miR-429 | 9 | 37 | 167 | 23 | 39 |
| 14 | cgr-miR-429 | 9 | 37 | 167 | 23 | 39 |
| 15 | cli-miR-429-3p | 9 | 37 | 167 | 23 | 39 |
| 16 | cpi-miR-429-3p | 9 | 37 | 167 | 23 | 39 |
| 17 | cpo-miR-429-3p | 9 | 37 | 167 | 23 | 39 |
| 18 | dno-miR-429-3p | 9 | 37 | 167 | 23 | 39 |
| 19 | dre-miR-429a | 9 | 37 | 167 | 23 | 39 |
| 20 | efu-miR-429 | 9 | 37 | 167 | 23 | 39 |
| 21 | fru-miR-429 | 9 | 37 | 167 | 23 | 39 |
| 22 | gga-miR-429-3p | 9 | 37 | 167 | 23 | 39 |
| 23 | gmo-miR-429-3p | 9 | 37 | 167 | 23 | 39 |
| 24 | mmu-miR-429-3p | 9 | 37 | 167 | 23 | 39 |
| 25 | mze-miR-429b | 9 | 37 | 167 | 23 | 39 |
| 26 | nbr-miR-429b | 9 | 37 | 167 | 23 | 39 |
| 27 | oan-miR-429-3p | 9 | 37 | 167 | 23 | 39 |
| 28 | oha-miR-429-3p | 9 | 37 | 167 | 23 | 39 |
| 29 | oni-miR-429b | 9 | 37 | 167 | 23 | 39 |
| 30 | pal-miR-429-3p | 9 | 37 | 167 | 23 | 39 |
| 31 | pbv-miR-429-3p | 9 | 37 | 167 | 23 | 39 |
| 32 | pony-miR-429b | 9 | 37 | 167 | 23 | 39 |
| 33 | rno-miR-429 | 9 | 37 | 167 | 23 | 39 |
| 34 | ssc-miR-429 | 9 | 37 | 167 | 23 | 39 |
| 35 | tni-miR-429 | 9 | 37 | 167 | 23 | 39 |
| 36 | xla-miR-429-3p | 9 | 37 | 167 | 23 | 39 |
| 37 | xtr-miR-429 | 9 | 37 | 167 | 23 | 39 |
| 38 | | | | | | |
| 39 | aof-miR166c | 101 | 1840 | 1341 | 461 | 530 |
| 40 | ath-miR165a-3p | 101 | 1840 | 1341 | 461 | 530 |
| 41 | ath-miR165b | 101 | 1840 | 1341 | 461 | 530 |
| 42 | bnm-miR166f | 101 | 1840 | 1341 | 461 | 530 |
| 43 | cas-miR165a | 101 | 1840 | 1341 | 461 | 530 |
| 44 | lus-miR166b | 101 | 1840 | 1341 | 461 | 530 |
| 45 | | | | | | |
| 46 | cli-let-7i-5p | 203 | 105 | 205 | 74 | 111 |
| 47 | abu-let-7i | 201 | 103 | 204 | 74 | 111 |
| 48 | aca-let-7i-5p | 201 | 103 | 204 | 74 | 111 |
| 49 | bta-let-7i | 201 | 103 | 204 | 74 | 111 |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | chi-let-7i-5p | 201 | 103 | 204 | 74 | 111 |
| 4 | cja-let-7i | 201 | 103 | 204 | 74 | 111 |
| 5 | cpi-let-7i-5p | 201 | 103 | 204 | 74 | 111 |
| 6 | cpo-let-7i-5p | 201 | 103 | 204 | 74 | 111 |
| 7 | dno-let-7i-5p | 201 | 103 | 204 | 74 | 111 |
| 8 | dre-let-7i | 201 | 103 | 204 | 74 | 111 |
| 9 | fru-let-7i | 201 | 103 | 204 | 74 | 111 |
| 10 | gmo-let-7i-5p | 201 | 103 | 204 | 74 | 111 |
| 11 | hsa-let-7i-5p | 201 | 103 | 204 | 74 | 111 |
| 12 | ipu-let-7i | 201 | 103 | 204 | 74 | 111 |
| 13 | mml-let-7i-5p | 201 | 103 | 204 | 74 | 111 |
| 14 | mmu-let-7i-5p | 201 | 103 | 204 | 74 | 111 |
| 15 | mze-let-7i | 201 | 103 | 204 | 74 | 111 |
| 16 | nbr-let-7i | 201 | 103 | 204 | 74 | 111 |
| 17 | nle-let-7i | 201 | 103 | 204 | 74 | 111 |
| 18 | oar-let-7i | 201 | 103 | 204 | 74 | 111 |
| 19 | ocu-let-7i-5p | 201 | 103 | 204 | 74 | 111 |
| 20 | oga-let-7i | 201 | 103 | 204 | 74 | 111 |
| 21 | oha-let-7i-5p | 201 | 103 | 204 | 74 | 111 |
| 22 | oni-let-7i | 201 | 103 | 204 | 74 | 111 |
| 23 | pal-let-7i-5p | 201 | 103 | 204 | 74 | 111 |
| 24 | pbv-let-7i-5p | 201 | 103 | 204 | 74 | 111 |
| 25 | pha-let-7i | 201 | 103 | 204 | 74 | 111 |
| 26 | ppy-let-7i | 201 | 103 | 204 | 74 | 111 |
| 27 | ppa-let-7i | 201 | 103 | 204 | 74 | 111 |
| 28 | ppp-let-7i | 201 | 103 | 204 | 74 | 111 |
| 29 | ptr-let-7i | 201 | 103 | 204 | 74 | 111 |
| 30 | rno-let-7i-5p | 201 | 103 | 204 | 74 | 111 |
| 31 | ssa-let-7i-5p | 201 | 103 | 204 | 74 | 111 |
| 32 | tch-let-7i-5p | 201 | 103 | 204 | 74 | 111 |
| 33 | tgu-let-7i-5p | 201 | 103 | 204 | 74 | 111 |
| 34 | tni-let-7i | 201 | 103 | 204 | 74 | 111 |
| 35 | ami-miR-30d-5p | 75 | 82 | 136 | 31 | 60 |
| 36 | bta-miR-30d | 75 | 82 | 136 | 31 | 60 |
| 37 | cfa-miR-30d | 75 | 82 | 136 | 31 | 60 |
| 38 | cli-miR-30d-5p | 75 | 82 | 136 | 31 | 60 |
| 39 | cpo-miR-30d-5p | 75 | 82 | 136 | 31 | 60 |
| 40 | dno-miR-30d-5p | 75 | 82 | 136 | 31 | 60 |
| 41 | gmo-miR-30a-5p | 75 | 82 | 136 | 31 | 60 |
| 42 | nle-miR-30d | 75 | 82 | 136 | 31 | 60 |
| 43 | ocu-miR-30d-5p | 75 | 82 | 136 | 31 | 60 |
| 44 | oga-miR-30d | 75 | 82 | 136 | 31 | 60 |
| 45 | oha-miR-30d-5p | 75 | 82 | 136 | 31 | 60 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|------------------|-----|----|-----|----|----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | pal-miR-30d-5p | 75 | 82 | 136 | 31 | 60 |
| 4 | pbv-miR-30d-5p | 75 | 82 | 136 | 31 | 60 |
| 5 | pha-miR-30d | 75 | 82 | 136 | 31 | 60 |
| 6 | ssa-miR-30b-5p | 75 | 82 | 136 | 31 | 60 |
| 7 | ssa-miR-30d | 75 | 82 | 136 | 31 | 60 |
| 8 | ssc-miR-30d | 75 | 82 | 136 | 31 | 60 |
| 9 | tgu-miR-30d-5p | 75 | 82 | 136 | 31 | 60 |
| 10 | xla-miR-30d-5p | 75 | 82 | 136 | 31 | 60 |
| 11 | cgr-miR-29a-3p | 88 | 63 | 108 | 32 | 67 |
| 12 | chi-miR-29a-3p | 88 | 63 | 108 | 32 | 67 |
| 13 | oar-miR-29a | 88 | 63 | 108 | 32 | 67 |
| 14 | tch-miR-29a-3p | 88 | 63 | 108 | 32 | 67 |
| 15 | ssa-miR-23b-3p | 101 | 31 | 58 | 21 | 45 |
| 16 | ami-miR-23b-3p | 98 | 30 | 57 | 21 | 45 |
| 17 | bta-miR-10174-3p | 98 | 30 | 57 | 21 | 45 |
| 18 | bta-miR-23b-3p | 98 | 30 | 57 | 21 | 45 |
| 19 | cpo-miR-23b-3p | 98 | 30 | 57 | 21 | 45 |
| 20 | dno-miR-23b-3p | 98 | 30 | 57 | 21 | 45 |
| 21 | dre-miR-23b-3p | 98 | 30 | 57 | 21 | 45 |
| 22 | efu-miR-23b | 98 | 30 | 57 | 21 | 45 |
| 23 | hsa-miR-23b-3p | 98 | 30 | 57 | 21 | 45 |
| 24 | ocu-miR-23b-3p | 98 | 30 | 57 | 21 | 45 |
| 25 | oga-miR-23b | 98 | 30 | 57 | 21 | 45 |
| 26 | oha-miR-23b-3p | 98 | 30 | 57 | 21 | 45 |
| 27 | ola-miR-23b | 98 | 30 | 57 | 21 | 45 |
| 28 | pbv-miR-23b-3p | 98 | 30 | 57 | 21 | 45 |
| 29 | pma-miR-23b | 98 | 30 | 57 | 21 | 45 |
| 30 | ppa-miR-23b | 98 | 30 | 57 | 21 | 45 |
| 31 | ppy-miR-23b | 98 | 30 | 57 | 21 | 45 |
| 32 | ptr-miR-23b | 98 | 30 | 57 | 21 | 45 |
| 33 | tch-miR-23b-3p | 98 | 30 | 57 | 21 | 45 |
| 34 | cfa-miR-29a | 117 | 82 | 137 | 45 | 82 |
| 35 | cja-miR-29a | 117 | 82 | 137 | 45 | 82 |
| 36 | cpo-miR-29a-3p | 117 | 82 | 137 | 45 | 82 |
| 37 | dma-miR-29a | 117 | 82 | 137 | 45 | 82 |
| 38 | dno-miR-29a-3p | 117 | 82 | 137 | 45 | 82 |
| 39 | eca-miR-29a | 117 | 82 | 137 | 45 | 82 |
| 40 | hsa-miR-29a-3p | 117 | 82 | 137 | 45 | 82 |
| 41 | mmr-miR-29a | 117 | 82 | 137 | 45 | 82 |
| 42 | mmu-miR-29a-3p | 117 | 82 | 137 | 45 | 82 |
| 43 | nle-miR-29a | 117 | 82 | 137 | 45 | 82 |
| 44 | ocu-miR-29a-3p | 117 | 82 | 137 | 45 | 82 |
| 45 | oga-miR-29a | 117 | 82 | 137 | 45 | 82 |
| 46 | pal-miR-29a-3p | 117 | 82 | 137 | 45 | 82 |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | pha-miR-29a | 117 | 82 | 137 | 45 | 82 |
| 4 | rno-miR-29a-3p | 117 | 82 | 137 | 45 | 82 |
| 5 | cli-miR-23b-3p | 99 | 30 | 57 | 22 | 45 |
| 6 | age-miR-29a | 170 | 93 | 148 | 58 | 108 |
| 7 | ggo-miR-29a | 170 | 93 | 148 | 58 | 108 |
| 8 | lla-miR-29a | 170 | 93 | 148 | 58 | 108 |
| 9 | mml-miR-29a-3p | 170 | 93 | 148 | 58 | 108 |
| 10 | mne-miR-29a | 170 | 93 | 148 | 58 | 108 |
| 11 | ppa-miR-29a | 170 | 93 | 148 | 58 | 108 |
| 12 | ppy-miR-29a | 170 | 93 | 148 | 58 | 108 |
| 13 | ptr-miR-29a | 170 | 93 | 148 | 58 | 108 |
| 14 | sbo-miR-29a | 170 | 93 | 148 | 58 | 108 |
| 15 | sla-miR-29a | 170 | 93 | 148 | 58 | 108 |
| 16 | gga-miR-126-3p | 752 | 501 | 671 | 291 | 487 |
| 17 | bta-miR-200c | 2 | 59 | 226 | 29 | 53 |
| 18 | cfa-miR-200c | 2 | 59 | 226 | 29 | 53 |
| 19 | cgr-miR-200c | 2 | 59 | 226 | 29 | 53 |
| 20 | chi-miR-200c | 2 | 59 | 226 | 29 | 53 |
| 21 | cja-miR-200c | 2 | 59 | 226 | 29 | 53 |
| 22 | cpo-miR-200c-3p | 2 | 59 | 226 | 29 | 53 |
| 23 | eca-miR-200c | 2 | 59 | 226 | 29 | 53 |
| 24 | efu-miR-200c | 2 | 59 | 226 | 29 | 53 |
| 25 | hsa-miR-200c-3p | 2 | 59 | 226 | 29 | 53 |
| 26 | mmu-miR-200c-3p | 2 | 59 | 226 | 29 | 53 |
| 27 | ocu-miR-200c-3p | 2 | 59 | 226 | 29 | 53 |
| 28 | pal-miR-200c-3p | 2 | 59 | 226 | 29 | 53 |
| 29 | ptr-miR-200c | 2 | 59 | 226 | 29 | 53 |
| 30 | tch-miR-200c-3p | 2 | 59 | 226 | 29 | 53 |
| 31 | aca-miR-126-3p | 752 | 499 | 671 | 291 | 487 |
| 32 | ami-miR-126-3p | 752 | 499 | 671 | 291 | 487 |
| 33 | cgr-miR-126a | 752 | 499 | 671 | 291 | 487 |
| 34 | cja-miR-126 | 752 | 499 | 671 | 291 | 487 |
| 35 | cli-miR-126-3p | 752 | 499 | 671 | 291 | 487 |
| 36 | cpi-miR-126-3p | 752 | 499 | 671 | 291 | 487 |
| 37 | cpo-miR-126-3p | 752 | 499 | 671 | 291 | 487 |
| 38 | dno-miR-126-3p | 752 | 499 | 671 | 291 | 487 |
| 39 | eca-miR-126-3p | 752 | 499 | 671 | 291 | 487 |
| 40 | hsa-miR-126-3p | 752 | 499 | 671 | 291 | 487 |
| 41 | mdo-miR-126-3p | 752 | 499 | 671 | 291 | 487 |
| 42 | mml-miR-126 | 752 | 499 | 671 | 291 | 487 |
| 43 | mmu-miR-126a-3p | 752 | 499 | 671 | 291 | 487 |
| 44 | oan-miR-126-3p | 752 | 499 | 671 | 291 | 487 |
| 45 | pbv-miR-126-3p | 752 | 499 | 671 | 291 | 487 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-----|-----|------|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ppy-miR-126 | 752 | 499 | 671 | 291 | 487 |
| 4 | ptr-miR-126 | 752 | 499 | 671 | 291 | 487 |
| 5 | rno-miR-126a-3p | 752 | 499 | 671 | 291 | 487 |
| 6 | ssc-miR-126-3p | 752 | 499 | 671 | 291 | 487 |
| 7 | ssc-miR-126-3p | 752 | 499 | 671 | 291 | 487 |
| 8 | tgu-miR-126-3p | 752 | 499 | 671 | 291 | 487 |
| 9 | tgu-miR-126-3p | 752 | 499 | 671 | 291 | 487 |
| 10 | ccr-miR-30d | 46 | 49 | 94 | 18 | 34 |
| 11 | cja-miR-30d | 46 | 49 | 94 | 18 | 34 |
| 12 | cpi-miR-30d-5p | 46 | 49 | 94 | 18 | 34 |
| 13 | cpi-miR-30d-5p | 46 | 49 | 94 | 18 | 34 |
| 14 | oan-miR-30d-5p | 46 | 49 | 94 | 18 | 34 |
| 15 | ola-miR-30d-5p | 46 | 49 | 94 | 18 | 34 |
| 16 | efu-miR-126 | 756 | 506 | 678 | 291 | 498 |
| 17 | efu-miR-126 | 756 | 506 | 678 | 291 | 498 |
| 18 | ccr-miR-100 | 126 | 30 | 25 | 38 | 32 |
| 19 | cgr-miR-100-5p | 126 | 30 | 25 | 38 | 32 |
| 20 | chi-miR-100-5p | 126 | 30 | 25 | 38 | 32 |
| 21 | chi-miR-100-5p | 126 | 30 | 25 | 38 | 32 |
| 22 | cpi-miR-100-5p | 126 | 30 | 25 | 38 | 32 |
| 23 | cpi-miR-100-5p | 126 | 30 | 25 | 38 | 32 |
| 24 | dma-miR-100 | 126 | 30 | 25 | 38 | 32 |
| 25 | mdo-miR-100-5p | 126 | 30 | 25 | 38 | 32 |
| 26 | pmi-miR-100-5p | 126 | 30 | 25 | 38 | 32 |
| 27 | sbo-miR-100 | 126 | 30 | 25 | 38 | 32 |
| 28 | sha-miR-100 | 126 | 30 | 25 | 38 | 32 |
| 29 | sha-miR-100 | 126 | 30 | 25 | 38 | 32 |
| 30 | tgu-miR-100-5p | 126 | 30 | 25 | 38 | 32 |
| 31 | efu-miR-29a | 207 | 117 | 182 | 73 | 128 |
| 32 | efu-miR-29a | 207 | 117 | 182 | 73 | 128 |
| 33 | gga-let-7g-5p | 27 | 68 | 130 | 39 | 56 |
| 34 | ggo-let-7g | 27 | 68 | 130 | 39 | 56 |
| 35 | mdo-let-7g-5p | 27 | 68 | 130 | 39 | 56 |
| 36 | oar-let-7g | 27 | 68 | 130 | 39 | 56 |
| 37 | oar-let-7g | 27 | 68 | 130 | 39 | 56 |
| 38 | sha-let-7g | 27 | 68 | 130 | 39 | 56 |
| 39 | bta-miR-29a | 200 | 114 | 179 | 73 | 124 |
| 40 | ssc-miR-29a-3p | 200 | 114 | 179 | 73 | 124 |
| 41 | ssc-miR-29a-3p | 200 | 114 | 179 | 73 | 124 |
| 42 | cpo-miR-16b-5p | 401 | 204 | 217 | 133 | 202 |
| 43 | dno-miR-16b-5p | 401 | 204 | 217 | 133 | 202 |
| 44 | dno-miR-16b-5p | 401 | 204 | 217 | 133 | 202 |
| 45 | efu-miR-16 | 401 | 204 | 217 | 133 | 202 |
| 46 | ocu-miR-16b-5p | 401 | 204 | 217 | 133 | 202 |
| 47 | bta-miR-375 | 12 | 470 | 1593 | 199 | 498 |
| 48 | efu-miR-375 | 12 | 470 | 1593 | 199 | 498 |
| 49 | efu-miR-375 | 12 | 470 | 1593 | 199 | 498 |
| 50 | mdo-miR-375 | 12 | 470 | 1593 | 199 | 498 |
| 51 | cfa-miR-375 | 12 | 464 | 1564 | 196 | 491 |
| 52 | cpo-miR-375-3p | 12 | 464 | 1564 | 196 | 491 |
| 53 | dno-miR-375-3p | 12 | 464 | 1564 | 196 | 491 |
| 54 | dno-miR-375-3p | 12 | 464 | 1564 | 196 | 491 |
| 55 | ggo-miR-375 | 12 | 464 | 1564 | 196 | 491 |
| 56 | hsa-miR-375-3p | 12 | 464 | 1564 | 196 | 491 |
| 57 | hsa-miR-375-3p | 12 | 464 | 1564 | 196 | 491 |
| 58 | mml-miR-375 | 12 | 464 | 1564 | 196 | 491 |
| 59 | mmu-miR-375-3p | 12 | 464 | 1564 | 196 | 491 |
| 60 | mmu-miR-375-3p | 12 | 464 | 1564 | 196 | 491 |

| | | | | | | |
|----|------------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ocu-miR-375-3p | 12 | 464 | 1564 | 196 | 491 |
| 4 | pal-miR-375-3p | 12 | 464 | 1564 | 196 | 491 |
| 5 | ppy-miR-375 | 12 | 464 | 1564 | 196 | 491 |
| 6 | ptr-miR-375 | 12 | 464 | 1564 | 196 | 491 |
| 7 | rno-miR-375-3p | 12 | 464 | 1564 | 196 | 491 |
| 8 | ssc-miR-375 | 12 | 464 | 1564 | 196 | 491 |
| 9 | gma-miR390a-3p | 6474 | 6483 | 8058 | 5160 | 4809 |
| 10 | gma-miR390c | 6474 | 6483 | 8058 | 5160 | 4809 |
| 11 | mes-miR390 | 6474 | 6483 | 8058 | 5160 | 4809 |
| 12 | nle-miR-148a | 0 | 84 | 241 | 41 | 76 |
| 13 | oga-miR-148a | 0 | 84 | 241 | 41 | 76 |
| 14 | pha-miR-148a | 0 | 84 | 241 | 41 | 76 |
| 15 | ppa-miR-148a | 0 | 84 | 241 | 41 | 76 |
| 16 | abu-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 17 | aca-miR-26-3-5p | 519 | 374 | 526 | 243 | 334 |
| 18 | ami-miR-26-5p | 519 | 374 | 526 | 243 | 334 |
| 19 | bta-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 20 | ccb-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 21 | cfa-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 22 | chi-miR-26a-5p | 519 | 374 | 526 | 243 | 334 |
| 23 | cja-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 24 | cli-miR-26-5p | 519 | 374 | 526 | 243 | 334 |
| 25 | cpi-miR-26-5p | 519 | 374 | 526 | 243 | 334 |
| 26 | cpo-miR-26a-5p | 519 | 374 | 526 | 243 | 334 |
| 27 | dma-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 28 | dno-miR-26a-5p | 519 | 374 | 526 | 243 | 334 |
| 29 | dre-miR-26a-5p | 519 | 374 | 526 | 243 | 334 |
| 30 | eca-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 31 | fru-miR-26 | 519 | 374 | 526 | 243 | 334 |
| 32 | gga-miR-26a-2-5p | 519 | 374 | 526 | 243 | 334 |
| 33 | ggo-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 34 | gmo-miR-26a-5p | 519 | 374 | 526 | 243 | 334 |
| 35 | hsa-miR-26a-5p | 519 | 374 | 526 | 243 | 334 |
| 36 | ipu-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 37 | lla-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 38 | mml-miR-26a-5p | 519 | 374 | 526 | 243 | 334 |
| 39 | mmr-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 40 | mmu-miR-26a-5p | 519 | 374 | 526 | 243 | 334 |
| 41 | mne-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 42 | mze-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 43 | nbr-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 44 | nle-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 45 | oan-miR-26-5p | 519 | 374 | 526 | 243 | 334 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | oar-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 4 | ocu-miR-26a-5p | 519 | 374 | 526 | 243 | 334 |
| 5 | oga-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 6 | oha-miR-26-5p | 519 | 374 | 526 | 243 | 334 |
| 7 | oni-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 8 | oni-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 9 | oni-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 10 | pal-miR-26a-5p | 519 | 374 | 526 | 243 | 334 |
| 11 | pbv-miR-26-5p | 519 | 374 | 526 | 243 | 334 |
| 12 | pha-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 13 | pha-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 14 | pma-miR-26a-5p | 519 | 374 | 526 | 243 | 334 |
| 15 | ppy-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 16 | ppa-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 17 | ppa-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 18 | ppy-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 19 | ptr-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 20 | ptr-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 21 | rno-miR-26a-5p | 519 | 374 | 526 | 243 | 334 |
| 22 | sbo-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 23 | ssa-miR-26a-5p | 519 | 374 | 526 | 243 | 334 |
| 24 | ssc-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 25 | ssc-miR-26a | 519 | 374 | 526 | 243 | 334 |
| 26 | tch-miR-26a-5p | 519 | 374 | 526 | 243 | 334 |
| 27 | tgu-miR-26-5p | 519 | 374 | 526 | 243 | 334 |
| 28 | tni-miR-26 | 519 | 374 | 526 | 243 | 334 |
| 29 | tni-miR-26 | 519 | 374 | 526 | 243 | 334 |
| 30 | xla-miR-26-5p | 519 | 374 | 526 | 243 | 334 |
| 31 | efu-miR-26a | 521 | 375 | 527 | 243 | 334 |
| 32 | efu-miR-26c | 521 | 375 | 527 | 243 | 334 |
| 33 | efu-miR-26c | 521 | 375 | 527 | 243 | 334 |
| 34 | gma-miR391-5p | 85 | 196 | 96 | 86 | 109 |
| 35 | aca-let-7g | 85 | 147 | 289 | 94 | 135 |
| 36 | ami-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 37 | ami-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 38 | bta-let-7g | 85 | 147 | 289 | 94 | 135 |
| 39 | cfa-let-7g | 85 | 147 | 289 | 94 | 135 |
| 40 | cgr-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 41 | cgr-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 42 | chi-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 43 | cja-let-7g | 85 | 147 | 289 | 94 | 135 |
| 44 | cli-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 45 | cli-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 46 | cpi-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 47 | cpo-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 48 | dma-let-7g | 85 | 147 | 289 | 94 | 135 |
| 49 | dma-let-7g | 85 | 147 | 289 | 94 | 135 |
| 50 | dno-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 51 | eca-let-7g | 85 | 147 | 289 | 94 | 135 |
| 52 | hsa-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 53 | hsa-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 54 | mml-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 55 | mmr-let-7g | 85 | 147 | 289 | 94 | 135 |
| 56 | mmu-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 57 | mmu-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 58 | nle-let-7g | 85 | 147 | 289 | 94 | 135 |
| 59 | oan-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ocu-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 4 | oga-let-7g | 85 | 147 | 289 | 94 | 135 |
| 5 | oha-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 6 | pal-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 7 | pal-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 8 | pbv-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 9 | pbv-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 10 | pha-let-7g | 85 | 147 | 289 | 94 | 135 |
| 11 | ppa-let-7g | 85 | 147 | 289 | 94 | 135 |
| 12 | ppy-let-7g | 85 | 147 | 289 | 94 | 135 |
| 13 | ppy-let-7g | 85 | 147 | 289 | 94 | 135 |
| 14 | ptr-let-7g | 85 | 147 | 289 | 94 | 135 |
| 15 | rno-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 16 | ssc-let-7g | 85 | 147 | 289 | 94 | 135 |
| 17 | ssc-let-7g | 85 | 147 | 289 | 94 | 135 |
| 18 | tch-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 19 | tgu-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 20 | tgu-let-7g-5p | 85 | 147 | 289 | 94 | 135 |
| 21 | aly-miR390a-3p | 7408 | 7479 | 8969 | 5907 | 5712 |
| 22 | ath-miR390a-3p | 7408 | 7479 | 8969 | 5907 | 5712 |
| 23 | cas-miR390a-3p | 7408 | 7479 | 8969 | 5907 | 5712 |
| 24 | csi-miR390a-3p | 7408 | 7479 | 8969 | 5907 | 5712 |
| 25 | csi-miR390a-3p | 7408 | 7479 | 8969 | 5907 | 5712 |
| 26 | lja-miR390a-3p | 7408 | 7479 | 8969 | 5907 | 5712 |
| 27 | lja-miR390b-3p | 7408 | 7479 | 8969 | 5907 | 5712 |
| 28 | sly-miR390b-3p | 7408 | 7479 | 8969 | 5907 | 5712 |
| 29 | sly-miR390b-3p | 7408 | 7479 | 8969 | 5907 | 5712 |
| 30 | pal-miR-126-3p | 144 | 117 | 122 | 63 | 112 |
| 31 | xla-miR-126-3p | 144 | 117 | 122 | 63 | 112 |
| 32 | aof-miR166a | 7981 | 8169 | 8133 | 5956 | 6604 |
| 33 | aof-miR166a | 7981 | 8169 | 8133 | 5956 | 6604 |
| 34 | atr-miR166b | 7981 | 8169 | 8133 | 5956 | 6604 |
| 35 | bdi-miR166f | 7981 | 8169 | 8133 | 5956 | 6604 |
| 36 | csi-miR166b-3p | 7981 | 8169 | 8133 | 5956 | 6604 |
| 37 | csi-miR166b-3p | 7981 | 8169 | 8133 | 5956 | 6604 |
| 38 | csi-miR166d-3p | 7981 | 8169 | 8133 | 5956 | 6604 |
| 39 | csi-miR166g-3p | 7981 | 8169 | 8133 | 5956 | 6604 |
| 40 | gma-miR166h-3p | 7981 | 8169 | 8133 | 5956 | 6604 |
| 41 | gma-miR166h-3p | 7981 | 8169 | 8133 | 5956 | 6604 |
| 42 | gma-miR166k | 7981 | 8169 | 8133 | 5956 | 6604 |
| 43 | pab-miR166e | 7981 | 8169 | 8133 | 5956 | 6604 |
| 44 | abu-let-7b | 225 | 214 | 386 | 156 | 214 |
| 45 | abu-let-7b | 225 | 214 | 386 | 156 | 214 |
| 46 | ami-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 47 | bta-let-7b | 225 | 214 | 386 | 156 | 214 |
| 48 | ccb-let-7b | 225 | 214 | 386 | 156 | 214 |
| 49 | ccb-let-7b | 225 | 214 | 386 | 156 | 214 |
| 50 | cfa-let-7b | 225 | 214 | 386 | 156 | 214 |
| 51 | cgr-let-7b | 225 | 214 | 386 | 156 | 214 |
| 52 | chi-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 53 | chi-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 54 | cja-let-7b | 225 | 214 | 386 | 156 | 214 |
| 55 | cpi-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 56 | cpi-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 57 | cpo-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 58 | dma-let-7b | 225 | 214 | 386 | 156 | 214 |
| 59 | dno-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 60 | | | | | | |

| | | | | | | |
|----|------------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | dre-let-7b | 225 | 214 | 386 | 156 | 214 |
| 4 | fru-let-7b | 225 | 214 | 386 | 156 | 214 |
| 5 | gga-let-7b | 225 | 214 | 386 | 156 | 214 |
| 6 | gga-let-7b | 225 | 214 | 386 | 156 | 214 |
| 7 | hsa-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 8 | mdo-let-7b | 225 | 214 | 386 | 156 | 214 |
| 9 | mml-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 10 | mml-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 11 | mmr-let-7b | 225 | 214 | 386 | 156 | 214 |
| 12 | mmu-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 13 | mmu-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 14 | mze-let-7b | 225 | 214 | 386 | 156 | 214 |
| 15 | nbr-let-7b | 225 | 214 | 386 | 156 | 214 |
| 16 | oan-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 17 | oan-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 18 | ocu-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 19 | oga-let-7b | 225 | 214 | 386 | 156 | 214 |
| 20 | oha-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 21 | oha-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 22 | oni-let-7b | 225 | 214 | 386 | 156 | 214 |
| 23 | pbv-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 24 | pha-let-7b | 225 | 214 | 386 | 156 | 214 |
| 25 | pha-let-7b | 225 | 214 | 386 | 156 | 214 |
| 26 | pony-let-7b | 225 | 214 | 386 | 156 | 214 |
| 27 | pol-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 28 | ppa-let-7b | 225 | 214 | 386 | 156 | 214 |
| 29 | ppa-let-7b | 225 | 214 | 386 | 156 | 214 |
| 30 | ppy-let-7b | 225 | 214 | 386 | 156 | 214 |
| 31 | ptr-let-7b | 225 | 214 | 386 | 156 | 214 |
| 32 | rno-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 33 | rno-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 34 | sbo-let-7b | 225 | 214 | 386 | 156 | 214 |
| 35 | ssa-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 36 | tgu-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 37 | tgu-let-7b-5p | 225 | 214 | 386 | 156 | 214 |
| 38 | tni-let-7b | 225 | 214 | 386 | 156 | 214 |
| 39 | bta-miR-126-3p | 144 | 115 | 122 | 63 | 112 |
| 40 | xla-miR-126-2-3p | 144 | 115 | 122 | 63 | 112 |
| 41 | xla-miR-126-2-3p | 144 | 115 | 122 | 63 | 112 |
| 42 | efu-miR-22 | 1415 | 908 | 1298 | 714 | 916 |
| 43 | xla-miR-22-3p | 1415 | 908 | 1298 | 714 | 916 |
| 44 | ama-miR156 | 4349 | 4087 | 2522 | 2892 | 2048 |
| 45 | aly-miR156a-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 46 | aly-miR156a-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 47 | aly-miR156b-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 48 | aly-miR156c-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 49 | aly-miR156c-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 50 | aly-miR156d-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 51 | aly-miR156e-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 52 | aly-miR156f-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 53 | aly-miR156f-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 54 | aof-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 55 | ata-miR156a-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 56 | ata-miR156b-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 57 | ata-miR156b-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 58 | ata-miR156c-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 59 | ata-miR156d-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ata-miR156e-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 4 | ath-miR156a-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 5 | ath-miR156b-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 6 | ath-miR156c-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 7 | ath-miR156d-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 8 | ath-miR156e | 4346 | 4087 | 2521 | 2892 | 2048 |
| 9 | ath-miR156f-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 10 | atr-miR156b | 4346 | 4087 | 2521 | 2892 | 2048 |
| 11 | atr-miR156d | 4346 | 4087 | 2521 | 2892 | 2048 |
| 12 | bdi-miR156b-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 13 | bdi-miR156c | 4346 | 4087 | 2521 | 2892 | 2048 |
| 14 | bdi-miR156d-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 15 | bdi-miR156e-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 16 | bdi-miR156f-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 17 | bdi-miR156g-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 18 | bdi-miR156h-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 19 | bdi-miR156i-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 20 | bna-miR156d | 4346 | 4087 | 2521 | 2892 | 2048 |
| 21 | bna-miR156e | 4346 | 4087 | 2521 | 2892 | 2048 |
| 22 | bna-miR156f | 4346 | 4087 | 2521 | 2892 | 2048 |
| 23 | bra-miR156a-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 24 | bra-miR156b-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 25 | bra-miR156c-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 26 | bra-miR156d-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 27 | bra-miR156e-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 28 | bra-miR156f-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 29 | bra-miR156g-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 30 | cas-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 31 | cas-miR156b-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 32 | cas-miR156c-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 33 | cas-miR156d-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 34 | cas-miR156e-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 35 | cas-miR156f-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 36 | cas-miR156k-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 37 | cca-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 38 | cme-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 39 | cme-miR156c | 4346 | 4087 | 2521 | 2892 | 2048 |
| 40 | cme-miR156d | 4346 | 4087 | 2521 | 2892 | 2048 |
| 41 | cme-miR156i | 4346 | 4087 | 2521 | 2892 | 2048 |
| 42 | cpa-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 43 | cpa-miR156b | 4346 | 4087 | 2521 | 2892 | 2048 |
| 44 | cpa-miR156c | 4346 | 4087 | 2521 | 2892 | 2048 |
| 45 | cpa-miR156d | 4346 | 4087 | 2521 | 2892 | 2048 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | csi-miR156a-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 4 | csi-miR156b-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 5 | csi-miR156c-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 6 | csi-miR156c-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 7 | ctr-miR156 | 4346 | 4087 | 2521 | 2892 | 2048 |
| 8 | dpr-miR156b | 4346 | 4087 | 2521 | 2892 | 2048 |
| 9 | dpr-miR156b | 4346 | 4087 | 2521 | 2892 | 2048 |
| 10 | fve-miR156d | 4346 | 4087 | 2521 | 2892 | 2048 |
| 11 | ghr-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 12 | ghr-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 13 | ghr-miR156b | 4346 | 4087 | 2521 | 2892 | 2048 |
| 14 | ghr-miR156d | 4346 | 4087 | 2521 | 2892 | 2048 |
| 15 | gma-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 16 | gma-miR156h | 4346 | 4087 | 2521 | 2892 | 2048 |
| 17 | gma-miR156h | 4346 | 4087 | 2521 | 2892 | 2048 |
| 18 | gma-miR156u | 4346 | 4087 | 2521 | 2892 | 2048 |
| 19 | gma-miR156v | 4346 | 4087 | 2521 | 2892 | 2048 |
| 20 | gma-miR156w | 4346 | 4087 | 2521 | 2892 | 2048 |
| 21 | gma-miR156w | 4346 | 4087 | 2521 | 2892 | 2048 |
| 22 | gma-miR156x | 4346 | 4087 | 2521 | 2892 | 2048 |
| 23 | gma-miR156y | 4346 | 4087 | 2521 | 2892 | 2048 |
| 24 | gma-miR156y | 4346 | 4087 | 2521 | 2892 | 2048 |
| 25 | han-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 26 | han-miR156b | 4346 | 4087 | 2521 | 2892 | 2048 |
| 27 | har-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 28 | har-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 29 | htu-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 30 | lus-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 31 | lus-miR156g | 4346 | 4087 | 2521 | 2892 | 2048 |
| 32 | mdm-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 33 | mdm-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 34 | mdm-miR156b | 4346 | 4087 | 2521 | 2892 | 2048 |
| 35 | mdm-miR156c | 4346 | 4087 | 2521 | 2892 | 2048 |
| 36 | mdm-miR156c | 4346 | 4087 | 2521 | 2892 | 2048 |
| 37 | mdm-miR156d | 4346 | 4087 | 2521 | 2892 | 2048 |
| 38 | mdm-miR156e | 4346 | 4087 | 2521 | 2892 | 2048 |
| 39 | mdm-miR156f | 4346 | 4087 | 2521 | 2892 | 2048 |
| 40 | mdm-miR156g | 4346 | 4087 | 2521 | 2892 | 2048 |
| 41 | mdm-miR156g | 4346 | 4087 | 2521 | 2892 | 2048 |
| 42 | mdm-miR156h | 4346 | 4087 | 2521 | 2892 | 2048 |
| 43 | mdm-miR156i | 4346 | 4087 | 2521 | 2892 | 2048 |
| 44 | mdm-miR156i | 4346 | 4087 | 2521 | 2892 | 2048 |
| 45 | mdm-miR156j | 4346 | 4087 | 2521 | 2892 | 2048 |
| 46 | mdm-miR156k | 4346 | 4087 | 2521 | 2892 | 2048 |
| 47 | mdm-miR156l | 4346 | 4087 | 2521 | 2892 | 2048 |
| 48 | mdm-miR156l | 4346 | 4087 | 2521 | 2892 | 2048 |
| 49 | mdm-miR156m | 4346 | 4087 | 2521 | 2892 | 2048 |
| 50 | mdm-miR156n | 4346 | 4087 | 2521 | 2892 | 2048 |
| 51 | mdm-miR156o | 4346 | 4087 | 2521 | 2892 | 2048 |
| 52 | mes-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 53 | mes-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 54 | mes-miR156b | 4346 | 4087 | 2521 | 2892 | 2048 |
| 55 | mes-miR156c | 4346 | 4087 | 2521 | 2892 | 2048 |
| 56 | mes-miR156d | 4346 | 4087 | 2521 | 2892 | 2048 |
| 57 | mes-miR156d | 4346 | 4087 | 2521 | 2892 | 2048 |
| 58 | mes-miR156e | 4346 | 4087 | 2521 | 2892 | 2048 |
| 59 | mes-miR156f | 4346 | 4087 | 2521 | 2892 | 2048 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | mes-miR156g | 4346 | 4087 | 2521 | 2892 | 2048 |
| 4 | mtr-miR156b-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 5 | mtr-miR156c-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 6 | mtr-miR156d-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 7 | mtr-miR156e-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 8 | nta-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 9 | nta-miR156b | 4346 | 4087 | 2521 | 2892 | 2048 |
| 10 | nta-miR156c | 4346 | 4087 | 2521 | 2892 | 2048 |
| 11 | nta-miR156d | 4346 | 4087 | 2521 | 2892 | 2048 |
| 12 | nta-miR156e | 4346 | 4087 | 2521 | 2892 | 2048 |
| 13 | osa-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 14 | osa-miR156b-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 15 | osa-miR156c-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 16 | osa-miR156d | 4346 | 4087 | 2521 | 2892 | 2048 |
| 17 | osa-miR156e | 4346 | 4087 | 2521 | 2892 | 2048 |
| 18 | osa-miR156f-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 19 | osa-miR156g-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 20 | osa-miR156h-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 21 | osa-miR156i | 4346 | 4087 | 2521 | 2892 | 2048 |
| 22 | osa-miR156j-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 23 | pab-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 24 | pab-miR156l | 4346 | 4087 | 2521 | 2892 | 2048 |
| 25 | ppe-miR156c | 4346 | 4087 | 2521 | 2892 | 2048 |
| 26 | ppe-miR156d | 4346 | 4087 | 2521 | 2892 | 2048 |
| 27 | ppe-miR156e | 4346 | 4087 | 2521 | 2892 | 2048 |
| 28 | ppt-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 29 | ppt-miR156b | 4346 | 4087 | 2521 | 2892 | 2048 |
| 30 | ppt-miR156c | 4346 | 4087 | 2521 | 2892 | 2048 |
| 31 | ptc-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 32 | ptc-miR156b | 4346 | 4087 | 2521 | 2892 | 2048 |
| 33 | ptc-miR156c | 4346 | 4087 | 2521 | 2892 | 2048 |
| 34 | ptc-miR156d | 4346 | 4087 | 2521 | 2892 | 2048 |
| 35 | ptc-miR156e | 4346 | 4087 | 2521 | 2892 | 2048 |
| 36 | ptc-miR156f | 4346 | 4087 | 2521 | 2892 | 2048 |
| 37 | sbi-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 38 | sbi-miR156b | 4346 | 4087 | 2521 | 2892 | 2048 |
| 39 | sbi-miR156c | 4346 | 4087 | 2521 | 2892 | 2048 |
| 40 | sbi-miR156f | 4346 | 4087 | 2521 | 2892 | 2048 |
| 41 | sbi-miR156g | 4346 | 4087 | 2521 | 2892 | 2048 |
| 42 | sbi-miR156h | 4346 | 4087 | 2521 | 2892 | 2048 |
| 43 | sbi-miR156i | 4346 | 4087 | 2521 | 2892 | 2048 |
| 44 | sly-miR156d-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 45 | sof-miR156 | 4346 | 4087 | 2521 | 2892 | 2048 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | stu-miR156e | 4346 | 4087 | 2521 | 2892 | 2048 |
| 4 | stu-miR156g-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 5 | stu-miR156h-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 6 | stu-miR156i-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 7 | stu-miR156j-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 8 | stu-miR156k-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 9 | stu-miR156l-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 10 | tcc-miR156b | 4346 | 4087 | 2521 | 2892 | 2048 |
| 11 | tcc-miR156c | 4346 | 4087 | 2521 | 2892 | 2048 |
| 12 | tcc-miR156d | 4346 | 4087 | 2521 | 2892 | 2048 |
| 13 | tcc-miR156g | 4346 | 4087 | 2521 | 2892 | 2048 |
| 14 | vca-miR156a-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 15 | vun-miR156a | 4346 | 4087 | 2521 | 2892 | 2048 |
| 16 | vvi-miR156b | 4346 | 4087 | 2521 | 2892 | 2048 |
| 17 | vvi-miR156c | 4346 | 4087 | 2521 | 2892 | 2048 |
| 18 | vvi-miR156d | 4346 | 4087 | 2521 | 2892 | 2048 |
| 19 | zma-miR156a-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 20 | zma-miR156b-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 21 | zma-miR156c | 4346 | 4087 | 2521 | 2892 | 2048 |
| 22 | zma-miR156d-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 23 | zma-miR156e-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 24 | zma-miR156f-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 25 | zma-miR156g-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 26 | zma-miR156h-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 27 | zma-miR156i-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 28 | zma-miR156l-5p | 4346 | 4087 | 2521 | 2892 | 2048 |
| 29 | cme-miR156j | 4473 | 4226 | 2603 | 2978 | 2127 |
| 30 | fve-miR156a | 4473 | 4226 | 2603 | 2978 | 2127 |
| 31 | fve-miR156b | 4473 | 4226 | 2603 | 2978 | 2127 |
| 32 | fve-miR156c | 4473 | 4226 | 2603 | 2978 | 2127 |
| 33 | fve-miR156e | 4473 | 4226 | 2603 | 2978 | 2127 |
| 34 | gma-miR156k | 4473 | 4226 | 2603 | 2978 | 2127 |
| 35 | gma-miR156n | 4473 | 4226 | 2603 | 2978 | 2127 |
| 36 | gma-miR156o | 4473 | 4226 | 2603 | 2978 | 2127 |
| 37 | bna-miR156a | 4370 | 4109 | 2532 | 2903 | 2073 |
| 38 | hvu-miR156a | 4370 | 4109 | 2532 | 2903 | 2073 |
| 39 | hvu-miR156b | 4370 | 4109 | 2532 | 2903 | 2073 |
| 40 | rco-miR156a | 4370 | 4109 | 2532 | 2903 | 2073 |
| 41 | rco-miR156b | 4370 | 4109 | 2532 | 2903 | 2073 |
| 42 | rco-miR156c | 4370 | 4109 | 2532 | 2903 | 2073 |
| 43 | rco-miR156d | 4370 | 4109 | 2532 | 2903 | 2073 |
| 44 | ssl-miR156 | 4370 | 4109 | 2532 | 2903 | 2073 |
| 45 | ssp-miR156 | 4370 | 4109 | 2532 | 2903 | 2073 |
| 46 | tae-miR156 | 4370 | 4109 | 2532 | 2903 | 2073 |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | gma-miR156q | 4361 | 4101 | 2529 | 2913 | 2052 |
| 4 | gma-miR156s | 4361 | 4101 | 2529 | 2913 | 2052 |
| 5 | aca-miR-148a-3p | 0 | 61 | 174 | 33 | 60 |
| 6 | bta-miR-148a | 0 | 61 | 174 | 33 | 60 |
| 7 | cfa-miR-148a | 0 | 61 | 174 | 33 | 60 |
| 8 | cgr-miR-148a | 0 | 61 | 174 | 33 | 60 |
| 9 | chi-miR-148a-3p | 0 | 61 | 174 | 33 | 60 |
| 10 | cja-miR-148a | 0 | 61 | 174 | 33 | 60 |
| 11 | cli-miR-148a-3p | 0 | 61 | 174 | 33 | 60 |
| 12 | cpi-miR-148a-3p | 0 | 61 | 174 | 33 | 60 |
| 13 | cpo-miR-148a-3p | 0 | 61 | 174 | 33 | 60 |
| 14 | dno-miR-148a-3p | 0 | 61 | 174 | 33 | 60 |
| 15 | eca-miR-148a | 0 | 61 | 174 | 33 | 60 |
| 16 | gga-miR-148a-3p | 0 | 61 | 174 | 33 | 60 |
| 17 | hsa-miR-148a-3p | 0 | 61 | 174 | 33 | 60 |
| 18 | mdo-miR-148-3p | 0 | 61 | 174 | 33 | 60 |
| 19 | mml-miR-148a-3p | 0 | 61 | 174 | 33 | 60 |
| 20 | mmu-miR-148a-3p | 0 | 61 | 174 | 33 | 60 |
| 21 | oan-miR-148-3p | 0 | 61 | 174 | 33 | 60 |
| 22 | oar-miR-148a | 0 | 61 | 174 | 33 | 60 |
| 23 | ocu-miR-148a-3p | 0 | 61 | 174 | 33 | 60 |
| 24 | pal-miR-148a-3p | 0 | 61 | 174 | 33 | 60 |
| 25 | pbv-miR-148a-3p | 0 | 61 | 174 | 33 | 60 |
| 26 | ppy-miR-148a | 0 | 61 | 174 | 33 | 60 |
| 27 | ptr-miR-148a | 0 | 61 | 174 | 33 | 60 |
| 28 | sbo-miR-148a | 0 | 61 | 174 | 33 | 60 |
| 29 | ssc-miR-148a-3p | 0 | 61 | 174 | 33 | 60 |
| 30 | tch-miR-148a-3p | 0 | 61 | 174 | 33 | 60 |
| 31 | tgu-miR-148a-3p | 0 | 61 | 174 | 33 | 60 |
| 32 | xtr-miR-148a | 0 | 61 | 174 | 33 | 60 |
| 33 | age-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 34 | aja-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 35 | cfa-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 36 | cgr-miR-22-3p | 1379 | 886 | 1272 | 702 | 902 |
| 37 | cja-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 38 | cli-miR-22-3p | 1379 | 886 | 1272 | 702 | 902 |
| 39 | cpi-miR-22-3p | 1379 | 886 | 1272 | 702 | 902 |
| 40 | cpo-miR-22-3p | 1379 | 886 | 1272 | 702 | 902 |
| 41 | dma-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 42 | dno-miR-22-3p | 1379 | 886 | 1272 | 702 | 902 |
| 43 | eca-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 44 | gga-miR-22-3p | 1379 | 886 | 1272 | 702 | 902 |
| 45 | hsa-miR-22-3p | 1379 | 886 | 1272 | 702 | 902 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | lca-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 4 | lla-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 5 | mml-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 6 | mmr-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 7 | mmr-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 8 | mmu-miR-22-3p | 1379 | 886 | 1272 | 702 | 902 |
| 9 | mmu-miR-22-3p | 1379 | 886 | 1272 | 702 | 902 |
| 10 | mne-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 11 | nle-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 12 | nle-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 13 | oan-miR-22-3p | 1379 | 886 | 1272 | 702 | 902 |
| 14 | ocu-miR-22-3p | 1379 | 886 | 1272 | 702 | 902 |
| 15 | oga-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 16 | oha-miR-22a | 1379 | 886 | 1272 | 702 | 902 |
| 17 | oha-miR-22a | 1379 | 886 | 1272 | 702 | 902 |
| 18 | pal-miR-22-3p | 1379 | 886 | 1272 | 702 | 902 |
| 19 | pbv-miR-22-3p | 1379 | 886 | 1272 | 702 | 902 |
| 20 | pbv-miR-22-3p | 1379 | 886 | 1272 | 702 | 902 |
| 21 | pha-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 22 | ppa-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 23 | ppy-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 24 | ptr-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 25 | ptr-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 26 | rno-miR-22-3p | 1379 | 886 | 1272 | 702 | 902 |
| 27 | sbo-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 28 | sla-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 29 | sla-miR-22 | 1379 | 886 | 1272 | 702 | 902 |
| 30 | ssc-miR-22-3p | 1379 | 886 | 1272 | 702 | 902 |
| 31 | tch-miR-22-3p | 1379 | 886 | 1272 | 702 | 902 |
| 32 | xtr-miR-22-3p | 1379 | 886 | 1272 | 702 | 902 |
| 33 | xtr-miR-22-3p | 1379 | 886 | 1272 | 702 | 902 |
| 34 | aly-miR170-5p | 8021 | 6868 | 7105 | 4211 | 6540 |
| 35 | aly-miR171a-5p | 8021 | 6868 | 7105 | 4211 | 6540 |
| 36 | ath-miR170-5p | 8021 | 6868 | 7105 | 4211 | 6540 |
| 37 | ath-miR170-5p | 8021 | 6868 | 7105 | 4211 | 6540 |
| 38 | ath-miR171a-5p | 8021 | 6868 | 7105 | 4211 | 6540 |
| 39 | cas-miR170 | 8021 | 6868 | 7105 | 4211 | 6540 |
| 40 | cas-miR171a-5p | 8021 | 6868 | 7105 | 4211 | 6540 |
| 41 | cas-miR171a-5p | 8021 | 6868 | 7105 | 4211 | 6540 |
| 42 | csi-miR171f-5p | 8021 | 6868 | 7105 | 4211 | 6540 |
| 43 | gma-miR171j-5p | 8021 | 6868 | 7105 | 4211 | 6540 |
| 44 | sly-miR171f | 8021 | 6868 | 7105 | 4211 | 6540 |
| 45 | stu-miR171a-5p | 8021 | 6868 | 7105 | 4211 | 6540 |
| 46 | stu-miR171a-5p | 8021 | 6868 | 7105 | 4211 | 6540 |
| 47 | stu-miR171c-5p | 8021 | 6868 | 7105 | 4211 | 6540 |
| 48 | age-miR-16 | 266 | 163 | 163 | 103 | 156 |
| 49 | cfa-miR-16 | 266 | 163 | 163 | 103 | 156 |
| 50 | cfa-miR-16 | 266 | 163 | 163 | 103 | 156 |
| 51 | cgr-miR-16-5p | 266 | 163 | 163 | 103 | 156 |
| 52 | cja-miR-16 | 266 | 163 | 163 | 103 | 156 |
| 53 | cja-miR-16 | 266 | 163 | 163 | 103 | 156 |
| 54 | cpi-miR-16a-5p | 266 | 163 | 163 | 103 | 156 |
| 55 | dma-miR-16 | 266 | 163 | 163 | 103 | 156 |
| 56 | eca-miR-16 | 266 | 163 | 163 | 103 | 156 |
| 57 | eca-miR-16 | 266 | 163 | 163 | 103 | 156 |
| 58 | ggo-miR-16 | 266 | 163 | 163 | 103 | 156 |
| 59 | hsa-miR-16-5p | 266 | 163 | 163 | 103 | 156 |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | lla-miR-16 | 266 | 163 | 163 | 103 | 156 |
| 4 | mdo-miR-16-5p | 266 | 163 | 163 | 103 | 156 |
| 5 | mml-miR-16-5p | 266 | 163 | 163 | 103 | 156 |
| 6 | mmu-miR-16-5p | 266 | 163 | 163 | 103 | 156 |
| 7 | mne-miR-16 | 266 | 163 | 163 | 103 | 156 |
| 8 | mze-miR-16a | 266 | 163 | 163 | 103 | 156 |
| 9 | nle-miR-16 | 266 | 163 | 163 | 103 | 156 |
| 10 | oan-miR-16a-5p | 266 | 163 | 163 | 103 | 156 |
| 11 | oga-miR-16 | 266 | 163 | 163 | 103 | 156 |
| 12 | oni-miR-16a | 266 | 163 | 163 | 103 | 156 |
| 13 | pal-miR-16-5p | 266 | 163 | 163 | 103 | 156 |
| 14 | pha-miR-16 | 266 | 163 | 163 | 103 | 156 |
| 15 | ppa-miR-16 | 266 | 163 | 163 | 103 | 156 |
| 16 | ptr-miR-16 | 266 | 163 | 163 | 103 | 156 |
| 17 | rno-miR-16-5p | 266 | 163 | 163 | 103 | 156 |
| 18 | sbo-miR-16 | 266 | 163 | 163 | 103 | 156 |
| 19 | sla-miR-16 | 266 | 163 | 163 | 103 | 156 |
| 20 | ssa-miR-16c-5p | 266 | 163 | 163 | 103 | 156 |
| 21 | ssc-miR-16 | 266 | 163 | 163 | 103 | 156 |
| 22 | xla-miR-148a-3p | 0 | 61 | 177 | 34 | 60 |
| 23 | efu-miR-133-3p | 331 | 233 | 127 | 128 | 219 |
| 24 | chi-miR-133a-3p | 324 | 223 | 125 | 127 | 212 |
| 25 | cli-miR-133a-3p | 324 | 223 | 125 | 127 | 212 |
| 26 | cpi-miR-133a-3p | 324 | 223 | 125 | 127 | 212 |
| 27 | cpo-miR-133a-3p | 324 | 223 | 125 | 127 | 212 |
| 28 | dno-miR-133a-3p | 324 | 223 | 125 | 127 | 212 |
| 29 | ocu-miR-133a-3p | 324 | 223 | 125 | 127 | 212 |
| 30 | pbv-miR-133a-3p | 324 | 223 | 125 | 127 | 212 |
| 31 | aca-miR-200a-3p | 2 | 58 | 166 | 41 | 61 |
| 32 | ami-miR-200a-3p | 2 | 58 | 166 | 41 | 61 |
| 33 | dre-miR-200a-3p | 2 | 58 | 166 | 41 | 61 |
| 34 | eca-miR-200a | 2 | 58 | 166 | 41 | 61 |
| 35 | fru-miR-200a | 2 | 58 | 166 | 41 | 61 |
| 36 | gga-miR-200a-3p | 2 | 58 | 166 | 41 | 61 |
| 37 | ggo-miR-200a | 2 | 58 | 166 | 41 | 61 |
| 38 | gmo-miR-200a-3p | 2 | 58 | 166 | 41 | 61 |
| 39 | hsa-miR-200a-3p | 2 | 58 | 166 | 41 | 61 |
| 40 | mdo-miR-200a-3p | 2 | 58 | 166 | 41 | 61 |
| 41 | mml-miR-200a-3p | 2 | 58 | 166 | 41 | 61 |
| 42 | mmu-miR-200a-3p | 2 | 58 | 166 | 41 | 61 |
| 43 | ppy-miR-200a | 2 | 58 | 166 | 41 | 61 |
| 44 | ptr-miR-200a | 2 | 58 | 166 | 41 | 61 |
| 45 | rno-miR-200a-3p | 2 | 58 | 166 | 41 | 61 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | tni-miR-200a | 2 | 58 | 166 | 41 | 61 |
| 4 | xtr-miR-200a | 2 | 58 | 166 | 41 | 61 |
| 5 | osa-miR159f | 1487 | 3915 | 3203 | 2104 | 1946 |
| 6 | aof-miR171b | 340 | 402 | 379 | 288 | 323 |
| 7 | fve-miR171f-3p | 340 | 402 | 379 | 288 | 323 |
| 8 | gma-miR171k-3p | 340 | 402 | 379 | 288 | 323 |
| 9 | lja-miR171d-5p | 340 | 402 | 379 | 288 | 323 |
| 10 | mdm-miR171j | 340 | 402 | 379 | 288 | 323 |
| 11 | mdm-miR171k | 340 | 402 | 379 | 288 | 323 |
| 12 | mdm-miR171l | 340 | 402 | 379 | 288 | 323 |
| 13 | mes-miR171e | 340 | 402 | 379 | 288 | 323 |
| 14 | nta-miR171b | 340 | 402 | 379 | 288 | 323 |
| 15 | pab-miR171b | 340 | 402 | 379 | 288 | 323 |
| 16 | pab-miR171c | 340 | 402 | 379 | 288 | 323 |
| 17 | ppe-miR171b | 340 | 402 | 379 | 288 | 323 |
| 18 | ssl-miR171b | 340 | 402 | 379 | 288 | 323 |
| 19 | vvi-miR171f | 340 | 402 | 379 | 288 | 323 |
| 20 | abu-miR-200a | 16 | 197 | 535 | 142 | 189 |
| 21 | bta-miR-200a | 16 | 197 | 535 | 142 | 189 |
| 22 | cgr-miR-200a | 16 | 197 | 535 | 142 | 189 |
| 23 | cli-miR-200a-3p | 16 | 197 | 535 | 142 | 189 |
| 24 | cpi-miR-200a-3p | 16 | 197 | 535 | 142 | 189 |
| 25 | cpo-miR-200a-3p | 16 | 197 | 535 | 142 | 189 |
| 26 | efu-miR-200a | 16 | 197 | 535 | 142 | 189 |
| 27 | mze-miR-200a | 16 | 197 | 535 | 142 | 189 |
| 28 | nbr-miR-200a | 16 | 197 | 535 | 142 | 189 |
| 29 | oan-miR-200a-3p | 16 | 197 | 535 | 142 | 189 |
| 30 | oha-miR-200a | 16 | 197 | 535 | 142 | 189 |
| 31 | oni-miR-200a | 16 | 197 | 535 | 142 | 189 |
| 32 | pal-miR-200a-3p | 16 | 197 | 535 | 142 | 189 |
| 33 | pbv-miR-200a-3p | 16 | 197 | 535 | 142 | 189 |
| 34 | pony-miR-200a | 16 | 197 | 535 | 142 | 189 |
| 35 | ssa-miR-200b-3p | 16 | 197 | 535 | 142 | 189 |
| 36 | tch-miR-200a-3p | 16 | 197 | 535 | 142 | 189 |
| 37 | tgu-miR-200a-3p | 16 | 197 | 535 | 142 | 189 |
| 38 | xla-miR-200a-3p | 16 | 197 | 535 | 142 | 189 |
| 39 | aca-miR-181a | 221 | 179 | 302 | 129 | 188 |
| 40 | ami-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 41 | cgr-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 42 | cja-miR-181a | 221 | 179 | 302 | 129 | 188 |
| 43 | cpi-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 44 | dma-miR-181a | 221 | 179 | 302 | 129 | 188 |
| 45 | dre-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | eca-miR-181a | 221 | 179 | 302 | 129 | 188 |
| 4 | fru-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 5 | gga-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 6 | ggo-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 7 | gmo-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 8 | hsa-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 9 | lla-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 10 | mdo-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 11 | mml-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 12 | mmu-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 13 | mne-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 14 | nle-miR-181a | 221 | 179 | 302 | 129 | 188 |
| 15 | oan-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 16 | oar-miR-181a | 221 | 179 | 302 | 129 | 188 |
| 17 | oga-miR-181a | 221 | 179 | 302 | 129 | 188 |
| 18 | pha-miR-181a | 221 | 179 | 302 | 129 | 188 |
| 19 | pma-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 20 | ppa-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 21 | ppy-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 22 | ptr-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 23 | rno-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 24 | sla-miR-181a | 221 | 179 | 302 | 129 | 188 |
| 25 | ssa-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 26 | tch-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 27 | tgu-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 28 | tni-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 29 | xtr-miR-181a-5p | 221 | 179 | 302 | 129 | 188 |
| 30 | bta-miR-181a | 264 | 202 | 337 | 151 | 211 |
| 31 | cli-miR-181a-5p | 264 | 202 | 337 | 151 | 211 |
| 32 | cpo-miR-181a-5p | 264 | 202 | 337 | 151 | 211 |
| 33 | dno-miR-181a-5p | 264 | 202 | 337 | 151 | 211 |
| 34 | ocu-miR-181a-5p | 264 | 202 | 337 | 151 | 211 |
| 35 | oha-miR-181a-5p | 264 | 202 | 337 | 151 | 211 |
| 36 | pal-miR-181a-5p | 264 | 202 | 337 | 151 | 211 |
| 37 | pbv-miR-181a-5p | 264 | 202 | 337 | 151 | 211 |
| 38 | ssc-miR-181a | 264 | 202 | 337 | 151 | 211 |
| 39 | abu-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 40 | ami-miR-221-3p | 90 | 49 | 41 | 42 | 43 |
| 41 | cgr-miR-221-3p | 90 | 49 | 41 | 42 | 43 |
| 42 | cpo-miR-221-3p | 90 | 49 | 41 | 42 | 43 |
| 43 | dma-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 44 | dno-miR-221-3p | 90 | 49 | 41 | 42 | 43 |
| 45 | dre-miR-221-3p | 90 | 49 | 41 | 42 | 43 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | eca-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 4 | fru-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 5 | gga-miR-221-3p | 90 | 49 | 41 | 42 | 43 |
| 6 | ggo-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 7 | ggo-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 8 | hsa-miR-221-3p | 90 | 49 | 41 | 42 | 43 |
| 9 | mdo-miR-221-3p | 90 | 49 | 41 | 42 | 43 |
| 10 | mml-miR-221-3p | 90 | 49 | 41 | 42 | 43 |
| 11 | mml-miR-221-3p | 90 | 49 | 41 | 42 | 43 |
| 12 | mml-miR-221-3p | 90 | 49 | 41 | 42 | 43 |
| 13 | mmr-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 14 | mmu-miR-221-3p | 90 | 49 | 41 | 42 | 43 |
| 15 | mze-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 16 | nbr-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 17 | nbr-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 18 | nle-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 19 | ocu-miR-221-3p | 90 | 49 | 41 | 42 | 43 |
| 20 | oga-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 21 | oga-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 22 | oha-miR-221-3p | 90 | 49 | 41 | 42 | 43 |
| 23 | ola-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 24 | oni-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 25 | oni-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 26 | pha-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 27 | phn-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 28 | ppa-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 29 | ppa-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 30 | ppy-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 31 | ptr-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 32 | ptr-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 33 | rno-miR-221-3p | 90 | 49 | 41 | 42 | 43 |
| 34 | sbo-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 35 | tgu-miR-221-3p | 90 | 49 | 41 | 42 | 43 |
| 36 | tni-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 37 | tni-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 38 | xtr-miR-221 | 90 | 49 | 41 | 42 | 43 |
| 39 | gma-miR159e-5p | 2364 | 1927 | 1599 | 1667 | 1619 |
| 40 | cli-miR-199-3p | 191 | 104 | 103 | 82 | 111 |
| 41 | cli-miR-199-3p | 191 | 104 | 103 | 82 | 111 |
| 42 | efu-miR-199 | 191 | 104 | 103 | 82 | 111 |
| 43 | dre-miR-199-3p | 182 | 97 | 95 | 75 | 108 |
| 44 | oha-miR-199c-3p | 182 | 97 | 95 | 75 | 108 |
| 45 | oha-miR-199c-3p | 182 | 97 | 95 | 75 | 108 |
| 46 | ssc-miR-199b-3p | 182 | 97 | 95 | 75 | 108 |
| 47 | xtr-miR-199a-3p | 182 | 97 | 95 | 75 | 108 |
| 48 | aca-miR-23a-3p | 177 | 117 | 122 | 81 | 117 |
| 49 | age-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 50 | age-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 51 | ccr-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 52 | cgr-miR-23a-3p | 177 | 117 | 122 | 81 | 117 |
| 53 | chi-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 54 | chi-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 55 | cpi-miR-23a-3p | 177 | 117 | 122 | 81 | 117 |
| 56 | eca-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 57 | ggo-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 58 | ggo-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 59 | hsa-miR-23a-3p | 177 | 117 | 122 | 81 | 117 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ipu-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 4 | lca-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 5 | mml-miR-23a-3p | 177 | 117 | 122 | 81 | 117 |
| 6 | mmu-miR-23a-3p | 177 | 117 | 122 | 81 | 117 |
| 7 | mne-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 8 | pbv-miR-23a-3p | 177 | 117 | 122 | 81 | 117 |
| 9 | pha-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 10 | phn-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 11 | pha-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 12 | phn-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 13 | ppa-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 14 | ppy-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 15 | ptr-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 16 | rno-miR-23a-3p | 177 | 117 | 122 | 81 | 117 |
| 17 | sla-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 18 | ssa-miR-23a-3p | 177 | 117 | 122 | 81 | 117 |
| 19 | ssc-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 20 | xla-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 21 | xtr-miR-23a | 177 | 117 | 122 | 81 | 117 |
| 22 | aly-miR168a-5p | 28942 | 22785 | 27536 | 20618 | 22487 |
| 23 | aly-miR168b-5p | 28942 | 22785 | 27536 | 20618 | 22487 |
| 24 | aof-miR168a | 28942 | 22785 | 27536 | 20618 | 22487 |
| 25 | ath-miR168a-5p | 28942 | 22785 | 27536 | 20618 | 22487 |
| 26 | ath-miR168b-5p | 28942 | 22785 | 27536 | 20618 | 22487 |
| 27 | atr-miR168 | 28942 | 22785 | 27536 | 20618 | 22487 |
| 28 | bna-miR168a | 28942 | 22785 | 27536 | 20618 | 22487 |
| 29 | bra-miR168a-5p | 28942 | 22785 | 27536 | 20618 | 22487 |
| 30 | cca-miR168a | 28942 | 22785 | 27536 | 20618 | 22487 |
| 31 | ccl-miR168 | 28942 | 22785 | 27536 | 20618 | 22487 |
| 32 | crt-miR168 | 28942 | 22785 | 27536 | 20618 | 22487 |
| 33 | csi-miR168-5p | 28942 | 22785 | 27536 | 20618 | 22487 |
| 34 | fve-miR168-5p | 28942 | 22785 | 27536 | 20618 | 22487 |
| 35 | gma-miR168a | 28942 | 22785 | 27536 | 20618 | 22487 |
| 36 | lus-miR168a | 28942 | 22785 | 27536 | 20618 | 22487 |
| 37 | lus-miR168b | 28942 | 22785 | 27536 | 20618 | 22487 |
| 38 | mdm-miR168a | 28942 | 22785 | 27536 | 20618 | 22487 |
| 39 | mdm-miR168b | 28942 | 22785 | 27536 | 20618 | 22487 |
| 40 | mes-miR168a | 28942 | 22785 | 27536 | 20618 | 22487 |
| 41 | mtr-miR168b | 28942 | 22785 | 27536 | 20618 | 22487 |
| 42 | mtr-miR168c-5p | 28942 | 22785 | 27536 | 20618 | 22487 |
| 43 | nta-miR168d | 28942 | 22785 | 27536 | 20618 | 22487 |
| 44 | nta-miR168e | 28942 | 22785 | 27536 | 20618 | 22487 |
| 45 | pab-miR168a | 28942 | 22785 | 27536 | 20618 | 22487 |
| 46 | ppe-miR168 | 28942 | 22785 | 27536 | 20618 | 22487 |
| 47 | ptc-miR168a-5p | 28942 | 22785 | 27536 | 20618 | 22487 |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ptc-miR168b-5p | 28942 | 22785 | 27536 | 20618 | 22487 |
| 4 | rco-miR168 | 28942 | 22785 | 27536 | 20618 | 22487 |
| 5 | tcc-miR168 | 28942 | 22785 | 27536 | 20618 | 22487 |
| 6 | vca-miR168a-5p | 28942 | 22785 | 27536 | 20618 | 22487 |
| 7 | vca-miR168b-5p | 28942 | 22785 | 27536 | 20618 | 22487 |
| 8 | vun-miR168 | 28942 | 22785 | 27536 | 20618 | 22487 |
| 9 | vvi-miR168 | 28942 | 22785 | 27536 | 20618 | 22487 |
| 10 | lja-miR168-5p | 29003 | 22843 | 27583 | 20701 | 22538 |
| 11 | oha-miR-1a-3p | 135 | 103 | 63 | 65 | 98 |
| 12 | pma-miR-1c-3p | 135 | 103 | 63 | 65 | 98 |
| 13 | ami-miR-27b-3p | 67 | 83 | 148 | 54 | 80 |
| 14 | dma-miR-27b | 67 | 83 | 148 | 54 | 80 |
| 15 | gmo-miR-27b-3p | 67 | 83 | 148 | 54 | 80 |
| 16 | nle-miR-27b | 67 | 83 | 148 | 54 | 80 |
| 17 | oga-miR-27b | 67 | 83 | 148 | 54 | 80 |
| 18 | pha-miR-27b | 67 | 83 | 148 | 54 | 80 |
| 19 | csi-miR167c-3p | 377 | 359 | 421 | 357 | 328 |
| 20 | aae-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 21 | abu-miR-133a | 206 | 143 | 77 | 83 | 146 |
| 22 | aga-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 23 | age-miR-133a | 206 | 143 | 77 | 83 | 146 |
| 24 | ame-miR-133-3p | 206 | 143 | 77 | 83 | 146 |
| 25 | bbe-miR-133-5p | 206 | 143 | 77 | 83 | 146 |
| 26 | bmo-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 27 | ccr-miR-133a-3p | 206 | 143 | 77 | 83 | 146 |
| 28 | cfa-miR-133a | 206 | 143 | 77 | 83 | 146 |
| 29 | cja-miR-133a | 206 | 143 | 77 | 83 | 146 |
| 30 | cqu-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 31 | cte-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 32 | dan-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 33 | der-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 34 | dgr-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 35 | dme-miR-133-3p | 206 | 143 | 77 | 83 | 146 |
| 36 | dmo-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 37 | dpe-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 38 | dps-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 39 | dpu-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 40 | dqu-miR-133-3p | 206 | 143 | 77 | 83 | 146 |
| 41 | dse-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 42 | dsi-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 43 | dvi-miR-133-3p | 206 | 143 | 77 | 83 | 146 |
| 44 | dwi-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 45 | dya-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-----|-----|----|----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | gga-miR-133a-3p | 206 | 143 | 77 | 83 | 146 |
| 4 | ggo-miR-133a | 206 | 143 | 77 | 83 | 146 |
| 5 | gmo-miR-133a-3p | 206 | 143 | 77 | 83 | 146 |
| 6 | ipu-miR-133a | 206 | 143 | 77 | 83 | 146 |
| 7 | isc-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 8 | lgi-miR-133-3p | 206 | 143 | 77 | 83 | 146 |
| 9 | lla-miR-133a | 206 | 143 | 77 | 83 | 146 |
| 10 | mdo-miR-133a-3p | 206 | 143 | 77 | 83 | 146 |
| 11 | mne-miR-133a | 206 | 143 | 77 | 83 | 146 |
| 12 | mse-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 13 | mze-miR-133a | 206 | 143 | 77 | 83 | 146 |
| 14 | nbr-miR-133a | 206 | 143 | 77 | 83 | 146 |
| 15 | ngi-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 16 | nlo-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 17 | nvi-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 18 | oan-miR-133a-3p | 206 | 143 | 77 | 83 | 146 |
| 19 | oar-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 20 | oni-miR-133a | 206 | 143 | 77 | 83 | 146 |
| 21 | pal-miR-133a-3p | 206 | 143 | 77 | 83 | 146 |
| 22 | pca-miR-133-3p | 206 | 143 | 77 | 83 | 146 |
| 23 | ppa-miR-133a | 206 | 143 | 77 | 83 | 146 |
| 24 | sko-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 25 | sla-miR-133a | 206 | 143 | 77 | 83 | 146 |
| 26 | ssa-miR-133a-3p | 206 | 143 | 77 | 83 | 146 |
| 27 | tca-miR-133-3p | 206 | 143 | 77 | 83 | 146 |
| 28 | tcf-miR-133 | 206 | 143 | 77 | 83 | 146 |
| 29 | tur-miR-133-3p | 206 | 143 | 77 | 83 | 146 |
| 30 | xla-miR-133a | 206 | 143 | 77 | 83 | 146 |
| 31 | xtr-miR-133a | 206 | 143 | 77 | 83 | 146 |
| 32 | ami-miR-199-3p | 152 | 98 | 96 | 73 | 100 |
| 33 | bta-miR-199a-3p | 152 | 98 | 96 | 73 | 100 |
| 34 | cpi-miR-199-3p | 152 | 98 | 96 | 73 | 100 |
| 35 | cpo-miR-199-3p | 152 | 98 | 96 | 73 | 100 |
| 36 | dno-miR-199-3p | 152 | 98 | 96 | 73 | 100 |
| 37 | eca-miR-199a-3p | 152 | 98 | 96 | 73 | 100 |
| 38 | eca-miR-199b-3p | 152 | 98 | 96 | 73 | 100 |
| 39 | gmo-miR-199-3p | 152 | 98 | 96 | 73 | 100 |
| 40 | hsa-miR-199a-3p | 152 | 98 | 96 | 73 | 100 |
| 41 | hsa-miR-199b-3p | 152 | 98 | 96 | 73 | 100 |
| 42 | mml-miR-199a-3p | 152 | 98 | 96 | 73 | 100 |
| 43 | mmu-miR-199a-3p | 152 | 98 | 96 | 73 | 100 |
| 44 | mmu-miR-199b-3p | 152 | 98 | 96 | 73 | 100 |
| 45 | ocu-miR-199a-3p | 152 | 98 | 96 | 73 | 100 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | oha-miR-199a-3p | 152 | 98 | 96 | 73 | 100 |
| 4 | ola-miR-199a-3p | 152 | 98 | 96 | 73 | 100 |
| 5 | pol-miR-199a-3p | 152 | 98 | 96 | 73 | 100 |
| 6 | ptr-miR-199a-3p | 152 | 98 | 96 | 73 | 100 |
| 7 | ptr-miR-199b | 152 | 98 | 96 | 73 | 100 |
| 8 | rno-miR-199a-3p | 152 | 98 | 96 | 73 | 100 |
| 9 | ssc-miR-199a-3p | 152 | 98 | 96 | 73 | 100 |
| 10 | xla-miR-199-3p | 152 | 98 | 96 | 73 | 100 |
| 11 | bdi-miR166e-3p | 1001 | 1255 | 1211 | 1048 | 894 |
| 12 | atr-miR319a | 4040 | 3144 | 2272 | 2517 | 2469 |
| 13 | atr-miR319c | 4040 | 3144 | 2272 | 2517 | 2469 |
| 14 | cme-miR319a | 4040 | 3144 | 2272 | 2517 | 2469 |
| 15 | cme-miR319b | 4040 | 3144 | 2272 | 2517 | 2469 |
| 16 | ctr-miR319 | 4040 | 3144 | 2272 | 2517 | 2469 |
| 17 | gma-miR319a | 4040 | 3144 | 2272 | 2517 | 2469 |
| 18 | gma-miR319b | 4040 | 3144 | 2272 | 2517 | 2469 |
| 19 | gma-miR319e | 4040 | 3144 | 2272 | 2517 | 2469 |
| 20 | lus-miR319b | 4040 | 3144 | 2272 | 2517 | 2469 |
| 21 | mtr-miR319a-3p | 4040 | 3144 | 2272 | 2517 | 2469 |
| 22 | mtr-miR319b-3p | 4040 | 3144 | 2272 | 2517 | 2469 |
| 23 | pab-miR319a | 4040 | 3144 | 2272 | 2517 | 2469 |
| 24 | pab-miR319b | 4040 | 3144 | 2272 | 2517 | 2469 |
| 25 | pab-miR319c | 4040 | 3144 | 2272 | 2517 | 2469 |
| 26 | pab-miR319f | 4040 | 3144 | 2272 | 2517 | 2469 |
| 27 | pab-miR319g | 4040 | 3144 | 2272 | 2517 | 2469 |
| 28 | pab-miR319i | 4040 | 3144 | 2272 | 2517 | 2469 |
| 29 | pab-miR319k | 4040 | 3144 | 2272 | 2517 | 2469 |
| 30 | pab-miR319l | 4040 | 3144 | 2272 | 2517 | 2469 |
| 31 | pab-miR319m | 4040 | 3144 | 2272 | 2517 | 2469 |
| 32 | pab-miR319n | 4040 | 3144 | 2272 | 2517 | 2469 |
| 33 | ppe-miR319a | 4040 | 3144 | 2272 | 2517 | 2469 |
| 34 | ptc-miR319a | 4040 | 3144 | 2272 | 2517 | 2469 |
| 35 | ptc-miR319b | 4040 | 3144 | 2272 | 2517 | 2469 |
| 36 | ptc-miR319c | 4040 | 3144 | 2272 | 2517 | 2469 |
| 37 | ptc-miR319d | 4040 | 3144 | 2272 | 2517 | 2469 |
| 38 | mes-miR166i | 65 | 161 | 139 | 108 | 79 |
| 39 | csi-miR159c-3p | 4060 | 3182 | 2307 | 2548 | 2498 |
| 40 | ppt-miR319c | 4060 | 3182 | 2307 | 2548 | 2498 |
| 41 | ppt-miR319d-3p | 4060 | 3182 | 2307 | 2548 | 2498 |
| 42 | ppt-miR319e | 4060 | 3182 | 2307 | 2548 | 2498 |
| 43 | abu-miR-199-3p | 144 | 91 | 88 | 66 | 97 |
| 44 | ccr-miR-199-3p | 144 | 91 | 88 | 66 | 97 |
| 45 | cfa-miR-199 | 144 | 91 | 88 | 66 | 97 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|------------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | cgr-miR-199a-3p | 144 | 91 | 88 | 66 | 97 |
| 4 | chi-miR-199a-3p | 144 | 91 | 88 | 66 | 97 |
| 5 | chi-miR-199b-3p | 144 | 91 | 88 | 66 | 97 |
| 6 | chi-miR-199c-3p | 144 | 91 | 88 | 66 | 97 |
| 7 | chi-miR-199c-3p | 144 | 91 | 88 | 66 | 97 |
| 8 | cja-miR-199 | 144 | 91 | 88 | 66 | 97 |
| 9 | cja-miR-199 | 144 | 91 | 88 | 66 | 97 |
| 10 | dma-miR-199 | 144 | 91 | 88 | 66 | 97 |
| 11 | gmo-miR-199-4-3p | 144 | 91 | 88 | 66 | 97 |
| 12 | ipu-miR-199a-3p | 144 | 91 | 88 | 66 | 97 |
| 13 | ipu-miR-199a-3p | 144 | 91 | 88 | 66 | 97 |
| 14 | mdo-miR-199b-3p | 144 | 91 | 88 | 66 | 97 |
| 15 | mmr-miR-199 | 144 | 91 | 88 | 66 | 97 |
| 16 | mze-miR-199 | 144 | 91 | 88 | 66 | 97 |
| 17 | mze-miR-199 | 144 | 91 | 88 | 66 | 97 |
| 18 | nbr-miR-199 | 144 | 91 | 88 | 66 | 97 |
| 19 | nle-miR-199a | 144 | 91 | 88 | 66 | 97 |
| 20 | nle-miR-199b | 144 | 91 | 88 | 66 | 97 |
| 21 | nle-miR-199b | 144 | 91 | 88 | 66 | 97 |
| 22 | oan-miR-199-3p | 144 | 91 | 88 | 66 | 97 |
| 23 | oar-miR-199a-3p | 144 | 91 | 88 | 66 | 97 |
| 24 | oga-miR-199 | 144 | 91 | 88 | 66 | 97 |
| 25 | oga-miR-199 | 144 | 91 | 88 | 66 | 97 |
| 26 | oni-miR-199a | 144 | 91 | 88 | 66 | 97 |
| 27 | pal-miR-199-3p | 144 | 91 | 88 | 66 | 97 |
| 28 | pbv-miR-199-3p | 144 | 91 | 88 | 66 | 97 |
| 29 | pbv-miR-199-3p | 144 | 91 | 88 | 66 | 97 |
| 30 | pha-miR-199 | 144 | 91 | 88 | 66 | 97 |
| 31 | phny-miR-199 | 144 | 91 | 88 | 66 | 97 |
| 32 | ppa-miR-199b | 144 | 91 | 88 | 66 | 97 |
| 33 | ppa-miR-199b | 144 | 91 | 88 | 66 | 97 |
| 34 | sbo-miR-199 | 144 | 91 | 88 | 66 | 97 |
| 35 | sha-miR-199a | 144 | 91 | 88 | 66 | 97 |
| 36 | ssa-miR-199a-3p | 144 | 91 | 88 | 66 | 97 |
| 37 | ssa-miR-199a-3p | 144 | 91 | 88 | 66 | 97 |
| 38 | tch-miR-199a-3p | 144 | 91 | 88 | 66 | 97 |
| 39 | tch-miR-199b-3p | 144 | 91 | 88 | 66 | 97 |
| 40 | tch-miR-199b-3p | 144 | 91 | 88 | 66 | 97 |
| 41 | tgu-miR-199-3p | 144 | 91 | 88 | 66 | 97 |
| 42 | mtr-miR319c-3p | 4046 | 3147 | 2279 | 2525 | 2473 |
| 43 | vvi-miR319g | 4046 | 3147 | 2279 | 2525 | 2473 |
| 44 | csi-miR396f-3p | 870 | 702 | 698 | 707 | 569 |
| 45 | csi-miR396f-3p | 870 | 702 | 698 | 707 | 569 |
| 46 | gma-miR396b-3p | 870 | 702 | 698 | 707 | 569 |
| 47 | gma-miR396k-3p | 870 | 702 | 698 | 707 | 569 |
| 48 | gma-miR396k-3p | 870 | 702 | 698 | 707 | 569 |
| 49 | mtr-miR396a-3p | 870 | 702 | 698 | 707 | 569 |
| 50 | cpo-miR-23a-3p | 264 | 180 | 170 | 131 | 175 |
| 51 | dno-miR-23a-3p | 264 | 180 | 170 | 131 | 175 |
| 52 | efu-miR-23a | 270 | 183 | 174 | 134 | 177 |
| 53 | efu-miR-23a | 270 | 183 | 174 | 134 | 177 |
| 54 | abu-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 55 | aca-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 56 | age-miR-92 | 107 | 89 | 126 | 64 | 97 |
| 57 | age-miR-92 | 107 | 89 | 126 | 64 | 97 |
| 58 | ami-miR-92a-3p | 107 | 89 | 126 | 64 | 97 |
| 59 | bta-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 60 | bta-miR-92a | 107 | 89 | 126 | 64 | 97 |

| | | | | | | |
|----|----------------|-----|----|-----|----|----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ccr-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 4 | cfa-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 5 | cgr-miR-92a-3p | 107 | 89 | 126 | 64 | 97 |
| 6 | chi-miR-92a-3p | 107 | 89 | 126 | 64 | 97 |
| 7 | chi-miR-92b | 107 | 89 | 126 | 64 | 97 |
| 8 | cja-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 9 | cli-miR-92-3p | 107 | 89 | 126 | 64 | 97 |
| 10 | cpo-miR-92a-3p | 107 | 89 | 126 | 64 | 97 |
| 11 | dma-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 12 | dno-miR-92a-3p | 107 | 89 | 126 | 64 | 97 |
| 13 | dre-miR-92a-3p | 107 | 89 | 126 | 64 | 97 |
| 14 | eca-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 15 | efu-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 16 | fru-miR-92 | 107 | 89 | 126 | 64 | 97 |
| 17 | ggo-miR-92 | 107 | 89 | 126 | 64 | 97 |
| 18 | hsa-miR-92a-3p | 107 | 89 | 126 | 64 | 97 |
| 19 | ipu-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 20 | lca-miR-92 | 107 | 89 | 126 | 64 | 97 |
| 21 | lla-miR-92 | 107 | 89 | 126 | 64 | 97 |
| 22 | mdo-miR-92a-3p | 107 | 89 | 126 | 64 | 97 |
| 23 | mml-miR-92a-3p | 107 | 89 | 126 | 64 | 97 |
| 24 | mmr-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 25 | mmr-miR-92b | 107 | 89 | 126 | 64 | 97 |
| 26 | mne-miR-92 | 107 | 89 | 126 | 64 | 97 |
| 27 | mze-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 28 | nbr-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 29 | nle-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 30 | oan-miR-92a-3p | 107 | 89 | 126 | 64 | 97 |
| 31 | ocu-miR-92a-3p | 107 | 89 | 126 | 64 | 97 |
| 32 | oga-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 33 | oha-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 34 | oha-miR-92a-3p | 107 | 89 | 126 | 64 | 97 |
| 35 | oni-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 36 | pal-miR-92a-3p | 107 | 89 | 126 | 64 | 97 |
| 37 | pbv-miR-92a-3p | 107 | 89 | 126 | 64 | 97 |
| 38 | pha-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 39 | pony-miR-92 | 107 | 89 | 126 | 64 | 97 |
| 40 | ppa-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 41 | ppy-miR-92 | 107 | 89 | 126 | 64 | 97 |
| 42 | ptr-miR-92 | 107 | 89 | 126 | 64 | 97 |
| 43 | sbo-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 44 | sla-miR-92 | 107 | 89 | 126 | 64 | 97 |
| 45 | ssa-miR-92a-3p | 107 | 89 | 126 | 64 | 97 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ssc-miR-92a | 107 | 89 | 126 | 64 | 97 |
| 4 | tch-miR-92a-3p | 107 | 89 | 126 | 64 | 97 |
| 5 | tgu-miR-92-3p | 107 | 89 | 126 | 64 | 97 |
| 6 | tni-miR-92 | 107 | 89 | 126 | 64 | 97 |
| 7 | tni-miR-92 | 107 | 89 | 126 | 64 | 97 |
| 8 | xla-miR-92a-3p | 107 | 89 | 126 | 64 | 97 |
| 9 | xla-miR-92a-3p | 107 | 89 | 126 | 64 | 97 |
| 10 | aau-miR319 | 5644 | 4160 | 3002 | 3409 | 3391 |
| 11 | aly-miR319a-3p | 5644 | 4160 | 3002 | 3409 | 3391 |
| 12 | aly-miR319b-3p | 5644 | 4160 | 3002 | 3409 | 3391 |
| 13 | aly-miR319b-3p | 5644 | 4160 | 3002 | 3409 | 3391 |
| 14 | amg-miR319 | 5644 | 4160 | 3002 | 3409 | 3391 |
| 15 | aof-miR319a | 5644 | 4160 | 3002 | 3409 | 3391 |
| 16 | aqc-miR319 | 5644 | 4160 | 3002 | 3409 | 3391 |
| 17 | aqc-miR319 | 5644 | 4160 | 3002 | 3409 | 3391 |
| 18 | ath-miR319a | 5644 | 4160 | 3002 | 3409 | 3391 |
| 19 | ath-miR319b | 5644 | 4160 | 3002 | 3409 | 3391 |
| 20 | bra-miR319-3p | 5644 | 4160 | 3002 | 3409 | 3391 |
| 21 | bra-miR319-3p | 5644 | 4160 | 3002 | 3409 | 3391 |
| 22 | cca-miR319 | 5644 | 4160 | 3002 | 3409 | 3391 |
| 23 | cca-miR319 | 5644 | 4160 | 3002 | 3409 | 3391 |
| 24 | gma-miR319h | 5644 | 4160 | 3002 | 3409 | 3391 |
| 25 | gma-miR319j | 5644 | 4160 | 3002 | 3409 | 3391 |
| 26 | gma-miR319k | 5644 | 4160 | 3002 | 3409 | 3391 |
| 27 | gma-miR319m | 5644 | 4160 | 3002 | 3409 | 3391 |
| 28 | gma-miR319m | 5644 | 4160 | 3002 | 3409 | 3391 |
| 29 | hbr-miR319 | 5644 | 4160 | 3002 | 3409 | 3391 |
| 30 | lus-miR319a | 5644 | 4160 | 3002 | 3409 | 3391 |
| 31 | mdm-miR319a | 5644 | 4160 | 3002 | 3409 | 3391 |
| 32 | mdm-miR319b-3p | 5644 | 4160 | 3002 | 3409 | 3391 |
| 33 | mdm-miR319b-3p | 5644 | 4160 | 3002 | 3409 | 3391 |
| 34 | mes-miR319a | 5644 | 4160 | 3002 | 3409 | 3391 |
| 35 | mes-miR319b | 5644 | 4160 | 3002 | 3409 | 3391 |
| 36 | mes-miR319c | 5644 | 4160 | 3002 | 3409 | 3391 |
| 37 | mes-miR319c | 5644 | 4160 | 3002 | 3409 | 3391 |
| 38 | mes-miR319d | 5644 | 4160 | 3002 | 3409 | 3391 |
| 39 | mes-miR319e | 5644 | 4160 | 3002 | 3409 | 3391 |
| 40 | mes-miR319e | 5644 | 4160 | 3002 | 3409 | 3391 |
| 41 | mtr-miR319d-3p | 5644 | 4160 | 3002 | 3409 | 3391 |
| 42 | nta-miR319a | 5644 | 4160 | 3002 | 3409 | 3391 |
| 43 | nta-miR319b | 5644 | 4160 | 3002 | 3409 | 3391 |
| 44 | nta-miR319b | 5644 | 4160 | 3002 | 3409 | 3391 |
| 45 | rco-miR319a | 5644 | 4160 | 3002 | 3409 | 3391 |
| 46 | rco-miR319b | 5644 | 4160 | 3002 | 3409 | 3391 |
| 47 | rco-miR319c | 5644 | 4160 | 3002 | 3409 | 3391 |
| 48 | rco-miR319c | 5644 | 4160 | 3002 | 3409 | 3391 |
| 49 | sly-miR319b | 5644 | 4160 | 3002 | 3409 | 3391 |
| 50 | stu-miR319a-3p | 5644 | 4160 | 3002 | 3409 | 3391 |
| 51 | tae-miR319 | 5644 | 4160 | 3002 | 3409 | 3391 |
| 52 | tae-miR319 | 5644 | 4160 | 3002 | 3409 | 3391 |
| 53 | vun-miR319a | 5644 | 4160 | 3002 | 3409 | 3391 |
| 54 | vvi-miR319b | 5644 | 4160 | 3002 | 3409 | 3391 |
| 55 | vvi-miR319c | 5644 | 4160 | 3002 | 3409 | 3391 |
| 56 | vvi-miR319f | 5644 | 4160 | 3002 | 3409 | 3391 |
| 57 | vvi-miR319f | 5644 | 4160 | 3002 | 3409 | 3391 |
| 58 | gma-miR5374-5p | 200 | 176 | 217 | 147 | 170 |
| 59 | abu-miR-23a | 257 | 176 | 161 | 129 | 171 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ami-miR-23a-3p | 257 | 176 | 161 | 129 | 171 |
| 4 | bta-miR-23a | 257 | 176 | 161 | 129 | 171 |
| 5 | cja-miR-23a | 257 | 176 | 161 | 129 | 171 |
| 6 | dre-miR-23a-3p | 257 | 176 | 161 | 129 | 171 |
| 7 | fru-miR-23a | 257 | 176 | 161 | 129 | 171 |
| 8 | gmo-miR-23a-3p | 257 | 176 | 161 | 129 | 171 |
| 9 | hhi-miR-23a | 257 | 176 | 161 | 129 | 171 |
| 10 | mze-miR-23a | 257 | 176 | 161 | 129 | 171 |
| 11 | nbr-miR-23a | 257 | 176 | 161 | 129 | 171 |
| 12 | oan-miR-23a-3p | 257 | 176 | 161 | 129 | 171 |
| 13 | oar-miR-23a | 257 | 176 | 161 | 129 | 171 |
| 14 | oga-miR-23a | 257 | 176 | 161 | 129 | 171 |
| 15 | oha-miR-23a-3p | 257 | 176 | 161 | 129 | 171 |
| 16 | ola-miR-23a | 257 | 176 | 161 | 129 | 171 |
| 17 | oni-miR-23a | 257 | 176 | 161 | 129 | 171 |
| 18 | pal-miR-23a-3p | 257 | 176 | 161 | 129 | 171 |
| 19 | tni-miR-23a | 257 | 176 | 161 | 129 | 171 |
| 20 | xla-miR-23a-3p | 257 | 176 | 161 | 129 | 171 |
| 21 | aly-miR171b-3p | 717 | 906 | 916 | 769 | 739 |
| 22 | aly-miR171c-3p | 717 | 906 | 916 | 769 | 739 |
| 23 | ata-miR171c-3p | 717 | 906 | 916 | 769 | 739 |
| 24 | ath-miR171b-3p | 717 | 906 | 916 | 769 | 739 |
| 25 | ath-miR171c-3p | 717 | 906 | 916 | 769 | 739 |
| 26 | bna-miR171a | 717 | 906 | 916 | 769 | 739 |
| 27 | bna-miR171b | 717 | 906 | 916 | 769 | 739 |
| 28 | bna-miR171c | 717 | 906 | 916 | 769 | 739 |
| 29 | bna-miR171d | 717 | 906 | 916 | 769 | 739 |
| 30 | bna-miR171e | 717 | 906 | 916 | 769 | 739 |
| 31 | bol-miR171a | 717 | 906 | 916 | 769 | 739 |
| 32 | bra-miR171a | 717 | 906 | 916 | 769 | 739 |
| 33 | bra-miR171b | 717 | 906 | 916 | 769 | 739 |
| 34 | bra-miR171c | 717 | 906 | 916 | 769 | 739 |
| 35 | bra-miR171d | 717 | 906 | 916 | 769 | 739 |
| 36 | cas-miR171b | 717 | 906 | 916 | 769 | 739 |
| 37 | cas-miR171c-3p | 717 | 906 | 916 | 769 | 739 |
| 38 | cme-miR171b | 717 | 906 | 916 | 769 | 739 |
| 39 | cme-miR171d | 717 | 906 | 916 | 769 | 739 |
| 40 | gma-miR171i-3p | 717 | 906 | 916 | 769 | 739 |
| 41 | lus-miR171i | 717 | 906 | 916 | 769 | 739 |
| 42 | mdm-miR171f-3p | 717 | 906 | 916 | 769 | 739 |
| 43 | mes-miR171b | 717 | 906 | 916 | 769 | 739 |
| 44 | mes-miR171c | 717 | 906 | 916 | 769 | 739 |
| 45 | mtr-miR171f | 717 | 906 | 916 | 769 | 739 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ptc-miR171a-3p | 717 | 906 | 916 | 769 | 739 |
| 4 | ptc-miR171b | 717 | 906 | 916 | 769 | 739 |
| 5 | rco-miR171a | 717 | 906 | 916 | 769 | 739 |
| 6 | rco-miR171b | 717 | 906 | 916 | 769 | 739 |
| 7 | sly-miR171b-3p | 717 | 906 | 916 | 769 | 739 |
| 8 | ssl-miR171a | 717 | 906 | 916 | 769 | 739 |
| 9 | stu-miR171d-3p | 717 | 906 | 916 | 769 | 739 |
| 10 | tae-miR171b | 717 | 906 | 916 | 769 | 739 |
| 11 | ptc-miR396e-3p | 559 | 463 | 485 | 488 | 383 |
| 12 | aly-miR390a-5p | 4718 | 5643 | 4258 | 4695 | 3692 |
| 13 | aly-miR390b-5p | 4718 | 5643 | 4258 | 4695 | 3692 |
| 14 | aof-miR390 | 4718 | 5643 | 4258 | 4695 | 3692 |
| 15 | ata-miR390-5p | 4718 | 5643 | 4258 | 4695 | 3692 |
| 16 | ath-miR390a-5p | 4718 | 5643 | 4258 | 4695 | 3692 |
| 17 | ath-miR390b-5p | 4718 | 5643 | 4258 | 4695 | 3692 |
| 18 | atr-miR390.2 | 4718 | 5643 | 4258 | 4695 | 3692 |
| 19 | bdi-miR390a-5p | 4718 | 5643 | 4258 | 4695 | 3692 |
| 20 | bna-miR390a | 4718 | 5643 | 4258 | 4695 | 3692 |
| 21 | bna-miR390b | 4718 | 5643 | 4258 | 4695 | 3692 |
| 22 | bna-miR390c | 4718 | 5643 | 4258 | 4695 | 3692 |
| 23 | bra-miR390-5p | 4718 | 5643 | 4258 | 4695 | 3692 |
| 24 | cas-miR390a-5p | 4718 | 5643 | 4258 | 4695 | 3692 |
| 25 | cas-miR390b | 4718 | 5643 | 4258 | 4695 | 3692 |
| 26 | cme-miR390a | 4718 | 5643 | 4258 | 4695 | 3692 |
| 27 | cme-miR390b | 4718 | 5643 | 4258 | 4695 | 3692 |
| 28 | cme-miR390c | 4718 | 5643 | 4258 | 4695 | 3692 |
| 29 | cme-miR390d | 4718 | 5643 | 4258 | 4695 | 3692 |
| 30 | cpa-miR390a | 4718 | 5643 | 4258 | 4695 | 3692 |
| 31 | cpa-miR390b | 4718 | 5643 | 4258 | 4695 | 3692 |
| 32 | csi-miR390a-5p | 4718 | 5643 | 4258 | 4695 | 3692 |
| 33 | fve-miR390a | 4718 | 5643 | 4258 | 4695 | 3692 |
| 34 | fve-miR390b | 4718 | 5643 | 4258 | 4695 | 3692 |
| 35 | ghr-miR390a | 4718 | 5643 | 4258 | 4695 | 3692 |
| 36 | ghr-miR390b | 4718 | 5643 | 4258 | 4695 | 3692 |
| 37 | ghr-miR390c | 4718 | 5643 | 4258 | 4695 | 3692 |
| 38 | gma-miR390a-5p | 4718 | 5643 | 4258 | 4695 | 3692 |
| 39 | gma-miR390f | 4718 | 5643 | 4258 | 4695 | 3692 |
| 40 | gma-miR390g | 4718 | 5643 | 4258 | 4695 | 3692 |
| 41 | hex-miR390a | 4718 | 5643 | 4258 | 4695 | 3692 |
| 42 | hex-miR390b | 4718 | 5643 | 4258 | 4695 | 3692 |
| 43 | lja-miR390a-5p | 4718 | 5643 | 4258 | 4695 | 3692 |
| 44 | lja-miR390b-5p | 4718 | 5643 | 4258 | 4695 | 3692 |
| 45 | lus-miR390a | 4718 | 5643 | 4258 | 4695 | 3692 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | lus-miR390b | 4718 | 5643 | 4258 | 4695 | 3692 |
| 4 | lus-miR390c | 4718 | 5643 | 4258 | 4695 | 3692 |
| 5 | lus-miR390d | 4718 | 5643 | 4258 | 4695 | 3692 |
| 6 | mdm-miR390a | 4718 | 5643 | 4258 | 4695 | 3692 |
| 7 | mdm-miR390b | 4718 | 5643 | 4258 | 4695 | 3692 |
| 8 | mdm-miR390c | 4718 | 5643 | 4258 | 4695 | 3692 |
| 9 | mdm-miR390d | 4718 | 5643 | 4258 | 4695 | 3692 |
| 10 | mdm-miR390e | 4718 | 5643 | 4258 | 4695 | 3692 |
| 11 | mdm-miR390f | 4718 | 5643 | 4258 | 4695 | 3692 |
| 12 | mes-miR390b | 4718 | 5643 | 4258 | 4695 | 3692 |
| 13 | mtr-miR390 | 4718 | 5643 | 4258 | 4695 | 3692 |
| 14 | nta-miR390b | 4718 | 5643 | 4258 | 4695 | 3692 |
| 15 | nta-miR390c | 4718 | 5643 | 4258 | 4695 | 3692 |
| 16 | osa-miR390-5p | 4718 | 5643 | 4258 | 4695 | 3692 |
| 17 | pab-miR390a | 4718 | 5643 | 4258 | 4695 | 3692 |
| 18 | pab-miR390b | 4718 | 5643 | 4258 | 4695 | 3692 |
| 19 | ppe-miR390 | 4718 | 5643 | 4258 | 4695 | 3692 |
| 20 | ppt-miR390a | 4718 | 5643 | 4258 | 4695 | 3692 |
| 21 | ppt-miR390b | 4718 | 5643 | 4258 | 4695 | 3692 |
| 22 | ptc-miR390a | 4718 | 5643 | 4258 | 4695 | 3692 |
| 23 | ptc-miR390b | 4718 | 5643 | 4258 | 4695 | 3692 |
| 24 | ptc-miR390c | 4718 | 5643 | 4258 | 4695 | 3692 |
| 25 | ptc-miR390d-5p | 4718 | 5643 | 4258 | 4695 | 3692 |
| 26 | rco-miR390a | 4718 | 5643 | 4258 | 4695 | 3692 |
| 27 | rco-miR390b | 4718 | 5643 | 4258 | 4695 | 3692 |
| 28 | sbi-miR390 | 4718 | 5643 | 4258 | 4695 | 3692 |
| 29 | sly-miR390b-5p | 4718 | 5643 | 4258 | 4695 | 3692 |
| 30 | tcc-miR390a | 4718 | 5643 | 4258 | 4695 | 3692 |
| 31 | tcc-miR390b | 4718 | 5643 | 4258 | 4695 | 3692 |
| 32 | vvi-miR390 | 4718 | 5643 | 4258 | 4695 | 3692 |
| 33 | zma-miR390a-5p | 4718 | 5643 | 4258 | 4695 | 3692 |
| 34 | zma-miR390b-5p | 4718 | 5643 | 4258 | 4695 | 3692 |
| 35 | aae-miR-125-5p | 89 | 54 | 61 | 42 | 55 |
| 36 | abu-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 37 | aca-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 38 | aga-miR-125 | 89 | 54 | 61 | 42 | 55 |
| 39 | age-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 40 | ami-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 41 | bbe-miR-125a-5p | 89 | 54 | 61 | 42 | 55 |
| 42 | bdo-miR-125 | 89 | 54 | 61 | 42 | 55 |
| 43 | bfl-miR-125a-5p | 89 | 54 | 61 | 42 | 55 |
| 44 | bta-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 45 | ccr-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|----|----|----|----|----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | cfa-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 4 | cgr-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 5 | cja-miR-125 | 89 | 54 | 61 | 42 | 55 |
| 6 | cja-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 7 | cli-miR-125-5p | 89 | 54 | 61 | 42 | 55 |
| 8 | cpi-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 9 | cpo-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 10 | cqu-miR-125-5p | 89 | 54 | 61 | 42 | 55 |
| 11 | cte-miR-125 | 89 | 54 | 61 | 42 | 55 |
| 12 | dan-miR-125 | 89 | 54 | 61 | 42 | 55 |
| 13 | der-miR-125 | 89 | 54 | 61 | 42 | 55 |
| 14 | dgr-miR-125 | 89 | 54 | 61 | 42 | 55 |
| 15 | dma-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 16 | dme-miR-125-5p | 89 | 54 | 61 | 42 | 55 |
| 17 | dmo-miR-125 | 89 | 54 | 61 | 42 | 55 |
| 18 | dno-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 19 | dpe-miR-125 | 89 | 54 | 61 | 42 | 55 |
| 20 | dps-miR-125 | 89 | 54 | 61 | 42 | 55 |
| 21 | dqu-miR-125-5p | 89 | 54 | 61 | 42 | 55 |
| 22 | dre-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 23 | dse-miR-125 | 89 | 54 | 61 | 42 | 55 |
| 24 | dsi-miR-125 | 89 | 54 | 61 | 42 | 55 |
| 25 | dwi-miR-125 | 89 | 54 | 61 | 42 | 55 |
| 26 | dya-miR-125 | 89 | 54 | 61 | 42 | 55 |
| 27 | eca-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 28 | efu-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 29 | fru-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 30 | gga-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 31 | ggo-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 32 | gmo-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 33 | hsa-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 34 | ipu-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 35 | lca-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 36 | lla-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 37 | lva-miR-125-5p | 89 | 54 | 61 | 42 | 55 |
| 38 | mdo-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 39 | mml-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 40 | mmr-miR-125a | 89 | 54 | 61 | 42 | 55 |
| 41 | mmu-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 42 | mne-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 43 | mze-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 44 | nbr-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 45 | nle-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|------|------|-------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | nlo-miR-125 | 89 | 54 | 61 | 42 | 55 |
| 4 | nvi-miR-125 | 89 | 54 | 61 | 42 | 55 |
| 5 | oan-miR-125-5p | 89 | 54 | 61 | 42 | 55 |
| 6 | ocu-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 7 | oga-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 8 | oha-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 9 | ola-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 10 | ola-miR-125c | 89 | 54 | 61 | 42 | 55 |
| 11 | oni-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 12 | pal-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 13 | pbv-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 14 | pha-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 15 | pma-miR-125-5p | 89 | 54 | 61 | 42 | 55 |
| 16 | pmi-miR-125-5p | 89 | 54 | 61 | 42 | 55 |
| 17 | ppy-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 18 | ppa-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 19 | ppp-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 20 | ptr-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 21 | rno-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 22 | sha-miR-125a | 89 | 54 | 61 | 42 | 55 |
| 23 | sko-miR-125a | 89 | 54 | 61 | 42 | 55 |
| 24 | sla-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 25 | spu-miR-125-5p | 89 | 54 | 61 | 42 | 55 |
| 26 | ssa-miR-125a-5p | 89 | 54 | 61 | 42 | 55 |
| 27 | ssc-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 28 | tca-miR-125-5p | 89 | 54 | 61 | 42 | 55 |
| 29 | tcf-miR-125 | 89 | 54 | 61 | 42 | 55 |
| 30 | tch-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 31 | tgu-miR-125-5p | 89 | 54 | 61 | 42 | 55 |
| 32 | tni-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 33 | xla-miR-125b-5p | 89 | 54 | 61 | 42 | 55 |
| 34 | xtr-miR-125b | 89 | 54 | 61 | 42 | 55 |
| 35 | cpa-miR166d | 9876 | 9912 | 11328 | 9107 | 9264 |
| 36 | gma-miR166j-3p | 9876 | 9912 | 11328 | 9107 | 9264 |
| 37 | crt-miR166a | 9887 | 9917 | 11339 | 9118 | 9271 |
| 38 | mes-miR166h | 9887 | 9917 | 11339 | 9118 | 9271 |
| 39 | atr-miR171b | 613 | 340 | 332 | 360 | 408 |
| 40 | gma-miR171c-3p | 613 | 340 | 332 | 360 | 408 |
| 41 | gma-miR171o-3p | 613 | 340 | 332 | 360 | 408 |
| 42 | gma-miR171q | 613 | 340 | 332 | 360 | 408 |
| 43 | mdm-miR171m | 613 | 340 | 332 | 360 | 408 |
| 44 | mdm-miR171n | 613 | 340 | 332 | 360 | 408 |
| 45 | zma-miR171f-3p | 613 | 340 | 332 | 360 | 408 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|------|-------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | gma-miR169e | 561 | 651 | 624 | 465 | 600 |
| 4 | mtr-miR169e-5p | 565 | 652 | 625 | 467 | 602 |
| 5 | vvi-miR169m | 565 | 652 | 625 | 467 | 602 |
| 6 | vvi-miR169n | 565 | 652 | 625 | 467 | 602 |
| 7 | vvi-miR169p | 565 | 652 | 625 | 467 | 602 |
| 8 | vvi-miR169q | 565 | 652 | 625 | 467 | 602 |
| 9 | ata-miR169h-5p | 566 | 657 | 625 | 469 | 603 |
| 10 | bdi-miR169b | 566 | 657 | 625 | 469 | 603 |
| 11 | mes-miR169f | 566 | 657 | 625 | 469 | 603 |
| 12 | osa-miR169e | 566 | 657 | 625 | 469 | 603 |
| 13 | sbi-miR169e | 566 | 657 | 625 | 469 | 603 |
| 14 | sbi-miR169j | 566 | 657 | 625 | 469 | 603 |
| 15 | ssp-miR169 | 566 | 657 | 625 | 469 | 603 |
| 16 | zma-miR169p-5p | 566 | 657 | 625 | 469 | 603 |
| 17 | cme-miR168 | 953 | 1082 | 894 | 850 | 845 |
| 18 | bra-miR168b-5p | 965 | 1101 | 912 | 870 | 854 |
| 19 | bra-miR168c-5p | 965 | 1101 | 912 | 870 | 854 |
| 20 | nta-miR168a | 965 | 1101 | 912 | 870 | 854 |
| 21 | nta-miR168b | 965 | 1101 | 912 | 870 | 854 |
| 22 | nta-miR168c | 965 | 1101 | 912 | 870 | 854 |
| 23 | sly-miR168a-5p | 965 | 1101 | 912 | 870 | 854 |
| 24 | sly-miR168b-5p | 965 | 1101 | 912 | 870 | 854 |
| 25 | aof-miR167b | 10888 | 9933 | 10539 | 8743 | 9558 |
| 26 | ata-miR167b-5p | 10888 | 9933 | 10539 | 8743 | 9558 |
| 27 | ata-miR167d-5p | 10888 | 9933 | 10539 | 8743 | 9558 |
| 28 | bdi-miR167c-5p | 10888 | 9933 | 10539 | 8743 | 9558 |
| 29 | bdi-miR167d-5p | 10888 | 9933 | 10539 | 8743 | 9558 |
| 30 | bdi-miR167e-5p | 10888 | 9933 | 10539 | 8743 | 9558 |
| 31 | bdi-miR167g | 10888 | 9933 | 10539 | 8743 | 9558 |
| 32 | ccl-miR167a | 10888 | 9933 | 10539 | 8743 | 9558 |
| 33 | ccl-miR167b | 10888 | 9933 | 10539 | 8743 | 9558 |
| 34 | cpa-miR167d | 10888 | 9933 | 10539 | 8743 | 9558 |
| 35 | ctr-miR167 | 10888 | 9933 | 10539 | 8743 | 9558 |
| 36 | eun-miR167a-5p | 10888 | 9933 | 10539 | 8743 | 9558 |
| 37 | gma-miR167g | 10888 | 9933 | 10539 | 8743 | 9558 |
| 38 | mes-miR167d | 10888 | 9933 | 10539 | 8743 | 9558 |
| 39 | mes-miR167e | 10888 | 9933 | 10539 | 8743 | 9558 |
| 40 | mes-miR167f | 10888 | 9933 | 10539 | 8743 | 9558 |
| 41 | ppe-miR167c | 10888 | 9933 | 10539 | 8743 | 9558 |
| 42 | vca-miR167a-5p | 10888 | 9933 | 10539 | 8743 | 9558 |
| 43 | vca-miR167b-5p | 10888 | 9933 | 10539 | 8743 | 9558 |
| 44 | aof-miR167c | 10502 | 9647 | 10322 | 8511 | 9280 |
| 45 | atr-miR167 | 10502 | 9647 | 10322 | 8511 | 9280 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|------|-------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | cme-miR167d | 10502 | 9647 | 10322 | 8511 | 9280 |
| 4 | cme-miR167f | 10502 | 9647 | 10322 | 8511 | 9280 |
| 5 | csi-miR167a-5p | 10502 | 9647 | 10322 | 8511 | 9280 |
| 6 | csi-miR167c-5p | 10502 | 9647 | 10322 | 8511 | 9280 |
| 7 | dpr-miR167c | 10502 | 9647 | 10322 | 8511 | 9280 |
| 8 | gma-miR167c | 10502 | 9647 | 10322 | 8511 | 9280 |
| 9 | gma-miR167j | 10502 | 9647 | 10322 | 8511 | 9280 |
| 10 | gso-miR167a | 10502 | 9647 | 10322 | 8511 | 9280 |
| 11 | lja-miR167 | 10502 | 9647 | 10322 | 8511 | 9280 |
| 12 | lus-miR167f | 10502 | 9647 | 10322 | 8511 | 9280 |
| 13 | lus-miR167g | 10502 | 9647 | 10322 | 8511 | 9280 |
| 14 | lus-miR167i | 10502 | 9647 | 10322 | 8511 | 9280 |
| 15 | mes-miR167a | 10502 | 9647 | 10322 | 8511 | 9280 |
| 16 | mtr-miR167b-5p | 10502 | 9647 | 10322 | 8511 | 9280 |
| 17 | osa-miR167d-5p | 10502 | 9647 | 10322 | 8511 | 9280 |
| 18 | osa-miR167e-5p | 10502 | 9647 | 10322 | 8511 | 9280 |
| 19 | osa-miR167f | 10502 | 9647 | 10322 | 8511 | 9280 |
| 20 | osa-miR167g | 10502 | 9647 | 10322 | 8511 | 9280 |
| 21 | osa-miR167h-5p | 10502 | 9647 | 10322 | 8511 | 9280 |
| 22 | osa-miR167i-5p | 10502 | 9647 | 10322 | 8511 | 9280 |
| 23 | osa-miR167j | 10502 | 9647 | 10322 | 8511 | 9280 |
| 24 | ptc-miR167e | 10502 | 9647 | 10322 | 8511 | 9280 |
| 25 | sbi-miR167c | 10502 | 9647 | 10322 | 8511 | 9280 |
| 26 | sbi-miR167d | 10502 | 9647 | 10322 | 8511 | 9280 |
| 27 | sbi-miR167e | 10502 | 9647 | 10322 | 8511 | 9280 |
| 28 | sbi-miR167f | 10502 | 9647 | 10322 | 8511 | 9280 |
| 29 | sbi-miR167g | 10502 | 9647 | 10322 | 8511 | 9280 |
| 30 | sbi-miR167h | 10502 | 9647 | 10322 | 8511 | 9280 |
| 31 | sof-miR167a | 10502 | 9647 | 10322 | 8511 | 9280 |
| 32 | sof-miR167b | 10502 | 9647 | 10322 | 8511 | 9280 |
| 33 | ssp-miR167b | 10502 | 9647 | 10322 | 8511 | 9280 |
| 34 | vvi-miR167a | 10502 | 9647 | 10322 | 8511 | 9280 |
| 35 | zma-miR167e-5p | 10502 | 9647 | 10322 | 8511 | 9280 |
| 36 | zma-miR167f-5p | 10502 | 9647 | 10322 | 8511 | 9280 |
| 37 | zma-miR167g-5p | 10502 | 9647 | 10322 | 8511 | 9280 |
| 38 | zma-miR167h-5p | 10502 | 9647 | 10322 | 8511 | 9280 |
| 39 | zma-miR167i-5p | 10502 | 9647 | 10322 | 8511 | 9280 |
| 40 | zma-miR167j-5p | 10502 | 9647 | 10322 | 8511 | 9280 |
| 41 | aca-let-7b-5p | 28 | 71 | 150 | 47 | 82 |
| 42 | ggo-let-7b | 28 | 71 | 150 | 47 | 82 |
| 43 | ipu-let-7b | 28 | 71 | 150 | 47 | 82 |
| 44 | oar-let-7b | 28 | 71 | 150 | 47 | 82 |
| 45 | ola-let-7b | 28 | 71 | 150 | 47 | 82 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|------|-------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ata-miR167f-5p | 10504 | 9649 | 10324 | 8514 | 9284 |
| 4 | tae-miR167c-5p | 10504 | 9649 | 10324 | 8514 | 9284 |
| 5 | ppt-miR390c-5p | 278 | 325 | 186 | 285 | 168 |
| 6 | efu-miR-99a | 203 | 319 | 406 | 196 | 297 |
| 7 | aof-miR166b | 356 | 315 | 387 | 316 | 314 |
| 8 | csi-miR390b-5p | 275 | 324 | 186 | 285 | 167 |
| 9 | gma-miR390e | 275 | 324 | 186 | 285 | 167 |
| 10 | abu-miR-27b | 109 | 114 | 188 | 89 | 124 |
| 11 | bta-miR-27b | 109 | 114 | 188 | 89 | 124 |
| 12 | cfa-miR-27b | 109 | 114 | 188 | 89 | 124 |
| 13 | cgr-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 14 | chi-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 15 | cja-miR-27b | 109 | 114 | 188 | 89 | 124 |
| 16 | cli-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 17 | cpi-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 18 | cpo-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 19 | dno-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 20 | eca-miR-27b | 109 | 114 | 188 | 89 | 124 |
| 21 | gga-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 22 | ggo-miR-27b | 109 | 114 | 188 | 89 | 124 |
| 23 | hsa-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 24 | ipu-miR-27b | 109 | 114 | 188 | 89 | 124 |
| 25 | mdo-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 26 | mml-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 27 | mmr-miR-27b | 109 | 114 | 188 | 89 | 124 |
| 28 | mmu-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 29 | mze-miR-27b | 109 | 114 | 188 | 89 | 124 |
| 30 | nbr-miR-27b | 109 | 114 | 188 | 89 | 124 |
| 31 | oan-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 32 | ocu-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 33 | oni-miR-27b | 109 | 114 | 188 | 89 | 124 |
| 34 | pal-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 35 | pbv-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 36 | pma-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 37 | pony-miR-27b | 109 | 114 | 188 | 89 | 124 |
| 38 | ppa-miR-27b | 109 | 114 | 188 | 89 | 124 |
| 39 | ppy-miR-27b | 109 | 114 | 188 | 89 | 124 |
| 40 | ptr-miR-27b | 109 | 114 | 188 | 89 | 124 |
| 41 | rno-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 42 | sbo-miR-27b | 109 | 114 | 188 | 89 | 124 |
| 43 | sha-miR-27b | 109 | 114 | 188 | 89 | 124 |
| 44 | ssa-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 45 | ssc-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | tch-miR-27b-3p | 109 | 114 | 188 | 89 | 124 |
| 4 | tgu-miR-27-3p | 109 | 114 | 188 | 89 | 124 |
| 5 | xtr-miR-27b | 109 | 114 | 188 | 89 | 124 |
| 6 | aca-miR-27b-3p | 116 | 124 | 192 | 94 | 134 |
| 7 | aca-miR-27b-3p | 116 | 124 | 192 | 94 | 134 |
| 8 | aca-miR-27b-3p | 116 | 124 | 192 | 94 | 134 |
| 9 | aca-miR-27b-3p | 116 | 124 | 192 | 94 | 134 |
| 10 | aca-miR-27b-3p | 116 | 124 | 192 | 94 | 134 |
| 11 | aca-miR-27b-3p | 116 | 124 | 192 | 94 | 134 |
| 12 | aca-miR-27b-3p | 116 | 124 | 192 | 94 | 134 |
| 13 | aca-miR-27b-3p | 116 | 124 | 192 | 94 | 134 |
| 14 | aca-miR-27b-3p | 116 | 124 | 192 | 94 | 134 |
| 15 | efu-miR-378 | 167 | 180 | 151 | 115 | 162 |
| 16 | ggo-miR-378a | 166 | 180 | 151 | 115 | 162 |
| 17 | ggo-miR-378a | 166 | 180 | 151 | 115 | 162 |
| 18 | gma-miR169n-5p | 387 | 611 | 589 | 332 | 607 |
| 19 | mtr-miR169c | 387 | 611 | 589 | 332 | 607 |
| 20 | aca-miR-99a-5p | 201 | 311 | 402 | 194 | 294 |
| 21 | ami-miR-99a-5p | 201 | 311 | 402 | 194 | 294 |
| 22 | ami-miR-99a-5p | 201 | 311 | 402 | 194 | 294 |
| 23 | cli-miR-99-5p | 201 | 311 | 402 | 194 | 294 |
| 24 | cpi-miR-99a-5p | 201 | 311 | 402 | 194 | 294 |
| 25 | cpi-miR-99a-5p | 201 | 311 | 402 | 194 | 294 |
| 26 | cpo-miR-99a-5p | 201 | 311 | 402 | 194 | 294 |
| 27 | dno-miR-99a-5p | 201 | 311 | 402 | 194 | 294 |
| 28 | dre-miR-99 | 201 | 311 | 402 | 194 | 294 |
| 29 | dre-miR-99 | 201 | 311 | 402 | 194 | 294 |
| 30 | eca-miR-99a | 201 | 311 | 402 | 194 | 294 |
| 31 | gga-miR-99a-5p | 201 | 311 | 402 | 194 | 294 |
| 32 | ggo-miR-99a | 201 | 311 | 402 | 194 | 294 |
| 33 | ggo-miR-99a | 201 | 311 | 402 | 194 | 294 |
| 34 | gmo-miR-99-5p | 201 | 311 | 402 | 194 | 294 |
| 35 | hsa-miR-99a-5p | 201 | 311 | 402 | 194 | 294 |
| 36 | ipu-miR-99a | 201 | 311 | 402 | 194 | 294 |
| 37 | ipu-miR-99a | 201 | 311 | 402 | 194 | 294 |
| 38 | lla-miR-99a | 201 | 311 | 402 | 194 | 294 |
| 39 | mml-miR-99a-5p | 201 | 311 | 402 | 194 | 294 |
| 40 | mmr-miR-99a | 201 | 311 | 402 | 194 | 294 |
| 41 | mmr-miR-99a | 201 | 311 | 402 | 194 | 294 |
| 42 | mmu-miR-99a-5p | 201 | 311 | 402 | 194 | 294 |
| 43 | mne-miR-99a | 201 | 311 | 402 | 194 | 294 |
| 44 | mze-miR-99b | 201 | 311 | 402 | 194 | 294 |
| 45 | mze-miR-99b | 201 | 311 | 402 | 194 | 294 |
| 46 | nbr-miR-99b | 201 | 311 | 402 | 194 | 294 |
| 47 | ocu-miR-99a-5p | 201 | 311 | 402 | 194 | 294 |
| 48 | oga-miR-99a | 201 | 311 | 402 | 194 | 294 |
| 49 | oga-miR-99a | 201 | 311 | 402 | 194 | 294 |
| 50 | oha-miR-99a-5p | 201 | 311 | 402 | 194 | 294 |
| 51 | oni-miR-99b | 201 | 311 | 402 | 194 | 294 |
| 52 | pbv-miR-99a-5p | 201 | 311 | 402 | 194 | 294 |
| 53 | pha-miR-99a | 201 | 311 | 402 | 194 | 294 |
| 54 | pha-miR-99a | 201 | 311 | 402 | 194 | 294 |
| 55 | ppy-miR-99b | 201 | 311 | 402 | 194 | 294 |
| 56 | ppa-miR-99a | 201 | 311 | 402 | 194 | 294 |
| 57 | ppy-miR-99a | 201 | 311 | 402 | 194 | 294 |
| 58 | ppy-miR-99a | 201 | 311 | 402 | 194 | 294 |
| 59 | ptr-miR-99a | 201 | 311 | 402 | 194 | 294 |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | rno-miR-99a-5p | 201 | 311 | 402 | 194 | 294 |
| 4 | ssa-miR-99-5p | 201 | 311 | 402 | 194 | 294 |
| 5 | ssc-miR-99a-5p | 201 | 311 | 402 | 194 | 294 |
| 6 | tch-miR-99a-5p | 201 | 311 | 402 | 194 | 294 |
| 7 | xtr-miR-99 | 201 | 311 | 402 | 194 | 294 |
| 8 | | | | | | |
| 9 | bnm-miR167d | 7576 | 6868 | 7151 | 6109 | 6451 |
| 10 | fve-miR167a | 7576 | 6868 | 7151 | 6109 | 6451 |
| 11 | fve-miR167b | 7576 | 6868 | 7151 | 6109 | 6451 |
| 12 | fve-miR167c | 7576 | 6868 | 7151 | 6109 | 6451 |
| 13 | gma-miR167l | 7576 | 6868 | 7151 | 6109 | 6451 |
| 14 | lja-miR167a | 7576 | 6868 | 7151 | 6109 | 6451 |
| 15 | lja-miR167b | 7576 | 6868 | 7151 | 6109 | 6451 |
| 16 | lja-miR167c | 7576 | 6868 | 7151 | 6109 | 6451 |
| 17 | mes-miR167b | 7576 | 6868 | 7151 | 6109 | 6451 |
| 18 | lus-miR167a | 7648 | 6940 | 7218 | 6183 | 6514 |
| 19 | vvi-miR167c | 7648 | 6940 | 7218 | 6183 | 6514 |
| 20 | fve-miR167d | 7696 | 6976 | 7256 | 6211 | 6559 |
| 21 | aca-miR-191-5p | 250 | 146 | 156 | 119 | 176 |
| 22 | bta-miR-191 | 250 | 146 | 156 | 119 | 176 |
| 23 | cgr-miR-191-5p | 250 | 146 | 156 | 119 | 176 |
| 24 | cja-miR-191 | 250 | 146 | 156 | 119 | 176 |
| 25 | cpo-miR-191-5p | 250 | 146 | 156 | 119 | 176 |
| 26 | dma-miR-191 | 250 | 146 | 156 | 119 | 176 |
| 27 | dno-miR-191-5p | 250 | 146 | 156 | 119 | 176 |
| 28 | eca-miR-191a | 250 | 146 | 156 | 119 | 176 |
| 29 | gga-miR-191-5p | 250 | 146 | 156 | 119 | 176 |
| 30 | hsa-miR-191-5p | 250 | 146 | 156 | 119 | 176 |
| 31 | mml-miR-191-5p | 250 | 146 | 156 | 119 | 176 |
| 32 | mmr-miR-191 | 250 | 146 | 156 | 119 | 176 |
| 33 | mmu-miR-191-5p | 250 | 146 | 156 | 119 | 176 |
| 34 | nle-miR-191 | 250 | 146 | 156 | 119 | 176 |
| 35 | ocu-miR-191-5p | 250 | 146 | 156 | 119 | 176 |
| 36 | oga-miR-191 | 250 | 146 | 156 | 119 | 176 |
| 37 | oha-miR-191-5p | 250 | 146 | 156 | 119 | 176 |
| 38 | pbv-miR-191-5p | 250 | 146 | 156 | 119 | 176 |
| 39 | pha-miR-191 | 250 | 146 | 156 | 119 | 176 |
| 40 | ppa-miR-191 | 250 | 146 | 156 | 119 | 176 |
| 41 | ppy-miR-191 | 250 | 146 | 156 | 119 | 176 |
| 42 | ptr-miR-191 | 250 | 146 | 156 | 119 | 176 |
| 43 | rno-miR-191a-5p | 250 | 146 | 156 | 119 | 176 |
| 44 | sbo-miR-191 | 250 | 146 | 156 | 119 | 176 |
| 45 | ssc-miR-191 | 250 | 146 | 156 | 119 | 176 |
| 46 | bta-miR-378 | 166 | 179 | 151 | 115 | 162 |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | cfa-miR-378 | 166 | 179 | 151 | 115 | 162 |
| 4 | cgr-miR-378-3p | 166 | 179 | 151 | 115 | 162 |
| 5 | chi-miR-378-3p | 166 | 179 | 151 | 115 | 162 |
| 6 | cja-miR-378 | 166 | 179 | 151 | 115 | 162 |
| 7 | cja-miR-378 | 166 | 179 | 151 | 115 | 162 |
| 8 | cpo-miR-378-3p | 166 | 179 | 151 | 115 | 162 |
| 9 | dno-miR-378-3p | 166 | 179 | 151 | 115 | 162 |
| 10 | dno-miR-378-3p | 166 | 179 | 151 | 115 | 162 |
| 11 | hsa-miR-378a-3p | 166 | 179 | 151 | 115 | 162 |
| 12 | nle-miR-378a | 166 | 179 | 151 | 115 | 162 |
| 13 | nle-miR-378a | 166 | 179 | 151 | 115 | 162 |
| 14 | ocu-miR-378-3p | 166 | 179 | 151 | 115 | 162 |
| 15 | oga-miR-378 | 166 | 179 | 151 | 115 | 162 |
| 16 | pal-miR-378-3p | 166 | 179 | 151 | 115 | 162 |
| 17 | pal-miR-378-3p | 166 | 179 | 151 | 115 | 162 |
| 18 | pha-miR-378 | 166 | 179 | 151 | 115 | 162 |
| 19 | ppa-miR-378a | 166 | 179 | 151 | 115 | 162 |
| 20 | ssc-miR-378 | 166 | 179 | 151 | 115 | 162 |
| 21 | ssc-miR-378 | 166 | 179 | 151 | 115 | 162 |
| 22 | tch-miR-378a-3p | 166 | 179 | 151 | 115 | 162 |
| 23 | ipu-miR-99b | 220 | 333 | 441 | 213 | 320 |
| 24 | abu-miR-99b | 90 | 189 | 250 | 100 | 172 |
| 25 | abu-miR-99b | 90 | 189 | 250 | 100 | 172 |
| 26 | bta-miR-99a-5p | 90 | 189 | 250 | 100 | 172 |
| 27 | ccr-miR-99 | 90 | 189 | 250 | 100 | 172 |
| 28 | cfa-miR-99a | 90 | 189 | 250 | 100 | 172 |
| 29 | cfa-miR-99a | 90 | 189 | 250 | 100 | 172 |
| 30 | cgr-miR-99a-5p | 90 | 189 | 250 | 100 | 172 |
| 31 | chi-miR-99a-5p | 90 | 189 | 250 | 100 | 172 |
| 32 | chi-miR-99a-5p | 90 | 189 | 250 | 100 | 172 |
| 33 | cja-miR-99 | 90 | 189 | 250 | 100 | 172 |
| 34 | nle-miR-99a | 90 | 189 | 250 | 100 | 172 |
| 35 | oan-miR-99-5p | 90 | 189 | 250 | 100 | 172 |
| 36 | pal-miR-99a-5p | 90 | 189 | 250 | 100 | 172 |
| 37 | pal-miR-99a-5p | 90 | 189 | 250 | 100 | 172 |
| 38 | sbo-miR-99a | 90 | 189 | 250 | 100 | 172 |
| 39 | tgu-miR-99-5p | 90 | 189 | 250 | 100 | 172 |
| 40 | xla-miR-99-5p | 90 | 189 | 250 | 100 | 172 |
| 41 | xla-miR-99-5p | 90 | 189 | 250 | 100 | 172 |
| 42 | abu-miR-30d | 42 | 53 | 90 | 31 | 65 |
| 43 | aca-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 44 | ami-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 45 | ami-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 46 | bta-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 47 | ccr-miR-30b | 42 | 53 | 90 | 31 | 65 |
| 48 | cfa-miR-30b | 42 | 53 | 90 | 31 | 65 |
| 49 | cfa-miR-30b | 42 | 53 | 90 | 31 | 65 |
| 50 | cgr-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 51 | chi-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 52 | chi-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 53 | cja-miR-30b | 42 | 53 | 90 | 31 | 65 |
| 54 | cpi-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 55 | cpi-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 56 | cpo-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 57 | dno-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 58 | dre-miR-30b | 42 | 53 | 90 | 31 | 65 |
| 59 | eca-miR-30b | 42 | 53 | 90 | 31 | 65 |
| 60 | eca-miR-30b | 42 | 53 | 90 | 31 | 65 |

| | | | | | | |
|----|----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | fru-miR-30b | 42 | 53 | 90 | 31 | 65 |
| 4 | gga-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 5 | gmo-miR-30c-5p | 42 | 53 | 90 | 31 | 65 |
| 6 | gmo-miR-30c-5p | 42 | 53 | 90 | 31 | 65 |
| 7 | hsa-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 8 | ipu-miR-30b | 42 | 53 | 90 | 31 | 65 |
| 9 | ipu-miR-30b | 42 | 53 | 90 | 31 | 65 |
| 10 | mdo-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 11 | mmu-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 12 | mmu-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 13 | mze-miR-30d | 42 | 53 | 90 | 31 | 65 |
| 14 | nbr-miR-30d | 42 | 53 | 90 | 31 | 65 |
| 15 | nle-miR-30b | 42 | 53 | 90 | 31 | 65 |
| 16 | oan-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 17 | oan-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 18 | ocu-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 19 | oga-miR-30b | 42 | 53 | 90 | 31 | 65 |
| 20 | oha-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 21 | oha-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 22 | oni-miR-30d | 42 | 53 | 90 | 31 | 65 |
| 23 | pal-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 24 | pbv-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 25 | pbv-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 26 | ppy-miR-30d | 42 | 53 | 90 | 31 | 65 |
| 27 | ppy-miR-30b | 42 | 53 | 90 | 31 | 65 |
| 28 | rno-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 29 | rno-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 30 | ssa-miR-30e-5p | 42 | 53 | 90 | 31 | 65 |
| 31 | ssc-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 32 | tch-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 33 | tch-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 34 | tgu-miR-30e | 42 | 53 | 90 | 31 | 65 |
| 35 | tni-miR-30b | 42 | 53 | 90 | 31 | 65 |
| 36 | xla-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 37 | xla-miR-30b-5p | 42 | 53 | 90 | 31 | 65 |
| 38 | xtr-miR-30b | 42 | 53 | 90 | 31 | 65 |
| 39 | mdo-miR-22-3p | 55 | 48 | 121 | 42 | 82 |
| 40 | crt-miR166b | 1477 | 1442 | 1546 | 1462 | 1248 |
| 41 | crt-miR166b | 1477 | 1442 | 1546 | 1462 | 1248 |
| 42 | cas-miR166e | 1471 | 1437 | 1540 | 1457 | 1243 |
| 43 | csi-miR166f-3p | 1471 | 1437 | 1540 | 1457 | 1243 |
| 44 | osa-miR166m | 1471 | 1437 | 1540 | 1457 | 1243 |
| 45 | osa-miR166m | 1471 | 1437 | 1540 | 1457 | 1243 |
| 46 | aly-miR166a-5p | 5486 | 4533 | 6616 | 5391 | 4363 |
| 47 | aly-miR166c-5p | 5486 | 4533 | 6616 | 5391 | 4363 |
| 48 | aly-miR166d-5p | 5486 | 4533 | 6616 | 5391 | 4363 |
| 49 | aly-miR166d-5p | 5486 | 4533 | 6616 | 5391 | 4363 |
| 50 | bdi-miR166e-5p | 5486 | 4533 | 6616 | 5391 | 4363 |
| 51 | cas-miR166a | 5486 | 4533 | 6616 | 5391 | 4363 |
| 52 | csi-miR166a-5p | 5486 | 4533 | 6616 | 5391 | 4363 |
| 53 | csi-miR166a-5p | 5486 | 4533 | 6616 | 5391 | 4363 |
| 54 | csi-miR166e-5p | 5486 | 4533 | 6616 | 5391 | 4363 |
| 55 | eun-miR166-5p | 5486 | 4533 | 6616 | 5391 | 4363 |
| 56 | gma-miR166a-5p | 5486 | 4533 | 6616 | 5391 | 4363 |
| 57 | gma-miR166c-5p | 5486 | 4533 | 6616 | 5391 | 4363 |
| 58 | gma-miR166c-5p | 5486 | 4533 | 6616 | 5391 | 4363 |
| 59 | gma-miR166l | 5486 | 4533 | 6616 | 5391 | 4363 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | mtr-miR166g-5p | 5486 | 4533 | 6616 | 5391 | 4363 |
| 4 | osa-miR166d-5p | 5486 | 4533 | 6616 | 5391 | 4363 |
| 5 | stu-miR166a-5p | 5486 | 4533 | 6616 | 5391 | 4363 |
| 6 | vca-miR166b-5p | 5486 | 4533 | 6616 | 5391 | 4363 |
| 7 | zma-miR166c-5p | 5486 | 4533 | 6616 | 5391 | 4363 |
| 8 | | | | | | |
| 9 | gma-miR169d | 678 | 740 | 699 | 522 | 697 |
| 10 | | | | | | |
| 11 | aly-miR167d-5p | 14528 | 13834 | 15655 | 12374 | 13711 |
| 12 | ath-miR167d | 14528 | 13834 | 15655 | 12374 | 13711 |
| 13 | cca-miR167 | 14528 | 13834 | 15655 | 12374 | 13711 |
| 14 | eun-miR167b-5p | 14528 | 13834 | 15655 | 12374 | 13711 |
| 15 | nta-miR167a | 14528 | 13834 | 15655 | 12374 | 13711 |
| 16 | nta-miR167b | 14528 | 13834 | 15655 | 12374 | 13711 |
| 17 | nta-miR167c | 14528 | 13834 | 15655 | 12374 | 13711 |
| 18 | pab-miR167b | 14528 | 13834 | 15655 | 12374 | 13711 |
| 19 | rco-miR167c | 14528 | 13834 | 15655 | 12374 | 13711 |
| 20 | mes-miR394c | 20373 | 13190 | 6876 | 10560 | 9404 |
| 21 | vvi-miR394a | 20373 | 13190 | 6876 | 10560 | 9404 |
| 22 | vvi-miR394c | 20373 | 13190 | 6876 | 10560 | 9404 |
| 23 | ahy-miR394 | 20361 | 13174 | 6869 | 10551 | 9394 |
| 24 | aly-miR394a-5p | 20361 | 13174 | 6869 | 10551 | 9394 |
| 25 | aly-miR394b-5p | 20361 | 13174 | 6869 | 10551 | 9394 |
| 26 | aof-miR394 | 20361 | 13174 | 6869 | 10551 | 9394 |
| 27 | ata-miR394-5p | 20361 | 13174 | 6869 | 10551 | 9394 |
| 28 | ath-miR394a | 20361 | 13174 | 6869 | 10551 | 9394 |
| 29 | ath-miR394b-5p | 20361 | 13174 | 6869 | 10551 | 9394 |
| 30 | atr-miR394 | 20361 | 13174 | 6869 | 10551 | 9394 |
| 31 | bdi-miR394 | 20361 | 13174 | 6869 | 10551 | 9394 |
| 32 | bna-miR394a | 20361 | 13174 | 6869 | 10551 | 9394 |
| 33 | bna-miR394b | 20361 | 13174 | 6869 | 10551 | 9394 |
| 34 | cca-miR394 | 20361 | 13174 | 6869 | 10551 | 9394 |
| 35 | cme-miR394a | 20361 | 13174 | 6869 | 10551 | 9394 |
| 36 | cme-miR394b | 20361 | 13174 | 6869 | 10551 | 9394 |
| 37 | cpa-miR394a | 20361 | 13174 | 6869 | 10551 | 9394 |
| 38 | cpa-miR394b | 20361 | 13174 | 6869 | 10551 | 9394 |
| 39 | csi-miR394a | 20361 | 13174 | 6869 | 10551 | 9394 |
| 40 | csi-miR394b-5p | 20361 | 13174 | 6869 | 10551 | 9394 |
| 41 | fve-miR394 | 20361 | 13174 | 6869 | 10551 | 9394 |
| 42 | ghr-miR394a | 20361 | 13174 | 6869 | 10551 | 9394 |
| 43 | ghr-miR394b | 20361 | 13174 | 6869 | 10551 | 9394 |
| 44 | gma-miR394a-5p | 20361 | 13174 | 6869 | 10551 | 9394 |
| 45 | gma-miR394b-5p | 20361 | 13174 | 6869 | 10551 | 9394 |
| 46 | gma-miR394c-5p | 20361 | 13174 | 6869 | 10551 | 9394 |
| 47 | gma-miR394d | 20361 | 13174 | 6869 | 10551 | 9394 |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | gma-miR394e | 20361 | 13174 | 6869 | 10551 | 9394 |
| 4 | gma-miR394f | 20361 | 13174 | 6869 | 10551 | 9394 |
| 5 | gma-miR394g | 20361 | 13174 | 6869 | 10551 | 9394 |
| 6 | lus-miR394a | 20361 | 13174 | 6869 | 10551 | 9394 |
| 7 | lus-miR394b | 20361 | 13174 | 6869 | 10551 | 9394 |
| 8 | mdm-miR394a | 20361 | 13174 | 6869 | 10551 | 9394 |
| 9 | mdm-miR394b | 20361 | 13174 | 6869 | 10551 | 9394 |
| 10 | mes-miR394a | 20361 | 13174 | 6869 | 10551 | 9394 |
| 11 | mes-miR394b | 20361 | 13174 | 6869 | 10551 | 9394 |
| 12 | mes-miR394c | 20361 | 13174 | 6869 | 10551 | 9394 |
| 13 | mes-miR394d | 20361 | 13174 | 6869 | 10551 | 9394 |
| 14 | mes-miR394e | 20361 | 13174 | 6869 | 10551 | 9394 |
| 15 | mes-miR394f | 20361 | 13174 | 6869 | 10551 | 9394 |
| 16 | mes-miR394g | 20361 | 13174 | 6869 | 10551 | 9394 |
| 17 | mes-miR394h | 20361 | 13174 | 6869 | 10551 | 9394 |
| 18 | mes-miR394i | 20361 | 13174 | 6869 | 10551 | 9394 |
| 19 | mes-miR394j | 20361 | 13174 | 6869 | 10551 | 9394 |
| 20 | mes-miR394k | 20361 | 13174 | 6869 | 10551 | 9394 |
| 21 | mes-miR394l | 20361 | 13174 | 6869 | 10551 | 9394 |
| 22 | mes-miR394m | 20361 | 13174 | 6869 | 10551 | 9394 |
| 23 | mes-miR394n | 20361 | 13174 | 6869 | 10551 | 9394 |
| 24 | mes-miR394o | 20361 | 13174 | 6869 | 10551 | 9394 |
| 25 | mes-miR394p | 20361 | 13174 | 6869 | 10551 | 9394 |
| 26 | mes-miR394q | 20361 | 13174 | 6869 | 10551 | 9394 |
| 27 | mes-miR394r | 20361 | 13174 | 6869 | 10551 | 9394 |
| 28 | mes-miR394s | 20361 | 13174 | 6869 | 10551 | 9394 |
| 29 | mes-miR394t | 20361 | 13174 | 6869 | 10551 | 9394 |
| 30 | mes-miR394u | 20361 | 13174 | 6869 | 10551 | 9394 |
| 31 | mes-miR394v | 20361 | 13174 | 6869 | 10551 | 9394 |
| 32 | mes-miR394w | 20361 | 13174 | 6869 | 10551 | 9394 |
| 33 | mes-miR394x | 20361 | 13174 | 6869 | 10551 | 9394 |
| 34 | mes-miR394y | 20361 | 13174 | 6869 | 10551 | 9394 |
| 35 | mes-miR394z | 20361 | 13174 | 6869 | 10551 | 9394 |
| 36 | osa-miR394 | 20361 | 13174 | 6869 | 10551 | 9394 |
| 37 | pab-miR394c | 20361 | 13174 | 6869 | 10551 | 9394 |
| 38 | ppe-miR394a | 20361 | 13174 | 6869 | 10551 | 9394 |
| 39 | ppe-miR394b | 20361 | 13174 | 6869 | 10551 | 9394 |
| 40 | ptc-miR394a-5p | 20361 | 13174 | 6869 | 10551 | 9394 |
| 41 | ptc-miR394b-5p | 20361 | 13174 | 6869 | 10551 | 9394 |
| 42 | sbi-miR394a | 20361 | 13174 | 6869 | 10551 | 9394 |
| 43 | sbi-miR394b | 20361 | 13174 | 6869 | 10551 | 9394 |
| 44 | sly-miR394-5p | 20361 | 13174 | 6869 | 10551 | 9394 |
| 45 | ssl-miR394 | 20361 | 13174 | 6869 | 10551 | 9394 |
| 46 | stu-miR384-5p | 20361 | 13174 | 6869 | 10551 | 9394 |
| 47 | tcc-miR394a | 20361 | 13174 | 6869 | 10551 | 9394 |
| 48 | tcc-miR394b | 20361 | 13174 | 6869 | 10551 | 9394 |
| 49 | vvi-miR394b | 20361 | 13174 | 6869 | 10551 | 9394 |
| 50 | zma-miR394a-5p | 20361 | 13174 | 6869 | 10551 | 9394 |
| 51 | zma-miR394b-5p | 20361 | 13174 | 6869 | 10551 | 9394 |
| 52 | aly-miR396a-3p | 248 | 215 | 161 | 180 | 207 |
| 53 | ath-miR396a-3p | 248 | 215 | 161 | 180 | 207 |
| 54 | csi-miR396b-3p | 248 | 215 | 161 | 180 | 207 |
| 55 | eun-miR396a-3p | 248 | 215 | 161 | 180 | 207 |
| 56 | fve-miR396a-3p | 248 | 215 | 161 | 180 | 207 |
| 57 | fve-miR396c-3p | 248 | 215 | 161 | 180 | 207 |
| 58 | gma-miR396i-3p | 248 | 215 | 161 | 180 | 207 |
| 59 | mtr-miR396b-3p | 248 | 215 | 161 | 180 | 207 |
| 60 | sly-miR396a-3p | 248 | 215 | 161 | 180 | 207 |
| 61 | cas-miR394 | 20411 | 13198 | 6897 | 10582 | 9441 |
| 62 | bna-miR167a | 13781 | 13587 | 11418 | 10576 | 12688 |
| 63 | bna-miR167b | 13781 | 13587 | 11418 | 10576 | 12688 |
| 64 | aly-miR167a-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 65 | aly-miR167b-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 66 | aof-miR167a | 13768 | 13581 | 11415 | 10571 | 12683 |
| 67 | ata-miR167a-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 68 | ata-miR167c-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 69 | | | | | | |
| 70 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ata-miR167e-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 4 | ath-miR167a-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 5 | ath-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 6 | ath-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 7 | bdi-miR167a | 13768 | 13581 | 11415 | 10571 | 12683 |
| 8 | bdi-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 9 | bdi-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 10 | bdi-miR167f | 13768 | 13581 | 11415 | 10571 | 12683 |
| 11 | bna-miR167c | 13768 | 13581 | 11415 | 10571 | 12683 |
| 12 | bra-miR167a | 13768 | 13581 | 11415 | 10571 | 12683 |
| 13 | bra-miR167a | 13768 | 13581 | 11415 | 10571 | 12683 |
| 14 | bra-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 15 | bra-miR167c | 13768 | 13581 | 11415 | 10571 | 12683 |
| 16 | bra-miR167c | 13768 | 13581 | 11415 | 10571 | 12683 |
| 17 | bra-miR167d | 13768 | 13581 | 11415 | 10571 | 12683 |
| 18 | cme-miR167a | 13768 | 13581 | 11415 | 10571 | 12683 |
| 19 | cme-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 20 | cpa-miR167a | 13768 | 13581 | 11415 | 10571 | 12683 |
| 21 | cpa-miR167a | 13768 | 13581 | 11415 | 10571 | 12683 |
| 22 | cpa-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 23 | csi-miR167d-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 24 | csi-miR167e-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 25 | csi-miR167e-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 26 | dpr-miR167a | 13768 | 13581 | 11415 | 10571 | 12683 |
| 27 | dpr-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 28 | dpr-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 29 | ghr-miR167a | 13768 | 13581 | 11415 | 10571 | 12683 |
| 30 | ghr-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 31 | ghr-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 32 | gma-miR167a | 13768 | 13581 | 11415 | 10571 | 12683 |
| 33 | gma-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 34 | gma-miR167d | 13768 | 13581 | 11415 | 10571 | 12683 |
| 35 | lus-miR167c | 13768 | 13581 | 11415 | 10571 | 12683 |
| 36 | lus-miR167d | 13768 | 13581 | 11415 | 10571 | 12683 |
| 37 | lus-miR167d | 13768 | 13581 | 11415 | 10571 | 12683 |
| 38 | lus-miR167e | 13768 | 13581 | 11415 | 10571 | 12683 |
| 39 | lus-miR167h | 13768 | 13581 | 11415 | 10571 | 12683 |
| 40 | mdm-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 41 | mdm-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 42 | mdm-miR167c | 13768 | 13581 | 11415 | 10571 | 12683 |
| 43 | mdm-miR167d | 13768 | 13581 | 11415 | 10571 | 12683 |
| 44 | mdm-miR167d | 13768 | 13581 | 11415 | 10571 | 12683 |
| 45 | mdm-miR167e | 13768 | 13581 | 11415 | 10571 | 12683 |
| 46 | mdm-miR167f | 13768 | 13581 | 11415 | 10571 | 12683 |
| 47 | mdm-miR167g | 13768 | 13581 | 11415 | 10571 | 12683 |
| 48 | mdm-miR167g | 13768 | 13581 | 11415 | 10571 | 12683 |
| 49 | mes-miR167c | 13768 | 13581 | 11415 | 10571 | 12683 |
| 50 | mtr-miR167a | 13768 | 13581 | 11415 | 10571 | 12683 |
| 51 | nta-miR167d | 13768 | 13581 | 11415 | 10571 | 12683 |
| 52 | nta-miR167d | 13768 | 13581 | 11415 | 10571 | 12683 |
| 53 | nta-miR167e | 13768 | 13581 | 11415 | 10571 | 12683 |
| 54 | osa-miR167a-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 55 | osa-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 56 | osa-miR167c-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 57 | osa-miR167c-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 58 | ppe-miR167a | 13768 | 13581 | 11415 | 10571 | 12683 |
| 59 | ppe-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|--------|-------|--------|--------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ptc-miR167a | 13768 | 13581 | 11415 | 10571 | 12683 |
| 4 | ptc-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 5 | ptc-miR167c | 13768 | 13581 | 11415 | 10571 | 12683 |
| 6 | ptc-miR167d | 13768 | 13581 | 11415 | 10571 | 12683 |
| 7 | ptc-miR167d | 13768 | 13581 | 11415 | 10571 | 12683 |
| 8 | rco-miR167a | 13768 | 13581 | 11415 | 10571 | 12683 |
| 9 | rco-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 10 | rco-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 11 | sbi-miR167a | 13768 | 13581 | 11415 | 10571 | 12683 |
| 12 | sbi-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 13 | sbi-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 14 | sbi-miR167i | 13768 | 13581 | 11415 | 10571 | 12683 |
| 15 | sly-miR167a | 13768 | 13581 | 11415 | 10571 | 12683 |
| 16 | stu-miR167a-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 17 | stu-miR167a-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 18 | stu-miR167b-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 19 | stu-miR167c-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 20 | stu-miR167d-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 21 | stu-miR167d-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 22 | tae-miR167a | 13768 | 13581 | 11415 | 10571 | 12683 |
| 23 | tcc-miR167a | 13768 | 13581 | 11415 | 10571 | 12683 |
| 24 | tcc-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 25 | tcc-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 26 | vvi-miR167b | 13768 | 13581 | 11415 | 10571 | 12683 |
| 27 | vvi-miR167d | 13768 | 13581 | 11415 | 10571 | 12683 |
| 28 | vvi-miR167e | 13768 | 13581 | 11415 | 10571 | 12683 |
| 29 | vvi-miR167e | 13768 | 13581 | 11415 | 10571 | 12683 |
| 30 | zma-miR167a-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 31 | zma-miR167b-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 32 | zma-miR167c-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 33 | zma-miR167c-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 34 | zma-miR167d-5p | 13768 | 13581 | 11415 | 10571 | 12683 |
| 35 | efu-miR-27b | 118 | 125 | 193 | 96 | 138 |
| 36 | gma-miR166u | 276 | 242 | 308 | 248 | 245 |
| 37 | gma-miR166u | 276 | 242 | 308 | 248 | 245 |
| 38 | ami-miR-191-5p | 140 | 88 | 106 | 70 | 105 |
| 39 | cfa-miR-191 | 140 | 88 | 106 | 70 | 105 |
| 40 | chi-miR-191-5p | 140 | 88 | 106 | 70 | 105 |
| 41 | chi-miR-191-5p | 140 | 88 | 106 | 70 | 105 |
| 42 | cpi-miR-191-5p | 140 | 88 | 106 | 70 | 105 |
| 43 | mdo-miR-191-5p | 140 | 88 | 106 | 70 | 105 |
| 44 | oan-miR-191-5p | 140 | 88 | 106 | 70 | 105 |
| 45 | oan-miR-191-5p | 140 | 88 | 106 | 70 | 105 |
| 46 | oar-miR-191 | 140 | 88 | 106 | 70 | 105 |
| 47 | pal-miR-191-5p | 140 | 88 | 106 | 70 | 105 |
| 48 | tch-miR-191-5p | 140 | 88 | 106 | 70 | 105 |
| 49 | tch-miR-191-5p | 140 | 88 | 106 | 70 | 105 |
| 50 | xla-miR-191-5p | 140 | 88 | 106 | 70 | 105 |
| 51 | xtr-miR-191 | 140 | 88 | 106 | 70 | 105 |
| 52 | aly-miR166a-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 53 | aly-miR166b-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 54 | aly-miR166b-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 55 | aly-miR166c-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 56 | aly-miR166d-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 57 | aly-miR166d-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 58 | aly-miR166e-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 59 | aly-miR166f-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|--------|-------|--------|--------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | aly-miR166g-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 4 | aly-miR166h-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 5 | aof-miR166d | 117790 | 98898 | 110407 | 105198 | 91820 |
| 6 | aqc-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 7 | aqc-miR166e | 117790 | 98898 | 110407 | 105198 | 91820 |
| 8 | ata-miR166a-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 9 | ata-miR166b-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 10 | ata-miR166d-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 11 | ata-miR166e-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 12 | ath-miR166a-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 13 | ath-miR166b-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 14 | ath-miR166c | 117790 | 98898 | 110407 | 105198 | 91820 |
| 15 | ath-miR166d | 117790 | 98898 | 110407 | 105198 | 91820 |
| 16 | ath-miR166e-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 17 | ath-miR166f | 117790 | 98898 | 110407 | 105198 | 91820 |
| 18 | ath-miR166g | 117790 | 98898 | 110407 | 105198 | 91820 |
| 19 | atr-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 20 | atr-miR166c | 117790 | 98898 | 110407 | 105198 | 91820 |
| 21 | gma-miR166i-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 22 | hpa-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 23 | hpe-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 24 | hvu-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 25 | hvu-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 26 | hvu-miR166c | 117790 | 98898 | 110407 | 105198 | 91820 |
| 27 | lus-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 28 | lus-miR166c | 117790 | 98898 | 110407 | 105198 | 91820 |
| 29 | lus-miR166d | 117790 | 98898 | 110407 | 105198 | 91820 |
| 30 | lus-miR166g | 117790 | 98898 | 110407 | 105198 | 91820 |
| 31 | lus-miR166h | 117790 | 98898 | 110407 | 105198 | 91820 |
| 32 | lus-miR166j | 117790 | 98898 | 110407 | 105198 | 91820 |
| 33 | mdm-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 34 | mdm-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 35 | mdm-miR166c | 117790 | 98898 | 110407 | 105198 | 91820 |
| 36 | mdm-miR166d | 117790 | 98898 | 110407 | 105198 | 91820 |
| 37 | mdm-miR166e | 117790 | 98898 | 110407 | 105198 | 91820 |
| 38 | mdm-miR166f | 117790 | 98898 | 110407 | 105198 | 91820 |
| 39 | mdm-miR166h | 117790 | 98898 | 110407 | 105198 | 91820 |
| 40 | mdm-miR166i | 117790 | 98898 | 110407 | 105198 | 91820 |
| 41 | mdm-miR166j | 117790 | 98898 | 110407 | 105198 | 91820 |
| 42 | mes-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 43 | mes-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 44 | mtr-miR166g-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 45 | nta-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|--------|-------|--------|--------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | nta-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 4 | osa-miR166b-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 5 | osa-miR166c-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 6 | osa-miR166c-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 7 | rco-miR166c | 117790 | 98898 | 110407 | 105198 | 91820 |
| 8 | atr-miR166d | 117790 | 98898 | 110407 | 105198 | 91820 |
| 9 | atr-miR166d | 117790 | 98898 | 110407 | 105198 | 91820 |
| 10 | bdi-miR166a-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 11 | bdi-miR166b-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 12 | bdi-miR166b-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 13 | bdi-miR166c-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 14 | bdi-miR166c-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 15 | bdi-miR166d-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 16 | bdi-miR166d-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 17 | bdi-miR166i-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 18 | bna-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 19 | bna-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 20 | bna-miR166c | 117790 | 98898 | 110407 | 105198 | 91820 |
| 21 | bna-miR166d | 117790 | 98898 | 110407 | 105198 | 91820 |
| 22 | bna-miR166e | 117790 | 98898 | 110407 | 105198 | 91820 |
| 23 | bna-miR166e | 117790 | 98898 | 110407 | 105198 | 91820 |
| 24 | cme-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 25 | cme-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 26 | cme-miR166c | 117790 | 98898 | 110407 | 105198 | 91820 |
| 27 | cme-miR166c | 117790 | 98898 | 110407 | 105198 | 91820 |
| 28 | cme-miR166d | 117790 | 98898 | 110407 | 105198 | 91820 |
| 29 | cme-miR166f | 117790 | 98898 | 110407 | 105198 | 91820 |
| 30 | cme-miR166h | 117790 | 98898 | 110407 | 105198 | 91820 |
| 31 | cpa-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 32 | cpa-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 33 | cpa-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 34 | cpa-miR166c | 117790 | 98898 | 110407 | 105198 | 91820 |
| 35 | csi-miR166e-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 36 | dpr-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 37 | dpr-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 38 | eun-miR166-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 39 | fve-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 40 | fve-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 41 | fve-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 42 | fve-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 43 | fve-miR166c | 117790 | 98898 | 110407 | 105198 | 91820 |
| 44 | fve-miR166d-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 45 | fve-miR166e | 117790 | 98898 | 110407 | 105198 | 91820 |
| 46 | fve-miR166e | 117790 | 98898 | 110407 | 105198 | 91820 |
| 47 | fve-miR166f | 117790 | 98898 | 110407 | 105198 | 91820 |
| 48 | ghr-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 49 | gma-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 50 | gma-miR166a-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 51 | gma-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 52 | gma-miR166c-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 53 | gma-miR166d | 117790 | 98898 | 110407 | 105198 | 91820 |
| 54 | gma-miR166d | 117790 | 98898 | 110407 | 105198 | 91820 |
| 55 | gma-miR166e | 117790 | 98898 | 110407 | 105198 | 91820 |
| 56 | gma-miR166f | 117790 | 98898 | 110407 | 105198 | 91820 |
| 57 | gma-miR166f | 117790 | 98898 | 110407 | 105198 | 91820 |
| 58 | gma-miR166g | 117790 | 98898 | 110407 | 105198 | 91820 |
| 59 | gma-miR166g | 117790 | 98898 | 110407 | 105198 | 91820 |
| 60 | gma-miR166n | 117790 | 98898 | 110407 | 105198 | 91820 |
| | gma-miR166o | 117790 | 98898 | 110407 | 105198 | 91820 |

| | | | | | | |
|----|----------------|--------|-------|--------|--------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | mdm-miR166g | 117790 | 98898 | 110407 | 105198 | 91820 |
| 4 | mes-miR166c | 117790 | 98898 | 110407 | 105198 | 91820 |
| 5 | mes-miR166d | 117790 | 98898 | 110407 | 105198 | 91820 |
| 6 | mes-miR166e | 117790 | 98898 | 110407 | 105198 | 91820 |
| 7 | mes-miR166f | 117790 | 98898 | 110407 | 105198 | 91820 |
| 8 | mes-miR166g | 117790 | 98898 | 110407 | 105198 | 91820 |
| 9 | mtr-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 10 | mtr-miR166e-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 11 | nta-miR166c | 117790 | 98898 | 110407 | 105198 | 91820 |
| 12 | nta-miR166d | 117790 | 98898 | 110407 | 105198 | 91820 |
| 13 | nta-miR166e | 117790 | 98898 | 110407 | 105198 | 91820 |
| 14 | nta-miR166f | 117790 | 98898 | 110407 | 105198 | 91820 |
| 15 | nta-miR166g | 117790 | 98898 | 110407 | 105198 | 91820 |
| 16 | nta-miR166h | 117790 | 98898 | 110407 | 105198 | 91820 |
| 17 | osa-miR166a-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 18 | osa-miR166d-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 19 | osa-miR166f | 117790 | 98898 | 110407 | 105198 | 91820 |
| 20 | osa-miR166j-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 21 | pab-miR166f | 117790 | 98898 | 110407 | 105198 | 91820 |
| 22 | pab-miR166g | 117790 | 98898 | 110407 | 105198 | 91820 |
| 23 | pab-miR166h | 117790 | 98898 | 110407 | 105198 | 91820 |
| 24 | pab-miR166i | 117790 | 98898 | 110407 | 105198 | 91820 |
| 25 | ppe-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 26 | ppe-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 27 | ppe-miR166c | 117790 | 98898 | 110407 | 105198 | 91820 |
| 28 | ppe-miR166d | 117790 | 98898 | 110407 | 105198 | 91820 |
| 29 | ppe-miR166e | 117790 | 98898 | 110407 | 105198 | 91820 |
| 30 | ppt-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 31 | ppt-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 32 | ppt-miR166c | 117790 | 98898 | 110407 | 105198 | 91820 |
| 33 | ppt-miR166d | 117790 | 98898 | 110407 | 105198 | 91820 |
| 34 | ppt-miR166e | 117790 | 98898 | 110407 | 105198 | 91820 |
| 35 | ppt-miR166f | 117790 | 98898 | 110407 | 105198 | 91820 |
| 36 | ppt-miR166g | 117790 | 98898 | 110407 | 105198 | 91820 |
| 37 | ppt-miR166h | 117790 | 98898 | 110407 | 105198 | 91820 |
| 38 | ppt-miR166i | 117790 | 98898 | 110407 | 105198 | 91820 |
| 39 | pta-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 40 | pta-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 41 | ptc-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 42 | ptc-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 43 | ptc-miR166c | 117790 | 98898 | 110407 | 105198 | 91820 |
| 44 | ptc-miR166d | 117790 | 98898 | 110407 | 105198 | 91820 |
| 45 | ptc-miR166e | 117790 | 98898 | 110407 | 105198 | 91820 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|--------|-------|--------|--------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ptc-miR166f | 117790 | 98898 | 110407 | 105198 | 91820 |
| 4 | ptc-miR166g | 117790 | 98898 | 110407 | 105198 | 91820 |
| 5 | ptc-miR166h | 117790 | 98898 | 110407 | 105198 | 91820 |
| 6 | ptc-miR166i | 117790 | 98898 | 110407 | 105198 | 91820 |
| 7 | ptc-miR166j | 117790 | 98898 | 110407 | 105198 | 91820 |
| 8 | ptc-miR166k | 117790 | 98898 | 110407 | 105198 | 91820 |
| 9 | ptc-miR166l | 117790 | 98898 | 110407 | 105198 | 91820 |
| 10 | ptc-miR166m | 117790 | 98898 | 110407 | 105198 | 91820 |
| 11 | pvu-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 12 | rco-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 13 | rco-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 14 | rco-miR166d | 117790 | 98898 | 110407 | 105198 | 91820 |
| 15 | rco-miR166e | 117790 | 98898 | 110407 | 105198 | 91820 |
| 16 | sly-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 17 | sly-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 18 | smo-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 19 | smo-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 20 | smo-miR166c | 117790 | 98898 | 110407 | 105198 | 91820 |
| 21 | ssl-miR166b | 117790 | 98898 | 110407 | 105198 | 91820 |
| 22 | ssp-miR166 | 117790 | 98898 | 110407 | 105198 | 91820 |
| 23 | stu-miR166a-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 24 | stu-miR166c-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 25 | stu-miR166d-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 26 | tcc-miR166a | 117790 | 98898 | 110407 | 105198 | 91820 |
| 27 | tcc-miR166d | 117790 | 98898 | 110407 | 105198 | 91820 |
| 28 | vca-miR166a-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 29 | vca-miR166b-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 30 | vca-miR166c-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 31 | vvi-miR166c | 117790 | 98898 | 110407 | 105198 | 91820 |
| 32 | vvi-miR166d | 117790 | 98898 | 110407 | 105198 | 91820 |
| 33 | vvi-miR166e | 117790 | 98898 | 110407 | 105198 | 91820 |
| 34 | vvi-miR166f | 117790 | 98898 | 110407 | 105198 | 91820 |
| 35 | vvi-miR166g | 117790 | 98898 | 110407 | 105198 | 91820 |
| 36 | vvi-miR166h | 117790 | 98898 | 110407 | 105198 | 91820 |
| 37 | zma-miR166a-3p | 117790 | 98898 | 110407 | 105198 | 91820 |
| 38 | csi-miR166a-3p | 117813 | 98934 | 110449 | 105238 | 91846 |
| 39 | ctr-miR166 | 117813 | 98934 | 110449 | 105238 | 91846 |
| 40 | hbr-miR166b | 117813 | 98934 | 110449 | 105238 | 91846 |
| 41 | lus-miR166i | 117813 | 98934 | 110449 | 105238 | 91846 |
| 42 | lus-miR166k | 117813 | 98934 | 110449 | 105238 | 91846 |
| 43 | cas-miR166c-3p | 118539 | 99568 | 111102 | 105947 | 92546 |
| 44 | cas-miR166d | 118539 | 99568 | 111102 | 105947 | 92546 |
| 45 | cas-miR166f-3p | 118539 | 99568 | 111102 | 105947 | 92546 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|--------|--------|--------|--------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | lja-miR166-3p | 122067 | 102434 | 113916 | 109193 | 95425 |
| 4 | bta-miR-22-3p | 51 | 45 | 113 | 42 | 74 |
| 5 | ggo-miR-22 | 51 | 45 | 113 | 42 | 74 |
| 6 | oar-miR-22-3p | 51 | 45 | 113 | 42 | 74 |
| 7 | abu-miR-499 | 79 | 68 | 58 | 44 | 65 |
| 8 | aca-miR-499-5p | 79 | 68 | 58 | 44 | 65 |
| 9 | cca-miR-499 | 79 | 68 | 58 | 44 | 65 |
| 10 | ccr-miR-499 | 79 | 68 | 58 | 44 | 65 |
| 11 | cgr-miR-499-5p | 79 | 68 | 58 | 44 | 65 |
| 12 | cpi-miR-499-5p | 79 | 68 | 58 | 44 | 65 |
| 13 | cpo-miR-499-5p | 79 | 68 | 58 | 44 | 65 |
| 14 | dno-miR-499-5p | 79 | 68 | 58 | 44 | 65 |
| 15 | dre-miR-499-5p | 79 | 68 | 58 | 44 | 65 |
| 16 | gmo-miR-499-5p | 79 | 68 | 58 | 44 | 65 |
| 17 | mze-miR-499 | 79 | 68 | 58 | 44 | 65 |
| 18 | nbr-miR-499 | 79 | 68 | 58 | 44 | 65 |
| 19 | ocu-miR-499-5p | 79 | 68 | 58 | 44 | 65 |
| 20 | oha-miR-499-5p | 79 | 68 | 58 | 44 | 65 |
| 21 | oni-miR-499 | 79 | 68 | 58 | 44 | 65 |
| 22 | pbv-miR-499-5p | 79 | 68 | 58 | 44 | 65 |
| 23 | ppy-miR-499 | 79 | 68 | 58 | 44 | 65 |
| 24 | ssa-miR-499b-5p | 79 | 68 | 58 | 44 | 65 |
| 25 | xla-miR-499-5p | 79 | 68 | 58 | 44 | 65 |
| 26 | xtr-miR-499 | 79 | 68 | 58 | 44 | 65 |
| 27 | cme-miR166g | 954 | 916 | 1017 | 975 | 810 |
| 28 | csi-miR166c-3p | 954 | 916 | 1017 | 975 | 810 |
| 29 | gma-miR166p | 954 | 916 | 1017 | 975 | 810 |
| 30 | gma-miR166q | 954 | 916 | 1017 | 975 | 810 |
| 31 | gma-miR166r | 954 | 916 | 1017 | 975 | 810 |
| 32 | gma-miR166s | 954 | 916 | 1017 | 975 | 810 |
| 33 | gma-miR166t | 954 | 916 | 1017 | 975 | 810 |
| 34 | sbi-miR166a | 954 | 916 | 1017 | 975 | 810 |
| 35 | sbi-miR166b | 954 | 916 | 1017 | 975 | 810 |
| 36 | sbi-miR166c | 954 | 916 | 1017 | 975 | 810 |
| 37 | sbi-miR166d | 954 | 916 | 1017 | 975 | 810 |
| 38 | sbi-miR166h | 954 | 916 | 1017 | 975 | 810 |
| 39 | sbi-miR166i | 954 | 916 | 1017 | 975 | 810 |
| 40 | sbi-miR166j | 954 | 916 | 1017 | 975 | 810 |
| 41 | tcc-miR166b | 954 | 916 | 1017 | 975 | 810 |
| 42 | zma-miR166b-3p | 954 | 916 | 1017 | 975 | 810 |
| 43 | zma-miR166c-3p | 954 | 916 | 1017 | 975 | 810 |
| 44 | zma-miR166d-3p | 954 | 916 | 1017 | 975 | 810 |
| 45 | zma-miR166e | 954 | 916 | 1017 | 975 | 810 |
| 46 | zma-miR166f | 954 | 916 | 1017 | 975 | 810 |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|------|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | zma-miR166g-3p | 954 | 916 | 1017 | 975 | 810 |
| 4 | zma-miR166h-3p | 954 | 916 | 1017 | 975 | 810 |
| 5 | zma-miR166i-3p | 954 | 916 | 1017 | 975 | 810 |
| 6 | zma-miR166i-3p | 954 | 916 | 1017 | 975 | 810 |
| 7 | ahy-miR156b-5p | 494 | 477 | 394 | 447 | 305 |
| 8 | aly-miR157a-5p | 494 | 477 | 394 | 447 | 305 |
| 9 | aly-miR157a-5p | 494 | 477 | 394 | 447 | 305 |
| 10 | aly-miR157b-5p | 494 | 477 | 394 | 447 | 305 |
| 11 | aly-miR157c-5p | 494 | 477 | 394 | 447 | 305 |
| 12 | aly-miR157c-5p | 494 | 477 | 394 | 447 | 305 |
| 13 | aof-miR156b | 494 | 477 | 394 | 447 | 305 |
| 14 | ath-miR157a-5p | 494 | 477 | 394 | 447 | 305 |
| 15 | ath-miR157b-5p | 494 | 477 | 394 | 447 | 305 |
| 16 | ath-miR157b-5p | 494 | 477 | 394 | 447 | 305 |
| 17 | ath-miR157c-5p | 494 | 477 | 394 | 447 | 305 |
| 18 | atr-miR156a | 494 | 477 | 394 | 447 | 305 |
| 19 | atr-miR156a | 494 | 477 | 394 | 447 | 305 |
| 20 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 21 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 22 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 23 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 24 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 25 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 26 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 27 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 28 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 29 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 30 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 31 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 32 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 33 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 34 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 35 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 36 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 37 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 38 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 39 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 40 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 41 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 42 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 43 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 44 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 45 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 46 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 47 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 48 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 49 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 50 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 51 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 52 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 53 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 54 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 55 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 56 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 57 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 58 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 59 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |
| 60 | atr-miR156c | 494 | 477 | 394 | 447 | 305 |

| | | | | | | |
|----|-----------------|------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | mes-miR156j | 494 | 477 | 394 | 447 | 305 |
| 4 | mtr-miR156e | 494 | 477 | 394 | 447 | 305 |
| 5 | mtr-miR156f | 494 | 477 | 394 | 447 | 305 |
| 6 | mtr-miR156h-5p | 494 | 477 | 394 | 447 | 305 |
| 7 | ppe-miR156g | 494 | 477 | 394 | 447 | 305 |
| 8 | ppe-miR156h | 494 | 477 | 394 | 447 | 305 |
| 9 | ppe-miR156i | 494 | 477 | 394 | 447 | 305 |
| 10 | ptc-miR156g | 494 | 477 | 394 | 447 | 305 |
| 11 | ptc-miR156h | 494 | 477 | 394 | 447 | 305 |
| 12 | ptc-miR156i | 494 | 477 | 394 | 447 | 305 |
| 13 | ptc-miR156j | 494 | 477 | 394 | 447 | 305 |
| 14 | rco-miR156f | 494 | 477 | 394 | 447 | 305 |
| 15 | rco-miR156g | 494 | 477 | 394 | 447 | 305 |
| 16 | rco-miR156h | 494 | 477 | 394 | 447 | 305 |
| 17 | sly-miR156a | 494 | 477 | 394 | 447 | 305 |
| 18 | sly-miR156b | 494 | 477 | 394 | 447 | 305 |
| 19 | sly-miR156c | 494 | 477 | 394 | 447 | 305 |
| 20 | stu-miR156a | 494 | 477 | 394 | 447 | 305 |
| 21 | stu-miR156b | 494 | 477 | 394 | 447 | 305 |
| 22 | stu-miR156c | 494 | 477 | 394 | 447 | 305 |
| 23 | stu-miR156d-5p | 494 | 477 | 394 | 447 | 305 |
| 24 | tcc-miR156e | 494 | 477 | 394 | 447 | 305 |
| 25 | tcc-miR156f | 494 | 477 | 394 | 447 | 305 |
| 26 | vca-miR156b-5p | 494 | 477 | 394 | 447 | 305 |
| 27 | vun-miR156b | 494 | 477 | 394 | 447 | 305 |
| 28 | vvi-miR156f | 494 | 477 | 394 | 447 | 305 |
| 29 | vvi-miR156g | 494 | 477 | 394 | 447 | 305 |
| 30 | vvi-miR156i | 494 | 477 | 394 | 447 | 305 |
| 31 | gma-miR169s-5p | 678 | 780 | 744 | 545 | 782 |
| 32 | mtr-miR169d-5p | 678 | 780 | 744 | 545 | 782 |
| 33 | pab-miR166j | 569 | 1967 | 1318 | 1082 | 984 |
| 34 | asu-miR-100a-5p | 531 | 277 | 204 | 309 | 269 |
| 35 | prd-miR-100-5p | 531 | 277 | 204 | 309 | 269 |
| 36 | bcy-miR156 | 494 | 477 | 394 | 447 | 305 |
| 37 | bgy-miR156 | 494 | 477 | 394 | 447 | 305 |
| 38 | bfl-miR-100-5p | 531 | 266 | 185 | 305 | 259 |
| 39 | dpu-miR-100 | 531 | 266 | 185 | 305 | 259 |
| 40 | hpo-miR-100-5p | 531 | 266 | 185 | 305 | 259 |
| 41 | isc-miR-100 | 531 | 266 | 185 | 305 | 259 |
| 42 | efu-miR-499 | 80 | 69 | 58 | 45 | 68 |
| 43 | aof-miR171a | 9653 | 12047 | 12181 | 10431 | 10297 |
| 44 | aqc-miR171a | 9653 | 12047 | 12181 | 10431 | 10297 |
| 45 | aqc-miR171b | 9653 | 12047 | 12181 | 10431 | 10297 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | aqc-miR171d | 9653 | 12047 | 12181 | 10431 | 10297 |
| 4 | ata-miR171b-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 5 | ata-miR171d-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 6 | ata-miR171d-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 7 | bdi-miR171b | 9653 | 12047 | 12181 | 10431 | 10297 |
| 8 | bdi-miR171c-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 9 | bdi-miR171c-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 10 | bdi-miR171d-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 11 | bdi-miR171e | 9653 | 12047 | 12181 | 10431 | 10297 |
| 12 | cme-miR171c | 9653 | 12047 | 12181 | 10431 | 10297 |
| 13 | cme-miR171c | 9653 | 12047 | 12181 | 10431 | 10297 |
| 14 | cme-miR171f | 9653 | 12047 | 12181 | 10431 | 10297 |
| 15 | cpa-miR171a | 9653 | 12047 | 12181 | 10431 | 10297 |
| 16 | cpa-miR171b | 9653 | 12047 | 12181 | 10431 | 10297 |
| 17 | cpa-miR171b | 9653 | 12047 | 12181 | 10431 | 10297 |
| 18 | cpa-miR171c | 9653 | 12047 | 12181 | 10431 | 10297 |
| 19 | cpa-miR171d | 9653 | 12047 | 12181 | 10431 | 10297 |
| 20 | crt-miR171 | 9653 | 12047 | 12181 | 10431 | 10297 |
| 21 | crt-miR171 | 9653 | 12047 | 12181 | 10431 | 10297 |
| 22 | csi-miR171c-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 23 | csi-miR171d-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 24 | csi-miR171d-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 25 | csi-miR171f-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 26 | csi-miR171h-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 27 | csi-miR171i-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 28 | far-miR171 | 9653 | 12047 | 12181 | 10431 | 10297 |
| 29 | far-miR171 | 9653 | 12047 | 12181 | 10431 | 10297 |
| 30 | fve-miR171a | 9653 | 12047 | 12181 | 10431 | 10297 |
| 31 | fve-miR171c-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 32 | fve-miR171d | 9653 | 12047 | 12181 | 10431 | 10297 |
| 33 | fve-miR171d | 9653 | 12047 | 12181 | 10431 | 10297 |
| 34 | fve-miR171e | 9653 | 12047 | 12181 | 10431 | 10297 |
| 35 | fve-miR171g | 9653 | 12047 | 12181 | 10431 | 10297 |
| 36 | fve-miR171g | 9653 | 12047 | 12181 | 10431 | 10297 |
| 37 | gma-miR171e | 9653 | 12047 | 12181 | 10431 | 10297 |
| 38 | gma-miR171f | 9653 | 12047 | 12181 | 10431 | 10297 |
| 39 | gma-miR171g | 9653 | 12047 | 12181 | 10431 | 10297 |
| 40 | gma-miR171j-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 41 | gma-miR171j-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 42 | gma-miR171u | 9653 | 12047 | 12181 | 10431 | 10297 |
| 43 | hpa-miR171a | 9653 | 12047 | 12181 | 10431 | 10297 |
| 44 | htu-miR171b | 9653 | 12047 | 12181 | 10431 | 10297 |
| 45 | htu-miR171b | 9653 | 12047 | 12181 | 10431 | 10297 |
| 46 | htu-miR171c | 9653 | 12047 | 12181 | 10431 | 10297 |
| 47 | hvu-miR171-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 48 | lja-miR171a | 9653 | 12047 | 12181 | 10431 | 10297 |
| 49 | lja-miR171a | 9653 | 12047 | 12181 | 10431 | 10297 |
| 50 | lus-miR171b | 9653 | 12047 | 12181 | 10431 | 10297 |
| 51 | lus-miR171c | 9653 | 12047 | 12181 | 10431 | 10297 |
| 52 | lus-miR171e | 9653 | 12047 | 12181 | 10431 | 10297 |
| 53 | mdm-miR171g | 9653 | 12047 | 12181 | 10431 | 10297 |
| 54 | mdm-miR171g | 9653 | 12047 | 12181 | 10431 | 10297 |
| 55 | mdm-miR171h | 9653 | 12047 | 12181 | 10431 | 10297 |
| 56 | mes-miR171g | 9653 | 12047 | 12181 | 10431 | 10297 |
| 57 | mes-miR171h | 9653 | 12047 | 12181 | 10431 | 10297 |
| 58 | mes-miR171h | 9653 | 12047 | 12181 | 10431 | 10297 |
| 59 | mes-miR171i | 9653 | 12047 | 12181 | 10431 | 10297 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | mes-miR171j | 9653 | 12047 | 12181 | 10431 | 10297 |
| 4 | mes-miR171k | 9653 | 12047 | 12181 | 10431 | 10297 |
| 5 | mtr-miR171d | 9653 | 12047 | 12181 | 10431 | 10297 |
| 6 | nta-miR171c | 9653 | 12047 | 12181 | 10431 | 10297 |
| 7 | nta-miR171c | 9653 | 12047 | 12181 | 10431 | 10297 |
| 8 | osa-miR171b | 9653 | 12047 | 12181 | 10431 | 10297 |
| 9 | osa-miR171b | 9653 | 12047 | 12181 | 10431 | 10297 |
| 10 | osa-miR171c-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 11 | osa-miR171d-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 12 | osa-miR171e-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 13 | osa-miR171e-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 14 | osa-miR171f-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 15 | pde-miR171 | 9653 | 12047 | 12181 | 10431 | 10297 |
| 16 | ppe-miR171a | 9653 | 12047 | 12181 | 10431 | 10297 |
| 17 | ppe-miR171a | 9653 | 12047 | 12181 | 10431 | 10297 |
| 18 | ppe-miR171c | 9653 | 12047 | 12181 | 10431 | 10297 |
| 19 | ppe-miR171f | 9653 | 12047 | 12181 | 10431 | 10297 |
| 20 | ppe-miR171g | 9653 | 12047 | 12181 | 10431 | 10297 |
| 21 | ppe-miR171g | 9653 | 12047 | 12181 | 10431 | 10297 |
| 22 | ptc-miR171e | 9653 | 12047 | 12181 | 10431 | 10297 |
| 23 | ptc-miR171f | 9653 | 12047 | 12181 | 10431 | 10297 |
| 24 | ptc-miR171g-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 25 | ptc-miR171g-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 26 | ptc-miR171h-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 27 | ptc-miR171i | 9653 | 12047 | 12181 | 10431 | 10297 |
| 28 | rco-miR171c | 9653 | 12047 | 12181 | 10431 | 10297 |
| 29 | rco-miR171c | 9653 | 12047 | 12181 | 10431 | 10297 |
| 30 | rco-miR171d | 9653 | 12047 | 12181 | 10431 | 10297 |
| 31 | rco-miR171e | 9653 | 12047 | 12181 | 10431 | 10297 |
| 32 | rco-miR171e | 9653 | 12047 | 12181 | 10431 | 10297 |
| 33 | rco-miR171f | 9653 | 12047 | 12181 | 10431 | 10297 |
| 34 | sbi-miR171a | 9653 | 12047 | 12181 | 10431 | 10297 |
| 35 | sbi-miR171b | 9653 | 12047 | 12181 | 10431 | 10297 |
| 36 | sbi-miR171b | 9653 | 12047 | 12181 | 10431 | 10297 |
| 37 | sbi-miR171d | 9653 | 12047 | 12181 | 10431 | 10297 |
| 38 | sbi-miR171i | 9653 | 12047 | 12181 | 10431 | 10297 |
| 39 | sbi-miR171k | 9653 | 12047 | 12181 | 10431 | 10297 |
| 40 | sly-miR171a | 9653 | 12047 | 12181 | 10431 | 10297 |
| 41 | sly-miR171a | 9653 | 12047 | 12181 | 10431 | 10297 |
| 42 | stu-miR171a-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 43 | stu-miR171e | 9653 | 12047 | 12181 | 10431 | 10297 |
| 44 | tae-miR171a | 9653 | 12047 | 12181 | 10431 | 10297 |
| 45 | tae-miR171a | 9653 | 12047 | 12181 | 10431 | 10297 |
| 46 | tcc-miR171d | 9653 | 12047 | 12181 | 10431 | 10297 |
| 47 | tcc-miR171e | 9653 | 12047 | 12181 | 10431 | 10297 |
| 48 | tcc-miR171e | 9653 | 12047 | 12181 | 10431 | 10297 |
| 49 | tcc-miR171f | 9653 | 12047 | 12181 | 10431 | 10297 |
| 50 | tcc-miR171g | 9653 | 12047 | 12181 | 10431 | 10297 |
| 51 | tcc-miR171h | 9653 | 12047 | 12181 | 10431 | 10297 |
| 52 | vvi-miR171a | 9653 | 12047 | 12181 | 10431 | 10297 |
| 53 | vvi-miR171c | 9653 | 12047 | 12181 | 10431 | 10297 |
| 54 | vvi-miR171c | 9653 | 12047 | 12181 | 10431 | 10297 |
| 55 | vvi-miR171d | 9653 | 12047 | 12181 | 10431 | 10297 |
| 56 | vvi-miR171i | 9653 | 12047 | 12181 | 10431 | 10297 |
| 57 | vvi-miR171i | 9653 | 12047 | 12181 | 10431 | 10297 |
| 58 | vvi-miR171j | 9653 | 12047 | 12181 | 10431 | 10297 |
| 59 | zma-miR171d-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|--------|--------|--------|--------|--------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | zma-miR171e-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 4 | zma-miR171i-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 5 | zma-miR171j-3p | 9653 | 12047 | 12181 | 10431 | 10297 |
| 6 | gma-miR166m | 458 | 1911 | 1254 | 1011 | 935 |
| 7 | mdm-miR167h | 332445 | 328666 | 280552 | 259175 | 328814 |
| 8 | mdm-miR167i | 332445 | 328666 | 280552 | 259175 | 328814 |
| 9 | mdm-miR167j | 332445 | 328666 | 280552 | 259175 | 328814 |
| 10 | ppe-miR167d | 332445 | 328666 | 280552 | 259175 | 328814 |
| 11 | ahy-miR159 | 124202 | 95587 | 114081 | 103220 | 93839 |
| 12 | aly-miR159a-3p | 124202 | 95587 | 114081 | 103220 | 93839 |
| 13 | aof-miR159 | 124202 | 95587 | 114081 | 103220 | 93839 |
| 14 | ath-miR159a | 124202 | 95587 | 114081 | 103220 | 93839 |
| 15 | atr-miR159 | 124202 | 95587 | 114081 | 103220 | 93839 |
| 16 | bnm-miR159 | 124202 | 95587 | 114081 | 103220 | 93839 |
| 17 | bra-miR159a | 124202 | 95587 | 114081 | 103220 | 93839 |
| 18 | cme-miR159a | 124202 | 95587 | 114081 | 103220 | 93839 |
| 19 | cpa-miR159a | 124202 | 95587 | 114081 | 103220 | 93839 |
| 20 | csi-miR159a-3p | 124202 | 95587 | 114081 | 103220 | 93839 |
| 21 | fve-miR159a-3p | 124202 | 95587 | 114081 | 103220 | 93839 |
| 22 | gma-miR159a-3p | 124202 | 95587 | 114081 | 103220 | 93839 |
| 23 | gma-miR159e-3p | 124202 | 95587 | 114081 | 103220 | 93839 |
| 24 | hbr-miR159a | 124202 | 95587 | 114081 | 103220 | 93839 |
| 25 | htu-miR159a | 124202 | 95587 | 114081 | 103220 | 93839 |
| 26 | mdm-miR159d | 124202 | 95587 | 114081 | 103220 | 93839 |
| 27 | mdm-miR159e | 124202 | 95587 | 114081 | 103220 | 93839 |
| 28 | mdm-miR159f | 124202 | 95587 | 114081 | 103220 | 93839 |
| 29 | mes-miR159a-3p | 124202 | 95587 | 114081 | 103220 | 93839 |
| 30 | mes-miR159b | 124202 | 95587 | 114081 | 103220 | 93839 |
| 31 | mtr-miR159a | 124202 | 95587 | 114081 | 103220 | 93839 |
| 32 | nta-miR159 | 124202 | 95587 | 114081 | 103220 | 93839 |
| 33 | ppe-miR159 | 124202 | 95587 | 114081 | 103220 | 93839 |
| 34 | ptc-miR159a | 124202 | 95587 | 114081 | 103220 | 93839 |
| 35 | ptc-miR159b | 124202 | 95587 | 114081 | 103220 | 93839 |
| 36 | pvu-miR159a.1 | 124202 | 95587 | 114081 | 103220 | 93839 |
| 37 | rco-miR159 | 124202 | 95587 | 114081 | 103220 | 93839 |
| 38 | sly-miR159 | 124202 | 95587 | 114081 | 103220 | 93839 |
| 39 | vca-miR159-3p | 124202 | 95587 | 114081 | 103220 | 93839 |
| 40 | vvi-miR159c | 124202 | 95587 | 114081 | 103220 | 93839 |
| 41 | tca-miR-100-5p | 477 | 244 | 170 | 288 | 241 |
| 42 | oha-miR-100-5p | 479 | 244 | 170 | 287 | 242 |
| 43 | csi-miR393b-5p | 200 | 229 | 175 | 202 | 173 |
| 44 | gma-miR393h | 200 | 229 | 175 | 202 | 173 |
| 45 | gma-miR393i | 200 | 229 | 175 | 202 | 173 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | gma-miR393j | 200 | 229 | 175 | 202 | 173 |
| 4 | gma-miR393k | 200 | 229 | 175 | 202 | 173 |
| 5 | aae-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 6 | abu-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 7 | aca-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 8 | aga-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 9 | age-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 10 | ame-miR-100-5p | 476 | 244 | 170 | 287 | 241 |
| 11 | ami-miR-100-5p | 476 | 244 | 170 | 287 | 241 |
| 12 | bbe-miR-100-5p | 476 | 244 | 170 | 287 | 241 |
| 13 | bma-miR-100b | 476 | 244 | 170 | 287 | 241 |
| 14 | bmo-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 15 | bta-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 16 | cja-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 17 | cli-miR-100-5p | 476 | 244 | 170 | 287 | 241 |
| 18 | cpo-miR-100-5p | 476 | 244 | 170 | 287 | 241 |
| 19 | cqu-miR-100-5p | 476 | 244 | 170 | 287 | 241 |
| 20 | dno-miR-100-5p | 476 | 244 | 170 | 287 | 241 |
| 21 | dre-miR-100-5p | 476 | 244 | 170 | 287 | 241 |
| 22 | eca-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 23 | fru-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 24 | gga-miR-100-5p | 476 | 244 | 170 | 287 | 241 |
| 25 | ggo-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 26 | gmo-miR-100a-5p | 476 | 244 | 170 | 287 | 241 |
| 27 | hsa-miR-100-5p | 476 | 244 | 170 | 287 | 241 |
| 28 | ipu-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 29 | lgi-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 30 | lla-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 31 | mml-miR-100-5p | 476 | 244 | 170 | 287 | 241 |
| 32 | mmr-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 33 | mmu-miR-100-5p | 476 | 244 | 170 | 287 | 241 |
| 34 | mse-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 35 | mze-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 36 | nbr-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 37 | nle-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 38 | nvi-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 39 | oan-miR-100-5p | 476 | 244 | 170 | 287 | 241 |
| 40 | ocu-miR-100-5p | 476 | 244 | 170 | 287 | 241 |
| 41 | oga-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 42 | oni-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 43 | pal-miR-100-5p | 476 | 244 | 170 | 287 | 241 |
| 44 | pbv-miR-100-5p | 476 | 244 | 170 | 287 | 241 |
| 45 | pha-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|--------|--------|--------|--------|--------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | pma-miR-100a-5p | 476 | 244 | 170 | 287 | 241 |
| 4 | ppy-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 5 | ppa-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 6 | ppa-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 7 | ppy-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 8 | pte-miR-100b-5p | 476 | 244 | 170 | 287 | 241 |
| 9 | ptr-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 10 | ptr-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 11 | rno-miR-100-5p | 476 | 244 | 170 | 287 | 241 |
| 12 | sko-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 13 | sko-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 14 | sla-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 15 | ssa-miR-100a-5p | 476 | 244 | 170 | 287 | 241 |
| 16 | ssc-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 17 | ssc-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 18 | tcf-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 19 | tch-miR-100-5p | 476 | 244 | 170 | 287 | 241 |
| 20 | tni-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 21 | tni-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 22 | xla-miR-100-5p | 476 | 244 | 170 | 287 | 241 |
| 23 | xtr-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 24 | xtr-miR-100 | 476 | 244 | 170 | 287 | 241 |
| 25 | ahy-miR167-5p | 125567 | 123159 | 109633 | 103163 | 121638 |
| 26 | cme-miR167c | 125567 | 123159 | 109633 | 103163 | 121638 |
| 27 | cpa-miR167c | 125567 | 123159 | 109633 | 103163 | 121638 |
| 28 | csi-miR167b-5p | 125567 | 123159 | 109633 | 103163 | 121638 |
| 29 | csi-miR167b-5p | 125567 | 123159 | 109633 | 103163 | 121638 |
| 30 | gma-miR167e | 125567 | 123159 | 109633 | 103163 | 121638 |
| 31 | gma-miR167f | 125567 | 123159 | 109633 | 103163 | 121638 |
| 32 | lus-miR167b | 125567 | 123159 | 109633 | 103163 | 121638 |
| 33 | lus-miR167b | 125567 | 123159 | 109633 | 103163 | 121638 |
| 34 | mes-miR167g | 125567 | 123159 | 109633 | 103163 | 121638 |
| 35 | mes-miR167h | 125567 | 123159 | 109633 | 103163 | 121638 |
| 36 | ptc-miR167f-5p | 125567 | 123159 | 109633 | 103163 | 121638 |
| 37 | ptc-miR167f-5p | 125567 | 123159 | 109633 | 103163 | 121638 |
| 38 | ptc-miR167g-5p | 125567 | 123159 | 109633 | 103163 | 121638 |
| 39 | tcc-miR167c | 125567 | 123159 | 109633 | 103163 | 121638 |
| 40 | gma-miR171n | 127 | 110 | 106 | 97 | 124 |
| 41 | gma-miR171n | 127 | 110 | 106 | 97 | 124 |
| 42 | gma-miR171p | 127 | 110 | 106 | 97 | 124 |
| 43 | aly-miR169b-5p | 6230 | 7972 | 6743 | 5589 | 7610 |
| 44 | aly-miR169c-5p | 6230 | 7972 | 6743 | 5589 | 7610 |
| 45 | aly-miR169c-5p | 6230 | 7972 | 6743 | 5589 | 7610 |
| 46 | aqc-miR169c | 6230 | 7972 | 6743 | 5589 | 7610 |
| 47 | ata-miR169d-5p | 6230 | 7972 | 6743 | 5589 | 7610 |
| 48 | ath-miR169b-5p | 6230 | 7972 | 6743 | 5589 | 7610 |
| 49 | ath-miR169c | 6230 | 7972 | 6743 | 5589 | 7610 |
| 50 | ath-miR169c | 6230 | 7972 | 6743 | 5589 | 7610 |
| 51 | bdi-miR169c-5p | 6230 | 7972 | 6743 | 5589 | 7610 |
| 52 | bdi-miR169f | 6230 | 7972 | 6743 | 5589 | 7610 |
| 53 | bdi-miR169f | 6230 | 7972 | 6743 | 5589 | 7610 |
| 54 | bna-miR169n | 6230 | 7972 | 6743 | 5589 | 7610 |
| 55 | cas-miR169b | 6230 | 7972 | 6743 | 5589 | 7610 |
| 56 | cme-miR169f | 6230 | 7972 | 6743 | 5589 | 7610 |
| 57 | cme-miR169h | 6230 | 7972 | 6743 | 5589 | 7610 |
| 58 | cme-miR169h | 6230 | 7972 | 6743 | 5589 | 7610 |
| 59 | csi-miR169g-5p | 6230 | 7972 | 6743 | 5589 | 7610 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | csi-miR169k-5p | 6230 | 7972 | 6743 | 5589 | 7610 |
| 4 | csi-miR169m-5p | 6230 | 7972 | 6743 | 5589 | 7610 |
| 5 | csi-miR169n-5p | 6230 | 7972 | 6743 | 5589 | 7610 |
| 6 | csi-miR169o-5p | 6230 | 7972 | 6743 | 5589 | 7610 |
| 7 | csi-miR169p-5p | 6230 | 7972 | 6743 | 5589 | 7610 |
| 8 | csi-miR169r-5p | 6230 | 7972 | 6743 | 5589 | 7610 |
| 9 | gma-miR169a | 6230 | 7972 | 6743 | 5589 | 7610 |
| 10 | gma-miR169f | 6230 | 7972 | 6743 | 5589 | 7610 |
| 11 | gma-miR169g | 6230 | 7972 | 6743 | 5589 | 7610 |
| 12 | gma-miR169m | 6230 | 7972 | 6743 | 5589 | 7610 |
| 13 | lus-miR169f | 6230 | 7972 | 6743 | 5589 | 7610 |
| 14 | lus-miR169h | 6230 | 7972 | 6743 | 5589 | 7610 |
| 15 | lus-miR169j | 6230 | 7972 | 6743 | 5589 | 7610 |
| 16 | mdm-miR169a | 6230 | 7972 | 6743 | 5589 | 7610 |
| 17 | mdm-miR169g | 6230 | 7972 | 6743 | 5589 | 7610 |
| 18 | mdm-miR169h | 6230 | 7972 | 6743 | 5589 | 7610 |
| 19 | mdm-miR169i | 6230 | 7972 | 6743 | 5589 | 7610 |
| 20 | mdm-miR169j | 6230 | 7972 | 6743 | 5589 | 7610 |
| 21 | mes-miR169a | 6230 | 7972 | 6743 | 5589 | 7610 |
| 22 | mes-miR169b | 6230 | 7972 | 6743 | 5589 | 7610 |
| 23 | mes-miR169c | 6230 | 7972 | 6743 | 5589 | 7610 |
| 24 | mes-miR169d | 6230 | 7972 | 6743 | 5589 | 7610 |
| 25 | mes-miR169e | 6230 | 7972 | 6743 | 5589 | 7610 |
| 26 | mtr-miR169b | 6230 | 7972 | 6743 | 5589 | 7610 |
| 27 | mtr-miR169g | 6230 | 7972 | 6743 | 5589 | 7610 |
| 28 | mtr-miR169l-5p | 6230 | 7972 | 6743 | 5589 | 7610 |
| 29 | nta-miR169q | 6230 | 7972 | 6743 | 5589 | 7610 |
| 30 | nta-miR169r | 6230 | 7972 | 6743 | 5589 | 7610 |
| 31 | nta-miR169s | 6230 | 7972 | 6743 | 5589 | 7610 |
| 32 | osa-miR169b | 6230 | 7972 | 6743 | 5589 | 7610 |
| 33 | osa-miR169c | 6230 | 7972 | 6743 | 5589 | 7610 |
| 34 | ppe-miR169a | 6230 | 7972 | 6743 | 5589 | 7610 |
| 35 | ppe-miR169b | 6230 | 7972 | 6743 | 5589 | 7610 |
| 36 | ppe-miR169c | 6230 | 7972 | 6743 | 5589 | 7610 |
| 37 | ptc-miR169d | 6230 | 7972 | 6743 | 5589 | 7610 |
| 38 | ptc-miR169e | 6230 | 7972 | 6743 | 5589 | 7610 |
| 39 | ptc-miR169f | 6230 | 7972 | 6743 | 5589 | 7610 |
| 40 | ptc-miR169g | 6230 | 7972 | 6743 | 5589 | 7610 |
| 41 | ptc-miR169h | 6230 | 7972 | 6743 | 5589 | 7610 |
| 42 | ptc-miR169p | 6230 | 7972 | 6743 | 5589 | 7610 |
| 43 | rco-miR169a | 6230 | 7972 | 6743 | 5589 | 7610 |
| 44 | rco-miR169b | 6230 | 7972 | 6743 | 5589 | 7610 |
| 45 | sbi-miR169b | 6230 | 7972 | 6743 | 5589 | 7610 |
| 46 | sbi-miR169k | 6230 | 7972 | 6743 | 5589 | 7610 |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | sly-miR169a | 6230 | 7972 | 6743 | 5589 | 7610 |
| 4 | tcc-miR169b | 6230 | 7972 | 6743 | 5589 | 7610 |
| 5 | tcc-miR169k | 6230 | 7972 | 6743 | 5589 | 7610 |
| 6 | tcc-miR169l | 6230 | 7972 | 6743 | 5589 | 7610 |
| 7 | tcc-miR169l | 6230 | 7972 | 6743 | 5589 | 7610 |
| 8 | vun-miR169 | 6230 | 7972 | 6743 | 5589 | 7610 |
| 9 | vun-miR169 | 6230 | 7972 | 6743 | 5589 | 7610 |
| 10 | vvi-miR169a | 6230 | 7972 | 6743 | 5589 | 7610 |
| 11 | vvi-miR169c | 6230 | 7972 | 6743 | 5589 | 7610 |
| 12 | vvi-miR169c | 6230 | 7972 | 6743 | 5589 | 7610 |
| 13 | vvi-miR169j | 6230 | 7972 | 6743 | 5589 | 7610 |
| 14 | vvi-miR169k | 6230 | 7972 | 6743 | 5589 | 7610 |
| 15 | vvi-miR169s | 6230 | 7972 | 6743 | 5589 | 7610 |
| 16 | vvi-miR169w | 6230 | 7972 | 6743 | 5589 | 7610 |
| 17 | vvi-miR169w | 6230 | 7972 | 6743 | 5589 | 7610 |
| 18 | zma-miR169c-5p | 6230 | 7972 | 6743 | 5589 | 7610 |
| 19 | zma-miR169r-5p | 6230 | 7972 | 6743 | 5589 | 7610 |
| 20 | zma-miR169r-5p | 6230 | 7972 | 6743 | 5589 | 7610 |
| 21 | gma-miR156f | 2621 | 2691 | 2018 | 2315 | 1867 |
| 22 | aly-miR164a-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 23 | aly-miR164b-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 24 | aly-miR164b-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 25 | aof-miR164 | 7094 | 4921 | 2155 | 4855 | 3374 |
| 26 | ata-miR164b-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 27 | ata-miR164c-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 28 | ath-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 29 | ath-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 30 | ath-miR164b-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 31 | atr-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 32 | atr-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 33 | atr-miR164b | 7094 | 4921 | 2155 | 4855 | 3374 |
| 34 | bdi-miR164a-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 35 | bdi-miR164b | 7094 | 4921 | 2155 | 4855 | 3374 |
| 36 | bdi-miR164b | 7094 | 4921 | 2155 | 4855 | 3374 |
| 37 | bdi-miR164e | 7094 | 4921 | 2155 | 4855 | 3374 |
| 38 | bna-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 39 | bra-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 40 | bra-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 41 | cas-miR164 | 7094 | 4921 | 2155 | 4855 | 3374 |
| 42 | cme-miR164c | 7094 | 4921 | 2155 | 4855 | 3374 |
| 43 | cme-miR164d | 7094 | 4921 | 2155 | 4855 | 3374 |
| 44 | cpa-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 45 | cpa-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 46 | cpa-miR164b | 7094 | 4921 | 2155 | 4855 | 3374 |
| 47 | cpa-miR164c | 7094 | 4921 | 2155 | 4855 | 3374 |
| 48 | csi-miR164a-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 49 | csi-miR164a-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 50 | csi-miR164b-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 51 | csi-miR164c-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 52 | csi-miR164d-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 53 | csi-miR164d-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 54 | ctr-miR164 | 7094 | 4921 | 2155 | 4855 | 3374 |
| 55 | fve-miR164a-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 56 | fve-miR164b | 7094 | 4921 | 2155 | 4855 | 3374 |
| 57 | fve-miR164b | 7094 | 4921 | 2155 | 4855 | 3374 |
| 58 | ghr-miR164 | 7094 | 4921 | 2155 | 4855 | 3374 |
| 59 | gma-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | gma-miR164e | 7094 | 4921 | 2155 | 4855 | 3374 |
| 4 | gma-miR164f | 7094 | 4921 | 2155 | 4855 | 3374 |
| 5 | gma-miR164g | 7094 | 4921 | 2155 | 4855 | 3374 |
| 6 | gma-miR164h | 7094 | 4921 | 2155 | 4855 | 3374 |
| 7 | gma-miR164i | 7094 | 4921 | 2155 | 4855 | 3374 |
| 8 | gma-miR164j | 7094 | 4921 | 2155 | 4855 | 3374 |
| 9 | gma-miR164k | 7094 | 4921 | 2155 | 4855 | 3374 |
| 10 | lus-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 11 | lus-miR164b | 7094 | 4921 | 2155 | 4855 | 3374 |
| 12 | lus-miR164c | 7094 | 4921 | 2155 | 4855 | 3374 |
| 13 | lus-miR164d | 7094 | 4921 | 2155 | 4855 | 3374 |
| 14 | lus-miR164e | 7094 | 4921 | 2155 | 4855 | 3374 |
| 15 | mdm-miR164b | 7094 | 4921 | 2155 | 4855 | 3374 |
| 16 | mdm-miR164c | 7094 | 4921 | 2155 | 4855 | 3374 |
| 17 | mdm-miR164d | 7094 | 4921 | 2155 | 4855 | 3374 |
| 18 | mdm-miR164e | 7094 | 4921 | 2155 | 4855 | 3374 |
| 19 | mdm-miR164f | 7094 | 4921 | 2155 | 4855 | 3374 |
| 20 | mes-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 21 | mes-miR164b | 7094 | 4921 | 2155 | 4855 | 3374 |
| 22 | mes-miR164c | 7094 | 4921 | 2155 | 4855 | 3374 |
| 23 | mtr-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 24 | mtr-miR164b | 7094 | 4921 | 2155 | 4855 | 3374 |
| 25 | mtr-miR164c | 7094 | 4921 | 2155 | 4855 | 3374 |
| 26 | nta-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 27 | nta-miR164b | 7094 | 4921 | 2155 | 4855 | 3374 |
| 28 | osa-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 29 | osa-miR164b | 7094 | 4921 | 2155 | 4855 | 3374 |
| 30 | osa-miR164f | 7094 | 4921 | 2155 | 4855 | 3374 |
| 31 | ppe-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 32 | ppe-miR164b | 7094 | 4921 | 2155 | 4855 | 3374 |
| 33 | ppe-miR164c | 7094 | 4921 | 2155 | 4855 | 3374 |
| 34 | ptc-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 35 | ptc-miR164b | 7094 | 4921 | 2155 | 4855 | 3374 |
| 36 | ptc-miR164c | 7094 | 4921 | 2155 | 4855 | 3374 |
| 37 | ptc-miR164d | 7094 | 4921 | 2155 | 4855 | 3374 |
| 38 | ptc-miR164e | 7094 | 4921 | 2155 | 4855 | 3374 |
| 39 | rco-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 40 | rco-miR164b | 7094 | 4921 | 2155 | 4855 | 3374 |
| 41 | rco-miR164c | 7094 | 4921 | 2155 | 4855 | 3374 |
| 42 | sbi-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 43 | sbi-miR164d | 7094 | 4921 | 2155 | 4855 | 3374 |
| 44 | sbi-miR164e | 7094 | 4921 | 2155 | 4855 | 3374 |
| 45 | sly-miR164a-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|-------|-------|------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | sly-miR164b-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 4 | ssl-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 5 | ssl-miR164b | 7094 | 4921 | 2155 | 4855 | 3374 |
| 6 | tae-miR164 | 7094 | 4921 | 2155 | 4855 | 3374 |
| 7 | tcc-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 8 | tcc-miR164b | 7094 | 4921 | 2155 | 4855 | 3374 |
| 9 | vvi-miR164a | 7094 | 4921 | 2155 | 4855 | 3374 |
| 10 | vvi-miR164c | 7094 | 4921 | 2155 | 4855 | 3374 |
| 11 | vvi-miR164d | 7094 | 4921 | 2155 | 4855 | 3374 |
| 12 | zma-miR164a-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 13 | zma-miR164b-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 14 | zma-miR164c-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 15 | zma-miR164d-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 16 | zma-miR164g-5p | 7094 | 4921 | 2155 | 4855 | 3374 |
| 17 | bra-miR164e-5p | 7101 | 4935 | 2160 | 4861 | 3386 |
| 18 | ahy-miR156c | 2606 | 2676 | 2010 | 2308 | 1861 |
| 19 | far-miR156b | 2606 | 2676 | 2010 | 2308 | 1861 |
| 20 | mdm-miR156t | 2606 | 2676 | 2010 | 2308 | 1861 |
| 21 | mdm-miR156u | 2606 | 2676 | 2010 | 2308 | 1861 |
| 22 | mdm-miR156v | 2606 | 2676 | 2010 | 2308 | 1861 |
| 23 | mdm-miR156w | 2606 | 2676 | 2010 | 2308 | 1861 |
| 24 | mes-miR156k | 2606 | 2676 | 2010 | 2308 | 1861 |
| 25 | aly-miR166g-5p | 364 | 304 | 383 | 343 | 358 |
| 26 | cas-miR166f-5p | 364 | 304 | 383 | 343 | 358 |
| 27 | csi-miR166b-5p | 364 | 304 | 383 | 343 | 358 |
| 28 | gma-miR166h-5p | 364 | 304 | 383 | 343 | 358 |
| 29 | gma-miR166j-5p | 364 | 304 | 383 | 343 | 358 |
| 30 | stu-miR166c-5p | 364 | 304 | 383 | 343 | 358 |
| 31 | gma-miR159d | 1575 | 1537 | 1275 | 1561 | 1314 |
| 32 | aof-miR398 | 8721 | 10351 | 12418 | 9258 | 10489 |
| 33 | aqc-miR398b | 8721 | 10351 | 12418 | 9258 | 10489 |
| 34 | bdi-miR398a | 8721 | 10351 | 12418 | 9258 | 10489 |
| 35 | cca-miR398 | 8721 | 10351 | 12418 | 9258 | 10489 |
| 36 | cme-miR398a | 8721 | 10351 | 12418 | 9258 | 10489 |
| 37 | csi-miR398b-3p | 8721 | 10351 | 12418 | 9258 | 10489 |
| 38 | gma-miR398c | 8721 | 10351 | 12418 | 9258 | 10489 |
| 39 | gma-miR398d | 8721 | 10351 | 12418 | 9258 | 10489 |
| 40 | lus-miR398a | 8721 | 10351 | 12418 | 9258 | 10489 |
| 41 | mdm-miR398b | 8721 | 10351 | 12418 | 9258 | 10489 |
| 42 | mdm-miR398c | 8721 | 10351 | 12418 | 9258 | 10489 |
| 43 | mes-miR398 | 8721 | 10351 | 12418 | 9258 | 10489 |
| 44 | mtr-miR398b | 8721 | 10351 | 12418 | 9258 | 10489 |
| 45 | mtr-miR398c | 8721 | 10351 | 12418 | 9258 | 10489 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | nta-miR398 | 8721 | 10351 | 12418 | 9258 | 10489 |
| 4 | osa-miR398b | 8721 | 10351 | 12418 | 9258 | 10489 |
| 5 | ppe-miR398a-3p | 8721 | 10351 | 12418 | 9258 | 10489 |
| 6 | ptc-miR398b | 8721 | 10351 | 12418 | 9258 | 10489 |
| 7 | ptc-miR398c-3p | 8721 | 10351 | 12418 | 9258 | 10489 |
| 8 | rco-miR398b | 8721 | 10351 | 12418 | 9258 | 10489 |
| 9 | tcc-miR398a | 8721 | 10351 | 12418 | 9258 | 10489 |
| 10 | vvi-miR398b | 8721 | 10351 | 12418 | 9258 | 10489 |
| 11 | vvi-miR398c | 8721 | 10351 | 12418 | 9258 | 10489 |
| 12 | abu-miR-222 | 350 | 182 | 148 | 265 | 177 |
| 13 | age-miR-222 | 350 | 182 | 148 | 265 | 177 |
| 14 | ami-miR-222a-3p | 350 | 182 | 148 | 265 | 177 |
| 15 | cgr-miR-222-3p | 350 | 182 | 148 | 265 | 177 |
| 16 | chi-miR-222-3p | 350 | 182 | 148 | 265 | 177 |
| 17 | cli-miR-222a-3p | 350 | 182 | 148 | 265 | 177 |
| 18 | cpo-miR-222-3p | 350 | 182 | 148 | 265 | 177 |
| 19 | dma-miR-222 | 350 | 182 | 148 | 265 | 177 |
| 20 | dno-miR-222-3p | 350 | 182 | 148 | 265 | 177 |
| 21 | dre-miR-222a-3p | 350 | 182 | 148 | 265 | 177 |
| 22 | fru-miR-222 | 350 | 182 | 148 | 265 | 177 |
| 23 | gga-miR-222a | 350 | 182 | 148 | 265 | 177 |
| 24 | mdo-miR-222a | 350 | 182 | 148 | 265 | 177 |
| 25 | mmr-miR-222 | 350 | 182 | 148 | 265 | 177 |
| 26 | mze-miR-222 | 350 | 182 | 148 | 265 | 177 |
| 27 | nbr-miR-222 | 350 | 182 | 148 | 265 | 177 |
| 28 | nle-miR-222 | 350 | 182 | 148 | 265 | 177 |
| 29 | ocu-miR-222-3p | 350 | 182 | 148 | 265 | 177 |
| 30 | oga-miR-222 | 350 | 182 | 148 | 265 | 177 |
| 31 | oha-miR-222a-3p | 350 | 182 | 148 | 265 | 177 |
| 32 | oni-miR-222 | 350 | 182 | 148 | 265 | 177 |
| 33 | pbv-miR-222a-3p | 350 | 182 | 148 | 265 | 177 |
| 34 | pha-miR-222 | 350 | 182 | 148 | 265 | 177 |
| 35 | ppy-miR-222 | 350 | 182 | 148 | 265 | 177 |
| 36 | ppa-miR-222 | 350 | 182 | 148 | 265 | 177 |
| 37 | ssa-miR-222a-3p | 350 | 182 | 148 | 265 | 177 |
| 38 | ssc-miR-222 | 350 | 182 | 148 | 265 | 177 |
| 39 | tgu-miR-222-3p | 350 | 182 | 148 | 265 | 177 |
| 40 | tni-miR-222 | 350 | 182 | 148 | 265 | 177 |
| 41 | xtr-miR-222 | 350 | 182 | 148 | 265 | 177 |
| 42 | lja-miR1511-3p | 49605 | 43469 | 45736 | 42592 | 43044 |
| 43 | aly-miR170-3p | 1478 | 1986 | 1879 | 1793 | 1706 |
| 44 | ath-miR170-3p | 1478 | 1986 | 1879 | 1793 | 1706 |
| 45 | stu-miR171c-3p | 1478 | 1986 | 1879 | 1793 | 1706 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | gma-miR159a-5p | 3882 | 3147 | 2995 | 3451 | 3205 |
| 4 | gma-miR319f | 134 | 171 | 91 | 133 | 95 |
| 5 | ahy-miR167-3p | 1040 | 1379 | 1214 | 1227 | 1117 |
| 6 | ahy-miR167-3p | 1040 | 1379 | 1214 | 1227 | 1117 |
| 7 | ptc-miR167f-3p | 1040 | 1379 | 1214 | 1227 | 1117 |
| 8 | ptc-miR167g-3p | 1040 | 1379 | 1214 | 1227 | 1117 |
| 9 | ptc-miR167h-3p | 1040 | 1379 | 1214 | 1227 | 1117 |
| 10 | ptc-miR167h-3p | 1040 | 1379 | 1214 | 1227 | 1117 |
| 11 | aja-miR-143 | 282 | 344 | 295 | 207 | 331 |
| 12 | bta-miR-143 | 282 | 344 | 295 | 207 | 331 |
| 13 | chi-miR-143-3p | 282 | 344 | 295 | 207 | 331 |
| 14 | chi-miR-143-3p | 282 | 344 | 295 | 207 | 331 |
| 15 | gga-miR-143-3p | 282 | 344 | 295 | 207 | 331 |
| 16 | mdo-miR-143-3p | 282 | 344 | 295 | 207 | 331 |
| 17 | mdo-miR-143-3p | 282 | 344 | 295 | 207 | 331 |
| 18 | tch-miR-143-3p | 282 | 344 | 295 | 207 | 331 |
| 19 | xtr-miR-143 | 282 | 344 | 295 | 207 | 331 |
| 20 | xtr-miR-143 | 282 | 344 | 295 | 207 | 331 |
| 21 | eca-miR-378 | 96 | 126 | 95 | 78 | 112 |
| 22 | mml-miR-378a | 96 | 126 | 95 | 78 | 112 |
| 23 | mmu-miR-378a-3p | 96 | 126 | 95 | 78 | 112 |
| 24 | ptr-miR-378a | 96 | 126 | 95 | 78 | 112 |
| 25 | ptr-miR-378a | 96 | 126 | 95 | 78 | 112 |
| 26 | rno-miR-378a-3p | 96 | 126 | 95 | 78 | 112 |
| 27 | efu-miR-143 | 283 | 345 | 298 | 208 | 334 |
| 28 | abu-miR-143 | 281 | 342 | 295 | 207 | 331 |
| 29 | abu-miR-143 | 281 | 342 | 295 | 207 | 331 |
| 30 | aca-miR-143-3p | 281 | 342 | 295 | 207 | 331 |
| 31 | ami-miR-143-3p | 281 | 342 | 295 | 207 | 331 |
| 32 | cfa-miR-143 | 281 | 342 | 295 | 207 | 331 |
| 33 | cfa-miR-143 | 281 | 342 | 295 | 207 | 331 |
| 34 | cgr-miR-143 | 281 | 342 | 295 | 207 | 331 |
| 35 | cli-miR-143-3p | 281 | 342 | 295 | 207 | 331 |
| 36 | cpi-miR-143-3p | 281 | 342 | 295 | 207 | 331 |
| 37 | cpi-miR-143-3p | 281 | 342 | 295 | 207 | 331 |
| 38 | cpo-miR-143-3p | 281 | 342 | 295 | 207 | 331 |
| 39 | dno-miR-143-3p | 281 | 342 | 295 | 207 | 331 |
| 40 | dre-miR-143 | 281 | 342 | 295 | 207 | 331 |
| 41 | dre-miR-143 | 281 | 342 | 295 | 207 | 331 |
| 42 | eca-miR-143 | 281 | 342 | 295 | 207 | 331 |
| 43 | hsa-miR-143-3p | 281 | 342 | 295 | 207 | 331 |
| 44 | ipu-miR-143 | 281 | 342 | 295 | 207 | 331 |
| 45 | ipu-miR-143 | 281 | 342 | 295 | 207 | 331 |
| 46 | mml-miR-143-3p | 281 | 342 | 295 | 207 | 331 |
| 47 | mmu-miR-143-3p | 281 | 342 | 295 | 207 | 331 |
| 48 | nle-miR-143 | 281 | 342 | 295 | 207 | 331 |
| 49 | nle-miR-143 | 281 | 342 | 295 | 207 | 331 |
| 50 | oan-miR-143-3p | 281 | 342 | 295 | 207 | 331 |
| 51 | oar-miR-143 | 281 | 342 | 295 | 207 | 331 |
| 52 | ocu-miR-143-3p | 281 | 342 | 295 | 207 | 331 |
| 53 | oga-miR-143 | 281 | 342 | 295 | 207 | 331 |
| 54 | oga-miR-143 | 281 | 342 | 295 | 207 | 331 |
| 55 | oni-miR-143 | 281 | 342 | 295 | 207 | 331 |
| 56 | pal-miR-143-3p | 281 | 342 | 295 | 207 | 331 |
| 57 | pbv-miR-143-3p | 281 | 342 | 295 | 207 | 331 |
| 58 | pbv-miR-143-3p | 281 | 342 | 295 | 207 | 331 |
| 59 | pha-miR-143 | 281 | 342 | 295 | 207 | 331 |
| 60 | pha-miR-143 | 281 | 342 | 295 | 207 | 331 |

| | | | | | | |
|----|-----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ssa-miR-143-3p | 281 | 342 | 295 | 207 | 331 |
| 4 | ssc-miR-143-3p | 281 | 342 | 295 | 207 | 331 |
| 5 | xla-miR-143-3p | 281 | 342 | 295 | 207 | 331 |
| 6 | | | | | | |
| 7 | gma-miR171m | 53026 | 54481 | 53808 | 50160 | 52786 |
| 8 | gma-miR171t | 53026 | 54481 | 53808 | 50160 | 52786 |
| 9 | | | | | | |
| 10 | dma-miR-143 | 294 | 397 | 330 | 230 | 360 |
| 11 | ggo-miR-143 | 294 | 397 | 330 | 230 | 360 |
| 12 | lla-miR-143 | 294 | 397 | 330 | 230 | 360 |
| 13 | oha-miR-143-3p | 294 | 397 | 330 | 230 | 360 |
| 14 | ppa-miR-143 | 294 | 397 | 330 | 230 | 360 |
| 15 | ppy-miR-143 | 294 | 397 | 330 | 230 | 360 |
| 16 | ptr-miR-143 | 294 | 397 | 330 | 230 | 360 |
| 17 | rno-miR-143-3p | 294 | 397 | 330 | 230 | 360 |
| 18 | | | | | | |
| 19 | bta-miR-99b | 96 | 69 | 60 | 61 | 73 |
| 20 | cfa-miR-99b | 96 | 69 | 60 | 61 | 73 |
| 21 | chi-miR-99b-5p | 96 | 69 | 60 | 61 | 73 |
| 22 | cpo-miR-99b-5p | 96 | 69 | 60 | 61 | 73 |
| 23 | eca-miR-99b | 96 | 69 | 60 | 61 | 73 |
| 24 | efu-miR-99b | 96 | 69 | 60 | 61 | 73 |
| 25 | hsa-miR-99b-5p | 96 | 69 | 60 | 61 | 73 |
| 26 | mml-miR-99b-5p | 96 | 69 | 60 | 61 | 73 |
| 27 | mmu-miR-99b-5p | 96 | 69 | 60 | 61 | 73 |
| 28 | oga-miR-99b | 96 | 69 | 60 | 61 | 73 |
| 29 | pal-miR-99b-5p | 96 | 69 | 60 | 61 | 73 |
| 30 | ptr-miR-99b | 96 | 69 | 60 | 61 | 73 |
| 31 | rno-miR-99b-5p | 96 | 69 | 60 | 61 | 73 |
| 32 | ssc-miR-99b | 96 | 69 | 60 | 61 | 73 |
| 33 | tch-miR-99b-5p | 96 | 69 | 60 | 61 | 73 |
| 34 | | | | | | |
| 35 | bbe-miR-216-5p | 0 | 53 | 196 | 23 | 82 |
| 36 | bfl-miR-216-5p | 0 | 53 | 196 | 23 | 82 |
| 37 | cpo-miR-216a-5p | 0 | 53 | 196 | 23 | 82 |
| 38 | dno-miR-216a-5p | 0 | 53 | 196 | 23 | 82 |
| 39 | ocu-miR-216a-5p | 0 | 53 | 196 | 23 | 82 |
| 40 | oha-miR-216-5p | 0 | 53 | 196 | 23 | 82 |
| 41 | ssc-miR-216 | 0 | 53 | 196 | 23 | 82 |
| 42 | xla-miR-216-5p | 0 | 53 | 196 | 23 | 82 |
| 43 | aca-miR-216a | 0 | 52 | 194 | 22 | 82 |
| 44 | bta-miR-216a | 0 | 52 | 194 | 22 | 82 |
| 45 | cja-miR-216a | 0 | 52 | 194 | 22 | 82 |
| 46 | cli-miR-216a-5p | 0 | 52 | 194 | 22 | 82 |
| 47 | cpi-miR-216a-5p | 0 | 52 | 194 | 22 | 82 |
| 48 | dre-miR-216a | 0 | 52 | 194 | 22 | 82 |
| 49 | eca-miR-216a | 0 | 52 | 194 | 22 | 82 |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|------------------|-------|------|-------|-------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | hsa-miR-216a-5p | 0 | 52 | 194 | 22 | 82 |
| 4 | ipu-miR-216a | 0 | 52 | 194 | 22 | 82 |
| 5 | mml-miR-216a-5p | 0 | 52 | 194 | 22 | 82 |
| 6 | mmu-miR-216a-5p | 0 | 52 | 194 | 22 | 82 |
| 7 | oan-miR-216a-5p | 0 | 52 | 194 | 22 | 82 |
| 8 | pbv-miR-216a-5p | 0 | 52 | 194 | 22 | 82 |
| 9 | rno-miR-216a-5p | 0 | 52 | 194 | 22 | 82 |
| 10 | ssa-miR-216b-5p | 0 | 52 | 194 | 22 | 82 |
| 11 | tgu-miR-216a-5p | 0 | 52 | 194 | 22 | 82 |
| 12 | ppt-miR160b | 140 | 221 | 113 | 163 | 136 |
| 13 | ppt-miR160i | 140 | 221 | 113 | 163 | 136 |
| 14 | gma-miR169k | 6868 | 8249 | 7252 | 5755 | 8943 |
| 15 | gma-miR169l-5p | 6868 | 8249 | 7252 | 5755 | 8943 |
| 16 | mes-miR169l | 6868 | 8249 | 7252 | 5755 | 8943 |
| 17 | mes-miR169m | 6868 | 8249 | 7252 | 5755 | 8943 |
| 18 | eun-miR167b-3p | 57 | 82 | 78 | 57 | 90 |
| 19 | aly-miR168a-3p | 11285 | 8749 | 11690 | 11552 | 9913 |
| 20 | ath-miR168a-3p | 11285 | 8749 | 11690 | 11552 | 9913 |
| 21 | bra-miR168b-3p | 11285 | 8749 | 11690 | 11552 | 9913 |
| 22 | bra-miR168c-3p | 11285 | 8749 | 11690 | 11552 | 9913 |
| 23 | cas-miR168 | 11285 | 8749 | 11690 | 11552 | 9913 |
| 24 | csi-miR168-3p | 11285 | 8749 | 11690 | 11552 | 9913 |
| 25 | fve-miR168-3p | 11285 | 8749 | 11690 | 11552 | 9913 |
| 26 | mtr-miR168c-3p | 11285 | 8749 | 11690 | 11552 | 9913 |
| 27 | ptc-miR168a-3p | 11285 | 8749 | 11690 | 11552 | 9913 |
| 28 | ptc-miR168b-3p | 11285 | 8749 | 11690 | 11552 | 9913 |
| 29 | sly-miR168b-3p | 11285 | 8749 | 11690 | 11552 | 9913 |
| 30 | lja-miR168-3p | 11316 | 8762 | 11718 | 11574 | 9938 |
| 31 | bdi-miR159b-3p.1 | 7101 | 5451 | 6272 | 6828 | 5467 |
| 32 | far-miR159 | 7101 | 5451 | 6272 | 6828 | 5467 |
| 33 | hvu-miR159a | 7101 | 5451 | 6272 | 6828 | 5467 |
| 34 | hvu-miR159b | 7101 | 5451 | 6272 | 6828 | 5467 |
| 35 | osa-miR159a.1 | 7101 | 5451 | 6272 | 6828 | 5467 |
| 36 | osa-miR159b | 7101 | 5451 | 6272 | 6828 | 5467 |
| 37 | sbi-miR159a | 7101 | 5451 | 6272 | 6828 | 5467 |
| 38 | sof-miR159a | 7101 | 5451 | 6272 | 6828 | 5467 |
| 39 | sof-miR159b | 7101 | 5451 | 6272 | 6828 | 5467 |
| 40 | sof-miR159d | 7101 | 5451 | 6272 | 6828 | 5467 |
| 41 | ssp-miR159a | 7101 | 5451 | 6272 | 6828 | 5467 |
| 42 | tae-miR159a | 7101 | 5451 | 6272 | 6828 | 5467 |
| 43 | tae-miR159b | 7101 | 5451 | 6272 | 6828 | 5467 |
| 44 | zma-miR159a-3p | 7101 | 5451 | 6272 | 6828 | 5467 |
| 45 | zma-miR159b-3p | 7101 | 5451 | 6272 | 6828 | 5467 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | zma-miR159f-3p | 7101 | 5451 | 6272 | 6828 | 5467 |
| 4 | zma-miR159j-3p | 7101 | 5451 | 6272 | 6828 | 5467 |
| 5 | zma-miR159k-3p | 7101 | 5451 | 6272 | 6828 | 5467 |
| 6 | zma-miR159k-3p | 7101 | 5451 | 6272 | 6828 | 5467 |
| 7 | cfa-miR-24 | 315 | 341 | 375 | 296 | 362 |
| 8 | cgr-miR-24-3p | 315 | 341 | 375 | 296 | 362 |
| 9 | ipu-miR-24 | 315 | 341 | 375 | 296 | 362 |
| 10 | ipu-miR-24 | 315 | 341 | 375 | 296 | 362 |
| 11 | oga-miR-24 | 315 | 341 | 375 | 296 | 362 |
| 12 | oga-miR-24 | 315 | 341 | 375 | 296 | 362 |
| 13 | oha-miR-24-3p | 315 | 341 | 375 | 296 | 362 |
| 14 | cpo-miR-27a-3p | 240 | 305 | 307 | 171 | 360 |
| 15 | tch-miR-27a-3p | 240 | 305 | 307 | 171 | 360 |
| 16 | abu-miR-24b-3p | 314 | 340 | 374 | 296 | 362 |
| 17 | abu-miR-24b-3p | 314 | 340 | 374 | 296 | 362 |
| 18 | aca-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 19 | ami-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 20 | ami-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 21 | bta-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 22 | ccb-miR-24 | 314 | 340 | 374 | 296 | 362 |
| 23 | cja-miR-24 | 314 | 340 | 374 | 296 | 362 |
| 24 | cja-miR-24 | 314 | 340 | 374 | 296 | 362 |
| 25 | cpo-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 26 | dno-miR-24a-3p | 314 | 340 | 374 | 296 | 362 |
| 27 | dre-miR-24 | 314 | 340 | 374 | 296 | 362 |
| 28 | eca-miR-24 | 314 | 340 | 374 | 296 | 362 |
| 29 | eca-miR-24 | 314 | 340 | 374 | 296 | 362 |
| 30 | fru-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 31 | gga-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 32 | ggo-miR-24 | 314 | 340 | 374 | 296 | 362 |
| 33 | ggo-miR-24 | 314 | 340 | 374 | 296 | 362 |
| 34 | hsa-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 35 | mml-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 36 | mmu-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 37 | mmu-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 38 | mne-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 39 | nbr-miR-24a | 314 | 340 | 374 | 296 | 362 |
| 40 | oan-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 41 | oan-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 42 | ocu-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 43 | ola-miR-24a | 314 | 340 | 374 | 296 | 362 |
| 44 | oni-miR-24a | 314 | 340 | 374 | 296 | 362 |
| 45 | oni-miR-24a | 314 | 340 | 374 | 296 | 362 |
| 46 | pbv-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 47 | pma-miR-24 | 314 | 340 | 374 | 296 | 362 |
| 48 | pony-miR-24a | 314 | 340 | 374 | 296 | 362 |
| 49 | pony-miR-24a | 314 | 340 | 374 | 296 | 362 |
| 50 | ppa-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 51 | ppy-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 52 | ptr-miR-24 | 314 | 340 | 374 | 296 | 362 |
| 53 | ptr-miR-24 | 314 | 340 | 374 | 296 | 362 |
| 54 | rno-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 55 | ssc-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 56 | tgu-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 57 | tgu-miR-24-3p | 314 | 340 | 374 | 296 | 362 |
| 58 | tni-miR-24 | 314 | 340 | 374 | 296 | 362 |
| 59 | xla-miR-24a-3p | 314 | 340 | 374 | 296 | 362 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | xtr-miR-24a-3p | 314 | 340 | 374 | 296 | 362 |
| 4 | dre-miR-27a-3p | 371 | 363 | 323 | 231 | 421 |
| 5 | ipu-miR-27a | 371 | 363 | 323 | 231 | 421 |
| 6 | ssa-miR-27a-3p | 371 | 363 | 323 | 231 | 421 |
| 7 | ssa-miR-27a-3p | 371 | 363 | 323 | 231 | 421 |
| 8 | gma-miR169u | 194 | 322 | 243 | 235 | 264 |
| 9 | gma-miR169u | 194 | 322 | 243 | 235 | 264 |
| 10 | aly-miR159b-3p | 7112 | 5791 | 6708 | 7202 | 5808 |
| 11 | ath-miR159b-3p | 7112 | 5791 | 6708 | 7202 | 5808 |
| 12 | ath-miR159b-3p | 7112 | 5791 | 6708 | 7202 | 5808 |
| 13 | cas-miR159b-3p | 7112 | 5791 | 6708 | 7202 | 5808 |
| 14 | cas-miR159c-3p | 7112 | 5791 | 6708 | 7202 | 5808 |
| 15 | lus-miR159c | 7112 | 5791 | 6708 | 7202 | 5808 |
| 16 | lus-miR159b | 6733 | 5459 | 6276 | 6835 | 5464 |
| 17 | lus-miR159b | 6733 | 5459 | 6276 | 6835 | 5464 |
| 18 | age-miR-27a | 322 | 338 | 307 | 213 | 395 |
| 19 | ggo-miR-27a | 322 | 338 | 307 | 213 | 395 |
| 20 | ggo-miR-27a | 322 | 338 | 307 | 213 | 395 |
| 21 | lca-miR-27a | 322 | 338 | 307 | 213 | 395 |
| 22 | mml-miR-27a-3p | 322 | 338 | 307 | 213 | 395 |
| 23 | mml-miR-27a-3p | 322 | 338 | 307 | 213 | 395 |
| 24 | mne-miR-27a | 322 | 338 | 307 | 213 | 395 |
| 25 | oha-miR-27a-3p | 322 | 338 | 307 | 213 | 395 |
| 26 | ppa-miR-27a | 322 | 338 | 307 | 213 | 395 |
| 27 | ppy-miR-27a | 322 | 338 | 307 | 213 | 395 |
| 28 | ptr-miR-27a | 322 | 338 | 307 | 213 | 395 |
| 29 | ptr-miR-27a | 322 | 338 | 307 | 213 | 395 |
| 30 | sla-miR-27a | 322 | 338 | 307 | 213 | 395 |
| 31 | gma-miR1515a | 8322 | 9086 | 9113 | 9201 | 9449 |
| 32 | gma-miR1515b | 8322 | 9086 | 9113 | 9201 | 9449 |
| 33 | gma-miR1515b | 8322 | 9086 | 9113 | 9201 | 9449 |
| 34 | abu-miR-27a | 321 | 336 | 307 | 212 | 395 |
| 35 | aca-miR-27a-3p | 321 | 336 | 307 | 212 | 395 |
| 36 | ami-miR-27a-3p | 321 | 336 | 307 | 212 | 395 |
| 37 | ami-miR-27a-3p | 321 | 336 | 307 | 212 | 395 |
| 38 | ccr-miR-27a | 321 | 336 | 307 | 212 | 395 |
| 39 | cgr-miR-27a-3p | 321 | 336 | 307 | 212 | 395 |
| 40 | cja-miR-27a | 321 | 336 | 307 | 212 | 395 |
| 41 | cja-miR-27a | 321 | 336 | 307 | 212 | 395 |
| 42 | cpi-miR-27a-3p | 321 | 336 | 307 | 212 | 395 |
| 43 | dno-miR-27a-3p | 321 | 336 | 307 | 212 | 395 |
| 44 | eca-miR-27a | 321 | 336 | 307 | 212 | 395 |
| 45 | eca-miR-27a | 321 | 336 | 307 | 212 | 395 |
| 46 | hsa-miR-27a-3p | 321 | 336 | 307 | 212 | 395 |
| 47 | mdo-miR-27a-3p | 321 | 336 | 307 | 212 | 395 |
| 48 | mmu-miR-27a-3p | 321 | 336 | 307 | 212 | 395 |
| 49 | mmu-miR-27a-3p | 321 | 336 | 307 | 212 | 395 |
| 50 | mze-miR-27a | 321 | 336 | 307 | 212 | 395 |
| 51 | nbr-miR-27a | 321 | 336 | 307 | 212 | 395 |
| 52 | oan-miR-27a-3p | 321 | 336 | 307 | 212 | 395 |
| 53 | oar-miR-27a | 321 | 336 | 307 | 212 | 395 |
| 54 | oar-miR-27a | 321 | 336 | 307 | 212 | 395 |
| 55 | oni-miR-27a | 321 | 336 | 307 | 212 | 395 |
| 56 | pbv-miR-27a-3p | 321 | 336 | 307 | 212 | 395 |
| 57 | pony-miR-27a | 321 | 336 | 307 | 212 | 395 |
| 58 | pony-miR-27a | 321 | 336 | 307 | 212 | 395 |
| 59 | rno-miR-27a-3p | 321 | 336 | 307 | 212 | 395 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | sbo-miR-27a | 321 | 336 | 307 | 212 | 395 |
| 4 | ssc-miR-27a | 321 | 336 | 307 | 212 | 395 |
| 5 | xtr-miR-27a | 321 | 336 | 307 | 212 | 395 |
| 6 | mtr-miR171c | 68 | 35 | 65 | 57 | 56 |
| 7 | csi-miR160a-5p | 143 | 213 | 110 | 176 | 127 |
| 8 | htu-miR171a | 66 | 32 | 63 | 54 | 54 |
| 9 | bta-miR-27a-3p | 186 | 259 | 253 | 146 | 314 |
| 10 | cfa-miR-27a | 186 | 259 | 253 | 146 | 314 |
| 11 | chi-miR-27a-3p | 186 | 259 | 253 | 146 | 314 |
| 12 | gmo-miR-27d-3p | 186 | 259 | 253 | 146 | 314 |
| 13 | oga-miR-27a | 186 | 259 | 253 | 146 | 314 |
| 14 | ola-miR-27a | 186 | 259 | 253 | 146 | 314 |
| 15 | pal-miR-27a-3p | 186 | 259 | 253 | 146 | 314 |
| 16 | xla-miR-27a-3p | 186 | 259 | 253 | 146 | 314 |
| 17 | ppe-miR398b | 90 | 204 | 173 | 190 | 132 |
| 18 | pvu-miR1514a | 6440 | 5014 | 5169 | 5730 | 6269 |
| 19 | lja-miR398-3p | 244 | 215 | 201 | 208 | 250 |
| 20 | stu-miR398b-3p | 244 | 215 | 201 | 208 | 250 |
| 21 | aof-miR171c | 558 | 594 | 556 | 633 | 559 |
| 22 | csi-miR171e-3p | 558 | 594 | 556 | 633 | 559 |
| 23 | csi-miR171g-3p | 558 | 594 | 556 | 633 | 559 |
| 24 | ctr-miR171 | 558 | 594 | 556 | 633 | 559 |
| 25 | fve-miR171h | 558 | 594 | 556 | 633 | 559 |
| 26 | mdm-miR171a | 558 | 594 | 556 | 633 | 559 |
| 27 | mdm-miR171b | 558 | 594 | 556 | 633 | 559 |
| 28 | mdm-miR171p | 558 | 594 | 556 | 633 | 559 |
| 29 | mes-miR171a | 558 | 594 | 556 | 633 | 559 |
| 30 | ppe-miR171h | 558 | 594 | 556 | 633 | 559 |
| 31 | gma-miR319p | 782 | 300 | 384 | 525 | 514 |
| 32 | cpi-miR-24-3p | 113 | 167 | 178 | 134 | 178 |
| 33 | sbo-miR-24 | 113 | 167 | 178 | 134 | 178 |
| 34 | sly-miR171e | 650 | 620 | 638 | 712 | 643 |
| 35 | stu-miR171b-3p | 650 | 620 | 638 | 712 | 643 |
| 36 | gma-miR169l-3p | 188 | 237 | 210 | 201 | 252 |
| 37 | bta-miR-451 | 2138 | 3477 | 2414 | 2108 | 3233 |
| 38 | cja-miR-451 | 2138 | 3477 | 2414 | 2108 | 3233 |
| 39 | cpo-miR-451-5p | 2138 | 3477 | 2414 | 2108 | 3233 |
| 40 | dno-miR-451-5p | 2138 | 3477 | 2414 | 2108 | 3233 |
| 41 | gga-miR-451 | 2138 | 3477 | 2414 | 2108 | 3233 |
| 42 | oan-miR-451 | 2138 | 3477 | 2414 | 2108 | 3233 |
| 43 | ocu-miR-451-5p | 2138 | 3477 | 2414 | 2108 | 3233 |
| 44 | oha-miR-451-?? | 2138 | 3477 | 2414 | 2108 | 3233 |
| 45 | tgu-miR-451 | 2138 | 3477 | 2414 | 2108 | 3233 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | aly-miR169a-5p | 156 | 232 | 193 | 178 | 222 |
| 4 | ata-miR169e-5p | 156 | 232 | 193 | 178 | 222 |
| 5 | ata-miR169f-5p | 156 | 232 | 193 | 178 | 222 |
| 6 | ata-miR169g-5p | 156 | 232 | 193 | 178 | 222 |
| 7 | ata-miR169g-5p | 156 | 232 | 193 | 178 | 222 |
| 8 | ath-miR169a-5p | 156 | 232 | 193 | 178 | 222 |
| 9 | ath-miR169a-5p | 156 | 232 | 193 | 178 | 222 |
| 10 | bdi-miR169a-5p | 156 | 232 | 193 | 178 | 222 |
| 11 | bna-miR169a | 156 | 232 | 193 | 178 | 222 |
| 12 | bna-miR169b | 156 | 232 | 193 | 178 | 222 |
| 13 | bna-miR169b | 156 | 232 | 193 | 178 | 222 |
| 14 | cas-miR169a | 156 | 232 | 193 | 178 | 222 |
| 15 | gma-miR169b | 156 | 232 | 193 | 178 | 222 |
| 16 | lus-miR169g | 156 | 232 | 193 | 178 | 222 |
| 17 | lus-miR169g | 156 | 232 | 193 | 178 | 222 |
| 18 | lus-miR169l | 156 | 232 | 193 | 178 | 222 |
| 19 | mes-miR169g | 156 | 232 | 193 | 178 | 222 |
| 20 | mes-miR169g | 156 | 232 | 193 | 178 | 222 |
| 21 | mtr-miR169a | 156 | 232 | 193 | 178 | 222 |
| 22 | nta-miR169a | 156 | 232 | 193 | 178 | 222 |
| 23 | nta-miR169a | 156 | 232 | 193 | 178 | 222 |
| 24 | nta-miR169b | 156 | 232 | 193 | 178 | 222 |
| 25 | nta-miR169c | 156 | 232 | 193 | 178 | 222 |
| 26 | nta-miR169d | 156 | 232 | 193 | 178 | 222 |
| 27 | nta-miR169e | 156 | 232 | 193 | 178 | 222 |
| 28 | nta-miR169f | 156 | 232 | 193 | 178 | 222 |
| 29 | nta-miR169f | 156 | 232 | 193 | 178 | 222 |
| 30 | nta-miR169g | 156 | 232 | 193 | 178 | 222 |
| 31 | nta-miR169g | 156 | 232 | 193 | 178 | 222 |
| 32 | nta-miR169h | 156 | 232 | 193 | 178 | 222 |
| 33 | nta-miR169i | 156 | 232 | 193 | 178 | 222 |
| 34 | nta-miR169j | 156 | 232 | 193 | 178 | 222 |
| 35 | nta-miR169k | 156 | 232 | 193 | 178 | 222 |
| 36 | nta-miR169l | 156 | 232 | 193 | 178 | 222 |
| 37 | nta-miR169l | 156 | 232 | 193 | 178 | 222 |
| 38 | nta-miR169m | 156 | 232 | 193 | 178 | 222 |
| 39 | nta-miR169o | 156 | 232 | 193 | 178 | 222 |
| 40 | nta-miR169p | 156 | 232 | 193 | 178 | 222 |
| 41 | nta-miR169p | 156 | 232 | 193 | 178 | 222 |
| 42 | osa-miR169a | 156 | 232 | 193 | 178 | 222 |
| 43 | ptc-miR169a | 156 | 232 | 193 | 178 | 222 |
| 44 | ptc-miR169a | 156 | 232 | 193 | 178 | 222 |
| 45 | ptc-miR169b-5p | 156 | 232 | 193 | 178 | 222 |
| 46 | ptc-miR169c | 156 | 232 | 193 | 178 | 222 |
| 47 | ptc-miR169c | 156 | 232 | 193 | 178 | 222 |
| 48 | sbi-miR169a | 156 | 232 | 193 | 178 | 222 |
| 49 | sly-miR169c | 156 | 232 | 193 | 178 | 222 |
| 50 | tcc-miR169a | 156 | 232 | 193 | 178 | 222 |
| 51 | tcc-miR169c | 156 | 232 | 193 | 178 | 222 |
| 52 | tcc-miR169c | 156 | 232 | 193 | 178 | 222 |
| 53 | tcc-miR169e | 156 | 232 | 193 | 178 | 222 |
| 54 | vvi-miR169f | 156 | 232 | 193 | 178 | 222 |
| 55 | vvi-miR169g | 156 | 232 | 193 | 178 | 222 |
| 56 | vvi-miR169g | 156 | 232 | 193 | 178 | 222 |
| 57 | zma-miR169a-5p | 156 | 232 | 193 | 178 | 222 |
| 58 | zma-miR169b-5p | 156 | 232 | 193 | 178 | 222 |
| 59 | lus-miR398f | 83 | 201 | 178 | 192 | 134 |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|--------|-------|--------|--------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | sly-miR156e-3p | 3491 | 2619 | 3494 | 3738 | 3412 |
| 4 | stu-miR156g-3p | 3491 | 2619 | 3494 | 3738 | 3412 |
| 5 | cas-miR156k-3p | 3496 | 2620 | 3499 | 3743 | 3418 |
| 6 | mtr-miR156c-3p | 3496 | 2620 | 3499 | 3743 | 3418 |
| 7 | ptc-miR169s | 152 | 230 | 188 | 178 | 217 |
| 8 | | | | | | |
| 9 | gma-miR2118a-3p | 4554 | 3424 | 4675 | 5118 | 4056 |
| 10 | gma-miR2118b-3p | 4554 | 3424 | 4675 | 5118 | 4056 |
| 11 | | | | | | |
| 12 | cme-miR169t | 55 | 85 | 57 | 55 | 76 |
| 13 | cme-miR169r | 55 | 85 | 56 | 55 | 74 |
| 14 | mes-miR169i | 55 | 85 | 56 | 55 | 74 |
| 15 | mes-miR169j | 55 | 85 | 56 | 55 | 74 |
| 16 | mes-miR169k | 55 | 85 | 56 | 55 | 74 |
| 17 | ptc-miR169t | 55 | 85 | 56 | 55 | 74 |
| 18 | smo-miR171a | 90 | 75 | 72 | 101 | 88 |
| 19 | | | | | | |
| 20 | gso-miR2218 | 208359 | 92323 | 117761 | 205633 | 84468 |
| 21 | | | | | | |
| 22 | pvu-miR2118 | 208359 | 92323 | 117761 | 205633 | 84468 |
| 23 | | | | | | |
| 24 | vun-miR2118 | 208359 | 92323 | 117761 | 205633 | 84468 |
| 25 | | | | | | |
| 26 | aly-miR164c-5p | 162 | 120 | 47 | 149 | 74 |
| 27 | ath-miR164c-5p | 162 | 120 | 47 | 149 | 74 |
| 28 | bnm-miR164b | 162 | 120 | 47 | 149 | 74 |
| 29 | bnm-miR164c | 162 | 120 | 47 | 149 | 74 |
| 30 | bnm-miR164d | 162 | 120 | 47 | 149 | 74 |
| 31 | bra-miR164b-5p | 162 | 120 | 47 | 149 | 74 |
| 32 | bra-miR164c-5p | 162 | 120 | 47 | 149 | 74 |
| 33 | bra-miR164d-5p | 162 | 120 | 47 | 149 | 74 |
| 34 | cln-miR164 | 162 | 120 | 47 | 149 | 74 |
| 35 | | | | | | |
| 36 | gma-miR403a | 7423 | 9152 | 8806 | 11066 | 9104 |
| 37 | gma-miR403b | 7423 | 9152 | 8806 | 11066 | 9104 |
| 38 | mes-miR319h | 246 | 211 | 206 | 260 | 191 |
| 39 | vun-miR319b | 246 | 211 | 206 | 260 | 191 |
| 40 | aly-miR319c-3p | 249 | 223 | 210 | 269 | 192 |
| 41 | aly-miR319d-3p | 249 | 223 | 210 | 269 | 192 |
| 42 | ath-miR319c | 249 | 223 | 210 | 269 | 192 |
| 43 | mes-miR319g | 249 | 223 | 210 | 269 | 192 |
| 44 | pvu-miR319c | 249 | 223 | 210 | 269 | 192 |
| 45 | rco-miR319d | 249 | 223 | 210 | 269 | 192 |
| 46 | sly-miR319c-3p | 249 | 223 | 210 | 269 | 192 |
| 47 | csi-miR858-3p | 197 | 158 | 133 | 206 | 178 |
| 48 | ppe-miR858 | 197 | 158 | 133 | 206 | 178 |
| 49 | csi-miR171a | 87 | 72 | 70 | 98 | 87 |
| 50 | zma-miR171b-3p | 87 | 72 | 70 | 98 | 87 |
| 51 | cme-miR319c | 236 | 200 | 198 | 246 | 186 |
| 52 | cme-miR319d | 236 | 200 | 198 | 246 | 186 |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | gma-miR319c | 236 | 200 | 198 | 246 | 186 |
| 4 | ptc-miR319e | 236 | 200 | 198 | 246 | 186 |
| 5 | ptc-miR319f | 236 | 200 | 198 | 246 | 186 |
| 6 | ptc-miR319g | 236 | 200 | 198 | 246 | 186 |
| 7 | ptc-miR319h | 236 | 200 | 198 | 246 | 186 |
| 8 | stu-miR319b | 236 | 200 | 198 | 246 | 186 |
| 9 | gma-miR164b | 161 | 118 | 44 | 147 | 74 |
| 10 | gma-miR164c | 161 | 118 | 44 | 147 | 74 |
| 11 | gma-miR164d | 161 | 118 | 44 | 147 | 74 |
| 12 | aca-miR-451-5p | 1022 | 2047 | 1417 | 1272 | 1853 |
| 13 | cfa-miR-451 | 1022 | 2047 | 1417 | 1272 | 1853 |
| 14 | cgr-miR-451a | 1022 | 2047 | 1417 | 1272 | 1853 |
| 15 | dre-miR-451 | 1022 | 2047 | 1417 | 1272 | 1853 |
| 16 | hsa-miR-451a | 1022 | 2047 | 1417 | 1272 | 1853 |
| 17 | mml-miR-451 | 1022 | 2047 | 1417 | 1272 | 1853 |
| 18 | mmu-miR-451a | 1022 | 2047 | 1417 | 1272 | 1853 |
| 19 | ppy-miR-451 | 1022 | 2047 | 1417 | 1272 | 1853 |
| 20 | ptr-miR-451 | 1022 | 2047 | 1417 | 1272 | 1853 |
| 21 | rno-miR-451-5p | 1022 | 2047 | 1417 | 1272 | 1853 |
| 22 | ssc-miR-451 | 1022 | 2047 | 1417 | 1272 | 1853 |
| 23 | xtr-miR-451 | 1022 | 2047 | 1417 | 1272 | 1853 |
| 24 | bta-miR-146b | 10 | 54 | 85 | 44 | 70 |
| 25 | chi-miR-146b-5p | 10 | 54 | 85 | 44 | 70 |
| 26 | cja-miR-146b | 10 | 54 | 85 | 44 | 70 |
| 27 | dno-miR-146b-5p | 10 | 54 | 85 | 44 | 70 |
| 28 | ggo-miR-146b | 10 | 54 | 85 | 44 | 70 |
| 29 | mmr-miR-146b | 10 | 54 | 85 | 44 | 70 |
| 30 | nle-miR-146b | 10 | 54 | 85 | 44 | 70 |
| 31 | pal-miR-146b-5p | 10 | 54 | 85 | 44 | 70 |
| 32 | pha-miR-146b | 10 | 54 | 85 | 44 | 70 |
| 33 | ppa-miR-146b | 10 | 54 | 85 | 44 | 70 |
| 34 | rno-miR-146b-5p | 10 | 54 | 85 | 44 | 70 |
| 35 | sbo-miR-146b | 10 | 54 | 85 | 44 | 70 |
| 36 | aqc-miR166a | 53 | 98 | 104 | 113 | 82 |
| 37 | aqc-miR166d | 53 | 98 | 104 | 113 | 82 |
| 38 | cme-miR166e | 53 | 98 | 104 | 113 | 82 |
| 39 | dpr-miR166a | 53 | 98 | 104 | 113 | 82 |
| 40 | lus-miR166e | 53 | 98 | 104 | 113 | 82 |
| 41 | mtr-miR166c | 53 | 98 | 104 | 113 | 82 |
| 42 | mtr-miR166f | 53 | 98 | 104 | 113 | 82 |
| 43 | osa-miR166g-3p | 53 | 98 | 104 | 113 | 82 |
| 44 | osa-miR166h-3p | 53 | 98 | 104 | 113 | 82 |
| 45 | pab-miR166a | 53 | 98 | 104 | 113 | 82 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | sbi-miR166f | 53 | 98 | 104 | 113 | 82 |
| 4 | sly-miR166c-3p | 53 | 98 | 104 | 113 | 82 |
| 5 | ssl-miR166a | 53 | 98 | 104 | 113 | 82 |
| 6 | ssl-miR166a | 53 | 98 | 104 | 113 | 82 |
| 7 | stu-miR166b | 53 | 98 | 104 | 113 | 82 |
| 8 | tcc-miR166c | 53 | 98 | 104 | 113 | 82 |
| 9 | tcc-miR166c | 53 | 98 | 104 | 113 | 82 |
| 10 | zma-miR166l-3p | 53 | 98 | 104 | 113 | 82 |
| 11 | zma-miR166m-3p | 53 | 98 | 104 | 113 | 82 |
| 12 | zma-miR166m-3p | 53 | 98 | 104 | 113 | 82 |
| 13 | cfa-miR-181a | 37 | 83 | 114 | 49 | 106 |
| 14 | ipu-miR-181a | 37 | 83 | 114 | 49 | 106 |
| 15 | mmr-miR-181a | 37 | 83 | 114 | 49 | 106 |
| 16 | oni-miR-181c | 37 | 83 | 114 | 49 | 106 |
| 17 | oni-miR-181c | 37 | 83 | 114 | 49 | 106 |
| 18 | sbo-miR-181a | 37 | 83 | 114 | 49 | 106 |
| 19 | gma-miR169j-5p | 52 | 92 | 58 | 58 | 81 |
| 20 | ata-miR164a-5p | 176 | 122 | 48 | 165 | 80 |
| 21 | ata-miR164a-5p | 176 | 122 | 48 | 165 | 80 |
| 22 | bdi-miR164c-5p | 176 | 122 | 48 | 165 | 80 |
| 23 | cme-miR164a | 176 | 122 | 48 | 165 | 80 |
| 24 | osa-miR164d | 176 | 122 | 48 | 165 | 80 |
| 25 | osa-miR164d | 176 | 122 | 48 | 165 | 80 |
| 26 | sbi-miR164b | 176 | 122 | 48 | 165 | 80 |
| 27 | zma-miR164f-5p | 176 | 122 | 48 | 165 | 80 |
| 28 | gma-miR319i | 236 | 227 | 265 | 341 | 247 |
| 29 | gma-miR319i | 236 | 227 | 265 | 341 | 247 |
| 30 | aof-miR319b | 4672 | 2814 | 3138 | 4518 | 3420 |
| 31 | atr-miR319b | 4672 | 2814 | 3138 | 4518 | 3420 |
| 32 | atr-miR319d | 4672 | 2814 | 3138 | 4518 | 3420 |
| 33 | atr-miR319d | 4672 | 2814 | 3138 | 4518 | 3420 |
| 34 | atr-miR319e | 4672 | 2814 | 3138 | 4518 | 3420 |
| 35 | cas-miR319c | 4672 | 2814 | 3138 | 4518 | 3420 |
| 36 | csi-miR159d | 4672 | 2814 | 3138 | 4518 | 3420 |
| 37 | csi-miR159d | 4672 | 2814 | 3138 | 4518 | 3420 |
| 38 | fve-miR319 | 4672 | 2814 | 3138 | 4518 | 3420 |
| 39 | tcc-miR319 | 4672 | 2814 | 3138 | 4518 | 3420 |
| 40 | vvi-miR319e | 4672 | 2814 | 3138 | 4518 | 3420 |
| 41 | vvi-miR319e | 4672 | 2814 | 3138 | 4518 | 3420 |
| 42 | gma-miR319d | 227 | 215 | 254 | 333 | 240 |
| 43 | gma-miR319o | 227 | 215 | 254 | 333 | 240 |
| 44 | efu-miR-93 | 47 | 76 | 69 | 48 | 88 |
| 45 | ccr-miR-181a | 16 | 73 | 83 | 36 | 79 |
| 46 | ccr-miR-181a | 16 | 73 | 83 | 36 | 79 |
| 47 | xla-miR-181a-5p | 16 | 73 | 83 | 36 | 79 |
| 48 | eun-miR160-3p | 61 | 100 | 57 | 105 | 75 |
| 49 | gma-miR160a-3p | 61 | 100 | 57 | 105 | 75 |
| 50 | gma-miR160a-3p | 61 | 100 | 57 | 105 | 75 |
| 51 | stu-miR160a-3p | 61 | 100 | 57 | 105 | 75 |
| 52 | gma-miR1511 | 7940 | 9451 | 8131 | 9671 | 9157 |
| 53 | ami-miR-93-5p | 43 | 75 | 65 | 46 | 87 |
| 54 | ami-miR-93-5p | 43 | 75 | 65 | 46 | 87 |
| 55 | cfa-miR-93 | 43 | 75 | 65 | 46 | 87 |
| 56 | cgr-miR-93-5p | 43 | 75 | 65 | 46 | 87 |
| 57 | chi-miR-93-5p | 43 | 75 | 65 | 46 | 87 |
| 58 | chi-miR-93-5p | 43 | 75 | 65 | 46 | 87 |
| 59 | cja-miR-93 | 43 | 75 | 65 | 46 | 87 |
| 60 | cja-miR-93 | 43 | 75 | 65 | 46 | 87 |

| | | | | | | |
|----|----------------|------|------|------|------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | cpo-miR-93-5p | 43 | 75 | 65 | 46 | 87 |
| 4 | dma-miR-93 | 43 | 75 | 65 | 46 | 87 |
| 5 | dno-miR-93-5p | 43 | 75 | 65 | 46 | 87 |
| 6 | eca-miR-93 | 43 | 75 | 65 | 46 | 87 |
| 7 | eca-miR-93 | 43 | 75 | 65 | 46 | 87 |
| 8 | hsa-miR-93-5p | 43 | 75 | 65 | 46 | 87 |
| 9 | hsa-miR-93-5p | 43 | 75 | 65 | 46 | 87 |
| 10 | mmu-miR-93-5p | 43 | 75 | 65 | 46 | 87 |
| 11 | nle-miR-93 | 43 | 75 | 65 | 46 | 87 |
| 12 | nle-miR-93 | 43 | 75 | 65 | 46 | 87 |
| 13 | ocu-miR-93-5p | 43 | 75 | 65 | 46 | 87 |
| 14 | oga-miR-93 | 43 | 75 | 65 | 46 | 87 |
| 15 | pal-miR-93-5p | 43 | 75 | 65 | 46 | 87 |
| 16 | pha-miR-93 | 43 | 75 | 65 | 46 | 87 |
| 17 | pha-miR-93 | 43 | 75 | 65 | 46 | 87 |
| 18 | rno-miR-93-5p | 43 | 75 | 65 | 46 | 87 |
| 19 | tch-miR-93-5p | 43 | 75 | 65 | 46 | 87 |
| 20 | tch-miR-93-5p | 43 | 75 | 65 | 46 | 87 |
| 21 | xla-miR-93-5p | 43 | 75 | 65 | 46 | 87 |
| 22 | aau-miR162 | 7770 | 6558 | 7618 | 8453 | 10462 |
| 23 | aly-miR162a-3p | 7770 | 6558 | 7618 | 8453 | 10462 |
| 24 | aly-miR162b-3p | 7770 | 6558 | 7618 | 8453 | 10462 |
| 25 | aly-miR162b-3p | 7770 | 6558 | 7618 | 8453 | 10462 |
| 26 | ath-miR162a-3p | 7770 | 6558 | 7618 | 8453 | 10462 |
| 27 | ath-miR162b-3p | 7770 | 6558 | 7618 | 8453 | 10462 |
| 28 | ath-miR162b-3p | 7770 | 6558 | 7618 | 8453 | 10462 |
| 29 | bra-miR162-3p | 7770 | 6558 | 7618 | 8453 | 10462 |
| 30 | cme-miR162 | 7770 | 6558 | 7618 | 8453 | 10462 |
| 31 | cpa-miR162a | 7770 | 6558 | 7618 | 8453 | 10462 |
| 32 | csi-miR162-3p | 7770 | 6558 | 7618 | 8453 | 10462 |
| 33 | csi-miR162-3p | 7770 | 6558 | 7618 | 8453 | 10462 |
| 34 | eun-miR162-3p | 7770 | 6558 | 7618 | 8453 | 10462 |
| 35 | fve-miR162-3p | 7770 | 6558 | 7618 | 8453 | 10462 |
| 36 | ghr-miR162a | 7770 | 6558 | 7618 | 8453 | 10462 |
| 37 | ghr-miR162a | 7770 | 6558 | 7618 | 8453 | 10462 |
| 38 | gma-miR162b | 7770 | 6558 | 7618 | 8453 | 10462 |
| 39 | gma-miR162c | 7770 | 6558 | 7618 | 8453 | 10462 |
| 40 | hpe-miR162a | 7770 | 6558 | 7618 | 8453 | 10462 |
| 41 | hpe-miR162a | 7770 | 6558 | 7618 | 8453 | 10462 |
| 42 | htu-miR162a | 7770 | 6558 | 7618 | 8453 | 10462 |
| 43 | lus-miR162a | 7770 | 6558 | 7618 | 8453 | 10462 |
| 44 | lus-miR162a | 7770 | 6558 | 7618 | 8453 | 10462 |
| 45 | lus-miR162b | 7770 | 6558 | 7618 | 8453 | 10462 |
| 46 | mdm-miR162a | 7770 | 6558 | 7618 | 8453 | 10462 |
| 47 | mdm-miR162b | 7770 | 6558 | 7618 | 8453 | 10462 |
| 48 | mes-miR162 | 7770 | 6558 | 7618 | 8453 | 10462 |
| 49 | mes-miR162 | 7770 | 6558 | 7618 | 8453 | 10462 |
| 50 | mtr-miR162 | 7770 | 6558 | 7618 | 8453 | 10462 |
| 51 | nta-miR162a | 7770 | 6558 | 7618 | 8453 | 10462 |
| 52 | nta-miR162b | 7770 | 6558 | 7618 | 8453 | 10462 |
| 53 | nta-miR162b | 7770 | 6558 | 7618 | 8453 | 10462 |
| 54 | osa-miR162a | 7770 | 6558 | 7618 | 8453 | 10462 |
| 55 | pde-miR162 | 7770 | 6558 | 7618 | 8453 | 10462 |
| 56 | ppe-miR162 | 7770 | 6558 | 7618 | 8453 | 10462 |
| 57 | ppe-miR162 | 7770 | 6558 | 7618 | 8453 | 10462 |
| 58 | ptc-miR162a | 7770 | 6558 | 7618 | 8453 | 10462 |
| 59 | ptc-miR162b | 7770 | 6558 | 7618 | 8453 | 10462 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | rco-miR162 | 7770 | 6558 | 7618 | 8453 | 10462 |
| 4 | sbi-miR162 | 7770 | 6558 | 7618 | 8453 | 10462 |
| 5 | sly-miR162 | 7770 | 6558 | 7618 | 8453 | 10462 |
| 6 | stu-miR162a-3p | 7770 | 6558 | 7618 | 8453 | 10462 |
| 7 | stu-miR162b-3p | 7770 | 6558 | 7618 | 8453 | 10462 |
| 8 | tcc-miR162 | 7770 | 6558 | 7618 | 8453 | 10462 |
| 9 | vun-miR162 | 7770 | 6558 | 7618 | 8453 | 10462 |
| 10 | vvi-miR162 | 7770 | 6558 | 7618 | 8453 | 10462 |
| 11 | aly-miR396b-5p | 9275 | 5516 | 6221 | 9477 | 8412 |
| 12 | ama-miR396-5p | 9275 | 5516 | 6221 | 9477 | 8412 |
| 13 | aqc-miR396b | 9275 | 5516 | 6221 | 9477 | 8412 |
| 14 | ata-miR396c-5p | 9275 | 5516 | 6221 | 9477 | 8412 |
| 15 | ath-miR396b-5p | 9275 | 5516 | 6221 | 9477 | 8412 |
| 16 | atr-miR396b | 9275 | 5516 | 6221 | 9477 | 8412 |
| 17 | atr-miR396c | 9275 | 5516 | 6221 | 9477 | 8412 |
| 18 | atr-miR396e | 9275 | 5516 | 6221 | 9477 | 8412 |
| 19 | bcy-miR396b | 9275 | 5516 | 6221 | 9477 | 8412 |
| 20 | bdi-miR396e-5p | 9275 | 5516 | 6221 | 9477 | 8412 |
| 21 | bgy-miR396b | 9275 | 5516 | 6221 | 9477 | 8412 |
| 22 | bna-miR396a | 9275 | 5516 | 6221 | 9477 | 8412 |
| 23 | bra-miR396-5p | 9275 | 5516 | 6221 | 9477 | 8412 |
| 24 | cas-miR396b | 9275 | 5516 | 6221 | 9477 | 8412 |
| 25 | cca-miR396a-5p | 9275 | 5516 | 6221 | 9477 | 8412 |
| 26 | ccl-miR396 | 9275 | 5516 | 6221 | 9477 | 8412 |
| 27 | cme-miR396a | 9275 | 5516 | 6221 | 9477 | 8412 |
| 28 | cme-miR396c | 9275 | 5516 | 6221 | 9477 | 8412 |
| 29 | cme-miR396d | 9275 | 5516 | 6221 | 9477 | 8412 |
| 30 | csi-miR396f-5p | 9275 | 5516 | 6221 | 9477 | 8412 |
| 31 | fve-miR396b-5p | 9275 | 5516 | 6221 | 9477 | 8412 |
| 32 | gma-miR396b-5p | 9275 | 5516 | 6221 | 9477 | 8412 |
| 33 | gma-miR396c | 9275 | 5516 | 6221 | 9477 | 8412 |
| 34 | gma-miR396k-5p | 9275 | 5516 | 6221 | 9477 | 8412 |
| 35 | lus-miR396b | 9275 | 5516 | 6221 | 9477 | 8412 |
| 36 | lus-miR396e | 9275 | 5516 | 6221 | 9477 | 8412 |
| 37 | mdm-miR396c | 9275 | 5516 | 6221 | 9477 | 8412 |
| 38 | mdm-miR396d | 9275 | 5516 | 6221 | 9477 | 8412 |
| 39 | mdm-miR396e | 9275 | 5516 | 6221 | 9477 | 8412 |
| 40 | mes-miR396c | 9275 | 5516 | 6221 | 9477 | 8412 |
| 41 | mes-miR396d | 9275 | 5516 | 6221 | 9477 | 8412 |
| 42 | mes-miR396e | 9275 | 5516 | 6221 | 9477 | 8412 |
| 43 | mes-miR396f | 9275 | 5516 | 6221 | 9477 | 8412 |
| 44 | mtr-miR396a-5p | 9275 | 5516 | 6221 | 9477 | 8412 |
| 45 | nta-miR396b | 9275 | 5516 | 6221 | 9477 | 8412 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | nta-miR396c | 9275 | 5516 | 6221 | 9477 | 8412 |
| 4 | osa-miR396c-5p | 9275 | 5516 | 6221 | 9477 | 8412 |
| 5 | pab-miR396g | 9275 | 5516 | 6221 | 9477 | 8412 |
| 6 | pab-miR396h | 9275 | 5516 | 6221 | 9477 | 8412 |
| 7 | ppe-miR396b | 9275 | 5516 | 6221 | 9477 | 8412 |
| 8 | pta-miR396 | 9275 | 5516 | 6221 | 9477 | 8412 |
| 9 | ptc-miR396c | 9275 | 5516 | 6221 | 9477 | 8412 |
| 10 | ptc-miR396d | 9275 | 5516 | 6221 | 9477 | 8412 |
| 11 | ptc-miR396e-5p | 9275 | 5516 | 6221 | 9477 | 8412 |
| 12 | rco-miR396 | 9275 | 5516 | 6221 | 9477 | 8412 |
| 13 | sbi-miR396c | 9275 | 5516 | 6221 | 9477 | 8412 |
| 14 | sly-miR396b | 9275 | 5516 | 6221 | 9477 | 8412 |
| 15 | stu-miR396-5p | 9275 | 5516 | 6221 | 9477 | 8412 |
| 16 | tcc-miR396c | 9275 | 5516 | 6221 | 9477 | 8412 |
| 17 | tcc-miR396e | 9275 | 5516 | 6221 | 9477 | 8412 |
| 18 | zma-miR396e-5p | 9275 | 5516 | 6221 | 9477 | 8412 |
| 19 | zma-miR396f-5p | 9275 | 5516 | 6221 | 9477 | 8412 |
| 20 | mes-miR160g | 11771 | 13787 | 9505 | 15781 | 13869 |
| 21 | mtr-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 22 | mtr-miR160d | 11715 | 13747 | 9463 | 15716 | 13825 |
| 23 | mtr-miR160e | 11715 | 13747 | 9463 | 15716 | 13825 |
| 24 | nta-miR160a | 11715 | 13747 | 9463 | 15716 | 13825 |
| 25 | nta-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 26 | nta-miR160c | 11715 | 13747 | 9463 | 15716 | 13825 |
| 27 | osa-miR160a-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 28 | osa-miR160b-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 29 | osa-miR160c-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 30 | osa-miR160d-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 31 | pab-miR160a | 11715 | 13747 | 9463 | 15716 | 13825 |
| 32 | pab-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 33 | pab-miR160d | 11715 | 13747 | 9463 | 15716 | 13825 |
| 34 | ppe-miR160a | 11715 | 13747 | 9463 | 15716 | 13825 |
| 35 | ppe-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 36 | ppt-miR160a | 11715 | 13747 | 9463 | 15716 | 13825 |
| 37 | ppt-miR160e | 11715 | 13747 | 9463 | 15716 | 13825 |
| 38 | ppt-miR160f | 11715 | 13747 | 9463 | 15716 | 13825 |
| 39 | ptc-miR160a | 11715 | 13747 | 9463 | 15716 | 13825 |
| 40 | ptc-miR160b-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 41 | ptc-miR160c-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 42 | ptc-miR160d | 11715 | 13747 | 9463 | 15716 | 13825 |
| 43 | rco-miR160a | 11715 | 13747 | 9463 | 15716 | 13825 |
| 44 | rco-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 45 | sbi-miR160a | 11715 | 13747 | 9463 | 15716 | 13825 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | sbi-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 4 | sbi-miR160c | 11715 | 13747 | 9463 | 15716 | 13825 |
| 5 | sbi-miR160d | 11715 | 13747 | 9463 | 15716 | 13825 |
| 6 | sbi-miR160e | 11715 | 13747 | 9463 | 15716 | 13825 |
| 7 | sly-miR160a | 11715 | 13747 | 9463 | 15716 | 13825 |
| 8 | sly-miR160a | 11715 | 13747 | 9463 | 15716 | 13825 |
| 9 | sly-miR160a | 11715 | 13747 | 9463 | 15716 | 13825 |
| 10 | smo-miR160a | 11715 | 13747 | 9463 | 15716 | 13825 |
| 11 | smo-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 12 | smo-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 13 | stu-miR160a-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 14 | stu-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 15 | tae-miR160 | 11715 | 13747 | 9463 | 15716 | 13825 |
| 16 | tcc-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 17 | tcc-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 18 | ttu-miR160 | 11715 | 13747 | 9463 | 15716 | 13825 |
| 19 | vun-miR160 | 11715 | 13747 | 9463 | 15716 | 13825 |
| 20 | vun-miR160 | 11715 | 13747 | 9463 | 15716 | 13825 |
| 21 | vvi-miR160c | 11715 | 13747 | 9463 | 15716 | 13825 |
| 22 | vvi-miR160d | 11715 | 13747 | 9463 | 15716 | 13825 |
| 23 | vvi-miR160e | 11715 | 13747 | 9463 | 15716 | 13825 |
| 24 | vvi-miR160e | 11715 | 13747 | 9463 | 15716 | 13825 |
| 25 | zma-miR160a-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 26 | zma-miR160b-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 27 | zma-miR160c-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 28 | zma-miR160d-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 29 | zma-miR160d-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 30 | zma-miR160e | 11715 | 13747 | 9463 | 15716 | 13825 |
| 31 | zma-miR160g-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 32 | zma-miR160g-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 33 | aly-miR160a-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 34 | aly-miR160b-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 35 | aly-miR160c-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 36 | aof-miR160c | 11715 | 13747 | 9463 | 15716 | 13825 |
| 37 | aof-miR160c | 11715 | 13747 | 9463 | 15716 | 13825 |
| 38 | aqc-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 39 | ata-miR160a-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 40 | ata-miR160b-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 41 | ata-miR160b-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 42 | ata-miR160c-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 43 | ath-miR160a-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 44 | ath-miR160a-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 45 | ath-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 46 | ath-miR160c-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 47 | atr-miR160 | 11715 | 13747 | 9463 | 15716 | 13825 |
| 48 | atr-miR160 | 11715 | 13747 | 9463 | 15716 | 13825 |
| 49 | bdi-miR160a-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 50 | bdi-miR160b-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 51 | bdi-miR160c-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 52 | bdi-miR160d-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 53 | bdi-miR160d-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 54 | bna-miR160a | 11715 | 13747 | 9463 | 15716 | 13825 |
| 55 | bna-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 56 | bna-miR160c | 11715 | 13747 | 9463 | 15716 | 13825 |
| 57 | bna-miR160c | 11715 | 13747 | 9463 | 15716 | 13825 |
| 58 | bna-miR160d | 11715 | 13747 | 9463 | 15716 | 13825 |
| 59 | bra-miR160a-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | cca-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 4 | cme-miR160a | 11715 | 13747 | 9463 | 15716 | 13825 |
| 5 | cme-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 6 | cme-miR160c | 11715 | 13747 | 9463 | 15716 | 13825 |
| 7 | cme-miR160c | 11715 | 13747 | 9463 | 15716 | 13825 |
| 8 | cpa-miR160a | 11715 | 13747 | 9463 | 15716 | 13825 |
| 9 | cpa-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 10 | cpa-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 11 | cpa-miR160c-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 12 | cpa-miR160e | 11715 | 13747 | 9463 | 15716 | 13825 |
| 13 | cpa-miR160e | 11715 | 13747 | 9463 | 15716 | 13825 |
| 14 | cpa-miR160f-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 15 | eun-miR160-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 16 | far-miR160 | 11715 | 13747 | 9463 | 15716 | 13825 |
| 17 | far-miR160 | 11715 | 13747 | 9463 | 15716 | 13825 |
| 18 | fve-miR160a | 11715 | 13747 | 9463 | 15716 | 13825 |
| 19 | fve-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 20 | fve-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 21 | gma-miR160a-5p | 11715 | 13747 | 9463 | 15716 | 13825 |
| 22 | gma-miR160f | 11715 | 13747 | 9463 | 15716 | 13825 |
| 23 | gma-miR160f | 11715 | 13747 | 9463 | 15716 | 13825 |
| 24 | lus-miR160a | 11715 | 13747 | 9463 | 15716 | 13825 |
| 25 | lus-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 26 | lus-miR160d | 11715 | 13747 | 9463 | 15716 | 13825 |
| 27 | lus-miR160e | 11715 | 13747 | 9463 | 15716 | 13825 |
| 28 | lus-miR160f | 11715 | 13747 | 9463 | 15716 | 13825 |
| 29 | lus-miR160f | 11715 | 13747 | 9463 | 15716 | 13825 |
| 30 | lus-miR160h | 11715 | 13747 | 9463 | 15716 | 13825 |
| 31 | lus-miR160i | 11715 | 13747 | 9463 | 15716 | 13825 |
| 32 | lus-miR160i | 11715 | 13747 | 9463 | 15716 | 13825 |
| 33 | lus-miR160j | 11715 | 13747 | 9463 | 15716 | 13825 |
| 34 | mdm-miR160a | 11715 | 13747 | 9463 | 15716 | 13825 |
| 35 | mdm-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 36 | mdm-miR160c | 11715 | 13747 | 9463 | 15716 | 13825 |
| 37 | mdm-miR160c | 11715 | 13747 | 9463 | 15716 | 13825 |
| 38 | mdm-miR160d | 11715 | 13747 | 9463 | 15716 | 13825 |
| 39 | mdm-miR160e | 11715 | 13747 | 9463 | 15716 | 13825 |
| 40 | mdm-miR160e | 11715 | 13747 | 9463 | 15716 | 13825 |
| 41 | mes-miR160a | 11715 | 13747 | 9463 | 15716 | 13825 |
| 42 | mes-miR160b | 11715 | 13747 | 9463 | 15716 | 13825 |
| 43 | mes-miR160d | 11715 | 13747 | 9463 | 15716 | 13825 |
| 44 | mes-miR160d | 11715 | 13747 | 9463 | 15716 | 13825 |
| 45 | mtr-miR160a | 11715 | 13747 | 9463 | 15716 | 13825 |
| 46 | mes-miR160h | 11832 | 13835 | 9531 | 15859 | 13897 |
| 47 | mtr-miR166e-5p | 339 | 293 | 315 | 457 | 332 |
| 48 | osa-miR166h-5p | 339 | 293 | 315 | 457 | 332 |
| 49 | osa-miR166h-5p | 339 | 293 | 315 | 457 | 332 |
| 50 | zma-miR166m-5p | 339 | 293 | 315 | 457 | 332 |
| 51 | abu-miR-19b | 19 | 71 | 82 | 57 | 84 |
| 52 | ami-miR-19b-3p | 19 | 71 | 82 | 57 | 84 |
| 53 | ami-miR-19b-3p | 19 | 71 | 82 | 57 | 84 |
| 54 | cfa-miR-19b | 19 | 71 | 82 | 57 | 84 |
| 55 | cpi-miR-19b-3p | 19 | 71 | 82 | 57 | 84 |
| 56 | dma-miR-19b | 19 | 71 | 82 | 57 | 84 |
| 57 | dma-miR-19b | 19 | 71 | 82 | 57 | 84 |
| 58 | mmr-miR-19b | 19 | 71 | 82 | 57 | 84 |
| 59 | mze-miR-19b | 19 | 71 | 82 | 57 | 84 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | nbr-miR-19b | 19 | 71 | 82 | 57 | 84 |
| 4 | nle-miR-19b | 19 | 71 | 82 | 57 | 84 |
| 5 | oga-miR-19b | 19 | 71 | 82 | 57 | 84 |
| 6 | oni-miR-19b | 19 | 71 | 82 | 57 | 84 |
| 7 | oni-miR-19b | 19 | 71 | 82 | 57 | 84 |
| 8 | pbv-miR-19b-3p | 19 | 71 | 82 | 57 | 84 |
| 9 | pha-miR-19b | 19 | 71 | 82 | 57 | 84 |
| 10 | pha-miR-19b | 19 | 71 | 82 | 57 | 84 |
| 11 | pony-miR-19b | 19 | 71 | 82 | 57 | 84 |
| 12 | ssa-miR-19c-3p | 19 | 71 | 82 | 57 | 84 |
| 13 | ssa-miR-19c-3p | 19 | 71 | 82 | 57 | 84 |
| 14 | bta-miR-93 | 32 | 63 | 53 | 40 | 75 |
| 15 | gmo-miR-451-5p | 273 | 833 | 548 | 505 | 753 |
| 16 | cpa-miR169 | 110 | 134 | 151 | 133 | 168 |
| 17 | cli-miR-451-5p | 47 | 54 | 35 | 45 | 64 |
| 18 | cli-miR-451-5p | 47 | 54 | 35 | 45 | 64 |
| 19 | gma-miR319g | 3386 | 2896 | 2088 | 3830 | 3074 |
| 20 | gma-miR319l | 3386 | 2896 | 2088 | 3830 | 3074 |
| 21 | gma-miR319l | 3386 | 2896 | 2088 | 3830 | 3074 |
| 22 | cpi-miR-93-5p | 30 | 58 | 53 | 38 | 72 |
| 23 | sha-miR-93 | 30 | 58 | 53 | 38 | 72 |
| 24 | sha-miR-93 | 30 | 58 | 53 | 38 | 72 |
| 25 | gma-miR319q | 3108 | 2667 | 1865 | 3525 | 2844 |
| 26 | csi-miR160b-5p | 213 | 172 | 140 | 262 | 200 |
| 27 | mes-miR160c | 213 | 172 | 140 | 262 | 200 |
| 28 | osa-miR160e-5p | 213 | 172 | 140 | 262 | 200 |
| 29 | osa-miR160e-5p | 213 | 172 | 140 | 262 | 200 |
| 30 | zma-miR160f-5p | 213 | 172 | 140 | 262 | 200 |
| 31 | zma-miR160f-5p | 213 | 172 | 140 | 262 | 200 |
| 32 | gma-miR482c-3p | 526 | 292 | 405 | 598 | 453 |
| 33 | gma-miR482a-3p | 41395 | 12714 | 21203 | 36812 | 21935 |
| 34 | vun-miR482 | 41395 | 12714 | 21203 | 36812 | 21935 |
| 35 | age-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 36 | bta-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 37 | bta-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 38 | cgr-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 39 | chi-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 40 | chi-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 41 | cja-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 42 | cli-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 43 | cpo-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 44 | dno-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 45 | dno-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 46 | dre-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 47 | eca-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 48 | efu-miR-19 | 22 | 77 | 92 | 65 | 95 |
| 49 | efu-miR-19 | 22 | 77 | 92 | 65 | 95 |
| 50 | fru-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 51 | gga-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 52 | ggo-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 53 | ggo-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 54 | gmo-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 55 | hsa-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 56 | lca-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 57 | lla-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 58 | lla-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 59 | mdo-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | mml-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 4 | mmu-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 5 | mne-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 6 | oan-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 7 | oar-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 8 | ocu-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 9 | oha-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 10 | pal-miR-19-3p | 22 | 77 | 92 | 65 | 95 |
| 11 | pma-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 12 | ppa-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 13 | ppy-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 14 | ptr-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 15 | rno-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 16 | sha-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 17 | sla-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 18 | ssc-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 19 | tch-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 20 | tgu-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 21 | tni-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 22 | xla-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 23 | xla-miR-19b-3p | 22 | 77 | 92 | 65 | 95 |
| 24 | xtr-miR-19b | 22 | 77 | 92 | 65 | 95 |
| 25 | dno-miR-146a-5p | 100 | 162 | 130 | 106 | 197 |
| 26 | vca-miR396-5p | 391 | 229 | 265 | 455 | 360 |
| 27 | vvi-miR396b | 391 | 229 | 265 | 455 | 360 |
| 28 | pab-miR396a-5p | 398 | 229 | 275 | 467 | 366 |
| 29 | vvi-miR396a | 398 | 229 | 275 | 467 | 366 |
| 30 | pvu-miR159a.2 | 134 | 136 | 90 | 158 | 147 |
| 31 | bdi-miR160f | 187 | 170 | 138 | 259 | 194 |
| 32 | cas-miR160a | 187 | 170 | 138 | 259 | 194 |
| 33 | cas-miR160b-5p | 187 | 170 | 138 | 259 | 194 |
| 34 | gma-miR160b | 187 | 170 | 138 | 259 | 194 |
| 35 | gma-miR160c | 187 | 170 | 138 | 259 | 194 |
| 36 | gma-miR160d | 187 | 170 | 138 | 259 | 194 |
| 37 | gma-miR160e | 187 | 170 | 138 | 259 | 194 |
| 38 | htu-miR160a | 187 | 170 | 138 | 259 | 194 |
| 39 | pab-miR160c | 187 | 170 | 138 | 259 | 194 |
| 40 | pab-miR160e | 187 | 170 | 138 | 259 | 194 |
| 41 | pab-miR160f | 187 | 170 | 138 | 259 | 194 |
| 42 | ahy-miR408-3p | 67 | 57 | 51 | 88 | 75 |
| 43 | aly-miR408-3p | 67 | 57 | 51 | 88 | 75 |
| 44 | ath-miR408-3p | 67 | 57 | 51 | 88 | 75 |
| 45 | cas-miR408 | 67 | 57 | 51 | 88 | 75 |
| 46 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | cme-miR408 | 67 | 57 | 51 | 88 | 75 |
| 4 | csi-miR408-3p | 67 | 57 | 51 | 88 | 75 |
| 5 | gma-miR408a-3p | 67 | 57 | 51 | 88 | 75 |
| 6 | gma-miR408b-3p | 67 | 57 | 51 | 88 | 75 |
| 7 | gma-miR408c-3p | 67 | 57 | 51 | 88 | 75 |
| 8 | lus-miR408a | 67 | 57 | 51 | 88 | 75 |
| 9 | mdm-miR408a | 67 | 57 | 51 | 88 | 75 |
| 10 | mes-miR408 | 67 | 57 | 51 | 88 | 75 |
| 11 | mtr-miR408-3p | 67 | 57 | 51 | 88 | 75 |
| 12 | pta-miR408 | 67 | 57 | 51 | 88 | 75 |
| 13 | ptc-miR408-3p | 67 | 57 | 51 | 88 | 75 |
| 14 | vun-miR408 | 67 | 57 | 51 | 88 | 75 |
| 15 | vvi-miR408 | 67 | 57 | 51 | 88 | 75 |
| 16 | ahy-miR160-5p | 46 | 54 | 41 | 76 | 49 |
| 17 | aof-miR160a | 46 | 54 | 41 | 76 | 49 |
| 18 | bdi-miR160e-5p | 46 | 54 | 41 | 76 | 49 |
| 19 | cme-miR160d | 46 | 54 | 41 | 76 | 49 |
| 20 | cpa-miR160d | 46 | 54 | 41 | 76 | 49 |
| 21 | mes-miR160e | 46 | 54 | 41 | 76 | 49 |
| 22 | mes-miR160f | 46 | 54 | 41 | 76 | 49 |
| 23 | mtr-miR160c | 46 | 54 | 41 | 76 | 49 |
| 24 | osa-miR160f-5p | 46 | 54 | 41 | 76 | 49 |
| 25 | ptc-miR160e-5p | 46 | 54 | 41 | 76 | 49 |
| 26 | ptc-miR160f | 46 | 54 | 41 | 76 | 49 |
| 27 | rco-miR160c | 46 | 54 | 41 | 76 | 49 |
| 28 | sbi-miR160f | 46 | 54 | 41 | 76 | 49 |
| 29 | tcc-miR160a | 46 | 54 | 41 | 76 | 49 |
| 30 | vca-miR160-5p | 46 | 54 | 41 | 76 | 49 |
| 31 | vvi-miR160a | 46 | 54 | 41 | 76 | 49 |
| 32 | vvi-miR160b | 46 | 54 | 41 | 76 | 49 |
| 33 | gma-miR396e | 964 | 595 | 612 | 1072 | 1081 |
| 34 | aaU-miR396 | 963 | 594 | 611 | 1071 | 1079 |
| 35 | aly-miR396a-5p | 963 | 594 | 611 | 1071 | 1079 |
| 36 | amg-miR396 | 963 | 594 | 611 | 1071 | 1079 |
| 37 | aof-miR396b | 963 | 594 | 611 | 1071 | 1079 |
| 38 | aqc-miR396a | 963 | 594 | 611 | 1071 | 1079 |
| 39 | ata-miR396e-5p | 963 | 594 | 611 | 1071 | 1079 |
| 40 | ath-miR396a-5p | 963 | 594 | 611 | 1071 | 1079 |
| 41 | bcy-miR396a | 963 | 594 | 611 | 1071 | 1079 |
| 42 | bdi-miR396c-5p | 963 | 594 | 611 | 1071 | 1079 |
| 43 | bdi-miR396d-5p | 963 | 594 | 611 | 1071 | 1079 |
| 44 | bgy-miR396a | 963 | 594 | 611 | 1071 | 1079 |
| 45 | cas-miR396a | 963 | 594 | 611 | 1071 | 1079 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-----|-----|-----|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | cme-miR396b | 963 | 594 | 611 | 1071 | 1079 |
| 4 | cpa-miR396 | 963 | 594 | 611 | 1071 | 1079 |
| 5 | csi-miR396a-5p | 963 | 594 | 611 | 1071 | 1079 |
| 6 | csi-miR396b-5p | 963 | 594 | 611 | 1071 | 1079 |
| 7 | dpr-miR396 | 963 | 594 | 611 | 1071 | 1079 |
| 8 | eun-miR396b-5p | 963 | 594 | 611 | 1071 | 1079 |
| 9 | fve-miR396a-5p | 963 | 594 | 611 | 1071 | 1079 |
| 10 | fve-miR396c-5p | 963 | 594 | 611 | 1071 | 1079 |
| 11 | fve-miR396d | 963 | 594 | 611 | 1071 | 1079 |
| 12 | ghr-miR396a | 963 | 594 | 611 | 1071 | 1079 |
| 13 | ghr-miR396b | 963 | 594 | 611 | 1071 | 1079 |
| 14 | gma-miR396a-5p | 963 | 594 | 611 | 1071 | 1079 |
| 15 | gma-miR396i-5p | 963 | 594 | 611 | 1071 | 1079 |
| 16 | hbr-miR396b | 963 | 594 | 611 | 1071 | 1079 |
| 17 | lja-miR396 | 963 | 594 | 611 | 1071 | 1079 |
| 18 | lus-miR396a | 963 | 594 | 611 | 1071 | 1079 |
| 19 | lus-miR396c | 963 | 594 | 611 | 1071 | 1079 |
| 20 | mdm-miR396b | 963 | 594 | 611 | 1071 | 1079 |
| 21 | mes-miR396a | 963 | 594 | 611 | 1071 | 1079 |
| 22 | mes-miR396b | 963 | 594 | 611 | 1071 | 1079 |
| 23 | mtr-miR396b-5p | 963 | 594 | 611 | 1071 | 1079 |
| 24 | nta-miR396a | 963 | 594 | 611 | 1071 | 1079 |
| 25 | osa-miR396a-5p | 963 | 594 | 611 | 1071 | 1079 |
| 26 | osa-miR396b-5p | 963 | 594 | 611 | 1071 | 1079 |
| 27 | ptc-miR396a | 963 | 594 | 611 | 1071 | 1079 |
| 28 | ptc-miR396b | 963 | 594 | 611 | 1071 | 1079 |
| 29 | sbi-miR396a | 963 | 594 | 611 | 1071 | 1079 |
| 30 | sbi-miR396b | 963 | 594 | 611 | 1071 | 1079 |
| 31 | sly-miR396a-5p | 963 | 594 | 611 | 1071 | 1079 |
| 32 | sof-miR396 | 963 | 594 | 611 | 1071 | 1079 |
| 33 | ssl-miR396 | 963 | 594 | 611 | 1071 | 1079 |
| 34 | ssp-miR396 | 963 | 594 | 611 | 1071 | 1079 |
| 35 | tcc-miR396a | 963 | 594 | 611 | 1071 | 1079 |
| 36 | tcc-miR396b | 963 | 594 | 611 | 1071 | 1079 |
| 37 | vvi-miR396c | 963 | 594 | 611 | 1071 | 1079 |
| 38 | vvi-miR396d | 963 | 594 | 611 | 1071 | 1079 |
| 39 | zma-miR396a-5p | 963 | 594 | 611 | 1071 | 1079 |
| 40 | zma-miR396b-5p | 963 | 594 | 611 | 1071 | 1079 |
| 41 | cli-miR-146a-5p | 57 | 144 | 112 | 93 | 177 |
| 42 | cpo-miR-146a-5p | 57 | 144 | 112 | 93 | 177 |
| 43 | ocu-miR-146a-5p | 57 | 144 | 112 | 93 | 177 |
| 44 | cfa-miR-146a | 57 | 142 | 110 | 93 | 175 |
| 45 | cgr-miR-146a | 57 | 142 | 110 | 93 | 175 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | cja-miR-146a | 57 | 142 | 110 | 93 | 175 |
| 4 | eca-miR-146a | 57 | 142 | 110 | 93 | 175 |
| 5 | gga-miR-146a-5p | 57 | 142 | 110 | 93 | 175 |
| 6 | hsa-miR-146a-5p | 57 | 142 | 110 | 93 | 175 |
| 7 | mdo-miR-146a-5p | 57 | 142 | 110 | 93 | 175 |
| 8 | mml-miR-146a-5p | 57 | 142 | 110 | 93 | 175 |
| 9 | mmr-miR-146a | 57 | 142 | 110 | 93 | 175 |
| 10 | mmu-miR-146a-5p | 57 | 142 | 110 | 93 | 175 |
| 11 | nle-miR-146a | 57 | 142 | 110 | 93 | 175 |
| 12 | pal-miR-146a-5p | 57 | 142 | 110 | 93 | 175 |
| 13 | pha-miR-146a | 57 | 142 | 110 | 93 | 175 |
| 14 | ppy-miR-146a | 57 | 142 | 110 | 93 | 175 |
| 15 | ptr-miR-146a | 57 | 142 | 110 | 93 | 175 |
| 16 | rno-miR-146a-5p | 57 | 142 | 110 | 93 | 175 |
| 17 | ssc-miR-146a-5p | 57 | 142 | 110 | 93 | 175 |
| 18 | tch-miR-146a-5p | 57 | 142 | 110 | 93 | 175 |
| 19 | tgu-miR-146c | 57 | 142 | 110 | 93 | 175 |
| 20 | pvu-miR482-3p | 324 | 179 | 265 | 440 | 347 |
| 21 | gma-miR482b-3p | 702 | 430 | 337 | 987 | 535 |
| 22 | gma-miR482d-3p | 702 | 430 | 337 | 987 | 535 |
| 23 | cme-miR172a | 183 | 184 | 189 | 324 | 359 |
| 24 | gma-miR172c | 183 | 184 | 189 | 324 | 359 |
| 25 | lus-miR172e | 183 | 184 | 189 | 324 | 359 |
| 26 | lus-miR172i | 183 | 184 | 189 | 324 | 359 |
| 27 | mdm-miR172l | 183 | 184 | 189 | 324 | 359 |
| 28 | mes-miR172e | 183 | 184 | 189 | 324 | 359 |
| 29 | mes-miR172f | 183 | 184 | 189 | 324 | 359 |
| 30 | ppe-miR172d | 183 | 184 | 189 | 324 | 359 |
| 31 | ptc-miR172g-3p | 183 | 184 | 189 | 324 | 359 |
| 32 | ptc-miR172h-3p | 183 | 184 | 189 | 324 | 359 |
| 33 | rco-miR172 | 183 | 184 | 189 | 324 | 359 |
| 34 | sly-miR172d | 183 | 184 | 189 | 324 | 359 |
| 35 | stu-miR172d-3p | 183 | 184 | 189 | 324 | 359 |
| 36 | vvi-miR172c | 183 | 184 | 189 | 324 | 359 |
| 37 | csi-miR172c-3p | 183 | 184 | 189 | 324 | 360 |
| 38 | gma-miR172d | 187 | 185 | 189 | 328 | 359 |
| 39 | gma-miR172e | 187 | 185 | 189 | 328 | 359 |
| 40 | ath-miR162a-5p | 82 | 49 | 39 | 95 | 127 |
| 41 | ath-miR162b-5p | 82 | 49 | 39 | 95 | 127 |
| 42 | csi-miR162-5p | 82 | 49 | 39 | 95 | 127 |
| 43 | ptc-miR6478 | 19612 | 41570 | 19446 | 47793 | 34975 |
| 44 | ath-miR8175 | 64 | 22 | 33 | 60 | 95 |
| 45 | csi-miR482d-3p | 1692 | 0 | 0 | 1 | 0 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|---|---|---|---|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ata-miR168-5p | 1231 | 1 | 1 | 1 | 0 |
| 4 | bdi-miR168-5p | 1231 | 1 | 1 | 1 | 0 |
| 5 | hvu-miR168-5p | 1231 | 1 | 1 | 1 | 0 |
| 6 | osa-miR168a-5p | 1231 | 1 | 1 | 1 | 0 |
| 7 | osa-miR168a-5p | 1231 | 1 | 1 | 1 | 0 |
| 8 | sbi-miR168 | 1231 | 1 | 1 | 1 | 0 |
| 9 | sbi-miR168 | 1231 | 1 | 1 | 1 | 0 |
| 10 | sof-miR168a | 1231 | 1 | 1 | 1 | 0 |
| 11 | ssp-miR168a | 1231 | 1 | 1 | 1 | 0 |
| 12 | ssp-miR168a | 1231 | 1 | 1 | 1 | 0 |
| 13 | zma-miR168a-5p | 1231 | 1 | 1 | 1 | 0 |
| 14 | zma-miR168b-5p | 1231 | 1 | 1 | 1 | 0 |
| 15 | csi-miR482a-3p | 370 | 0 | 0 | 0 | 0 |
| 16 | csi-miR482g-3p | 370 | 0 | 0 | 0 | 0 |
| 17 | csi-miR482g-3p | 370 | 0 | 0 | 0 | 0 |
| 18 | osa-miR444b.1 | 359 | 0 | 0 | 0 | 0 |
| 19 | osa-miR444c.1 | 359 | 0 | 0 | 0 | 0 |
| 20 | | | | | | |
| 21 | | | | | | |
| 22 | | | | | | |
| 23 | | | | | | |
| 24 | | | | | | |
| 25 | | | | | | |
| 26 | | | | | | |
| 27 | | | | | | |
| 28 | | | | | | |
| 29 | | | | | | |
| 30 | | | | | | |
| 31 | | | | | | |
| 32 | | | | | | |
| 33 | | | | | | |
| 34 | | | | | | |
| 35 | | | | | | |
| 36 | | | | | | |
| 37 | | | | | | |
| 38 | | | | | | |
| 39 | | | | | | |
| 40 | | | | | | |
| 41 | | | | | | |
| 42 | | | | | | |
| 43 | | | | | | |
| 44 | | | | | | |
| 45 | | | | | | |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

Do not distribute

| | | | | | | | |
|----|-----|-----|-----|-----|----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 4 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 5 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 6 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 7 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 8 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 9 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 10 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 11 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 12 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 13 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 14 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 15 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 16 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 17 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 18 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 19 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 20 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 21 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 22 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 23 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 24 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 25 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 26 | 125 | 83 | 106 | 427 | 72 | 86 | 115 |
| 27 | 126 | 151 | 116 | 351 | 62 | 110 | 115 |
| 28 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 29 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 30 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 31 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 32 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 33 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 34 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 35 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 36 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 37 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 38 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 39 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 40 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 41 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 42 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 43 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 44 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 45 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 46 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 47 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 48 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 49 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 50 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 51 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 52 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 53 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 54 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 55 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 56 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 57 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 58 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 59 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 4 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 5 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 6 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 7 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 8 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 9 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 10 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 11 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 12 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 13 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 14 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 15 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 16 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 17 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 18 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 19 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 20 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 21 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 22 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 23 | 125 | 149 | 114 | 350 | 62 | 110 | 115 |
| 24 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 25 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 26 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 27 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 28 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 29 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 30 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 31 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 32 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 33 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 34 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 35 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 36 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 37 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 38 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 39 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 40 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 41 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 42 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 43 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 44 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 45 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 46 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 47 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 48 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 49 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 50 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 51 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 52 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 53 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 54 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 55 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 56 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 57 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 58 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 59 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 4 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 5 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 6 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 7 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 8 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 9 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 10 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 11 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 12 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 13 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 14 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 15 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 16 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 17 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 18 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 19 | 394 | 481 | 699 | 421 | 126 | 276 | 361 |
| 20 | 364 | 441 | 619 | 380 | 111 | 250 | 334 |
| 21 | 364 | 441 | 619 | 380 | 111 | 250 | 334 |
| 22 | 364 | 441 | 619 | 380 | 111 | 250 | 334 |
| 23 | 364 | 441 | 619 | 380 | 111 | 250 | 334 |
| 24 | 364 | 441 | 619 | 379 | 111 | 250 | 334 |
| 25 | 364 | 441 | 619 | 379 | 111 | 250 | 334 |
| 26 | 364 | 441 | 619 | 379 | 111 | 250 | 334 |
| 27 | 364 | 441 | 619 | 379 | 111 | 250 | 334 |
| 28 | 57 | 63 | 44 | 157 | 32 | 44 | 52 |
| 29 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 30 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 31 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 32 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 33 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 34 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 35 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 36 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 37 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 38 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 39 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 40 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 41 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 42 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 43 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 44 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 45 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 46 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 47 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 48 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 49 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 50 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 51 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 52 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 53 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 54 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 55 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 56 | 56 | 56 | 43 | 153 | 30 | 44 | 51 |
| 57 | 139 | 343 | 275 | 182 | 169 | 111 | 127 |
| 58 | 2512 | 4793 | 1921 | 4544 | 1785 | 1955 | 2302 |
| 59 | | | | | | | |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 2512 | 4793 | 1921 | 4544 | 1785 | 1955 | 2302 |
| 4 | 2512 | 4793 | 1921 | 4544 | 1785 | 1955 | 2302 |
| 5 | 2512 | 4793 | 1921 | 4544 | 1785 | 1955 | 2302 |
| 6 | 2512 | 4793 | 1921 | 4544 | 1785 | 1955 | 2302 |
| 7 | 2512 | 4793 | 1921 | 4544 | 1785 | 1955 | 2302 |
| 8 | 2500 | 4760 | 1911 | 4516 | 1775 | 1942 | 2291 |
| 9 | 2500 | 4760 | 1911 | 4516 | 1775 | 1942 | 2291 |
| 10 | 2500 | 4760 | 1911 | 4516 | 1775 | 1942 | 2291 |
| 11 | 2500 | 4760 | 1911 | 4516 | 1775 | 1942 | 2291 |
| 12 | 2500 | 4760 | 1911 | 4516 | 1775 | 1942 | 2291 |
| 13 | 2500 | 4760 | 1911 | 4516 | 1775 | 1942 | 2291 |
| 14 | 2500 | 4760 | 1911 | 4516 | 1775 | 1942 | 2291 |
| 15 | 2500 | 4760 | 1911 | 4516 | 1775 | 1942 | 2291 |
| 16 | 2500 | 4760 | 1911 | 4516 | 1775 | 1942 | 2291 |
| 17 | 2500 | 4760 | 1911 | 4516 | 1775 | 1942 | 2291 |
| 18 | 2500 | 4760 | 1911 | 4516 | 1775 | 1942 | 2291 |
| 19 | 2500 | 4760 | 1911 | 4516 | 1775 | 1942 | 2291 |
| 20 | 2500 | 4760 | 1911 | 4516 | 1775 | 1942 | 2291 |
| 21 | 2500 | 4760 | 1911 | 4516 | 1775 | 1942 | 2291 |
| 22 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 23 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 24 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 25 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 26 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 27 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 28 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 29 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 30 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 31 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 32 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 33 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 34 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 35 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 36 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 37 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 38 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 39 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 40 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 41 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 42 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 43 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 44 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 45 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 46 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 47 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 48 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 49 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 50 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 51 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 52 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 53 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 54 | 432 | 1120 | 402 | 399 | 287 | 370 | 396 |
| 55 | 112 | 152 | 94 | 204 | 78 | 90 | 103 |
| 56 | 112 | 151 | 94 | 203 | 78 | 90 | 103 |
| 57 | 112 | 151 | 94 | 203 | 78 | 90 | 103 |
| 58 | 112 | 151 | 94 | 203 | 78 | 90 | 103 |
| 59 | 112 | 151 | 94 | 203 | 78 | 90 | 103 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|----|-----|----|----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 112 | 151 | 94 | 203 | 78 | 90 | 103 |
| 4 | 112 | 151 | 94 | 203 | 78 | 90 | 103 |
| 5 | 112 | 151 | 94 | 203 | 78 | 90 | 103 |
| 6 | 112 | 151 | 94 | 203 | 78 | 90 | 103 |
| 7 | 112 | 151 | 94 | 203 | 78 | 90 | 103 |
| 8 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 9 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 10 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 11 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 12 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 13 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 14 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 15 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 16 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 17 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 18 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 19 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 20 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 21 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 22 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 23 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 24 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 25 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 26 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 27 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 28 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 29 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 30 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 31 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 32 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 33 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 34 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 35 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 36 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 37 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 38 | 80 | 69 | 74 | 188 | 64 | 66 | 73 |
| 39 | 81 | 69 | 74 | 188 | 64 | 67 | 74 |
| 40 | 81 | 69 | 74 | 188 | 64 | 67 | 74 |
| 41 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 42 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 43 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 44 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 45 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 46 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 47 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 48 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 49 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 50 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 51 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 52 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 53 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 54 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 55 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 56 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 57 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 58 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 59 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 4 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 5 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 6 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 7 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 8 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 9 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 10 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 11 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 12 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 13 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 14 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 15 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 16 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 17 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 18 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 19 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 20 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 21 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 22 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 23 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 24 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 25 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 26 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 27 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 28 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 29 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 30 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 31 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 32 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 33 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 34 | 91 | 116 | 75 | 174 | 67 | 78 | 83 |
| 35 | 224 | 245 | 199 | 498 | 203 | 194 | 205 |
| 36 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 37 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 38 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 39 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 40 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 41 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 42 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 43 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 44 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 45 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 46 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 47 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 48 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 49 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 50 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 51 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 52 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 53 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 54 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 55 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 56 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 57 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 58 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 59 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 4 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 5 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 6 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 7 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 8 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 9 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 10 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 11 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 12 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 13 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 14 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 15 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 16 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 17 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 18 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 19 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 20 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 21 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 22 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 23 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 24 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 25 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 26 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 27 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 28 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 29 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 30 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 31 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 32 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 33 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 34 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 35 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 36 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 37 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 38 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 39 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 40 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 41 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 42 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 43 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 44 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 45 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 46 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 47 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 48 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 49 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 50 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 51 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 52 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 53 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 54 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 55 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 56 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 57 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 58 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 59 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|------|------|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 4 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 5 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 6 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 7 | 219 | 239 | 193 | 487 | 198 | 192 | 201 |
| 8 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 9 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 10 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 11 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 12 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 13 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 14 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 15 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 16 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 17 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 18 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 19 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 20 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 21 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 22 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 23 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 24 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 25 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 26 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 27 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 28 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 29 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 30 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 31 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 32 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 33 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 34 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 35 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 36 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 37 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 38 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 39 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 40 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 41 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 42 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 43 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 44 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 45 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 46 | 64 | 8 | 37 | 154 | 28 | 41 | 59 |
| 47 | 1032 | 88 | 1818 | 1238 | 554 | 554 | 946 |
| 48 | 1032 | 88 | 1818 | 1238 | 554 | 554 | 946 |
| 49 | 1032 | 88 | 1818 | 1238 | 554 | 554 | 946 |
| 50 | 1032 | 88 | 1818 | 1238 | 554 | 554 | 946 |
| 51 | 1032 | 88 | 1818 | 1238 | 554 | 554 | 946 |
| 52 | 1032 | 88 | 1818 | 1238 | 554 | 554 | 946 |
| 53 | 1032 | 88 | 1818 | 1238 | 554 | 554 | 946 |
| 54 | 1032 | 88 | 1818 | 1238 | 554 | 554 | 946 |
| 55 | 137 | 176 | 104 | 189 | 89 | 116 | 126 |
| 56 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 57 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 58 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 59 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 4 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 5 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 6 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 7 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 8 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 9 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 10 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 11 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 12 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 13 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 14 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 15 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 16 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 17 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 18 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 19 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 20 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 21 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 22 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 23 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 24 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 25 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 26 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 27 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 28 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 29 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 30 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 31 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 32 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 33 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 34 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 35 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 36 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 37 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 38 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 39 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 40 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 41 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 42 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 43 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 44 | 136 | 174 | 102 | 188 | 89 | 116 | 125 |
| 45 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 46 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 47 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 48 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 49 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 50 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 51 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 52 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 53 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 54 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 55 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 56 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 57 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 58 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 59 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|----|-----|----|----|----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 4 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 5 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 6 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 7 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 8 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 9 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 10 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 11 | 104 | 65 | 81 | 126 | 37 | 63 | 95 |
| 12 | 69 | 76 | 62 | 100 | 38 | 70 | 63 |
| 13 | 69 | 76 | 62 | 100 | 38 | 70 | 63 |
| 14 | 69 | 76 | 62 | 100 | 38 | 70 | 63 |
| 15 | 69 | 76 | 62 | 100 | 38 | 70 | 63 |
| 16 | 69 | 76 | 62 | 100 | 38 | 70 | 63 |
| 17 | 69 | 76 | 62 | 100 | 38 | 70 | 63 |
| 18 | 58 | 88 | 31 | 54 | 25 | 47 | 53 |
| 19 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 20 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 21 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 22 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 23 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 24 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 25 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 26 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 27 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 28 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 29 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 30 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 31 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 32 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 33 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 34 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 35 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 36 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 37 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 38 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 39 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 40 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 41 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 42 | 57 | 85 | 30 | 53 | 25 | 47 | 52 |
| 43 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 44 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 45 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 46 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 47 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 48 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 49 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 50 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 51 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 52 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 53 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 54 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 55 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 56 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 57 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 58 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 59 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 4 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 5 | 99 | 101 | 81 | 126 | 54 | 86 | 91 |
| 6 | 57 | 86 | 30 | 53 | 26 | 47 | 52 |
| 7 | 109 | 147 | 92 | 137 | 70 | 113 | 100 |
| 8 | 109 | 147 | 92 | 137 | 70 | 113 | 100 |
| 9 | 109 | 147 | 92 | 137 | 70 | 113 | 100 |
| 10 | 109 | 147 | 92 | 137 | 70 | 113 | 100 |
| 11 | 109 | 147 | 92 | 137 | 70 | 113 | 100 |
| 12 | 109 | 147 | 92 | 137 | 70 | 113 | 100 |
| 13 | 109 | 147 | 92 | 137 | 70 | 113 | 100 |
| 14 | 109 | 147 | 92 | 137 | 70 | 113 | 100 |
| 15 | 109 | 147 | 92 | 137 | 70 | 113 | 100 |
| 16 | 109 | 147 | 92 | 137 | 70 | 113 | 100 |
| 17 | 109 | 147 | 92 | 137 | 70 | 113 | 100 |
| 18 | 109 | 147 | 92 | 137 | 70 | 113 | 100 |
| 19 | 109 | 147 | 92 | 137 | 70 | 113 | 100 |
| 20 | 518 | 652 | 495 | 619 | 350 | 509 | 475 |
| 21 | 123 | 2 | 58 | 209 | 35 | 55 | 113 |
| 22 | 123 | 2 | 58 | 209 | 35 | 55 | 113 |
| 23 | 123 | 2 | 58 | 209 | 35 | 55 | 113 |
| 24 | 123 | 2 | 58 | 209 | 35 | 55 | 113 |
| 25 | 123 | 2 | 58 | 209 | 35 | 55 | 113 |
| 26 | 123 | 2 | 58 | 209 | 35 | 55 | 113 |
| 27 | 123 | 2 | 58 | 209 | 35 | 55 | 113 |
| 28 | 123 | 2 | 58 | 209 | 35 | 55 | 113 |
| 29 | 123 | 2 | 58 | 209 | 35 | 55 | 113 |
| 30 | 123 | 2 | 58 | 209 | 35 | 55 | 113 |
| 31 | 123 | 2 | 58 | 209 | 35 | 55 | 113 |
| 32 | 123 | 2 | 58 | 209 | 35 | 55 | 113 |
| 33 | 123 | 2 | 58 | 209 | 35 | 55 | 113 |
| 34 | 123 | 2 | 58 | 209 | 35 | 55 | 113 |
| 35 | 123 | 2 | 58 | 209 | 35 | 55 | 113 |
| 36 | 123 | 2 | 58 | 209 | 35 | 55 | 113 |
| 37 | 123 | 2 | 58 | 209 | 35 | 55 | 113 |
| 38 | 123 | 2 | 58 | 209 | 35 | 55 | 113 |
| 39 | 123 | 2 | 58 | 209 | 35 | 55 | 113 |
| 40 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 41 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 42 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 43 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 44 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 45 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 46 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 47 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 48 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 49 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 50 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 51 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 52 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 53 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 54 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 55 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 56 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 57 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 58 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 59 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|------|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | | | | | | | |
| 4 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 5 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 6 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 7 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 8 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 9 | 518 | 652 | 493 | 619 | 350 | 509 | 475 |
| 10 | 80 | 40 | 48 | 87 | 22 | 36 | 73 |
| 11 | 80 | 40 | 48 | 87 | 22 | 36 | 73 |
| 12 | 80 | 40 | 48 | 87 | 22 | 36 | 73 |
| 13 | 80 | 40 | 48 | 87 | 22 | 36 | 73 |
| 14 | 80 | 40 | 48 | 87 | 22 | 36 | 73 |
| 15 | 80 | 40 | 48 | 87 | 22 | 36 | 73 |
| 16 | 80 | 40 | 48 | 87 | 22 | 36 | 73 |
| 17 | 527 | 656 | 500 | 626 | 350 | 520 | 483 |
| 18 | 49 | 109 | 30 | 23 | 46 | 33 | 45 |
| 19 | 49 | 109 | 30 | 23 | 46 | 33 | 45 |
| 20 | 49 | 109 | 30 | 23 | 46 | 33 | 45 |
| 21 | 49 | 109 | 30 | 23 | 46 | 33 | 45 |
| 22 | 49 | 109 | 30 | 23 | 46 | 33 | 45 |
| 23 | 49 | 109 | 30 | 23 | 46 | 33 | 45 |
| 24 | 49 | 109 | 30 | 23 | 46 | 33 | 45 |
| 25 | 49 | 109 | 30 | 23 | 46 | 33 | 45 |
| 26 | 49 | 109 | 30 | 23 | 46 | 33 | 45 |
| 27 | 49 | 109 | 30 | 23 | 46 | 33 | 45 |
| 28 | 49 | 109 | 30 | 23 | 46 | 33 | 45 |
| 29 | 49 | 109 | 30 | 23 | 46 | 33 | 45 |
| 30 | 49 | 109 | 30 | 23 | 46 | 33 | 45 |
| 31 | 143 | 180 | 116 | 168 | 88 | 134 | 131 |
| 32 | 62 | 23 | 67 | 120 | 47 | 58 | 57 |
| 33 | 62 | 23 | 67 | 120 | 47 | 58 | 57 |
| 34 | 62 | 23 | 67 | 120 | 47 | 58 | 57 |
| 35 | 62 | 23 | 67 | 120 | 47 | 58 | 57 |
| 36 | 62 | 23 | 67 | 120 | 47 | 58 | 57 |
| 37 | 62 | 23 | 67 | 120 | 47 | 58 | 57 |
| 38 | 62 | 23 | 67 | 120 | 47 | 58 | 57 |
| 39 | 142 | 173 | 113 | 165 | 88 | 130 | 130 |
| 40 | 142 | 173 | 113 | 165 | 88 | 130 | 130 |
| 41 | 142 | 173 | 113 | 165 | 88 | 130 | 130 |
| 42 | 236 | 348 | 202 | 200 | 160 | 211 | 216 |
| 43 | 236 | 348 | 202 | 200 | 160 | 211 | 216 |
| 44 | 236 | 348 | 202 | 200 | 160 | 211 | 216 |
| 45 | 236 | 348 | 202 | 200 | 160 | 211 | 216 |
| 46 | 236 | 348 | 202 | 200 | 160 | 211 | 216 |
| 47 | 844 | 10 | 464 | 1470 | 239 | 520 | 774 |
| 48 | 844 | 10 | 464 | 1470 | 239 | 520 | 774 |
| 49 | 844 | 10 | 464 | 1470 | 239 | 520 | 774 |
| 50 | 844 | 10 | 464 | 1470 | 239 | 520 | 774 |
| 51 | 833 | 10 | 459 | 1443 | 235 | 513 | 764 |
| 52 | 833 | 10 | 459 | 1443 | 235 | 513 | 764 |
| 53 | 833 | 10 | 459 | 1443 | 235 | 513 | 764 |
| 54 | 833 | 10 | 459 | 1443 | 235 | 513 | 764 |
| 55 | 833 | 10 | 459 | 1443 | 235 | 513 | 764 |
| 56 | 833 | 10 | 459 | 1443 | 235 | 513 | 764 |
| 57 | 833 | 10 | 459 | 1443 | 235 | 513 | 764 |
| 58 | 833 | 10 | 459 | 1443 | 235 | 513 | 764 |
| 59 | 833 | 10 | 459 | 1443 | 235 | 513 | 764 |
| 60 | 833 | 10 | 459 | 1443 | 235 | 513 | 764 |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 833 | 10 | 459 | 1443 | 235 | 513 | 764 |
| 4 | 833 | 10 | 459 | 1443 | 235 | 513 | 764 |
| 5 | 833 | 10 | 459 | 1443 | 235 | 513 | 764 |
| 6 | 833 | 10 | 459 | 1443 | 235 | 513 | 764 |
| 7 | 833 | 10 | 459 | 1443 | 235 | 513 | 764 |
| 8 | 833 | 10 | 459 | 1443 | 235 | 513 | 764 |
| 9 | 833 | 10 | 459 | 1443 | 235 | 513 | 764 |
| 10 | 833 | 10 | 459 | 1443 | 235 | 513 | 764 |
| 11 | 5004 | 5614 | 6406 | 7437 | 6198 | 5023 | 4587 |
| 12 | 5004 | 5614 | 6406 | 7437 | 6198 | 5023 | 4587 |
| 13 | 5004 | 5614 | 6406 | 7437 | 6198 | 5023 | 4587 |
| 14 | 5004 | 5614 | 6406 | 7437 | 6198 | 5023 | 4587 |
| 15 | 131 | 0 | 83 | 222 | 49 | 79 | 120 |
| 16 | 131 | 0 | 83 | 222 | 49 | 79 | 120 |
| 17 | 131 | 0 | 83 | 222 | 49 | 79 | 120 |
| 18 | 131 | 0 | 83 | 222 | 49 | 79 | 120 |
| 19 | 131 | 0 | 83 | 222 | 49 | 79 | 120 |
| 20 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 21 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 22 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 23 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 24 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 25 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 26 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 27 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 28 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 29 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 30 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 31 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 32 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 33 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 34 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 35 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 36 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 37 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 38 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 39 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 40 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 41 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 42 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 43 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 44 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 45 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 46 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 47 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 48 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 49 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 50 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 51 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 52 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 53 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 54 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 55 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 56 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 57 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 58 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 59 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | | | | | | | |
| 4 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 5 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 6 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 7 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 8 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 9 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 10 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 11 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 12 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 13 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 14 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 15 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 16 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 17 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 18 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 19 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 20 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 21 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 22 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 23 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 24 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 25 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 26 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 27 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 28 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 29 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 30 | 458 | 450 | 370 | 485 | 292 | 349 | 420 |
| 31 | 461 | 452 | 371 | 486 | 292 | 349 | 423 |
| 32 | 461 | 452 | 371 | 486 | 292 | 349 | 423 |
| 33 | | | | | | | |
| 34 | 88 | 74 | 194 | 89 | 103 | 114 | 81 |
| 35 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 36 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 37 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 38 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 39 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 40 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 41 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 42 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 43 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 44 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 45 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 46 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 47 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 48 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 49 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 50 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 51 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 52 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 53 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 54 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 55 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 56 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 57 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 58 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 59 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 4 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 5 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 6 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 7 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 8 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 9 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 10 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 11 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 12 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 13 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 14 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 15 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 16 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 17 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 18 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 19 | 166 | 74 | 145 | 267 | 113 | 141 | 152 |
| 20 | 5838 | 6424 | 7391 | 8277 | 7096 | 5966 | 5351 |
| 21 | 5838 | 6424 | 7391 | 8277 | 7096 | 5966 | 5351 |
| 22 | 5838 | 6424 | 7391 | 8277 | 7096 | 5966 | 5351 |
| 23 | 5838 | 6424 | 7391 | 8277 | 7096 | 5966 | 5351 |
| 24 | 5838 | 6424 | 7391 | 8277 | 7096 | 5966 | 5351 |
| 25 | 5838 | 6424 | 7391 | 8277 | 7096 | 5966 | 5351 |
| 26 | 5838 | 6424 | 7391 | 8277 | 7096 | 5966 | 5351 |
| 27 | 5838 | 6424 | 7391 | 8277 | 7096 | 5966 | 5351 |
| 28 | 5838 | 6424 | 7391 | 8277 | 7096 | 5966 | 5351 |
| 29 | 112 | 125 | 116 | 113 | 76 | 117 | 103 |
| 30 | 112 | 125 | 116 | 113 | 76 | 117 | 103 |
| 31 | 5298 | 6921 | 8072 | 7506 | 7155 | 6898 | 4856 |
| 32 | 5298 | 6921 | 8072 | 7506 | 7155 | 6898 | 4856 |
| 33 | 5298 | 6921 | 8072 | 7506 | 7155 | 6898 | 4856 |
| 34 | 5298 | 6921 | 8072 | 7506 | 7155 | 6898 | 4856 |
| 35 | 5298 | 6921 | 8072 | 7506 | 7155 | 6898 | 4856 |
| 36 | 5298 | 6921 | 8072 | 7506 | 7155 | 6898 | 4856 |
| 37 | 5298 | 6921 | 8072 | 7506 | 7155 | 6898 | 4856 |
| 38 | 5298 | 6921 | 8072 | 7506 | 7155 | 6898 | 4856 |
| 39 | 5298 | 6921 | 8072 | 7506 | 7155 | 6898 | 4856 |
| 40 | 5298 | 6921 | 8072 | 7506 | 7155 | 6898 | 4856 |
| 41 | 5298 | 6921 | 8072 | 7506 | 7155 | 6898 | 4856 |
| 42 | 5298 | 6921 | 8072 | 7506 | 7155 | 6898 | 4856 |
| 43 | 5298 | 6921 | 8072 | 7506 | 7155 | 6898 | 4856 |
| 44 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 45 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 46 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 47 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 48 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 49 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 50 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 51 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 52 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 53 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 54 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 55 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 56 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 57 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 58 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 59 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 4 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 5 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 6 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 7 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 8 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 9 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 10 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 11 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 12 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 13 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 14 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 15 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 16 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 17 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 18 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 19 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 20 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 21 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 22 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 23 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 24 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 25 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 26 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 27 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 28 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 29 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 30 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 31 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 32 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 33 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 34 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 35 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 36 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 37 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 38 | 253 | 195 | 211 | 356 | 187 | 224 | 232 |
| 39 | 112 | 125 | 114 | 113 | 76 | 117 | 103 |
| 40 | 112 | 125 | 114 | 113 | 76 | 117 | 103 |
| 41 | | | | | | | |
| 42 | 1087 | 1227 | 897 | 1198 | 858 | 957 | 996 |
| 43 | 1087 | 1227 | 897 | 1198 | 858 | 957 | 996 |
| 44 | 3261 | 3772 | 4039 | 2328 | 3474 | 2139 | 2989 |
| 45 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 46 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 47 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 48 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 49 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 50 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 51 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 52 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 53 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 54 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 55 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 56 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 57 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 58 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 59 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 4 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 5 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 6 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 7 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 8 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 9 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 10 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 11 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 12 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 13 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 14 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 15 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 16 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 17 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 18 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 19 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 20 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 21 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 22 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 23 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 24 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 25 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 26 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 27 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 28 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 29 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 30 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 31 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 32 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 33 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 34 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 35 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 36 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 37 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 38 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 39 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 40 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 41 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 42 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 43 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 44 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 45 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 46 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 47 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 48 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 49 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 50 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 51 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 52 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 53 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 54 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 55 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 56 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 57 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 58 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 59 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | | | | | | | |
| 4 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 5 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 6 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 7 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 8 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 9 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 10 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 11 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 12 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 13 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 14 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 15 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 16 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 17 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 18 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 19 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 20 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 21 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 22 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 23 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 24 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 25 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 26 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 27 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 28 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 29 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 30 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 31 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 32 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 33 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 34 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 35 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 36 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 37 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 38 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 39 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 40 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 41 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 42 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 43 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 44 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 45 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 46 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 47 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 48 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 49 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 50 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 51 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 52 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 53 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 54 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 55 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 56 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 57 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 58 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 59 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 4 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 5 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 6 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 7 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 8 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 9 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 10 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 11 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 12 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 13 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 14 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 15 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 16 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 17 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 18 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 19 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 20 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 21 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 22 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 23 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 24 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 25 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 26 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 27 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 28 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 29 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 30 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 31 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 32 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 33 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 34 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 35 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 36 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 37 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 38 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 39 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 40 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 41 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 42 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 43 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 44 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 45 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 46 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 47 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 48 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 49 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 50 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 51 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 52 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 53 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 54 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 55 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 56 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 57 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 58 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 59 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 4 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 5 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 6 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 7 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 8 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 9 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 10 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 11 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 12 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 13 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 14 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 15 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 16 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 17 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 18 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 19 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 20 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 21 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 22 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 23 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 24 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 25 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 26 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 27 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 28 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 29 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 30 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 31 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 32 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 33 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 34 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 35 | 3261 | 3769 | 4039 | 2327 | 3474 | 2139 | 2989 |
| 36 | 3364 | 3879 | 4176 | 2402 | 3577 | 2222 | 3083 |
| 37 | 3364 | 3879 | 4176 | 2402 | 3577 | 2222 | 3083 |
| 38 | 3364 | 3879 | 4176 | 2402 | 3577 | 2222 | 3083 |
| 39 | 3364 | 3879 | 4176 | 2402 | 3577 | 2222 | 3083 |
| 40 | 3364 | 3879 | 4176 | 2402 | 3577 | 2222 | 3083 |
| 41 | 3364 | 3879 | 4176 | 2402 | 3577 | 2222 | 3083 |
| 42 | 3364 | 3879 | 4176 | 2402 | 3577 | 2222 | 3083 |
| 43 | 3364 | 3879 | 4176 | 2402 | 3577 | 2222 | 3083 |
| 44 | 3364 | 3879 | 4176 | 2402 | 3577 | 2222 | 3083 |
| 45 | 3364 | 3879 | 4176 | 2402 | 3577 | 2222 | 3083 |
| 46 | 3364 | 3879 | 4176 | 2402 | 3577 | 2222 | 3083 |
| 47 | 3277 | 3790 | 4060 | 2337 | 3487 | 2165 | 3004 |
| 48 | 3277 | 3790 | 4060 | 2337 | 3487 | 2165 | 3004 |
| 49 | 3277 | 3790 | 4060 | 2337 | 3487 | 2165 | 3004 |
| 50 | 3277 | 3790 | 4060 | 2337 | 3487 | 2165 | 3004 |
| 51 | 3277 | 3790 | 4060 | 2337 | 3487 | 2165 | 3004 |
| 52 | 3277 | 3790 | 4060 | 2337 | 3487 | 2165 | 3004 |
| 53 | 3277 | 3790 | 4060 | 2337 | 3487 | 2165 | 3004 |
| 54 | 3277 | 3790 | 4060 | 2337 | 3487 | 2165 | 3004 |
| 55 | 3277 | 3790 | 4060 | 2337 | 3487 | 2165 | 3004 |
| 56 | 3277 | 3790 | 4060 | 2337 | 3487 | 2165 | 3004 |
| 57 | 3277 | 3790 | 4060 | 2337 | 3487 | 2165 | 3004 |
| 58 | 3277 | 3790 | 4060 | 2337 | 3487 | 2165 | 3004 |
| 59 | 3277 | 3790 | 4060 | 2337 | 3487 | 2165 | 3004 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 3274 | 3782 | 4052 | 2334 | 3499 | 2143 | 3001 |
| 4 | 3274 | 3782 | 4052 | 2334 | 3499 | 2143 | 3001 |
| 5 | 3274 | 3782 | 4052 | 2334 | 3499 | 2143 | 3001 |
| 6 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 7 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 8 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 9 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 10 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 11 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 12 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 13 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 14 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 15 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 16 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 17 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 18 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 19 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 20 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 21 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 22 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 23 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 24 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 25 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 26 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 27 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 28 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 29 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 30 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 31 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 32 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 33 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 34 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 35 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 36 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 37 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 38 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 39 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 40 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 41 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 42 | 94 | 0 | 60 | 161 | 40 | 63 | 86 |
| 43 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 44 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 45 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 46 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 47 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 48 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 49 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 50 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 51 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 52 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 53 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 54 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 55 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 56 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 57 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 58 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 59 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 4 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 5 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 6 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 7 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 8 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 9 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 10 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 11 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 12 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 13 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 14 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 15 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 16 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 17 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 18 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 19 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 20 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 21 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 22 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 23 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 24 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 25 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 26 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 27 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 28 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 29 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 30 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 31 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 32 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 33 | 1072 | 1196 | 876 | 1174 | 843 | 942 | 983 |
| 34 | 5982 | 6956 | 6787 | 6557 | 5058 | 6831 | 5483 |
| 35 | 5982 | 6956 | 6787 | 6557 | 5058 | 6831 | 5483 |
| 36 | 5982 | 6956 | 6787 | 6557 | 5058 | 6831 | 5483 |
| 37 | 5982 | 6956 | 6787 | 6557 | 5058 | 6831 | 5483 |
| 38 | 5982 | 6956 | 6787 | 6557 | 5058 | 6831 | 5483 |
| 39 | 5982 | 6956 | 6787 | 6557 | 5058 | 6831 | 5483 |
| 40 | 5982 | 6956 | 6787 | 6557 | 5058 | 6831 | 5483 |
| 41 | 5982 | 6956 | 6787 | 6557 | 5058 | 6831 | 5483 |
| 42 | 5982 | 6956 | 6787 | 6557 | 5058 | 6831 | 5483 |
| 43 | 5982 | 6956 | 6787 | 6557 | 5058 | 6831 | 5483 |
| 44 | 5982 | 6956 | 6787 | 6557 | 5058 | 6831 | 5483 |
| 45 | 5982 | 6956 | 6787 | 6557 | 5058 | 6831 | 5483 |
| 46 | 5982 | 6956 | 6787 | 6557 | 5058 | 6831 | 5483 |
| 47 | 5982 | 6956 | 6787 | 6557 | 5058 | 6831 | 5483 |
| 48 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 49 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 50 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 51 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 52 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 53 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 54 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 55 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 56 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 57 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 58 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 59 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 4 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 5 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 6 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 7 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 8 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 9 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 10 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 11 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 12 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 13 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 14 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 15 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 16 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 17 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 18 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 19 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 20 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 21 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 22 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 23 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 24 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 25 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 26 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 27 | 198 | 231 | 161 | 150 | 124 | 163 | 181 |
| 28 | 97 | 0 | 60 | 163 | 41 | 63 | 89 |
| 29 | | | | | | | |
| 30 | 180 | 287 | 230 | 117 | 154 | 229 | 165 |
| 31 | 177 | 281 | 220 | 115 | 153 | 221 | 162 |
| 32 | 177 | 281 | 220 | 115 | 153 | 221 | 162 |
| 33 | 177 | 281 | 220 | 115 | 153 | 221 | 162 |
| 34 | 177 | 281 | 220 | 115 | 153 | 221 | 162 |
| 35 | 177 | 281 | 220 | 115 | 153 | 221 | 162 |
| 36 | 177 | 281 | 220 | 115 | 153 | 221 | 162 |
| 37 | 177 | 281 | 220 | 115 | 153 | 221 | 162 |
| 38 | 177 | 281 | 220 | 115 | 153 | 221 | 162 |
| 39 | 177 | 281 | 220 | 115 | 153 | 221 | 162 |
| 40 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 41 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 42 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 43 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 44 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 45 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 46 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 47 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 48 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 49 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 50 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 51 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 52 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 53 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 54 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 55 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 56 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 57 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 58 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 59 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 4 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 5 | 80 | 2 | 57 | 153 | 49 | 64 | 73 |
| 6 | 2793 | 1290 | 3869 | 2956 | 2527 | 2033 | 2560 |
| 7 | 257 | 295 | 397 | 350 | 346 | 337 | 236 |
| 8 | 257 | 295 | 397 | 350 | 346 | 337 | 236 |
| 9 | 257 | 295 | 397 | 350 | 346 | 337 | 236 |
| 10 | 257 | 295 | 397 | 350 | 346 | 337 | 236 |
| 11 | 257 | 295 | 397 | 350 | 346 | 337 | 236 |
| 12 | 257 | 295 | 397 | 350 | 346 | 337 | 236 |
| 13 | 257 | 295 | 397 | 350 | 346 | 337 | 236 |
| 14 | 257 | 295 | 397 | 350 | 346 | 337 | 236 |
| 15 | 257 | 295 | 397 | 350 | 346 | 337 | 236 |
| 16 | 257 | 295 | 397 | 350 | 346 | 337 | 236 |
| 17 | 257 | 295 | 397 | 350 | 346 | 337 | 236 |
| 18 | 257 | 295 | 397 | 350 | 346 | 337 | 236 |
| 19 | 257 | 295 | 397 | 350 | 346 | 337 | 236 |
| 20 | 257 | 295 | 397 | 350 | 346 | 337 | 236 |
| 21 | 257 | 295 | 397 | 350 | 346 | 337 | 236 |
| 22 | 257 | 295 | 397 | 350 | 346 | 337 | 236 |
| 23 | 257 | 295 | 397 | 350 | 346 | 337 | 236 |
| 24 | 257 | 295 | 397 | 350 | 346 | 337 | 236 |
| 25 | 257 | 295 | 397 | 350 | 346 | 337 | 236 |
| 26 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 27 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 28 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 29 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 30 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 31 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 32 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 33 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 34 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 35 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 36 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 37 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 38 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 39 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 40 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 41 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 42 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 43 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 44 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 45 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 46 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 47 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 48 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 49 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 50 | 275 | 14 | 195 | 494 | 171 | 197 | 252 |
| 51 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 52 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 53 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 54 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 55 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 56 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 57 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 58 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 59 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 4 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 5 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 6 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 7 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 8 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 9 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 10 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 11 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 12 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 13 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 14 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 15 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 16 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 17 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 18 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 19 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 20 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 21 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 22 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 23 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 24 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 25 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 26 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 27 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 28 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 29 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 30 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 31 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 32 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 33 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 34 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 35 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 36 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 37 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 38 | 246 | 192 | 177 | 279 | 155 | 196 | 225 |
| 39 | 283 | 229 | 200 | 311 | 181 | 220 | 259 |
| 40 | 283 | 229 | 200 | 311 | 181 | 220 | 259 |
| 41 | 283 | 229 | 200 | 311 | 181 | 220 | 259 |
| 42 | 283 | 229 | 200 | 311 | 181 | 220 | 259 |
| 43 | 283 | 229 | 200 | 311 | 181 | 220 | 259 |
| 44 | 283 | 229 | 200 | 311 | 181 | 220 | 259 |
| 45 | 283 | 229 | 200 | 311 | 181 | 220 | 259 |
| 46 | 283 | 229 | 200 | 311 | 181 | 220 | 259 |
| 47 | 283 | 229 | 200 | 311 | 181 | 220 | 259 |
| 48 | 283 | 229 | 200 | 311 | 181 | 220 | 259 |
| 49 | 283 | 229 | 200 | 311 | 181 | 220 | 259 |
| 50 | 283 | 229 | 200 | 311 | 181 | 220 | 259 |
| 51 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 52 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 53 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 54 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 55 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 56 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 57 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 58 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 59 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 4 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 5 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 6 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 7 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 8 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 9 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 10 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 11 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 12 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 13 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 14 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 15 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 16 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 17 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 18 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 19 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 20 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 21 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 22 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 23 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 24 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 25 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 26 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 27 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 28 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 29 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 30 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 31 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 32 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 33 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 34 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 35 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 36 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 37 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 38 | 56 | 78 | 48 | 38 | 50 | 45 | 51 |
| 39 | 1397 | 2050 | 1904 | 1476 | 2002 | 1691 | 1280 |
| 40 | 129 | 166 | 103 | 95 | 99 | 116 | 118 |
| 41 | 129 | 166 | 103 | 95 | 99 | 116 | 118 |
| 42 | 129 | 166 | 103 | 95 | 99 | 116 | 118 |
| 43 | 122 | 158 | 96 | 88 | 90 | 113 | 112 |
| 44 | 122 | 158 | 96 | 88 | 90 | 113 | 112 |
| 45 | 122 | 158 | 96 | 88 | 90 | 113 | 112 |
| 46 | 122 | 158 | 96 | 88 | 90 | 113 | 112 |
| 47 | 122 | 158 | 96 | 88 | 90 | 113 | 112 |
| 48 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 49 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 50 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 51 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 52 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 53 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 54 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 55 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 56 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 57 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 58 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 59 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|-------|-------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 4 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 5 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 6 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 7 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 8 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 9 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 10 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 11 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 12 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 13 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 14 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 15 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 16 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 17 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 18 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 19 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 20 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 21 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 22 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 23 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 24 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 25 | 143 | 153 | 116 | 113 | 97 | 122 | 131 |
| 26 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 27 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 28 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 29 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 30 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 31 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 32 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 33 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 34 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 35 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 36 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 37 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 38 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 39 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 40 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 41 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 42 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 43 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 44 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 45 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 46 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 47 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 48 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 49 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 50 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 51 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 52 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 53 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 54 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 55 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 56 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 57 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 58 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 59 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|-------|-------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 4 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 5 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 6 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 7 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 8 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 9 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 10 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 11 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 12 | 20760 | 25099 | 22515 | 25413 | 24767 | 23487 | 19028 |
| 13 | 20811 | 25152 | 22573 | 25456 | 24867 | 23541 | 19075 |
| 14 | 83 | 117 | 102 | 58 | 78 | 102 | 76 |
| 15 | 83 | 117 | 102 | 58 | 78 | 102 | 76 |
| 16 | 117 | 58 | 82 | 137 | 65 | 84 | 107 |
| 17 | 117 | 58 | 82 | 137 | 65 | 84 | 107 |
| 18 | 117 | 58 | 82 | 137 | 65 | 84 | 107 |
| 19 | 117 | 58 | 82 | 137 | 65 | 84 | 107 |
| 20 | 117 | 58 | 82 | 137 | 65 | 84 | 107 |
| 21 | 117 | 58 | 82 | 137 | 65 | 84 | 107 |
| 22 | 117 | 58 | 82 | 137 | 65 | 84 | 107 |
| 23 | 117 | 58 | 82 | 137 | 65 | 84 | 107 |
| 24 | 117 | 58 | 82 | 137 | 65 | 84 | 107 |
| 25 | 239 | 327 | 355 | 389 | 429 | 343 | 219 |
| 26 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 27 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 28 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 29 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 30 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 31 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 32 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 33 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 34 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 35 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 36 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 37 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 38 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 39 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 40 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 41 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 42 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 43 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 44 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 45 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 46 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 47 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 48 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 49 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 50 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 51 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 52 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 53 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 54 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 55 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 56 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 57 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 58 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 59 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 4 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 5 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 6 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 7 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 8 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 9 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 10 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 11 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 12 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 13 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 14 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 15 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 16 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 17 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 18 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 19 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 20 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 21 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 22 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 23 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 24 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 25 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 26 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 27 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 28 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 29 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 30 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 31 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 32 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 33 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 34 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 35 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 36 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 37 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 38 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 39 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 40 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 41 | 122 | 179 | 141 | 71 | 100 | 152 | 112 |
| 42 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 43 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 44 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 45 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 46 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 47 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 48 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 49 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 50 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 51 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 52 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 53 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 54 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 55 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 56 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 57 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 58 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 59 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 4 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 5 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 6 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 7 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 8 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 9 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 10 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 11 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 12 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 13 | 114 | 132 | 97 | 89 | 88 | 104 | 104 |
| 14 | 903 | 868 | 1240 | 1118 | 1259 | 934 | 828 |
| 15 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 16 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 17 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 18 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 19 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 20 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 21 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 22 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 23 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 24 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 25 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 26 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 27 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 28 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 29 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 30 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 31 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 32 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 33 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 34 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 35 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 36 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 37 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 38 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 39 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 40 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 41 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 42 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 43 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 44 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 45 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 46 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 47 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 48 | 2803 | 3504 | 3107 | 2097 | 3024 | 2579 | 2569 |
| 49 | 118 | 56 | 159 | 128 | 130 | 83 | 108 |
| 50 | 2825 | 3521 | 3144 | 2129 | 3061 | 2609 | 2589 |
| 51 | 2825 | 3521 | 3144 | 2129 | 3061 | 2609 | 2589 |
| 52 | 2825 | 3521 | 3144 | 2129 | 3061 | 2609 | 2589 |
| 53 | 2825 | 3521 | 3144 | 2129 | 3061 | 2609 | 2589 |
| 54 | 2825 | 3521 | 3144 | 2129 | 3061 | 2609 | 2589 |
| 55 | 2825 | 3521 | 3144 | 2129 | 3061 | 2609 | 2589 |
| 56 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 57 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 58 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 59 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 4 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 5 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 6 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 7 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 8 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 9 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 10 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 11 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 12 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 13 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 14 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 15 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 16 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 17 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 18 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 19 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 20 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 21 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 22 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 23 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 24 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 25 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 26 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 27 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 28 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 29 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 30 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 31 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 32 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 33 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 34 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 35 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 36 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 37 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 38 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 39 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 40 | 108 | 125 | 90 | 81 | 79 | 101 | 99 |
| 41 | | | | | | | |
| 42 | 2812 | 3509 | 3110 | 2103 | 3033 | 2583 | 2577 |
| 43 | 2812 | 3509 | 3110 | 2103 | 3033 | 2583 | 2577 |
| 44 | 569 | 754 | 694 | 644 | 849 | 594 | 522 |
| 45 | 569 | 754 | 694 | 644 | 849 | 594 | 522 |
| 46 | 569 | 754 | 694 | 644 | 849 | 594 | 522 |
| 47 | 569 | 754 | 694 | 644 | 849 | 594 | 522 |
| 48 | 569 | 754 | 694 | 644 | 849 | 594 | 522 |
| 49 | 209 | 229 | 178 | 157 | 157 | 183 | 192 |
| 50 | 209 | 229 | 178 | 157 | 157 | 183 | 192 |
| 51 | 209 | 229 | 178 | 157 | 157 | 183 | 192 |
| 52 | 216 | 234 | 181 | 161 | 161 | 185 | 198 |
| 53 | | | | | | | |
| 54 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 55 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 56 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 57 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 58 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 59 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|----|----|-----|----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 4 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 5 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 6 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 7 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 8 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 9 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 10 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 11 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 12 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 13 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 14 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 15 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 16 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 17 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 18 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 19 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 20 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 21 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 22 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 23 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 24 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 25 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 26 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 27 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 28 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 29 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 30 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 31 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 32 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 33 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 34 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 35 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 36 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 37 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 38 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 39 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 40 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 41 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 42 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 43 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 44 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 45 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 46 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 47 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 48 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 49 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 50 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 51 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 52 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 53 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 54 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 55 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 56 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 57 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 58 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 59 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 4 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 5 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 6 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 7 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 8 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 9 | 114 | 93 | 88 | 116 | 77 | 101 | 104 |
| 10 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 11 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 12 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 13 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 14 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 15 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 16 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 17 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 18 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 19 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 20 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 21 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 22 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 23 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 24 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 25 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 26 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 27 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 28 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 29 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 30 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 31 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 32 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 33 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 34 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 35 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 36 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 37 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 38 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 39 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 40 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 41 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 42 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 43 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 44 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 45 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 46 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 47 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 48 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 49 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 50 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 51 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 52 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 53 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 54 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 55 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 56 | 3894 | 4895 | 4111 | 2771 | 4095 | 3542 | 3569 |
| 57 | 181 | 173 | 174 | 200 | 177 | 178 | 166 |
| 58 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 59 | | | | | | | |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | | | | | | | |
| 4 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 5 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 6 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 7 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 8 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 9 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 10 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 11 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 12 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 13 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 14 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 15 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 16 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 17 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 18 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 19 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 20 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 21 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 22 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 23 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 24 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 25 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 26 | 204 | 223 | 174 | 149 | 155 | 179 | 187 |
| 27 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 28 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 29 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 30 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 31 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 32 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 33 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 34 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 35 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 36 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 37 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 38 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 39 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 40 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 41 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 42 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 43 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 44 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 45 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 46 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 47 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 48 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 49 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 50 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 51 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 52 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 53 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 54 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 55 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 56 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 57 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 58 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 59 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 4 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 5 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 6 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 7 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 8 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 9 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 10 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 11 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 12 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 13 | 621 | 622 | 895 | 845 | 924 | 772 | 569 |
| 14 | 386 | 485 | 458 | 448 | 586 | 400 | 354 |
| 15 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 16 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 17 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 18 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 19 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 20 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 21 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 22 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 23 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 24 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 25 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 26 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 27 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 28 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 29 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 30 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 31 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 32 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 33 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 34 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 35 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 36 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 37 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 38 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 39 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 40 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 41 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 42 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 43 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 44 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 45 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 46 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 47 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 48 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 49 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 50 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 51 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 52 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 53 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 54 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 55 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 56 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 57 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 58 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 59 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 4 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 5 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 6 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 7 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 8 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 9 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 10 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 11 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 12 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 13 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 14 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 15 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 16 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 17 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 18 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 19 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 20 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 21 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 22 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 23 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 24 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 25 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 26 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 27 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 28 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 29 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 30 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 31 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 32 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 33 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 34 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 35 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 36 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 37 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 38 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 39 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 40 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 41 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 42 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 43 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 44 | 3974 | 4092 | 5576 | 3930 | 5640 | 3856 | 3642 |
| 45 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 46 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 47 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 48 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 49 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 50 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 51 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 52 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 53 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 54 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 55 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 56 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 57 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 58 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 59 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----|----|----|----|----|----|----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 4 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 5 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 6 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 7 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 8 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 9 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 10 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 11 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 12 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 13 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 14 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 15 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 16 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 17 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 18 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 19 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 20 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 21 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 22 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 23 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 24 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 25 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 26 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 27 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 28 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 29 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 30 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 31 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 32 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 33 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 34 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 35 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 36 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 37 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 38 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 39 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 40 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 41 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 42 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 43 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 44 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 45 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 46 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 47 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 48 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 49 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 50 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 51 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 52 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 53 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 54 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 55 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 56 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 57 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 58 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 59 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|-------|-------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 4 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 5 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 6 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 7 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 8 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 9 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 10 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 11 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 12 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 13 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 14 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 15 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 16 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 17 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 18 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 19 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 20 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 21 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 22 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 23 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 24 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 25 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 26 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 27 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 28 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 29 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 30 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 31 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 32 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 33 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 34 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 35 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 36 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 37 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 38 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 39 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 40 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 41 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 42 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 43 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 44 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 45 | 81 | 77 | 53 | 56 | 50 | 57 | 74 |
| 46 | 8056 | 8565 | 9795 | 10455 | 10940 | 9676 | 7384 |
| 47 | 8056 | 8565 | 9795 | 10455 | 10940 | 9676 | 7384 |
| 48 | 8061 | 8574 | 9800 | 10465 | 10953 | 9683 | 7388 |
| 49 | 8061 | 8574 | 9800 | 10465 | 10953 | 9683 | 7388 |
| 50 | 8061 | 8574 | 9800 | 10465 | 10953 | 9683 | 7388 |
| 51 | 321 | 532 | 336 | 306 | 432 | 426 | 294 |
| 52 | 321 | 532 | 336 | 306 | 432 | 426 | 294 |
| 53 | 321 | 532 | 336 | 306 | 432 | 426 | 294 |
| 54 | 321 | 532 | 336 | 306 | 432 | 426 | 294 |
| 55 | 321 | 532 | 336 | 306 | 432 | 426 | 294 |
| 56 | 321 | 532 | 336 | 306 | 432 | 426 | 294 |
| 57 | 321 | 532 | 336 | 306 | 432 | 426 | 294 |
| 58 | 321 | 532 | 336 | 306 | 432 | 426 | 294 |
| 59 | 321 | 532 | 336 | 306 | 432 | 426 | 294 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|-------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 535 | 487 | 643 | 576 | 559 | 627 | 490 |
| 4 | 535 | 490 | 644 | 577 | 561 | 629 | 490 |
| 5 | 535 | 490 | 644 | 577 | 561 | 629 | 490 |
| 6 | 535 | 490 | 644 | 577 | 561 | 629 | 490 |
| 7 | 535 | 490 | 644 | 577 | 561 | 629 | 490 |
| 8 | 535 | 490 | 644 | 577 | 561 | 629 | 490 |
| 9 | 535 | 490 | 644 | 577 | 561 | 629 | 490 |
| 10 | 535 | 490 | 644 | 577 | 561 | 629 | 490 |
| 11 | 539 | 491 | 649 | 577 | 563 | 630 | 494 |
| 12 | 539 | 491 | 649 | 577 | 563 | 630 | 494 |
| 13 | 539 | 491 | 649 | 577 | 563 | 630 | 494 |
| 14 | 539 | 491 | 649 | 577 | 563 | 630 | 494 |
| 15 | 539 | 491 | 649 | 577 | 563 | 630 | 494 |
| 16 | 539 | 491 | 649 | 577 | 563 | 630 | 494 |
| 17 | 539 | 491 | 649 | 577 | 563 | 630 | 494 |
| 18 | 539 | 491 | 649 | 577 | 563 | 630 | 494 |
| 19 | 539 | 491 | 649 | 577 | 563 | 630 | 494 |
| 20 | 539 | 491 | 649 | 577 | 563 | 630 | 494 |
| 21 | 539 | 491 | 649 | 577 | 563 | 630 | 494 |
| 22 | 843 | 826 | 1069 | 825 | 1021 | 883 | 773 |
| 23 | 856 | 837 | 1088 | 842 | 1045 | 892 | 785 |
| 24 | 856 | 837 | 1088 | 842 | 1045 | 892 | 785 |
| 25 | 856 | 837 | 1088 | 842 | 1045 | 892 | 785 |
| 26 | 856 | 837 | 1088 | 842 | 1045 | 892 | 785 |
| 27 | 856 | 837 | 1088 | 842 | 1045 | 892 | 785 |
| 28 | 856 | 837 | 1088 | 842 | 1045 | 892 | 785 |
| 29 | 856 | 837 | 1088 | 842 | 1045 | 892 | 785 |
| 30 | 856 | 837 | 1088 | 842 | 1045 | 892 | 785 |
| 31 | 856 | 837 | 1088 | 842 | 1045 | 892 | 785 |
| 32 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 33 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 34 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 35 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 36 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 37 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 38 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 39 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 40 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 41 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 42 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 43 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 44 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 45 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 46 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 47 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 48 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 49 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 50 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 51 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 52 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 53 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 54 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 55 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 56 | 8808 | 9442 | 9816 | 9726 | 10502 | 9983 | 8073 |
| 57 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 58 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 59 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|-------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 4 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 5 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 6 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 7 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 8 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 9 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 10 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 11 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 12 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 13 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 14 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 15 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 16 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 17 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 18 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 19 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 20 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 21 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 22 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 23 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 24 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 25 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 26 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 27 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 28 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 29 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 30 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 31 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 32 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 33 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 34 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 35 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 36 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 37 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 38 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 39 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 40 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 41 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 42 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 43 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 44 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 45 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 46 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 47 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 48 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 49 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 50 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 51 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 52 | 8601 | 9108 | 9533 | 9526 | 10224 | 9693 | 7883 |
| 53 | 94 | 24 | 70 | 138 | 56 | 86 | 86 |
| 54 | 94 | 24 | 70 | 138 | 56 | 86 | 86 |
| 55 | 94 | 24 | 70 | 138 | 56 | 86 | 86 |
| 56 | 94 | 24 | 70 | 138 | 56 | 86 | 86 |
| 57 | 94 | 24 | 70 | 138 | 56 | 86 | 86 |
| 58 | 94 | 24 | 70 | 138 | 56 | 86 | 86 |
| 59 | 94 | 24 | 70 | 138 | 56 | 86 | 86 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|-------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 8603 | 9109 | 9535 | 9528 | 10227 | 9697 | 7885 |
| 4 | 8603 | 9109 | 9535 | 9528 | 10227 | 9697 | 7885 |
| 5 | 8603 | 9109 | 9535 | 9528 | 10227 | 9697 | 7885 |
| 6 | 227 | 241 | 321 | 172 | 342 | 175 | 208 |
| 7 | 343 | 176 | 315 | 375 | 235 | 310 | 314 |
| 8 | 285 | 309 | 311 | 357 | 380 | 328 | 261 |
| 9 | 227 | 238 | 320 | 172 | 342 | 174 | 208 |
| 10 | 227 | 238 | 320 | 172 | 342 | 174 | 208 |
| 11 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 12 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 13 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 14 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 15 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 16 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 17 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 18 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 19 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 20 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 21 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 22 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 23 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 24 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 25 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 26 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 27 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 28 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 29 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 30 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 31 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 32 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 33 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 34 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 35 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 36 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 37 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 38 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 39 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 40 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 41 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 42 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 43 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 44 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 45 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 46 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 47 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 48 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 49 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 50 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 51 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 52 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 53 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 54 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 55 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 56 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 57 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 58 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 59 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 4 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 5 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 6 | 153 | 95 | 113 | 174 | 107 | 130 | 140 |
| 7 | 160 | 101 | 123 | 177 | 113 | 140 | 147 |
| 8 | 160 | 101 | 123 | 177 | 113 | 140 | 147 |
| 9 | 160 | 101 | 123 | 177 | 113 | 140 | 147 |
| 10 | 160 | 101 | 123 | 177 | 113 | 140 | 147 |
| 11 | 160 | 101 | 123 | 177 | 113 | 140 | 147 |
| 12 | 160 | 101 | 123 | 177 | 113 | 140 | 147 |
| 13 | 160 | 101 | 123 | 177 | 113 | 140 | 147 |
| 14 | 160 | 101 | 123 | 177 | 113 | 140 | 147 |
| 15 | 165 | 145 | 178 | 139 | 138 | 169 | 151 |
| 16 | 165 | 144 | 178 | 139 | 138 | 169 | 151 |
| 17 | 487 | 336 | 604 | 544 | 399 | 634 | 446 |
| 18 | 487 | 336 | 604 | 544 | 399 | 634 | 446 |
| 19 | 487 | 336 | 604 | 544 | 399 | 634 | 446 |
| 20 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 21 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 22 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 23 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 24 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 25 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 26 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 27 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 28 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 29 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 30 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 31 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 32 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 33 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 34 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 35 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 36 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 37 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 38 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 39 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 40 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 41 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 42 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 43 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 44 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 45 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 46 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 47 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 48 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 49 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 50 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 51 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 52 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 53 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 54 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 55 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 56 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 57 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 58 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 59 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 4 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 5 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 6 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 7 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 8 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 9 | 337 | 174 | 307 | 371 | 233 | 307 | 309 |
| 10 | 6378 | 6570 | 6787 | 6600 | 7338 | 6738 | 5846 |
| 11 | 6378 | 6570 | 6787 | 6600 | 7338 | 6738 | 5846 |
| 12 | 6378 | 6570 | 6787 | 6600 | 7338 | 6738 | 5846 |
| 13 | 6378 | 6570 | 6787 | 6600 | 7338 | 6738 | 5846 |
| 14 | 6378 | 6570 | 6787 | 6600 | 7338 | 6738 | 5846 |
| 15 | 6378 | 6570 | 6787 | 6600 | 7338 | 6738 | 5846 |
| 16 | 6378 | 6570 | 6787 | 6600 | 7338 | 6738 | 5846 |
| 17 | 6378 | 6570 | 6787 | 6600 | 7338 | 6738 | 5846 |
| 18 | 6378 | 6570 | 6787 | 6600 | 7338 | 6738 | 5846 |
| 19 | 6378 | 6570 | 6787 | 6600 | 7338 | 6738 | 5846 |
| 20 | 6378 | 6570 | 6787 | 6600 | 7338 | 6738 | 5846 |
| 21 | 6378 | 6570 | 6787 | 6600 | 7338 | 6738 | 5846 |
| 22 | 6443 | 6633 | 6858 | 6661 | 7427 | 6804 | 5905 |
| 23 | 6443 | 6633 | 6858 | 6661 | 7427 | 6804 | 5905 |
| 24 | 6492 | 6674 | 6893 | 6697 | 7461 | 6851 | 5950 |
| 25 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 26 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 27 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 28 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 29 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 30 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 31 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 32 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 33 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 34 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 35 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 36 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 37 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 38 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 39 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 40 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 41 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 42 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 43 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 44 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 45 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 46 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 47 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 48 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 49 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 50 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 51 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 52 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 53 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 54 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 55 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 56 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 57 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 58 | 192 | 217 | 144 | 144 | 143 | 184 | 176 |
| 59 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 4 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 5 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 6 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 7 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 8 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 9 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 10 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 11 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 12 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 13 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 14 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 15 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 16 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 17 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 18 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 19 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 20 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 21 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 22 | 165 | 144 | 177 | 139 | 138 | 169 | 151 |
| 23 | 369 | 191 | 329 | 407 | 256 | 334 | 338 |
| 24 | 212 | 78 | 187 | 231 | 120 | 180 | 194 |
| 25 | 212 | 78 | 187 | 231 | 120 | 180 | 194 |
| 26 | 212 | 78 | 187 | 231 | 120 | 180 | 194 |
| 27 | 212 | 78 | 187 | 231 | 120 | 180 | 194 |
| 28 | 212 | 78 | 187 | 231 | 120 | 180 | 194 |
| 29 | 212 | 78 | 187 | 231 | 120 | 180 | 194 |
| 30 | 212 | 78 | 187 | 231 | 120 | 180 | 194 |
| 31 | 212 | 78 | 187 | 231 | 120 | 180 | 194 |
| 32 | 212 | 78 | 187 | 231 | 120 | 180 | 194 |
| 33 | 212 | 78 | 187 | 231 | 120 | 180 | 194 |
| 34 | 212 | 78 | 187 | 231 | 120 | 180 | 194 |
| 35 | 212 | 78 | 187 | 231 | 120 | 180 | 194 |
| 36 | 212 | 78 | 187 | 231 | 120 | 180 | 194 |
| 37 | 212 | 78 | 187 | 231 | 120 | 180 | 194 |
| 38 | 212 | 78 | 187 | 231 | 120 | 180 | 194 |
| 39 | 212 | 78 | 187 | 231 | 120 | 180 | 194 |
| 40 | 212 | 78 | 187 | 231 | 120 | 180 | 194 |
| 41 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 42 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 43 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 44 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 45 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 46 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 47 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 48 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 49 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 50 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 51 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 52 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 53 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 54 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 55 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 56 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 57 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 58 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 59 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 4 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 5 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 6 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 7 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 8 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 9 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 10 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 11 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 12 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 13 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 14 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 15 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 16 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 17 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 18 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 19 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 20 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 21 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 22 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 23 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 24 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 25 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 26 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 27 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 28 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 29 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 30 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 31 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 32 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 33 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 34 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 35 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 36 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 37 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 38 | 72 | 36 | 52 | 83 | 37 | 68 | 66 |
| 39 | 77 | 48 | 47 | 112 | 50 | 86 | 71 |
| 40 | 1173 | 1281 | 1425 | 1427 | 1756 | 1304 | 1075 |
| 41 | 1168 | 1276 | 1420 | 1421 | 1750 | 1298 | 1071 |
| 42 | 1168 | 1276 | 1420 | 1421 | 1750 | 1298 | 1071 |
| 43 | 1168 | 1276 | 1420 | 1421 | 1750 | 1298 | 1071 |
| 44 | 1168 | 1276 | 1420 | 1421 | 1750 | 1298 | 1071 |
| 45 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 46 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 47 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 48 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 49 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 50 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 51 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 52 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 53 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 54 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 55 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 56 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 57 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 58 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 59 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|-------|-------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | | | | | | | |
| 4 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 5 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 6 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 7 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 8 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 9 | 4749 | 4758 | 4479 | 6106 | 6476 | 4557 | 4353 |
| 10 | 672 | 588 | 731 | 645 | 627 | 728 | 616 |
| 11 | 12743 | 12599 | 13670 | 14448 | 14864 | 14321 | 11680 |
| 12 | 12743 | 12599 | 13670 | 14448 | 14864 | 14321 | 11680 |
| 13 | 12743 | 12599 | 13670 | 14448 | 14864 | 14321 | 11680 |
| 14 | 12743 | 12599 | 13670 | 14448 | 14864 | 14321 | 11680 |
| 15 | 12743 | 12599 | 13670 | 14448 | 14864 | 14321 | 11680 |
| 16 | 12743 | 12599 | 13670 | 14448 | 14864 | 14321 | 11680 |
| 17 | 12743 | 12599 | 13670 | 14448 | 14864 | 14321 | 11680 |
| 18 | 12743 | 12599 | 13670 | 14448 | 14864 | 14321 | 11680 |
| 19 | 12743 | 12599 | 13670 | 14448 | 14864 | 14321 | 11680 |
| 20 | 12743 | 12599 | 13670 | 14448 | 14864 | 14321 | 11680 |
| 21 | 12743 | 12599 | 13670 | 14448 | 14864 | 14321 | 11680 |
| 22 | 12743 | 12599 | 13670 | 14448 | 14864 | 14321 | 11680 |
| 23 | 16055 | 17668 | 13034 | 6346 | 12685 | 9822 | 14716 |
| 24 | 16055 | 17668 | 13034 | 6346 | 12685 | 9822 | 14716 |
| 25 | 16055 | 17668 | 13034 | 6346 | 12685 | 9822 | 14716 |
| 26 | 16055 | 17668 | 13034 | 6346 | 12685 | 9822 | 14716 |
| 27 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 28 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 29 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 30 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 31 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 32 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 33 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 34 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 35 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 36 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 37 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 38 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 39 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 40 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 41 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 42 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 43 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 44 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 45 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 46 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 47 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 48 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 49 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 50 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 51 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 52 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 53 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 54 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 55 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 56 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 57 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 58 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 59 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|-------|-------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 4 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 5 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 6 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 7 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 8 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 9 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 10 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 11 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 12 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 13 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 14 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 15 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 16 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 17 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 18 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 19 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 20 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 21 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 22 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 23 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 24 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 25 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 26 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 27 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 28 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 29 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 30 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 31 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 32 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 33 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 34 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 35 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 36 | 16048 | 17658 | 13018 | 6339 | 12674 | 9812 | 14709 |
| 37 | 159 | 215 | 212 | 149 | 216 | 216 | 146 |
| 38 | 159 | 215 | 212 | 149 | 216 | 216 | 146 |
| 39 | 159 | 215 | 212 | 149 | 216 | 216 | 146 |
| 40 | 159 | 215 | 212 | 149 | 216 | 216 | 146 |
| 41 | 159 | 215 | 212 | 149 | 216 | 216 | 146 |
| 42 | 159 | 215 | 212 | 149 | 216 | 216 | 146 |
| 43 | 159 | 215 | 212 | 149 | 216 | 216 | 146 |
| 44 | 159 | 215 | 212 | 149 | 216 | 216 | 146 |
| 45 | 159 | 215 | 212 | 149 | 216 | 216 | 146 |
| 46 | 159 | 215 | 212 | 149 | 216 | 216 | 146 |
| 47 | 159 | 215 | 212 | 149 | 216 | 216 | 146 |
| 48 | 159 | 215 | 212 | 149 | 216 | 216 | 146 |
| 49 | 16080 | 17701 | 13042 | 6365 | 12711 | 9861 | 14738 |
| 50 | 11090 | 11951 | 13426 | 10538 | 12704 | 13252 | 10165 |
| 51 | 11090 | 11951 | 13426 | 10538 | 12704 | 13252 | 10165 |
| 52 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 53 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 54 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 55 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 56 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 57 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 58 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 59 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|--------|-------|--------|--------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 4 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 5 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 6 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 7 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 8 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 9 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 10 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 11 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 12 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 13 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 14 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 15 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 16 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 17 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 18 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 19 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 20 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 21 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 22 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 23 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 24 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 25 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 26 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 27 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 28 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 29 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 30 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 31 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 32 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 33 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 34 | 11084 | 11940 | 13420 | 10535 | 12698 | 13247 | 10159 |
| 35 | 162 | 102 | 124 | 178 | 115 | 144 | 148 |
| 36 | 234 | 239 | 239 | 284 | 298 | 256 | 214 |
| 37 | 125 | 121 | 87 | 98 | 84 | 110 | 115 |
| 38 | 125 | 121 | 87 | 98 | 84 | 110 | 115 |
| 39 | 125 | 121 | 87 | 98 | 84 | 110 | 115 |
| 40 | 125 | 121 | 87 | 98 | 84 | 110 | 115 |
| 41 | 125 | 121 | 87 | 98 | 84 | 110 | 115 |
| 42 | 125 | 121 | 87 | 98 | 84 | 110 | 115 |
| 43 | 125 | 121 | 87 | 98 | 84 | 110 | 115 |
| 44 | 125 | 121 | 87 | 98 | 84 | 110 | 115 |
| 45 | 125 | 121 | 87 | 98 | 84 | 110 | 115 |
| 46 | 125 | 121 | 87 | 98 | 84 | 110 | 115 |
| 47 | 125 | 121 | 87 | 98 | 84 | 110 | 115 |
| 48 | 125 | 121 | 87 | 98 | 84 | 110 | 115 |
| 49 | 125 | 121 | 87 | 98 | 84 | 110 | 115 |
| 50 | 125 | 121 | 87 | 98 | 84 | 110 | 115 |
| 51 | 125 | 121 | 87 | 98 | 84 | 110 | 115 |
| 52 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 53 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 54 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 55 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 56 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 57 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 58 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 59 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|--------|-------|--------|--------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 4 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 5 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 6 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 7 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 8 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 9 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 10 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 11 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 12 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 13 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 14 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 15 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 16 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 17 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 18 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 19 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 20 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 21 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 22 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 23 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 24 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 25 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 26 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 27 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 28 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 29 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 30 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 31 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 32 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 33 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 34 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 35 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 36 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 37 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 38 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 39 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 40 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 41 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 42 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 43 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 44 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 45 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 46 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 47 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 48 | 90088 | 102150 | 97728 | 101894 | 126367 | 95904 | 82572 |
| 49 | 90125 | 102170 | 97764 | 101933 | 126415 | 95931 | 82606 |
| 50 | 90125 | 102170 | 97764 | 101933 | 126415 | 95931 | 82606 |
| 51 | 90125 | 102170 | 97764 | 101933 | 126415 | 95931 | 82606 |
| 52 | 90125 | 102170 | 97764 | 101933 | 126415 | 95931 | 82606 |
| 53 | 90125 | 102170 | 97764 | 101933 | 126415 | 95931 | 82606 |
| 54 | 90125 | 102170 | 97764 | 101933 | 126415 | 95931 | 82606 |
| 55 | 90125 | 102170 | 97764 | 101933 | 126415 | 95931 | 82606 |
| 56 | 90633 | 102800 | 98390 | 102536 | 127267 | 96663 | 83072 |
| 57 | 90633 | 102800 | 98390 | 102536 | 127267 | 96663 | 83072 |
| 58 | 90633 | 102800 | 98390 | 102536 | 127267 | 96663 | 83072 |
| 59 | 90633 | 102800 | 98390 | 102536 | 127267 | 96663 | 83072 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|--------|--------|--------|--------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 93500 | 105859 | 101222 | 105133 | 131166 | 99670 | 85699 |
| 4 | 74 | 44 | 44 | 104 | 50 | 77 | 68 |
| 5 | 74 | 44 | 44 | 104 | 50 | 77 | 68 |
| 6 | 74 | 44 | 44 | 104 | 50 | 77 | 68 |
| 7 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 8 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 9 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 10 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 11 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 12 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 13 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 14 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 15 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 16 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 17 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 18 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 19 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 20 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 21 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 22 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 23 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 24 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 25 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 26 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 27 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 28 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 29 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 30 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 31 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 32 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 33 | 77 | 69 | 67 | 54 | 53 | 68 | 71 |
| 34 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 35 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 36 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 37 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 38 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 39 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 40 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 41 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 42 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 43 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 44 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 45 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 46 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 47 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 48 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 49 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 50 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 51 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 52 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 53 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 54 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 55 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 56 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 57 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 58 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 59 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|------|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 4 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 5 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 6 | 768 | 827 | 905 | 939 | 1171 | 846 | 704 |
| 7 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 8 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 9 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 10 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 11 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 12 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 13 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 14 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 15 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 16 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 17 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 18 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 19 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 20 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 21 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 22 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 23 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 24 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 25 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 26 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 27 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 28 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 29 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 30 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 31 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 32 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 33 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 34 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 35 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 36 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 37 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 38 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 39 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 40 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 41 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 42 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 43 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 44 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 45 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 46 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 47 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 48 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 49 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 50 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 51 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 52 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 53 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 54 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 55 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 56 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 57 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 58 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 59 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|------|-------|-------|-------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 4 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 5 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 6 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 7 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 8 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 9 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 10 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 11 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 12 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 13 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 14 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 15 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 16 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 17 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 18 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 19 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 20 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 21 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 22 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 23 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 24 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 25 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 26 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 27 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 28 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 29 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 30 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 31 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 32 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 33 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 34 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 35 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 36 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 37 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 38 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 39 | 478 | 428 | 471 | 364 | 537 | 319 | 438 |
| 40 | 683 | 588 | 771 | 687 | 655 | 817 | 626 |
| 41 | 683 | 588 | 771 | 687 | 655 | 817 | 626 |
| 42 | 683 | 588 | 771 | 687 | 655 | 817 | 626 |
| 43 | 1547 | 493 | 1944 | 1216 | 1300 | 1028 | 1418 |
| 44 | 321 | 460 | 274 | 188 | 371 | 281 | 294 |
| 45 | 321 | 460 | 274 | 188 | 371 | 281 | 294 |
| 46 | 321 | 460 | 274 | 188 | 371 | 281 | 294 |
| 47 | 479 | 428 | 471 | 364 | 537 | 319 | 439 |
| 48 | 479 | 428 | 471 | 364 | 537 | 319 | 439 |
| 49 | 306 | 460 | 263 | 171 | 366 | 271 | 280 |
| 50 | 306 | 460 | 263 | 171 | 366 | 271 | 280 |
| 51 | 306 | 460 | 263 | 171 | 366 | 271 | 280 |
| 52 | 306 | 460 | 263 | 171 | 366 | 271 | 280 |
| 53 | 306 | 460 | 263 | 171 | 366 | 271 | 280 |
| 54 | 306 | 460 | 263 | 171 | 366 | 271 | 280 |
| 55 | 79 | 69 | 68 | 54 | 54 | 71 | 72 |
| 56 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 57 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 58 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 59 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|------|-------|-------|-------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 4 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 5 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 6 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 7 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 8 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 9 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 10 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 11 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 12 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 13 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 14 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 15 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 16 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 17 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 18 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 19 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 20 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 21 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 22 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 23 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 24 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 25 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 26 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 27 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 28 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 29 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 30 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 31 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 32 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 33 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 34 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 35 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 36 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 37 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 38 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 39 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 40 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 41 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 42 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 43 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 44 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 45 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 46 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 47 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 48 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 49 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 50 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 51 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 52 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 53 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 54 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 55 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 56 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 57 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 58 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 59 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|------|-------|-------|-------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 4 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 5 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 6 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 7 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 8 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 9 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 10 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 11 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 12 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 13 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 14 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 15 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 16 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 17 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 18 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 19 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 20 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 21 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 22 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 23 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 24 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 25 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 26 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 27 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 28 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 29 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 30 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 31 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 32 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 33 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 34 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 35 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 36 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 37 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 38 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 39 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 40 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 41 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 42 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 43 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 44 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 45 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 46 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 47 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 48 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 49 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 50 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 51 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 52 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 53 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 54 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 55 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 56 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 57 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 58 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 59 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|--------|--------|--------|--------|--------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 4 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 5 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 6 | 10172 | 8371 | 11905 | 11242 | 12530 | 10755 | 9323 |
| 7 | 1511 | 397 | 1888 | 1157 | 1214 | 977 | 1385 |
| 8 | | | | | | | |
| 9 | 278851 | 288304 | 324778 | 258921 | 311329 | 343440 | 255587 |
| 10 | 278851 | 288304 | 324778 | 258921 | 311329 | 343440 | 255587 |
| 11 | 278851 | 288304 | 324778 | 258921 | 311329 | 343440 | 255587 |
| 12 | 278851 | 288304 | 324778 | 258921 | 311329 | 343440 | 255587 |
| 13 | 278851 | 288304 | 324778 | 258921 | 311329 | 343440 | 255587 |
| 14 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 15 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 16 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 17 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 18 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 19 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 20 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 21 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 22 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 23 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 24 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 25 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 26 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 27 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 28 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 29 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 30 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 31 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 32 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 33 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 34 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 35 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 36 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 37 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 38 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 39 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 40 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 41 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 42 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 43 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 44 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 45 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 46 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 47 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 48 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 49 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 50 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 51 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 52 | 109314 | 107711 | 94456 | 105285 | 123991 | 98013 | 100194 |
| 53 | | | | | | | |
| 54 | 276 | 414 | 241 | 157 | 346 | 252 | 253 |
| 55 | 276 | 415 | 241 | 157 | 345 | 253 | 253 |
| 56 | 179 | 173 | 226 | 162 | 243 | 181 | 164 |
| 57 | 179 | 173 | 226 | 162 | 243 | 181 | 164 |
| 58 | 179 | 173 | 226 | 162 | 243 | 181 | 164 |
| 59 | 179 | 173 | 226 | 162 | 243 | 181 | 164 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | | | | | | | |
| 4 | 179 | 173 | 226 | 162 | 243 | 181 | 164 |
| 5 | 179 | 173 | 226 | 162 | 243 | 181 | 164 |
| 6 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 7 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 8 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 9 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 10 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 11 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 12 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 13 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 14 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 15 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 16 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 17 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 18 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 19 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 20 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 21 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 22 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 23 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 24 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 25 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 26 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 27 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 28 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 29 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 30 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 31 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 32 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 33 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 34 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 35 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 36 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 37 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 38 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 39 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 40 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 41 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 42 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 43 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 44 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 45 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 46 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 47 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 48 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 49 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 50 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 51 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 52 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 53 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 54 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 55 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 56 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 57 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 58 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 59 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|--------|--------|--------|--------|--------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 4 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 5 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 6 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 7 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 8 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 9 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 10 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 11 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 12 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 13 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 14 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 15 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 16 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 17 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 18 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 19 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 20 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 21 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 22 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 23 | 276 | 413 | 241 | 157 | 345 | 252 | 253 |
| 24 | 106747 | 108895 | 121702 | 101180 | 123923 | 127049 | 97841 |
| 25 | 106747 | 108895 | 121702 | 101180 | 123923 | 127049 | 97841 |
| 26 | 106747 | 108895 | 121702 | 101180 | 123923 | 127049 | 97841 |
| 27 | 106747 | 108895 | 121702 | 101180 | 123923 | 127049 | 97841 |
| 28 | 106747 | 108895 | 121702 | 101180 | 123923 | 127049 | 97841 |
| 29 | 106747 | 108895 | 121702 | 101180 | 123923 | 127049 | 97841 |
| 30 | 106747 | 108895 | 121702 | 101180 | 123923 | 127049 | 97841 |
| 31 | 106747 | 108895 | 121702 | 101180 | 123923 | 127049 | 97841 |
| 32 | 106747 | 108895 | 121702 | 101180 | 123923 | 127049 | 97841 |
| 33 | 106747 | 108895 | 121702 | 101180 | 123923 | 127049 | 97841 |
| 34 | 106747 | 108895 | 121702 | 101180 | 123923 | 127049 | 97841 |
| 35 | 106747 | 108895 | 121702 | 101180 | 123923 | 127049 | 97841 |
| 36 | 106747 | 108895 | 121702 | 101180 | 123923 | 127049 | 97841 |
| 37 | 106747 | 108895 | 121702 | 101180 | 123923 | 127049 | 97841 |
| 38 | 106747 | 108895 | 121702 | 101180 | 123923 | 127049 | 97841 |
| 39 | 106747 | 108895 | 121702 | 101180 | 123923 | 127049 | 97841 |
| 40 | 97 | 110 | 109 | 98 | 117 | 130 | 89 |
| 41 | 97 | 110 | 109 | 98 | 117 | 130 | 89 |
| 42 | 97 | 110 | 109 | 98 | 117 | 130 | 89 |
| 43 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 44 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 45 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 46 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 47 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 48 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 49 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 50 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 51 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 52 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 53 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 54 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 55 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 56 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 57 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 58 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 59 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | | | | | | | |
| 4 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 5 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 6 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 7 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 8 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 9 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 10 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 11 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 12 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 13 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 14 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 15 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 16 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 17 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 18 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 19 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 20 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 21 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 22 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 23 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 24 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 25 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 26 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 27 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 28 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 29 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 30 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 31 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 32 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 33 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 34 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 35 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 36 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 37 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 38 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 39 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 40 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 41 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 42 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 43 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 44 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 45 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 46 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 47 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 48 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 49 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 50 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 51 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 52 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 53 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 54 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 55 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 56 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 57 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 58 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 59 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 4 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 5 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 6 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 7 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 8 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 9 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 10 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 11 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 12 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 13 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 14 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 15 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 16 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 17 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 18 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 19 | 6612 | 5403 | 7878 | 6223 | 6714 | 7948 | 6060 |
| 20 | 2741 | 2273 | 2659 | 1862 | 2781 | 1950 | 2512 |
| 21 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 22 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 23 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 24 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 25 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 26 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 27 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 28 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 29 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 30 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 31 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 32 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 33 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 34 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 35 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 36 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 37 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 38 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 39 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 40 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 41 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 42 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 43 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 44 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 45 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 46 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 47 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 48 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 49 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 50 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 51 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 52 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 53 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 54 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 55 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 56 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 57 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 58 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 59 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 4 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 5 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 6 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 7 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 8 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 9 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 10 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 11 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 12 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 13 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 14 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 15 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 16 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 17 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 18 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 19 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 20 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 21 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 22 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 23 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 24 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 25 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 26 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 27 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 28 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 29 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 30 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 31 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 32 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 33 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 34 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 35 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 36 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 37 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 38 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 39 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 40 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 41 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 42 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 43 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 44 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 45 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 46 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 47 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 48 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 49 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 50 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 51 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 52 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 53 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 54 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 55 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 56 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 57 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 58 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 59 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|------|-------|-------|-------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 4 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 5 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 6 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 7 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 8 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 9 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 10 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 11 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 12 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 13 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 14 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 15 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 16 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 17 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 18 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 19 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 20 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 21 | 4918 | 6152 | 4863 | 1989 | 5832 | 3524 | 4508 |
| 22 | 4928 | 6158 | 4877 | 1993 | 5839 | 3537 | 4517 |
| 23 | 2731 | 2260 | 2644 | 1855 | 2772 | 1944 | 2503 |
| 24 | 2731 | 2260 | 2644 | 1855 | 2772 | 1944 | 2503 |
| 25 | 2731 | 2260 | 2644 | 1855 | 2772 | 1944 | 2503 |
| 26 | 2731 | 2260 | 2644 | 1855 | 2772 | 1944 | 2503 |
| 27 | 2731 | 2260 | 2644 | 1855 | 2772 | 1944 | 2503 |
| 28 | 2731 | 2260 | 2644 | 1855 | 2772 | 1944 | 2503 |
| 29 | 2731 | 2260 | 2644 | 1855 | 2772 | 1944 | 2503 |
| 30 | 2731 | 2260 | 2644 | 1855 | 2772 | 1944 | 2503 |
| 31 | 2731 | 2260 | 2644 | 1855 | 2772 | 1944 | 2503 |
| 32 | 274 | 316 | 300 | 353 | 412 | 374 | 251 |
| 33 | 274 | 316 | 300 | 353 | 412 | 374 | 251 |
| 34 | 274 | 316 | 300 | 353 | 412 | 374 | 251 |
| 35 | 274 | 316 | 300 | 353 | 412 | 374 | 251 |
| 36 | 274 | 316 | 300 | 353 | 412 | 374 | 251 |
| 37 | 274 | 316 | 300 | 353 | 412 | 374 | 251 |
| 38 | 274 | 316 | 300 | 353 | 412 | 374 | 251 |
| 39 | 274 | 316 | 300 | 353 | 412 | 374 | 251 |
| 40 | 1215 | 1366 | 1519 | 1177 | 1875 | 1372 | 1114 |
| 41 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 42 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 43 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 44 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 45 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 46 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 47 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 48 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 49 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 50 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 51 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 52 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 53 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 54 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 55 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 56 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 57 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 58 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 59 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|-------|-------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 4 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 5 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 6 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 7 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 8 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 9 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 10 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 11 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 12 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 13 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 14 | 10193 | 7563 | 10229 | 11461 | 11121 | 10956 | 9343 |
| 15 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 16 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 17 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 18 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 19 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 20 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 21 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 22 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 23 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 24 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 25 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 26 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 27 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 28 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 29 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 30 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 31 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 32 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 33 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 34 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 35 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 36 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 37 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 38 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 39 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 40 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 41 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 42 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 43 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 44 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 45 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 46 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 47 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 48 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 49 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 50 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 51 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 52 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 53 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 54 | 180 | 304 | 180 | 137 | 318 | 185 | 165 |
| 55 | 46114 | 43019 | 42955 | 42210 | 51163 | 44959 | 42267 |
| 56 | 1600 | 1282 | 1963 | 1734 | 2154 | 1782 | 1467 |
| 57 | 1600 | 1282 | 1963 | 1734 | 2154 | 1782 | 1467 |
| 58 | 1600 | 1282 | 1963 | 1734 | 2154 | 1782 | 1467 |
| 59 | 1600 | 1282 | 1963 | 1734 | 2154 | 1782 | 1467 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 2797 | 3367 | 3110 | 2764 | 4145 | 3348 | 2564 |
| 4 | 156 | 116 | 169 | 84 | 160 | 99 | 143 |
| 5 | 1144 | 902 | 1363 | 1120 | 1474 | 1167 | 1049 |
| 6 | 1144 | 902 | 1363 | 1120 | 1474 | 1167 | 1049 |
| 7 | 1144 | 902 | 1363 | 1120 | 1474 | 1167 | 1049 |
| 8 | 1144 | 902 | 1363 | 1120 | 1474 | 1167 | 1049 |
| 9 | 1144 | 902 | 1363 | 1120 | 1474 | 1167 | 1049 |
| 10 | 1144 | 902 | 1363 | 1120 | 1474 | 1167 | 1049 |
| 11 | 373 | 245 | 340 | 272 | 249 | 346 | 342 |
| 12 | 373 | 245 | 340 | 272 | 249 | 346 | 342 |
| 13 | 373 | 245 | 340 | 272 | 249 | 346 | 342 |
| 14 | 373 | 245 | 340 | 272 | 249 | 346 | 342 |
| 15 | 373 | 245 | 340 | 272 | 249 | 346 | 342 |
| 16 | 373 | 245 | 340 | 272 | 249 | 346 | 342 |
| 17 | 373 | 245 | 340 | 272 | 249 | 346 | 342 |
| 18 | 373 | 245 | 340 | 272 | 249 | 346 | 342 |
| 19 | 373 | 245 | 340 | 272 | 249 | 346 | 342 |
| 20 | 122 | 83 | 125 | 88 | 94 | 117 | 112 |
| 21 | 122 | 83 | 125 | 88 | 94 | 117 | 112 |
| 22 | 122 | 83 | 125 | 88 | 94 | 117 | 112 |
| 23 | 122 | 83 | 125 | 88 | 94 | 117 | 112 |
| 24 | 122 | 83 | 125 | 88 | 94 | 117 | 112 |
| 25 | 122 | 83 | 125 | 88 | 94 | 117 | 112 |
| 26 | 122 | 83 | 125 | 88 | 94 | 117 | 112 |
| 27 | 374 | 245 | 341 | 275 | 250 | 349 | 343 |
| 28 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 29 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 30 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 31 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 32 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 33 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 34 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 35 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 36 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 37 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 38 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 39 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 40 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 41 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 42 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 43 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 44 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 45 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 46 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 47 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 48 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 49 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 50 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 51 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 52 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 53 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 54 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 55 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 56 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 57 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 58 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 59 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|-------|-------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 4 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 5 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 6 | 372 | 244 | 338 | 272 | 249 | 346 | 341 |
| 7 | 53371 | 45985 | 53837 | 49659 | 60254 | 55134 | 48918 |
| 8 | 53371 | 45985 | 53837 | 49659 | 60254 | 55134 | 48918 |
| 9 | 430 | 255 | 392 | 305 | 276 | 376 | 394 |
| 10 | 430 | 255 | 392 | 305 | 276 | 376 | 394 |
| 11 | 430 | 255 | 392 | 305 | 276 | 376 | 394 |
| 12 | 430 | 255 | 392 | 305 | 276 | 376 | 394 |
| 13 | 430 | 255 | 392 | 305 | 276 | 376 | 394 |
| 14 | 430 | 255 | 392 | 305 | 276 | 376 | 394 |
| 15 | 430 | 255 | 392 | 305 | 276 | 376 | 394 |
| 16 | 430 | 255 | 392 | 305 | 276 | 376 | 394 |
| 17 | 430 | 255 | 392 | 305 | 276 | 376 | 394 |
| 18 | 430 | 255 | 392 | 305 | 276 | 376 | 394 |
| 19 | 430 | 255 | 392 | 305 | 276 | 376 | 394 |
| 20 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 21 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 22 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 23 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 24 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 25 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 26 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 27 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 28 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 29 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 30 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 31 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 32 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 33 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 34 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 35 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 36 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 37 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 38 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 39 | 85 | 83 | 68 | 55 | 73 | 76 | 78 |
| 40 | 158 | 0 | 52 | 181 | 28 | 86 | 145 |
| 41 | 158 | 0 | 52 | 181 | 28 | 86 | 145 |
| 42 | 158 | 0 | 52 | 181 | 28 | 86 | 145 |
| 43 | 158 | 0 | 52 | 181 | 28 | 86 | 145 |
| 44 | 158 | 0 | 52 | 181 | 28 | 86 | 145 |
| 45 | 158 | 0 | 52 | 181 | 28 | 86 | 145 |
| 46 | 158 | 0 | 52 | 181 | 28 | 86 | 145 |
| 47 | 158 | 0 | 52 | 181 | 28 | 86 | 145 |
| 48 | 158 | 0 | 52 | 181 | 28 | 86 | 145 |
| 49 | 158 | 0 | 52 | 181 | 28 | 86 | 145 |
| 50 | 158 | 0 | 52 | 181 | 28 | 86 | 145 |
| 51 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 52 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 53 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 54 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 55 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 56 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 57 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 58 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 59 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|-------|-------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 4 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 5 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 6 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 7 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 8 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 9 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 10 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 11 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 12 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 13 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 14 | 157 | 0 | 51 | 179 | 26 | 86 | 144 |
| 15 | 169 | 121 | 218 | 104 | 196 | 142 | 155 |
| 16 | 169 | 121 | 218 | 104 | 196 | 142 | 155 |
| 17 | | | | | | | |
| 18 | 7544 | 5956 | 8151 | 6693 | 6913 | 9341 | 6915 |
| 19 | 7544 | 5956 | 8151 | 6693 | 6913 | 9341 | 6915 |
| 20 | 7544 | 5956 | 8151 | 6693 | 6913 | 9341 | 6915 |
| 21 | 7544 | 5956 | 8151 | 6693 | 6913 | 9341 | 6915 |
| 22 | 7544 | 5956 | 8151 | 6693 | 6913 | 9341 | 6915 |
| 23 | 68 | 49 | 81 | 72 | 68 | 94 | 62 |
| 24 | 9284 | 9787 | 8646 | 10789 | 13877 | 10354 | 8509 |
| 25 | 9284 | 9787 | 8646 | 10789 | 13877 | 10354 | 8509 |
| 26 | 9284 | 9787 | 8646 | 10789 | 13877 | 10354 | 8509 |
| 27 | 9284 | 9787 | 8646 | 10789 | 13877 | 10354 | 8509 |
| 28 | 9284 | 9787 | 8646 | 10789 | 13877 | 10354 | 8509 |
| 29 | 9284 | 9787 | 8646 | 10789 | 13877 | 10354 | 8509 |
| 30 | 9284 | 9787 | 8646 | 10789 | 13877 | 10354 | 8509 |
| 31 | 9284 | 9787 | 8646 | 10789 | 13877 | 10354 | 8509 |
| 32 | 9284 | 9787 | 8646 | 10789 | 13877 | 10354 | 8509 |
| 33 | 9284 | 9787 | 8646 | 10789 | 13877 | 10354 | 8509 |
| 34 | 9284 | 9787 | 8646 | 10789 | 13877 | 10354 | 8509 |
| 35 | 9284 | 9787 | 8646 | 10789 | 13877 | 10354 | 8509 |
| 36 | 9284 | 9787 | 8646 | 10789 | 13877 | 10354 | 8509 |
| 37 | 9284 | 9787 | 8646 | 10789 | 13877 | 10354 | 8509 |
| 38 | 9284 | 9787 | 8646 | 10789 | 13877 | 10354 | 8509 |
| 39 | 9303 | 9814 | 8658 | 10815 | 13903 | 10380 | 8527 |
| 40 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 41 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 42 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 43 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 44 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 45 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 46 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 47 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 48 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 49 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 50 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 51 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 52 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 53 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 54 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 55 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 56 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 57 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 58 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 59 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 4 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 5 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 6 | 6147 | 6158 | 5387 | 5788 | 8202 | 5710 | 5634 |
| 7 | 378 | 273 | 337 | 346 | 356 | 378 | 346 |
| 8 | 378 | 273 | 337 | 346 | 356 | 378 | 346 |
| 9 | 378 | 273 | 337 | 346 | 356 | 378 | 346 |
| 10 | 378 | 273 | 337 | 346 | 356 | 378 | 346 |
| 11 | 378 | 273 | 337 | 346 | 356 | 378 | 346 |
| 12 | 378 | 273 | 337 | 346 | 356 | 378 | 346 |
| 13 | 378 | 273 | 337 | 346 | 356 | 378 | 346 |
| 14 | 341 | 208 | 301 | 283 | 205 | 376 | 313 |
| 15 | 341 | 208 | 301 | 283 | 205 | 376 | 313 |
| 16 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 17 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 18 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 19 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 20 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 21 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 22 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 23 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 24 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 25 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 26 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 27 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 28 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 29 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 30 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 31 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 32 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 33 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 34 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 35 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 36 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 37 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 38 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 39 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 40 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 41 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 42 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 43 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 44 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 45 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 46 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 47 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 48 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 49 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 50 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 51 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 52 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 53 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 54 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 55 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 56 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 57 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 58 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 59 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|-------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 377 | 272 | 336 | 345 | 356 | 378 | 346 |
| 4 | 429 | 322 | 359 | 298 | 277 | 440 | 393 |
| 5 | 429 | 322 | 359 | 298 | 277 | 440 | 393 |
| 6 | 429 | 322 | 359 | 298 | 277 | 440 | 393 |
| 7 | 429 | 322 | 359 | 298 | 277 | 440 | 393 |
| 8 | 277 | 168 | 318 | 224 | 282 | 276 | 254 |
| 9 | | | | | | | |
| 10 | 6502 | 6168 | 5723 | 6191 | 8651 | 6066 | 5960 |
| 11 | 6502 | 6168 | 5723 | 6191 | 8651 | 6066 | 5960 |
| 12 | 6502 | 6168 | 5723 | 6191 | 8651 | 6066 | 5960 |
| 13 | 6502 | 6168 | 5723 | 6191 | 8651 | 6066 | 5960 |
| 14 | 6502 | 6168 | 5723 | 6191 | 8651 | 6066 | 5960 |
| 15 | 6502 | 6168 | 5723 | 6191 | 8651 | 6066 | 5960 |
| 16 | 6154 | 5839 | 5394 | 5792 | 8210 | 5707 | 5641 |
| 17 | 397 | 279 | 334 | 283 | 256 | 413 | 364 |
| 18 | 397 | 279 | 334 | 283 | 256 | 413 | 364 |
| 19 | 397 | 279 | 334 | 283 | 256 | 413 | 364 |
| 20 | 397 | 279 | 334 | 283 | 256 | 413 | 364 |
| 21 | 397 | 279 | 334 | 283 | 256 | 413 | 364 |
| 22 | 397 | 279 | 334 | 283 | 256 | 413 | 364 |
| 23 | 397 | 279 | 334 | 283 | 256 | 413 | 364 |
| 24 | 397 | 279 | 334 | 283 | 256 | 413 | 364 |
| 25 | 397 | 279 | 334 | 283 | 256 | 413 | 364 |
| 26 | 397 | 279 | 334 | 283 | 256 | 413 | 364 |
| 27 | 397 | 279 | 334 | 283 | 256 | 413 | 364 |
| 28 | 397 | 279 | 334 | 283 | 256 | 413 | 364 |
| 29 | 397 | 279 | 334 | 283 | 256 | 413 | 364 |
| 30 | 397 | 279 | 334 | 283 | 256 | 413 | 364 |
| 31 | 8120 | 7217 | 8979 | 8410 | 11053 | 9869 | 7443 |
| 32 | 8120 | 7217 | 8979 | 8410 | 11053 | 9869 | 7443 |
| 33 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 34 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 35 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 36 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 37 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 38 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 39 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 40 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 41 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 42 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 43 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 44 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 45 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 46 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 47 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 48 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 49 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 50 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 51 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 52 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 53 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 54 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 55 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 56 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 57 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 58 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 59 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | | | | | | | |
| 4 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 5 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 6 | 397 | 278 | 332 | 283 | 255 | 413 | 364 |
| 7 | 55 | 59 | 35 | 60 | 68 | 58 | 50 |
| 8 | 174 | 124 | 210 | 102 | 211 | 133 | 159 |
| 9 | 53 | 57 | 32 | 58 | 65 | 56 | 49 |
| 10 | 289 | 161 | 256 | 233 | 175 | 328 | 265 |
| 11 | 289 | 161 | 256 | 233 | 175 | 328 | 265 |
| 12 | 289 | 161 | 256 | 233 | 175 | 328 | 265 |
| 13 | 289 | 161 | 256 | 233 | 175 | 328 | 265 |
| 14 | 289 | 161 | 256 | 233 | 175 | 328 | 265 |
| 15 | 289 | 161 | 256 | 233 | 175 | 328 | 265 |
| 16 | 289 | 161 | 256 | 233 | 175 | 328 | 265 |
| 17 | 289 | 161 | 256 | 233 | 175 | 328 | 265 |
| 18 | 289 | 161 | 256 | 233 | 175 | 328 | 265 |
| 19 | 289 | 161 | 256 | 233 | 175 | 328 | 265 |
| 20 | 289 | 161 | 256 | 233 | 175 | 328 | 265 |
| 21 | 289 | 161 | 256 | 233 | 175 | 328 | 265 |
| 22 | 170 | 78 | 202 | 160 | 228 | 138 | 156 |
| 23 | 5320 | 5585 | 4955 | 4770 | 6883 | 6548 | 4876 |
| 24 | 239 | 212 | 212 | 186 | 250 | 261 | 219 |
| 25 | 239 | 212 | 212 | 186 | 250 | 261 | 219 |
| 26 | 239 | 212 | 212 | 186 | 250 | 261 | 219 |
| 27 | 610 | 484 | 587 | 513 | 760 | 584 | 559 |
| 28 | 610 | 484 | 587 | 513 | 760 | 584 | 559 |
| 29 | 610 | 484 | 587 | 513 | 760 | 584 | 559 |
| 30 | 610 | 484 | 587 | 513 | 760 | 584 | 559 |
| 31 | 610 | 484 | 587 | 513 | 760 | 584 | 559 |
| 32 | 610 | 484 | 587 | 513 | 760 | 584 | 559 |
| 33 | 610 | 484 | 587 | 513 | 760 | 584 | 559 |
| 34 | 610 | 484 | 587 | 513 | 760 | 584 | 559 |
| 35 | 610 | 484 | 587 | 513 | 760 | 584 | 559 |
| 36 | 610 | 484 | 587 | 513 | 760 | 584 | 559 |
| 37 | 610 | 484 | 587 | 513 | 760 | 584 | 559 |
| 38 | 610 | 484 | 587 | 513 | 760 | 584 | 559 |
| 39 | 610 | 484 | 587 | 513 | 760 | 584 | 559 |
| 40 | 468 | 678 | 296 | 354 | 631 | 537 | 429 |
| 41 | 184 | 98 | 165 | 164 | 161 | 186 | 169 |
| 42 | 184 | 98 | 165 | 164 | 161 | 186 | 169 |
| 43 | 184 | 98 | 165 | 164 | 161 | 186 | 169 |
| 44 | 676 | 564 | 613 | 589 | 855 | 672 | 620 |
| 45 | 676 | 564 | 613 | 589 | 855 | 672 | 620 |
| 46 | 676 | 564 | 613 | 589 | 855 | 672 | 620 |
| 47 | 238 | 163 | 234 | 194 | 241 | 263 | 218 |
| 48 | 3588 | 1854 | 3436 | 2228 | 2532 | 3377 | 3289 |
| 49 | 3588 | 1854 | 3436 | 2228 | 2532 | 3377 | 3289 |
| 50 | 3588 | 1854 | 3436 | 2228 | 2532 | 3377 | 3289 |
| 51 | 3588 | 1854 | 3436 | 2228 | 2532 | 3377 | 3289 |
| 52 | 3588 | 1854 | 3436 | 2228 | 2532 | 3377 | 3289 |
| 53 | 3588 | 1854 | 3436 | 2228 | 2532 | 3377 | 3289 |
| 54 | 3588 | 1854 | 3436 | 2228 | 2532 | 3377 | 3289 |
| 55 | 3588 | 1854 | 3436 | 2228 | 2532 | 3377 | 3289 |
| 56 | 3588 | 1854 | 3436 | 2228 | 2532 | 3377 | 3289 |
| 57 | 3588 | 1854 | 3436 | 2228 | 2532 | 3377 | 3289 |
| 58 | 3588 | 1854 | 3436 | 2228 | 2532 | 3377 | 3289 |
| 59 | 3588 | 1854 | 3436 | 2228 | 2532 | 3377 | 3289 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 4 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 5 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 6 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 7 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 8 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 9 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 10 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 11 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 12 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 13 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 14 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 15 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 16 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 17 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 18 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 19 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 20 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 21 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 22 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 23 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 24 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 25 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 26 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 27 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 28 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 29 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 30 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 31 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 32 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 33 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 34 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 35 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 36 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 37 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 38 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 39 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 40 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 41 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 42 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 43 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 44 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 45 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 46 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 47 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 48 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 49 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 50 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 51 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 52 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 53 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 54 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 55 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 56 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 57 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 58 | 239 | 135 | 229 | 178 | 214 | 232 | 219 |
| 59 | 179 | 72 | 199 | 164 | 231 | 140 | 164 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|--------|-------|--------|--------|-------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 3054 | 3027 | 2588 | 3225 | 4490 | 3564 | 2799 |
| 4 | 3054 | 3027 | 2588 | 3225 | 4490 | 3564 | 2799 |
| 5 | 3054 | 3027 | 2588 | 3225 | 4490 | 3564 | 2799 |
| 6 | 3056 | 3032 | 2589 | 3229 | 4496 | 3570 | 2801 |
| 7 | 3056 | 3032 | 2589 | 3229 | 4496 | 3570 | 2801 |
| 8 | 235 | 132 | 227 | 174 | 214 | 227 | 215 |
| 9 | 4435 | 3949 | 3383 | 4315 | 6148 | 4236 | 4065 |
| 10 | 4435 | 3949 | 3383 | 4315 | 6148 | 4236 | 4065 |
| 11 | 93 | 48 | 84 | 53 | 66 | 79 | 85 |
| 12 | 93 | 48 | 84 | 52 | 66 | 77 | 85 |
| 13 | 93 | 48 | 84 | 52 | 66 | 77 | 85 |
| 14 | 93 | 48 | 84 | 52 | 66 | 77 | 85 |
| 15 | 93 | 48 | 84 | 52 | 66 | 77 | 85 |
| 16 | 93 | 48 | 84 | 52 | 66 | 77 | 85 |
| 17 | 93 | 48 | 84 | 52 | 66 | 77 | 85 |
| 18 | 93 | 48 | 84 | 52 | 66 | 77 | 85 |
| 19 | 93 | 48 | 84 | 52 | 66 | 77 | 85 |
| 20 | 65 | 78 | 74 | 66 | 121 | 92 | 60 |
| 21 | | | | | | | |
| 22 | 153334 | 180694 | 91231 | 108681 | 247013 | 88225 | 140542 |
| 23 | 153334 | 180694 | 91231 | 108681 | 247013 | 88225 | 140542 |
| 24 | 153334 | 180694 | 91231 | 108681 | 247013 | 88225 | 140542 |
| 25 | | | | | | | |
| 26 | 137 | 140 | 119 | 43 | 179 | 77 | 126 |
| 27 | 137 | 140 | 119 | 43 | 179 | 77 | 126 |
| 28 | 137 | 140 | 119 | 43 | 179 | 77 | 126 |
| 29 | 137 | 140 | 119 | 43 | 179 | 77 | 126 |
| 30 | 137 | 140 | 119 | 43 | 179 | 77 | 126 |
| 31 | 137 | 140 | 119 | 43 | 179 | 77 | 126 |
| 32 | 137 | 140 | 119 | 43 | 179 | 77 | 126 |
| 33 | 137 | 140 | 119 | 43 | 179 | 77 | 126 |
| 34 | 137 | 140 | 119 | 43 | 179 | 77 | 126 |
| 35 | 137 | 140 | 119 | 43 | 179 | 77 | 126 |
| 36 | 137 | 140 | 119 | 43 | 179 | 77 | 126 |
| 37 | | | | | | | |
| 38 | 7536 | 6437 | 9044 | 8127 | 13293 | 9509 | 6907 |
| 39 | 7536 | 6437 | 9044 | 8127 | 13293 | 9509 | 6907 |
| 40 | | | | | | | |
| 41 | 283 | 213 | 209 | 190 | 312 | 199 | 259 |
| 42 | 283 | 213 | 209 | 190 | 312 | 199 | 259 |
| 43 | 298 | 216 | 220 | 194 | 323 | 201 | 273 |
| 44 | 298 | 216 | 220 | 194 | 323 | 201 | 273 |
| 45 | 298 | 216 | 220 | 194 | 323 | 201 | 273 |
| 46 | 298 | 216 | 220 | 194 | 323 | 201 | 273 |
| 47 | 298 | 216 | 220 | 194 | 323 | 201 | 273 |
| 48 | 298 | 216 | 220 | 194 | 323 | 201 | 273 |
| 49 | 298 | 216 | 220 | 194 | 323 | 201 | 273 |
| 50 | 298 | 216 | 220 | 194 | 323 | 201 | 273 |
| 51 | 298 | 216 | 220 | 194 | 323 | 201 | 273 |
| 52 | 149 | 171 | 156 | 123 | 247 | 186 | 137 |
| 53 | 149 | 171 | 156 | 123 | 247 | 186 | 137 |
| 54 | | | | | | | |
| 55 | 64 | 75 | 71 | 65 | 118 | 91 | 59 |
| 56 | 64 | 75 | 71 | 65 | 118 | 91 | 59 |
| 57 | | | | | | | |
| 58 | 277 | 205 | 198 | 183 | 296 | 194 | 254 |
| 59 | 277 | 205 | 198 | 183 | 296 | 194 | 254 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 277 | 205 | 198 | 183 | 296 | 194 | 254 |
| 4 | 277 | 205 | 198 | 183 | 296 | 194 | 254 |
| 5 | 277 | 205 | 198 | 183 | 296 | 194 | 254 |
| 6 | 277 | 205 | 198 | 183 | 296 | 194 | 254 |
| 7 | 277 | 205 | 198 | 183 | 296 | 194 | 254 |
| 8 | 277 | 205 | 198 | 183 | 296 | 194 | 254 |
| 9 | 277 | 205 | 198 | 183 | 296 | 194 | 254 |
| 10 | 277 | 205 | 198 | 183 | 296 | 194 | 254 |
| 11 | 134 | 140 | 117 | 41 | 177 | 77 | 123 |
| 12 | 134 | 140 | 117 | 41 | 177 | 77 | 123 |
| 13 | 134 | 140 | 117 | 41 | 177 | 77 | 123 |
| 14 | 134 | 140 | 117 | 41 | 177 | 77 | 123 |
| 15 | 2152 | 886 | 2023 | 1308 | 1528 | 1935 | 1972 |
| 16 | 2152 | 886 | 2023 | 1308 | 1528 | 1935 | 1972 |
| 17 | 2152 | 886 | 2023 | 1308 | 1528 | 1935 | 1972 |
| 18 | 2152 | 886 | 2023 | 1308 | 1528 | 1935 | 1972 |
| 19 | 2152 | 886 | 2023 | 1308 | 1528 | 1935 | 1972 |
| 20 | 2152 | 886 | 2023 | 1308 | 1528 | 1935 | 1972 |
| 21 | 2152 | 886 | 2023 | 1308 | 1528 | 1935 | 1972 |
| 22 | 2152 | 886 | 2023 | 1308 | 1528 | 1935 | 1972 |
| 23 | 2152 | 886 | 2023 | 1308 | 1528 | 1935 | 1972 |
| 24 | 2152 | 886 | 2023 | 1308 | 1528 | 1935 | 1972 |
| 25 | 2152 | 886 | 2023 | 1308 | 1528 | 1935 | 1972 |
| 26 | 2152 | 886 | 2023 | 1308 | 1528 | 1935 | 1972 |
| 27 | 2152 | 886 | 2023 | 1308 | 1528 | 1935 | 1972 |
| 28 | 2152 | 886 | 2023 | 1308 | 1528 | 1935 | 1972 |
| 29 | 2152 | 886 | 2023 | 1308 | 1528 | 1935 | 1972 |
| 30 | 2152 | 886 | 2023 | 1308 | 1528 | 1935 | 1972 |
| 31 | 63 | 9 | 53 | 78 | 53 | 73 | 58 |
| 32 | 63 | 9 | 53 | 78 | 53 | 73 | 58 |
| 33 | 63 | 9 | 53 | 78 | 53 | 73 | 58 |
| 34 | 63 | 9 | 53 | 78 | 53 | 73 | 58 |
| 35 | 63 | 9 | 53 | 78 | 53 | 73 | 58 |
| 36 | 63 | 9 | 53 | 78 | 53 | 73 | 58 |
| 37 | 63 | 9 | 53 | 78 | 53 | 73 | 58 |
| 38 | 63 | 9 | 53 | 78 | 53 | 73 | 58 |
| 39 | 63 | 9 | 53 | 78 | 53 | 73 | 58 |
| 40 | 63 | 9 | 53 | 78 | 53 | 73 | 58 |
| 41 | 63 | 9 | 53 | 78 | 53 | 73 | 58 |
| 42 | 63 | 9 | 53 | 78 | 53 | 73 | 58 |
| 43 | 63 | 9 | 53 | 78 | 53 | 73 | 58 |
| 44 | 63 | 9 | 53 | 78 | 53 | 73 | 58 |
| 45 | 63 | 9 | 53 | 78 | 53 | 73 | 58 |
| 46 | 63 | 9 | 53 | 78 | 53 | 73 | 58 |
| 47 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 48 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 49 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 50 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 51 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 52 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 53 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 54 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 55 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 56 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 57 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 58 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 59 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|------|------|------|-------|------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 4 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 5 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 6 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 7 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 8 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 9 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 10 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 11 | 97 | 46 | 97 | 96 | 136 | 86 | 89 |
| 12 | 125 | 32 | 82 | 105 | 59 | 111 | 115 |
| 13 | 125 | 32 | 82 | 105 | 59 | 111 | 115 |
| 14 | 125 | 32 | 82 | 105 | 59 | 111 | 115 |
| 15 | 125 | 32 | 82 | 105 | 59 | 111 | 115 |
| 16 | 125 | 32 | 82 | 105 | 59 | 111 | 115 |
| 17 | 125 | 32 | 82 | 105 | 59 | 111 | 115 |
| 18 | 125 | 32 | 82 | 105 | 59 | 111 | 115 |
| 19 | 98 | 45 | 91 | 54 | 70 | 85 | 90 |
| 20 | 145 | 153 | 121 | 44 | 198 | 84 | 133 |
| 21 | 145 | 153 | 121 | 44 | 198 | 84 | 133 |
| 22 | 145 | 153 | 121 | 44 | 198 | 84 | 133 |
| 23 | 145 | 153 | 121 | 44 | 198 | 84 | 133 |
| 24 | 145 | 153 | 121 | 44 | 198 | 84 | 133 |
| 25 | 145 | 153 | 121 | 44 | 198 | 84 | 133 |
| 26 | 145 | 153 | 121 | 44 | 198 | 84 | 133 |
| 27 | 145 | 153 | 121 | 44 | 198 | 84 | 133 |
| 28 | 237 | 205 | 224 | 245 | 410 | 258 | 217 |
| 29 | 4146 | 4052 | 2781 | 2896 | 5427 | 3572 | 3800 |
| 30 | 4146 | 4052 | 2781 | 2896 | 5427 | 3572 | 3800 |
| 31 | 4146 | 4052 | 2781 | 2896 | 5427 | 3572 | 3800 |
| 32 | 4146 | 4052 | 2781 | 2896 | 5427 | 3572 | 3800 |
| 33 | 4146 | 4052 | 2781 | 2896 | 5427 | 3572 | 3800 |
| 34 | 4146 | 4052 | 2781 | 2896 | 5427 | 3572 | 3800 |
| 35 | 4146 | 4052 | 2781 | 2896 | 5427 | 3572 | 3800 |
| 36 | 4146 | 4052 | 2781 | 2896 | 5427 | 3572 | 3800 |
| 37 | 4146 | 4052 | 2781 | 2896 | 5427 | 3572 | 3800 |
| 38 | 4146 | 4052 | 2781 | 2896 | 5427 | 3572 | 3800 |
| 39 | 4146 | 4052 | 2781 | 2896 | 5427 | 3572 | 3800 |
| 40 | 4146 | 4052 | 2781 | 2896 | 5427 | 3572 | 3800 |
| 41 | 221 | 197 | 212 | 234 | 400 | 251 | 203 |
| 42 | 221 | 197 | 212 | 234 | 400 | 251 | 203 |
| 43 | 99 | 41 | 75 | 64 | 58 | 92 | 91 |
| 44 | 101 | 14 | 72 | 77 | 43 | 83 | 93 |
| 45 | 101 | 14 | 72 | 77 | 43 | 83 | 93 |
| 46 | 77 | 53 | 99 | 53 | 126 | 78 | 71 |
| 47 | 77 | 53 | 99 | 53 | 126 | 78 | 71 |
| 48 | 77 | 53 | 99 | 53 | 126 | 78 | 71 |
| 49 | 77 | 53 | 99 | 53 | 126 | 78 | 71 |
| 50 | 77 | 53 | 99 | 53 | 126 | 78 | 71 |
| 51 | 12196 | 6886 | 9339 | 7504 | 11617 | 9564 | 11179 |
| 52 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 53 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 54 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 55 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 56 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 57 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 58 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 59 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|-------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 4 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 5 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 6 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 7 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 8 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 9 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 10 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 11 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 12 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 13 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 14 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 15 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 16 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 17 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 18 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 19 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 20 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 21 | 95 | 37 | 74 | 60 | 55 | 91 | 87 |
| 22 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 23 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 24 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 25 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 26 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 27 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 28 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 29 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 30 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 31 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 32 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 33 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 34 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 35 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 36 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 37 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 38 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 39 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 40 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 41 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 42 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 43 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 44 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 45 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 46 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 47 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 48 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 49 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 50 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 51 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 52 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 53 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 54 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 55 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 56 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 57 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 58 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 59 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|-------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | | | | | | | |
| 4 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 5 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 6 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 7 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 8 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 9 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 10 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 11 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 12 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 13 | 7354 | 6738 | 6480 | 7031 | 10154 | 10927 | 6740 |
| 14 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 15 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 16 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 17 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 18 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 19 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 20 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 21 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 22 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 23 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 24 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 25 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 26 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 27 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 28 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 29 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 30 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 31 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 32 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 33 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 34 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 35 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 36 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 37 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 38 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 39 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 40 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 41 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 42 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 43 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 44 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 45 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 46 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 47 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 48 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 49 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 50 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 51 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 52 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 53 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 54 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 55 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 56 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 57 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 58 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 59 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|------|-------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 4 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 5 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 6 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 7 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 8 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 9 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 10 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 11 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 12 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 13 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 14 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 15 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 16 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 17 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 18 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 19 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 20 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 21 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 22 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 23 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 24 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 25 | 6851 | 8043 | 5451 | 5741 | 11384 | 8786 | 6279 |
| 26 | 12651 | 10208 | 13624 | 8772 | 18957 | 14486 | 11596 |
| 27 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 28 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 29 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 30 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 31 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 32 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 33 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 34 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 35 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 36 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 37 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 38 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 39 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 40 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 41 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 42 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 43 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 44 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 45 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 46 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 47 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 48 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 49 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 50 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 51 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 52 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 53 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 54 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 55 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 56 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 57 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 58 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 59 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|------|-------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 4 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 5 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 6 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 7 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 8 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 9 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 10 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 11 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 12 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 13 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 14 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 15 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 16 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 17 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 18 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 19 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 20 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 21 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 22 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 23 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 24 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 25 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 26 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 27 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 28 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 29 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 30 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 31 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 32 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 33 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 34 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 35 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 36 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 37 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 38 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 39 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 40 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 41 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 42 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 43 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 44 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 45 | 12608 | 10160 | 13584 | 8733 | 18879 | 14440 | 11556 |
| 46 | 12714 | 10261 | 13671 | 8796 | 19050 | 14515 | 11653 |
| 47 | 346 | 294 | 290 | 291 | 549 | 347 | 317 |
| 48 | 346 | 294 | 290 | 291 | 549 | 347 | 317 |
| 49 | 346 | 294 | 290 | 291 | 549 | 347 | 317 |
| 50 | 346 | 294 | 290 | 291 | 549 | 347 | 317 |
| 51 | 78 | 16 | 70 | 76 | 68 | 88 | 71 |
| 52 | 78 | 16 | 70 | 76 | 68 | 88 | 71 |
| 53 | 78 | 16 | 70 | 76 | 68 | 88 | 71 |
| 54 | 78 | 16 | 70 | 76 | 68 | 88 | 71 |
| 55 | 78 | 16 | 70 | 76 | 68 | 88 | 71 |
| 56 | 78 | 16 | 70 | 76 | 68 | 88 | 71 |
| 57 | 78 | 16 | 70 | 76 | 68 | 88 | 71 |
| 58 | 78 | 16 | 70 | 76 | 68 | 88 | 71 |
| 59 | 78 | 16 | 70 | 76 | 68 | 88 | 71 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 4 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 5 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 6 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 7 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 8 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 9 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 10 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 11 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 12 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 13 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 14 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 15 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 16 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 17 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 18 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 19 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 20 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 21 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 22 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 23 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 24 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 25 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 26 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 27 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 28 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 29 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 30 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 31 | 94 | 19 | 76 | 85 | 78 | 99 | 86 |
| 32 | 226 | 87 | 160 | 120 | 127 | 206 | 207 |
| 33 | 312 | 339 | 226 | 245 | 547 | 376 | 286 |
| 34 | 312 | 339 | 226 | 245 | 547 | 376 | 286 |
| 35 | 312 | 339 | 226 | 245 | 547 | 376 | 286 |
| 36 | 317 | 345 | 226 | 254 | 561 | 382 | 291 |
| 37 | 317 | 345 | 226 | 254 | 561 | 382 | 291 |
| 38 | 317 | 345 | 226 | 254 | 561 | 382 | 291 |
| 39 | 168 | 116 | 134 | 83 | 190 | 154 | 154 |
| 40 | 187 | 162 | 168 | 127 | 311 | 203 | 171 |
| 41 | 187 | 162 | 168 | 127 | 311 | 203 | 171 |
| 42 | 187 | 162 | 168 | 127 | 311 | 203 | 171 |
| 43 | 187 | 162 | 168 | 127 | 311 | 203 | 171 |
| 44 | 187 | 162 | 168 | 127 | 311 | 203 | 171 |
| 45 | 187 | 162 | 168 | 127 | 311 | 203 | 171 |
| 46 | 187 | 162 | 168 | 127 | 311 | 203 | 171 |
| 47 | 187 | 162 | 168 | 127 | 311 | 203 | 171 |
| 48 | 187 | 162 | 168 | 127 | 311 | 203 | 171 |
| 49 | 187 | 162 | 168 | 127 | 311 | 203 | 171 |
| 50 | 187 | 162 | 168 | 127 | 311 | 203 | 171 |
| 51 | 187 | 162 | 168 | 127 | 311 | 203 | 171 |
| 52 | 187 | 162 | 168 | 127 | 311 | 203 | 171 |
| 53 | 187 | 162 | 168 | 127 | 311 | 203 | 171 |
| 54 | 187 | 162 | 168 | 127 | 311 | 203 | 171 |
| 55 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 56 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 57 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 58 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 59 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|------|------|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 4 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 5 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 6 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 7 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 8 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 9 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 10 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 11 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 12 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 13 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 14 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 15 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 16 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 17 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 18 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 19 | 66 | 58 | 56 | 47 | 106 | 78 | 60 |
| 20 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 21 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 22 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 23 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 24 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 25 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 26 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 27 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 28 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 29 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 30 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 31 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 32 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 33 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 34 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 35 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 36 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 37 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 38 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 39 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 40 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 41 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 42 | 68 | 40 | 53 | 38 | 91 | 51 | 62 |
| 43 | 840 | 836 | 588 | 565 | 1288 | 1129 | 770 |
| 44 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 45 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 46 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 47 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 48 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 49 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 50 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 51 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 52 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 53 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 54 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 55 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 56 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 57 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 58 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 59 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|------|------|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 4 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 5 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 6 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 7 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 8 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 9 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 10 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 11 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 12 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 13 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 14 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 15 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 16 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 17 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 18 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 19 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 20 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 21 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 22 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 23 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 24 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 25 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 26 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 27 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 28 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 29 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 30 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 31 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 32 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 33 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 34 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 35 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 36 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 37 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 38 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 39 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 40 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 41 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 42 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 43 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 44 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 45 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 46 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 47 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 48 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 49 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 50 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 51 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 52 | 840 | 835 | 587 | 564 | 1287 | 1127 | 770 |
| 53 | 199 | 49 | 142 | 103 | 112 | 185 | 182 |
| 54 | 199 | 49 | 142 | 103 | 112 | 185 | 182 |
| 55 | 199 | 49 | 142 | 103 | 112 | 185 | 182 |
| 56 | 199 | 49 | 142 | 103 | 112 | 185 | 182 |
| 57 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 58 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 59 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|-------|-------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 4 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 5 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 6 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 7 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 8 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 9 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 10 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 11 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 12 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 13 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 14 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 15 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 16 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 17 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 18 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 19 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 20 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 21 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 22 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 23 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 24 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 25 | 198 | 49 | 140 | 102 | 112 | 183 | 181 |
| 26 | 331 | 281 | 177 | 245 | 529 | 362 | 303 |
| 27 | 711 | 609 | 425 | 311 | 1186 | 559 | 652 |
| 28 | 711 | 609 | 425 | 311 | 1186 | 559 | 652 |
| 29 | 222 | 159 | 182 | 174 | 389 | 375 | 203 |
| 30 | 222 | 159 | 182 | 174 | 389 | 375 | 203 |
| 31 | 222 | 159 | 182 | 174 | 389 | 375 | 203 |
| 32 | 222 | 159 | 182 | 174 | 389 | 375 | 203 |
| 33 | 222 | 159 | 182 | 174 | 389 | 375 | 203 |
| 34 | 222 | 159 | 182 | 174 | 389 | 375 | 203 |
| 35 | 222 | 159 | 182 | 174 | 389 | 375 | 203 |
| 36 | 222 | 159 | 182 | 174 | 389 | 375 | 203 |
| 37 | 222 | 159 | 182 | 174 | 389 | 375 | 203 |
| 38 | 222 | 159 | 182 | 174 | 389 | 375 | 203 |
| 39 | 222 | 159 | 182 | 174 | 389 | 375 | 203 |
| 40 | 222 | 159 | 182 | 174 | 389 | 375 | 203 |
| 41 | 222 | 159 | 182 | 174 | 389 | 375 | 203 |
| 42 | 222 | 159 | 182 | 174 | 389 | 375 | 203 |
| 43 | 222 | 159 | 182 | 174 | 389 | 375 | 203 |
| 44 | 222 | 159 | 182 | 174 | 389 | 375 | 203 |
| 45 | 222 | 159 | 182 | 174 | 389 | 375 | 203 |
| 46 | 222 | 159 | 182 | 174 | 389 | 375 | 203 |
| 47 | 222 | 159 | 182 | 174 | 389 | 375 | 203 |
| 48 | 222 | 159 | 182 | 174 | 389 | 376 | 203 |
| 49 | 226 | 162 | 183 | 174 | 394 | 375 | 207 |
| 50 | 226 | 162 | 183 | 174 | 394 | 375 | 207 |
| 51 | 53 | 71 | 48 | 36 | 114 | 133 | 49 |
| 52 | 53 | 71 | 48 | 36 | 114 | 133 | 49 |
| 53 | 53 | 71 | 48 | 36 | 114 | 133 | 49 |
| 54 | 53 | 71 | 48 | 36 | 114 | 133 | 49 |
| 55 | 53 | 71 | 48 | 36 | 114 | 133 | 49 |
| 56 | 61152 | 17008 | 41078 | 17947 | 57410 | 36531 | 56050 |
| 57 | 82 | 56 | 22 | 30 | 72 | 99 | 75 |
| 58 | 0 | 1467 | 0 | 0 | 1 | 0 | 0 |
| 59 | | | | | | | |
| 60 | | | | | | | |

| | | | | | | | | |
|----|---|------|---|---|---|---|---|--|
| 1 | | | | | | | | |
| 2 | | | | | | | | |
| 3 | 0 | 1068 | 1 | 1 | 1 | 0 | 0 | |
| 4 | 0 | 1068 | 1 | 1 | 1 | 0 | 0 | |
| 5 | 0 | 1068 | 1 | 1 | 1 | 0 | 0 | |
| 6 | 0 | 1068 | 1 | 1 | 1 | 0 | 0 | |
| 7 | 0 | 1068 | 1 | 1 | 1 | 0 | 0 | |
| 8 | 0 | 1068 | 1 | 1 | 1 | 0 | 0 | |
| 9 | 0 | 1068 | 1 | 1 | 1 | 0 | 0 | |
| 10 | 0 | 1068 | 1 | 1 | 1 | 0 | 0 | |
| 11 | 0 | 1068 | 1 | 1 | 1 | 0 | 0 | |
| 12 | 0 | 1068 | 1 | 1 | 1 | 0 | 0 | |
| 13 | 0 | 1068 | 1 | 1 | 1 | 0 | 0 | |
| 14 | 0 | 1068 | 1 | 1 | 1 | 0 | 0 | |
| 15 | 0 | 321 | 0 | 0 | 0 | 0 | 0 | |
| 16 | 0 | 321 | 0 | 0 | 0 | 0 | 0 | |
| 17 | 0 | 311 | 0 | 0 | 0 | 0 | 0 | |
| 18 | 0 | 311 | 0 | 0 | 0 | 0 | 0 | |
| 19 | 0 | 311 | 0 | 0 | 0 | 0 | 0 | |
| 20 | | | | | | | | |
| 21 | | | | | | | | |
| 22 | | | | | | | | |
| 23 | | | | | | | | |
| 24 | | | | | | | | |
| 25 | | | | | | | | |
| 26 | | | | | | | | |
| 27 | | | | | | | | |
| 28 | | | | | | | | |
| 29 | | | | | | | | |
| 30 | | | | | | | | |
| 31 | | | | | | | | |
| 32 | | | | | | | | |
| 33 | | | | | | | | |
| 34 | | | | | | | | |
| 35 | | | | | | | | |
| 36 | | | | | | | | |
| 37 | | | | | | | | |
| 38 | | | | | | | | |
| 39 | | | | | | | | |
| 40 | | | | | | | | |
| 41 | | | | | | | | |
| 42 | | | | | | | | |
| 43 | | | | | | | | |
| 44 | | | | | | | | |
| 45 | | | | | | | | |
| 46 | | | | | | | | |
| 47 | | | | | | | | |
| 48 | | | | | | | | |
| 49 | | | | | | | | |
| 50 | | | | | | | | |
| 51 | | | | | | | | |
| 52 | | | | | | | | |
| 53 | | | | | | | | |
| 54 | | | | | | | | |
| 55 | | | | | | | | |
| 56 | | | | | | | | |
| 57 | | | | | | | | |
| 58 | | | | | | | | |
| 59 | | | | | | | | |
| 60 | | | | | | | | |

Do not distribute

| | baseMean | H2O | Xcf | FoldChange | log2FoldChange | stat | pvalue |
|----|----------|-----|-----|------------|----------------|------------|-------------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | | | | | | | |
| 4 | | | | | | | |
| 5 | 71.47 | | 142 | 1 | 0.992 | -7.1497471 | -1.983 NA |
| 6 | 46.12 | | 91 | 1 | 0.993 | -6.5077946 | -2.123 NA |
| 7 | 46.12 | | 91 | 1 | 0.993 | -6.5077946 | -2.123 NA |
| 8 | 46.12 | | 91 | 1 | 0.993 | -6.5077946 | -2.123 NA |
| 9 | 46.12 | | 91 | 1 | 0.993 | -6.5077946 | -2.123 NA |
| 10 | 46.12 | | 91 | 1 | 0.993 | -6.5077946 | -2.123 NA |
| 11 | 46.12 | | 91 | 1 | 0.993 | -6.5077946 | -2.123 NA |
| 12 | 46.12 | | 91 | 1 | 0.993 | -6.5077946 | -2.123 NA |
| 13 | 46.12 | | 91 | 1 | 0.993 | -6.5077946 | -2.123 NA |
| 14 | 46.12 | | 91 | 1 | 0.993 | -6.5077946 | -2.123 NA |
| 15 | 46.12 | | 91 | 1 | 0.993 | -6.5077946 | -2.123 NA |
| 16 | 46.12 | | 91 | 1 | 0.993 | -6.5077946 | -2.123 NA |
| 17 | 46.12 | | 91 | 1 | 0.993 | -6.5077946 | -2.123 NA |
| 18 | 50.8 | | 74 | 27 | 0.998 | -1.4545659 | -2.374 0.01758514 |
| 19 | 50.8 | | 74 | 27 | 0.998 | -1.4545659 | -2.374 0.01758514 |
| 20 | 50.8 | | 74 | 27 | 0.998 | -1.4545659 | -2.374 0.01758514 |
| 21 | 50.8 | | 74 | 27 | 0.998 | -1.4545659 | -2.374 0.01758514 |
| 22 | 156.27 | | 217 | 96 | 0.998 | -1.1765887 | -2.259 0.02385415 |
| 23 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 24 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 25 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 26 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 27 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 28 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 29 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 30 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 31 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 32 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 33 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 34 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 35 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 36 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 37 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 38 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 39 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 40 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 41 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 42 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 43 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 44 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 45 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 46 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 47 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 48 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 49 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 50 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 51 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 52 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 53 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 54 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 55 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 56 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 57 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 58 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 59 | 148.1 | | 205 | 91 | 0.998 | -1.1716855 | -2.236 0.02535544 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|----|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 4 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 5 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 6 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 7 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 8 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 9 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 10 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 11 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 12 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 13 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 14 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 15 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 16 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 17 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 18 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 19 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 20 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 21 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 22 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 23 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 24 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 25 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 26 | 148.1 | 205 | 91 | 0.998 | -1.1716855 | -2.236 | 0.02535544 |
| 27 | 150.81 | 206 | 96 | 0.998 | -1.101538 | -2.472 | 0.01344867 |
| 28 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 29 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 30 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 31 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 32 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 33 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 34 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 35 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 36 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 37 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 38 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 39 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 40 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 41 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 42 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 43 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 44 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 45 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 46 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 47 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 48 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 49 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 50 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 51 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 52 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 53 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 54 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 55 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 56 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 57 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 58 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 59 | 149.88 | 204 | 96 | 0.998 | -1.0874628 | -2.447 | 0.01439291 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 393.96 | 534 | 254 | 0.997 | -1.0720112 | -2.789 | 0.00528842 |
| 4 | 393.96 | 534 | 254 | 0.997 | -1.0720112 | -2.789 | 0.00528842 |
| 5 | 393.96 | 534 | 254 | 0.997 | -1.0720112 | -2.789 | 0.00528842 |
| 6 | 393.96 | 534 | 254 | 0.997 | -1.0720112 | -2.789 | 0.00528842 |
| 7 | 393.96 | 534 | 254 | 0.997 | -1.0720112 | -2.789 | 0.00528842 |
| 8 | 393.96 | 534 | 254 | 0.997 | -1.0720112 | -2.789 | 0.00528842 |
| 9 | 393.96 | 534 | 254 | 0.997 | -1.0720112 | -2.789 | 0.00528842 |
| 10 | 393.96 | 534 | 254 | 0.997 | -1.0720112 | -2.789 | 0.00528842 |
| 11 | 393.96 | 534 | 254 | 0.997 | -1.0720112 | -2.789 | 0.00528842 |
| 12 | 393.96 | 534 | 254 | 0.997 | -1.0720112 | -2.789 | 0.00528842 |
| 13 | 393.96 | 534 | 254 | 0.997 | -1.0720112 | -2.789 | 0.00528842 |
| 14 | 393.96 | 534 | 254 | 0.997 | -1.0720112 | -2.789 | 0.00528842 |
| 15 | 393.96 | 534 | 254 | 0.997 | -1.0720112 | -2.789 | 0.00528842 |
| 16 | 393.96 | 534 | 254 | 0.997 | -1.0720112 | -2.789 | 0.00528842 |
| 17 | 393.96 | 534 | 254 | 0.997 | -1.0720112 | -2.789 | 0.00528842 |
| 18 | 393.96 | 534 | 254 | 0.997 | -1.0720112 | -2.789 | 0.00528842 |
| 19 | 393.96 | 534 | 254 | 0.997 | -1.0720112 | -2.789 | 0.00528842 |
| 20 | 393.96 | 534 | 254 | 0.997 | -1.0720112 | -2.789 | 0.00528842 |
| 21 | 355.67 | 480 | 232 | 0.997 | -1.0489096 | -2.704 | 0.00684464 |
| 22 | 355.67 | 480 | 232 | 0.997 | -1.0489096 | -2.704 | 0.00684464 |
| 23 | 355.67 | 480 | 232 | 0.997 | -1.0489096 | -2.704 | 0.00684464 |
| 24 | 355.52 | 480 | 232 | 0.997 | -1.0489096 | -2.701 | 0.00691441 |
| 25 | 355.52 | 480 | 232 | 0.997 | -1.0489096 | -2.701 | 0.00691441 |
| 26 | 355.52 | 480 | 232 | 0.997 | -1.0489096 | -2.701 | 0.00691441 |
| 27 | 355.52 | 480 | 232 | 0.997 | -1.0489096 | -2.701 | 0.00691441 |
| 28 | 65.54 | 88 | 43 | 0.998 | -1.0331669 | -2.034 | 0.04198944 |
| 29 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 30 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 31 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 32 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 33 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 34 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 35 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 36 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 37 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 38 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 39 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 40 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 41 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 42 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 43 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 44 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 45 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 46 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 47 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 48 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 49 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 50 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 51 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 52 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 53 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 54 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 55 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 56 | 63.05 | 84 | 42 | 0.999 | -1 | -1.935 | 0.05293459 |
| 57 | 201.09 | 267 | 136 | 0.997 | -0.9732331 | -2.801 | 0.00508989 |
| 58 | 2883.54 | 3753 | 2014 | 0.997 | -0.8979806 | -2.626 | 0.00863824 |
| 59 | | | | | | | |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 2883.54 | 3753 | 2014 | 0.997 | -0.8979806 | -2.626 | 0.00863824 |
| 4 | 2883.54 | 3753 | 2014 | 0.997 | -0.8979806 | -2.626 | 0.00863824 |
| 5 | 2883.54 | 3753 | 2014 | 0.997 | -0.8979806 | -2.626 | 0.00863824 |
| 6 | 2883.54 | 3753 | 2014 | 0.997 | -0.8979806 | -2.626 | 0.00863824 |
| 7 | 2883.54 | 3753 | 2014 | 0.997 | -0.8979806 | -2.626 | 0.00863824 |
| 8 | 2865.93 | 3729 | 2003 | 0.997 | -0.8966264 | -2.624 | 0.00868082 |
| 9 | 2865.93 | 3729 | 2003 | 0.997 | -0.8966264 | -2.624 | 0.00868082 |
| 10 | 2865.93 | 3729 | 2003 | 0.997 | -0.8966264 | -2.624 | 0.00868082 |
| 11 | 2865.93 | 3729 | 2003 | 0.997 | -0.8966264 | -2.624 | 0.00868082 |
| 12 | 2865.93 | 3729 | 2003 | 0.997 | -0.8966264 | -2.624 | 0.00868082 |
| 13 | 2865.93 | 3729 | 2003 | 0.997 | -0.8966264 | -2.624 | 0.00868082 |
| 14 | 2865.93 | 3729 | 2003 | 0.997 | -0.8966264 | -2.624 | 0.00868082 |
| 15 | 2865.93 | 3729 | 2003 | 0.997 | -0.8966264 | -2.624 | 0.00868082 |
| 16 | 2865.93 | 3729 | 2003 | 0.997 | -0.8966264 | -2.624 | 0.00868082 |
| 17 | 2865.93 | 3729 | 2003 | 0.997 | -0.8966264 | -2.624 | 0.00868082 |
| 18 | 2865.93 | 3729 | 2003 | 0.997 | -0.8966264 | -2.624 | 0.00868082 |
| 19 | 2865.93 | 3729 | 2003 | 0.997 | -0.8966264 | -2.624 | 0.00868082 |
| 20 | 2865.93 | 3729 | 2003 | 0.997 | -0.8966264 | -2.624 | 0.00868082 |
| 21 | 2865.93 | 3729 | 2003 | 0.997 | -0.8966264 | -2.624 | 0.00868082 |
| 22 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 23 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 24 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 25 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 26 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 27 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 28 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 29 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 30 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 31 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 32 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 33 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 34 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 35 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 36 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 37 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 38 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 39 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 40 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 41 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 42 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 43 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 44 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 45 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 46 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 47 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 48 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 49 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 50 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 51 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 52 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 53 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 54 | 495.69 | 640 | 351 | 0.998 | -0.8666009 | -2.178 | 0.02938607 |
| 55 | 120.03 | 150 | 90 | 0.998 | -0.7369656 | -1.922 | 0.05465553 |
| 56 | 119.73 | 149 | 90 | 0.998 | -0.7273154 | -1.908 | 0.05633446 |
| 57 | 119.73 | 149 | 90 | 0.998 | -0.7273154 | -1.908 | 0.05633446 |
| 58 | 119.73 | 149 | 90 | 0.998 | -0.7273154 | -1.908 | 0.05633446 |
| 59 | 119.73 | 149 | 90 | 0.998 | -0.7273154 | -1.908 | 0.05633446 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|----|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 119.73 | 149 | 90 | 0.998 | -0.7273154 | -1.908 | 0.05633446 |
| 4 | 119.73 | 149 | 90 | 0.998 | -0.7273154 | -1.908 | 0.05633446 |
| 5 | 119.73 | 149 | 90 | 0.998 | -0.7273154 | -1.908 | 0.05633446 |
| 6 | 119.73 | 149 | 90 | 0.998 | -0.7273154 | -1.908 | 0.05633446 |
| 7 | 119.73 | 149 | 90 | 0.998 | -0.7273154 | -1.908 | 0.05633446 |
| 8 | | | | | | | |
| 9 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 10 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 11 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 12 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 13 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 14 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 15 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 16 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 17 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 18 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 19 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 20 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 21 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 22 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 23 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 24 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 25 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 26 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 27 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 28 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 29 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 30 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 31 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 32 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 33 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 34 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 35 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 36 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 37 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 38 | 89.09 | 110 | 68 | 0.999 | -0.6938969 | -1.576 | 0.11491311 |
| 39 | 89.42 | 110 | 68 | 0.999 | -0.6938969 | -1.546 | 0.1220541 |
| 40 | 89.42 | 110 | 68 | 0.999 | -0.6938969 | -1.546 | 0.1220541 |
| 41 | | | | | | | |
| 42 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 43 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 44 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 45 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 46 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 47 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 48 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 49 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 50 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 51 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 52 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 53 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 54 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 55 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 56 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 57 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 58 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 59 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 4 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 5 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 6 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 7 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 8 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 9 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 10 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 11 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 12 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 13 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 14 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 15 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 16 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 17 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 18 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 19 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 20 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 21 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 22 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 23 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 24 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 25 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 26 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 27 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 28 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 29 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 30 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 31 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 32 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 33 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 34 | 99.12 | 122 | 76 | 0.999 | -0.6828098 | -1.686 | 0.09188525 |
| 35 | 257.5 | 314 | 201 | 0.998 | -0.6435691 | -1.744 | 0.08120503 |
| 36 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 37 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 38 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 39 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 40 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 41 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 42 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 43 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 44 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 45 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 46 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 47 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 48 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 49 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 50 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 51 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 52 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 53 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 54 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 55 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 56 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 57 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 58 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 59 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|------|-----|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 4 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 5 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 6 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 7 | 251.74 | 306 | 197 | 0.998 | -0.635336 | -1.715 | 0.08641366 |
| 8 | | | | | | | |
| 9 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 10 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 11 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 12 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 13 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 14 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 15 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 16 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 17 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 18 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 19 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 20 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 21 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 22 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 23 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 24 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 25 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 26 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 27 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 28 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 29 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 30 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 31 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 32 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 33 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 34 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 35 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 36 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 37 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 38 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 39 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 40 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 41 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 42 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 43 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 44 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 45 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 46 | 54.25 | 66 | 43 | 1 | -0.6181294 | -0.883 | 0.37716247 |
| 47 | 866.11 | 1048 | 685 | 1 | -0.6134628 | -0.588 | 0.5562651 |
| 48 | 866.11 | 1048 | 685 | 1 | -0.6134628 | -0.588 | 0.5562651 |
| 49 | 866.11 | 1048 | 685 | 1 | -0.6134628 | -0.588 | 0.5562651 |
| 50 | 866.11 | 1048 | 685 | 1 | -0.6134628 | -0.588 | 0.5562651 |
| 51 | 866.11 | 1048 | 685 | 1 | -0.6134628 | -0.588 | 0.5562651 |
| 52 | 866.11 | 1048 | 685 | 1 | -0.6134628 | -0.588 | 0.5562651 |
| 53 | 866.11 | 1048 | 685 | 1 | -0.6134628 | -0.588 | 0.5562651 |
| 54 | 866.11 | 1048 | 685 | 1 | -0.6134628 | -0.588 | 0.5562651 |
| 55 | 133.23 | 156 | 110 | 0.999 | -0.5040425 | -1.394 | 0.16338548 |
| 56 | 132.31 | 155 | 110 | 0.999 | -0.4947647 | -1.36 | 0.17387296 |
| 57 | 132.31 | 155 | 110 | 0.999 | -0.4947647 | -1.36 | 0.17387296 |
| 58 | 132.31 | 155 | 110 | 0.999 | -0.4947647 | -1.36 | 0.17387296 |
| 59 | 132.31 | 155 | 110 | 0.999 | -0.4947647 | -1.36 | 0.17387296 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-----|----|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 77.8 | 91 | 65 | 0.999 | -0.4854268 | -1.04 | 0.29854745 |
| 4 | 77.8 | 91 | 65 | 0.999 | -0.4854268 | -1.04 | 0.29854745 |
| 5 | 77.8 | 91 | 65 | 0.999 | -0.4854268 | -1.04 | 0.29854745 |
| 6 | 77.8 | 91 | 65 | 0.999 | -0.4854268 | -1.04 | 0.29854745 |
| 7 | 77.8 | 91 | 65 | 0.999 | -0.4854268 | -1.04 | 0.29854745 |
| 8 | 77.8 | 91 | 65 | 0.999 | -0.4854268 | -1.04 | 0.29854745 |
| 9 | 77.8 | 91 | 65 | 0.999 | -0.4854268 | -1.04 | 0.29854745 |
| 10 | 77.8 | 91 | 65 | 0.999 | -0.4854268 | -1.04 | 0.29854745 |
| 11 | 77.8 | 91 | 65 | 0.999 | -0.4854268 | -1.04 | 0.29854745 |
| 12 | 68.32 | 79 | 57 | 0.999 | -0.4708907 | -1.121 | 0.26249418 |
| 13 | 68.32 | 79 | 57 | 0.999 | -0.4708907 | -1.121 | 0.26249418 |
| 14 | 68.32 | 79 | 57 | 0.999 | -0.4708907 | -1.121 | 0.26249418 |
| 15 | 68.32 | 79 | 57 | 0.999 | -0.4708907 | -1.121 | 0.26249418 |
| 16 | 68.32 | 79 | 57 | 0.999 | -0.4708907 | -1.121 | 0.26249418 |
| 17 | 68.32 | 79 | 57 | 0.999 | -0.4708907 | -1.121 | 0.26249418 |
| 18 | 49.52 | 58 | 42 | 0.999 | -0.4656636 | -0.875 | 0.38167002 |
| 19 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 20 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 21 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 22 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 23 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 24 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 25 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 26 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 27 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 28 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 29 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 30 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 31 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 32 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 33 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 34 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 35 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 36 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 37 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 38 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 39 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 40 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 41 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 42 | 48.62 | 56 | 41 | 0.999 | -0.4498029 | -0.82 | 0.4122912 |
| 43 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 44 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 45 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 46 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 47 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 48 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 49 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 50 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 51 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 52 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 53 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 54 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 55 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 56 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 57 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 58 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 59 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 4 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 5 | 89.9 | 103 | 77 | 0.999 | -0.419714 | -1.087 | 0.27699077 |
| 6 | 48.96 | 56 | 42 | 0.999 | -0.4150375 | -0.812 | 0.41681107 |
| 7 | 109.72 | 125 | 94 | 0.999 | -0.4111954 | -1.113 | 0.26587994 |
| 8 | 109.72 | 125 | 94 | 0.999 | -0.4111954 | -1.113 | 0.26587994 |
| 9 | 109.72 | 125 | 94 | 0.999 | -0.4111954 | -1.113 | 0.26587994 |
| 10 | 109.72 | 125 | 94 | 0.999 | -0.4111954 | -1.113 | 0.26587994 |
| 11 | 109.72 | 125 | 94 | 0.999 | -0.4111954 | -1.113 | 0.26587994 |
| 12 | 109.72 | 125 | 94 | 0.999 | -0.4111954 | -1.113 | 0.26587994 |
| 13 | 109.72 | 125 | 94 | 0.999 | -0.4111954 | -1.113 | 0.26587994 |
| 14 | 109.72 | 125 | 94 | 0.999 | -0.4111954 | -1.113 | 0.26587994 |
| 15 | 109.72 | 125 | 94 | 0.999 | -0.4111954 | -1.113 | 0.26587994 |
| 16 | 109.72 | 125 | 94 | 0.999 | -0.4111954 | -1.113 | 0.26587994 |
| 17 | 109.72 | 125 | 94 | 0.999 | -0.4111954 | -1.113 | 0.26587994 |
| 18 | 109.72 | 125 | 94 | 0.999 | -0.4111954 | -1.113 | 0.26587994 |
| 19 | 109.72 | 125 | 94 | 0.999 | -0.4111954 | -1.113 | 0.26587994 |
| 20 | 109.72 | 125 | 94 | 0.999 | -0.4111954 | -1.113 | 0.26587994 |
| 21 | 516.58 | 589 | 445 | 0.998 | -0.4044623 | -1.436 | 0.15106432 |
| 22 | 78.59 | 90 | 68 | 1 | -0.4043903 | -0.284 | 0.77668962 |
| 23 | 78.59 | 90 | 68 | 1 | -0.4043903 | -0.284 | 0.77668962 |
| 24 | 78.59 | 90 | 68 | 1 | -0.4043903 | -0.284 | 0.77668962 |
| 25 | 78.59 | 90 | 68 | 1 | -0.4043903 | -0.284 | 0.77668962 |
| 26 | 78.59 | 90 | 68 | 1 | -0.4043903 | -0.284 | 0.77668962 |
| 27 | 78.59 | 90 | 68 | 1 | -0.4043903 | -0.284 | 0.77668962 |
| 28 | 78.59 | 90 | 68 | 1 | -0.4043903 | -0.284 | 0.77668962 |
| 29 | 78.59 | 90 | 68 | 1 | -0.4043903 | -0.284 | 0.77668962 |
| 30 | 78.59 | 90 | 68 | 1 | -0.4043903 | -0.284 | 0.77668962 |
| 31 | 78.59 | 90 | 68 | 1 | -0.4043903 | -0.284 | 0.77668962 |
| 32 | 78.59 | 90 | 68 | 1 | -0.4043903 | -0.284 | 0.77668962 |
| 33 | 78.59 | 90 | 68 | 1 | -0.4043903 | -0.284 | 0.77668962 |
| 34 | 78.59 | 90 | 68 | 1 | -0.4043903 | -0.284 | 0.77668962 |
| 35 | 78.59 | 90 | 68 | 1 | -0.4043903 | -0.284 | 0.77668962 |
| 36 | 78.59 | 90 | 68 | 1 | -0.4043903 | -0.284 | 0.77668962 |
| 37 | 78.59 | 90 | 68 | 1 | -0.4043903 | -0.284 | 0.77668962 |
| 38 | 78.59 | 90 | 68 | 1 | -0.4043903 | -0.284 | 0.77668962 |
| 39 | 78.59 | 90 | 68 | 1 | -0.4043903 | -0.284 | 0.77668962 |
| 40 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 41 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 42 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 43 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 44 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 45 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 46 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 47 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 48 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 49 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 50 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 51 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 52 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 53 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 54 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 55 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 56 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 57 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 58 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 59 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 4 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 5 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 6 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 7 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 8 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 9 | 516.25 | 588 | 445 | 0.998 | -0.4020108 | -1.428 | 0.15317999 |
| 10 | 50.92 | 58 | 44 | 0.999 | -0.3985494 | -0.774 | 0.43909009 |
| 11 | 50.92 | 58 | 44 | 0.999 | -0.3985494 | -0.774 | 0.43909009 |
| 12 | 50.92 | 58 | 44 | 0.999 | -0.3985494 | -0.774 | 0.43909009 |
| 13 | 50.92 | 58 | 44 | 0.999 | -0.3985494 | -0.774 | 0.43909009 |
| 14 | 50.92 | 58 | 44 | 0.999 | -0.3985494 | -0.774 | 0.43909009 |
| 15 | 50.92 | 58 | 44 | 0.999 | -0.3985494 | -0.774 | 0.43909009 |
| 16 | 50.92 | 58 | 44 | 0.999 | -0.3985494 | -0.774 | 0.43909009 |
| 17 | 522.35 | 594 | 451 | 0.998 | -0.3973355 | -1.395 | 0.16306794 |
| 18 | 47.66 | 54 | 41 | 1 | -0.3973355 | -0.662 | 0.50787169 |
| 19 | 47.66 | 54 | 41 | 1 | -0.3973355 | -0.662 | 0.50787169 |
| 20 | 47.66 | 54 | 41 | 1 | -0.3973355 | -0.662 | 0.50787169 |
| 21 | 47.66 | 54 | 41 | 1 | -0.3973355 | -0.662 | 0.50787169 |
| 22 | 47.66 | 54 | 41 | 1 | -0.3973355 | -0.662 | 0.50787169 |
| 23 | 47.66 | 54 | 41 | 1 | -0.3973355 | -0.662 | 0.50787169 |
| 24 | 47.66 | 54 | 41 | 1 | -0.3973355 | -0.662 | 0.50787169 |
| 25 | 47.66 | 54 | 41 | 1 | -0.3973355 | -0.662 | 0.50787169 |
| 26 | 47.66 | 54 | 41 | 1 | -0.3973355 | -0.662 | 0.50787169 |
| 27 | 47.66 | 54 | 41 | 1 | -0.3973355 | -0.662 | 0.50787169 |
| 28 | 47.66 | 54 | 41 | 1 | -0.3973355 | -0.662 | 0.50787169 |
| 29 | 47.66 | 54 | 41 | 1 | -0.3973355 | -0.662 | 0.50787169 |
| 30 | 47.66 | 54 | 41 | 1 | -0.3973355 | -0.662 | 0.50787169 |
| 31 | 135.93 | 155 | 118 | 0.999 | -0.3934814 | -1.118 | 0.26368155 |
| 32 | 62.13 | 70 | 54 | 1 | -0.3743955 | -0.704 | 0.48146024 |
| 33 | 62.13 | 70 | 54 | 1 | -0.3743955 | -0.704 | 0.48146024 |
| 34 | 62.13 | 70 | 54 | 1 | -0.3743955 | -0.704 | 0.48146024 |
| 35 | 62.13 | 70 | 54 | 1 | -0.3743955 | -0.704 | 0.48146024 |
| 36 | 62.13 | 70 | 54 | 1 | -0.3743955 | -0.704 | 0.48146024 |
| 37 | 62.13 | 70 | 54 | 1 | -0.3743955 | -0.704 | 0.48146024 |
| 38 | 62.13 | 70 | 54 | 1 | -0.3743955 | -0.704 | 0.48146024 |
| 39 | 133.11 | 150 | 116 | 0.999 | -0.3708377 | -1.073 | 0.2832042 |
| 40 | 133.11 | 150 | 116 | 0.999 | -0.3708377 | -1.073 | 0.2832042 |
| 41 | 222.78 | 250 | 196 | 0.999 | -0.3510744 | -1.043 | 0.29680673 |
| 42 | 222.78 | 250 | 196 | 0.999 | -0.3510744 | -1.043 | 0.29680673 |
| 43 | 222.78 | 250 | 196 | 0.999 | -0.3510744 | -1.043 | 0.29680673 |
| 44 | 222.78 | 250 | 196 | 0.999 | -0.3510744 | -1.043 | 0.29680673 |
| 45 | 222.78 | 250 | 196 | 0.999 | -0.3510744 | -1.043 | 0.29680673 |
| 46 | 222.78 | 250 | 196 | 0.999 | -0.3510744 | -1.043 | 0.29680673 |
| 47 | 579.63 | 648 | 511 | 1 | -0.3426705 | -0.238 | 0.8116487 |
| 48 | 579.63 | 648 | 511 | 1 | -0.3426705 | -0.238 | 0.8116487 |
| 49 | 579.63 | 648 | 511 | 1 | -0.3426705 | -0.238 | 0.8116487 |
| 50 | 579.63 | 648 | 511 | 1 | -0.3426705 | -0.238 | 0.8116487 |
| 51 | 570.69 | 637 | 504 | 1 | -0.3378696 | -0.236 | 0.813742 |
| 52 | 570.69 | 637 | 504 | 1 | -0.3378696 | -0.236 | 0.813742 |
| 53 | 570.69 | 637 | 504 | 1 | -0.3378696 | -0.236 | 0.813742 |
| 54 | 570.69 | 637 | 504 | 1 | -0.3378696 | -0.236 | 0.813742 |
| 55 | 570.69 | 637 | 504 | 1 | -0.3378696 | -0.236 | 0.813742 |
| 56 | 570.69 | 637 | 504 | 1 | -0.3378696 | -0.236 | 0.813742 |
| 57 | 570.69 | 637 | 504 | 1 | -0.3378696 | -0.236 | 0.813742 |
| 58 | 570.69 | 637 | 504 | 1 | -0.3378696 | -0.236 | 0.813742 |
| 59 | 570.69 | 637 | 504 | 1 | -0.3378696 | -0.236 | 0.813742 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 570.69 | 637 | 504 | 1 | -0.3378696 | -0.236 | 0.813742 |
| 4 | 570.69 | 637 | 504 | 1 | -0.3378696 | -0.236 | 0.813742 |
| 5 | 570.69 | 637 | 504 | 1 | -0.3378696 | -0.236 | 0.813742 |
| 6 | 570.69 | 637 | 504 | 1 | -0.3378696 | -0.236 | 0.813742 |
| 7 | 570.69 | 637 | 504 | 1 | -0.3378696 | -0.236 | 0.813742 |
| 8 | 570.69 | 637 | 504 | 1 | -0.3378696 | -0.236 | 0.813742 |
| 9 | 570.69 | 637 | 504 | 1 | -0.3378696 | -0.236 | 0.813742 |
| 10 | 570.69 | 637 | 504 | 1 | -0.3378696 | -0.236 | 0.813742 |
| 11 | 5877.54 | 6486 | 5269 | 0.998 | -0.2997998 | -1.171 | 0.24161443 |
| 12 | 5877.54 | 6486 | 5269 | 0.998 | -0.2997998 | -1.171 | 0.24161443 |
| 13 | 5877.54 | 6486 | 5269 | 0.998 | -0.2997998 | -1.171 | 0.24161443 |
| 14 | 5877.54 | 6486 | 5269 | 0.998 | -0.2997998 | -1.171 | 0.24161443 |
| 15 | 92.35 | 102 | 83 | 1 | -0.2973859 | -0.164 | 0.86953914 |
| 16 | 92.35 | 102 | 83 | 1 | -0.2973859 | -0.164 | 0.86953914 |
| 17 | 92.35 | 102 | 83 | 1 | -0.2973859 | -0.164 | 0.86953914 |
| 18 | 92.35 | 102 | 83 | 1 | -0.2973859 | -0.164 | 0.86953914 |
| 19 | 92.35 | 102 | 83 | 1 | -0.2973859 | -0.164 | 0.86953914 |
| 20 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 21 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 22 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 23 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 24 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 25 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 26 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 27 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 28 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 29 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 30 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 31 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 32 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 33 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 34 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 35 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 36 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 37 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 38 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 39 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 40 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 41 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 42 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 43 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 44 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 45 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 46 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 47 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 48 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 49 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 50 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 51 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 52 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 53 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 54 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 55 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 56 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 57 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 58 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 59 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 4 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 5 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 6 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 7 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 8 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 9 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 10 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 11 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 12 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 13 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 14 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 15 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 16 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 17 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 18 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 19 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 20 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 21 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 22 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 23 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 24 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 25 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 26 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 27 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 28 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 29 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 30 | 394.28 | 435 | 354 | 0.999 | -0.297266 | -1.046 | 0.29548296 |
| 31 | 395.34 | 436 | 355 | 0.999 | -0.2965091 | -1.045 | 0.29591636 |
| 32 | 395.34 | 436 | 355 | 0.999 | -0.2965091 | -1.045 | 0.29591636 |
| 33 | 108.97 | 119 | 99 | 1 | -0.2654611 | -0.603 | 0.5464287 |
| 34 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 35 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 36 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 37 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 38 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 39 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 40 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 41 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 42 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 43 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 44 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 45 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 46 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 47 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 48 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 49 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 50 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 51 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 52 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 53 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 54 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 55 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 56 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 57 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 58 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 59 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 4 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 5 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 6 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 7 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 8 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 9 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 10 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 11 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 12 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 13 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 14 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 15 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 16 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 17 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 18 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 19 | 148.63 | 162 | 135 | 1 | -0.2630344 | -0.591 | 0.55445819 |
| 20 | 6750.85 | 7364 | 6138 | 0.999 | -0.262721 | -1.047 | 0.2951539 |
| 21 | 6750.85 | 7364 | 6138 | 0.999 | -0.262721 | -1.047 | 0.2951539 |
| 22 | 6750.85 | 7364 | 6138 | 0.999 | -0.262721 | -1.047 | 0.2951539 |
| 23 | 6750.85 | 7364 | 6138 | 0.999 | -0.262721 | -1.047 | 0.2951539 |
| 24 | 6750.85 | 7364 | 6138 | 0.999 | -0.262721 | -1.047 | 0.2951539 |
| 25 | 6750.85 | 7364 | 6138 | 0.999 | -0.262721 | -1.047 | 0.2951539 |
| 26 | 6750.85 | 7364 | 6138 | 0.999 | -0.262721 | -1.047 | 0.2951539 |
| 27 | 6750.85 | 7364 | 6138 | 0.999 | -0.262721 | -1.047 | 0.2951539 |
| 28 | 6750.85 | 7364 | 6138 | 0.999 | -0.262721 | -1.047 | 0.2951539 |
| 29 | 108.07 | 118 | 99 | 0.999 | -0.2532864 | -0.74 | 0.45937141 |
| 30 | 108.07 | 118 | 99 | 0.999 | -0.2532864 | -0.74 | 0.45937141 |
| 31 | 6901.32 | 7500 | 6303 | 0.999 | -0.2508519 | -0.969 | 0.33260102 |
| 32 | 6901.32 | 7500 | 6303 | 0.999 | -0.2508519 | -0.969 | 0.33260102 |
| 33 | 6901.32 | 7500 | 6303 | 0.999 | -0.2508519 | -0.969 | 0.33260102 |
| 34 | 6901.32 | 7500 | 6303 | 0.999 | -0.2508519 | -0.969 | 0.33260102 |
| 35 | 6901.32 | 7500 | 6303 | 0.999 | -0.2508519 | -0.969 | 0.33260102 |
| 36 | 6901.32 | 7500 | 6303 | 0.999 | -0.2508519 | -0.969 | 0.33260102 |
| 37 | 6901.32 | 7500 | 6303 | 0.999 | -0.2508519 | -0.969 | 0.33260102 |
| 38 | 6901.32 | 7500 | 6303 | 0.999 | -0.2508519 | -0.969 | 0.33260102 |
| 39 | 6901.32 | 7500 | 6303 | 0.999 | -0.2508519 | -0.969 | 0.33260102 |
| 40 | 6901.32 | 7500 | 6303 | 0.999 | -0.2508519 | -0.969 | 0.33260102 |
| 41 | 6901.32 | 7500 | 6303 | 0.999 | -0.2508519 | -0.969 | 0.33260102 |
| 42 | 6901.32 | 7500 | 6303 | 0.999 | -0.2508519 | -0.969 | 0.33260102 |
| 43 | 6901.32 | 7500 | 6303 | 0.999 | -0.2508519 | -0.969 | 0.33260102 |
| 44 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 45 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 46 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 47 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 48 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 49 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 50 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 51 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 52 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 53 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 54 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 55 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 56 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 57 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 58 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 59 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 4 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 5 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 6 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 7 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 8 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 9 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 10 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 11 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 12 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 13 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 14 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 15 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 16 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 17 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 18 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 19 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 20 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 21 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 22 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 23 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 24 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 25 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 26 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 27 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 28 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 29 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 30 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 31 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 32 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 33 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 34 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 35 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 36 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 37 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 38 | 234.27 | 254 | 214 | 0.999 | -0.2472177 | -0.74 | 0.45949415 |
| 39 | 107.74 | 117 | 99 | 0.999 | -0.2410081 | -0.716 | 0.47411965 |
| 40 | 107.74 | 117 | 99 | 0.999 | -0.2410081 | -0.716 | 0.47411965 |
| 41 | | | | | | | |
| 42 | 1022.17 | 1107 | 937 | 0.999 | -0.2405343 | -0.929 | 0.35310181 |
| 43 | 1022.17 | 1107 | 937 | 0.999 | -0.2405343 | -0.929 | 0.35310181 |
| 44 | 3123.29 | 3380 | 2867 | 0.999 | -0.2374813 | -0.778 | 0.43684888 |
| 45 | 3122.71 | 3378 | 2867 | 0.999 | -0.2366274 | -0.776 | 0.43784626 |
| 46 | 3122.71 | 3378 | 2867 | 0.999 | -0.2366274 | -0.776 | 0.43784626 |
| 47 | 3122.71 | 3378 | 2867 | 0.999 | -0.2366274 | -0.776 | 0.43784626 |
| 48 | 3122.71 | 3378 | 2867 | 0.999 | -0.2366274 | -0.776 | 0.43784626 |
| 49 | 3122.71 | 3378 | 2867 | 0.999 | -0.2366274 | -0.776 | 0.43784626 |
| 50 | 3122.71 | 3378 | 2867 | 0.999 | -0.2366274 | -0.776 | 0.43784626 |
| 51 | 3122.71 | 3378 | 2867 | 0.999 | -0.2366274 | -0.776 | 0.43784626 |
| 52 | 3122.71 | 3378 | 2867 | 0.999 | -0.2366274 | -0.776 | 0.43784626 |
| 53 | 3122.71 | 3378 | 2867 | 0.999 | -0.2366274 | -0.776 | 0.43784626 |
| 54 | 3122.71 | 3378 | 2867 | 0.999 | -0.2366274 | -0.776 | 0.43784626 |
| 55 | 3122.71 | 3378 | 2867 | 0.999 | -0.2366274 | -0.776 | 0.43784626 |
| 56 | 3122.71 | 3378 | 2867 | 0.999 | -0.2366274 | -0.776 | 0.43784626 |
| 57 | 3122.71 | 3378 | 2867 | 0.999 | -0.2366274 | -0.776 | 0.43784626 |
| 58 | 3122.71 | 3378 | 2867 | 0.999 | -0.2366274 | -0.776 | 0.43784626 |
| 59 | 3122.71 | 3378 | 2867 | 0.999 | -0.2366274 | -0.776 | 0.43784626 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 3135.3 | 3389 | 2881 | 0.999 | -0.23429 | -0.768 | 0.44255331 |
| 4 | 3135.3 | 3389 | 2881 | 0.999 | -0.23429 | -0.768 | 0.44255331 |
| 5 | 3135.3 | 3389 | 2881 | 0.999 | -0.23429 | -0.768 | 0.44255331 |
| 6 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 7 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 8 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 9 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 10 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 11 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 12 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 13 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 14 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 15 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 16 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 17 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 18 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 19 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 20 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 21 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 22 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 23 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 24 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 25 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 26 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 27 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 28 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 29 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 30 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 31 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 32 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 33 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 34 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 35 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 36 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 37 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 38 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 39 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 40 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 41 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 42 | 68.22 | 74 | 63 | 1 | -0.2321734 | -0.131 | 0.89568917 |
| 43 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 44 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 45 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 46 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 47 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 48 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 49 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 50 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 51 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 52 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 53 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 54 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 55 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 56 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 57 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 58 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 59 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 4 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 5 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 6 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 7 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 8 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 9 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 10 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 11 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 12 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 13 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 14 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 15 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 16 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 17 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 18 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 19 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 20 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 21 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 22 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 23 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 24 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 25 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 26 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 27 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 28 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 29 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 30 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 31 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 32 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 33 | 1002.22 | 1082 | 923 | 0.999 | -0.2292979 | -0.882 | 0.37779 |
| 34 | 6278.7 | 6767 | 5791 | 0.999 | -0.2247039 | -0.92 | 0.3575076 |
| 35 | 6278.7 | 6767 | 5791 | 0.999 | -0.2247039 | -0.92 | 0.3575076 |
| 36 | 6278.7 | 6767 | 5791 | 0.999 | -0.2247039 | -0.92 | 0.3575076 |
| 37 | 6278.7 | 6767 | 5791 | 0.999 | -0.2247039 | -0.92 | 0.3575076 |
| 38 | 6278.7 | 6767 | 5791 | 0.999 | -0.2247039 | -0.92 | 0.3575076 |
| 39 | 6278.7 | 6767 | 5791 | 0.999 | -0.2247039 | -0.92 | 0.3575076 |
| 40 | 6278.7 | 6767 | 5791 | 0.999 | -0.2247039 | -0.92 | 0.3575076 |
| 41 | 6278.7 | 6767 | 5791 | 0.999 | -0.2247039 | -0.92 | 0.3575076 |
| 42 | 6278.7 | 6767 | 5791 | 0.999 | -0.2247039 | -0.92 | 0.3575076 |
| 43 | 6278.7 | 6767 | 5791 | 0.999 | -0.2247039 | -0.92 | 0.3575076 |
| 44 | 6278.7 | 6767 | 5791 | 0.999 | -0.2247039 | -0.92 | 0.3575076 |
| 45 | 6278.7 | 6767 | 5791 | 0.999 | -0.2247039 | -0.92 | 0.3575076 |
| 46 | 6278.7 | 6767 | 5791 | 0.999 | -0.2247039 | -0.92 | 0.3575076 |
| 47 | 6278.7 | 6767 | 5791 | 0.999 | -0.2247039 | -0.92 | 0.3575076 |
| 48 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 49 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 50 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 51 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 52 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 53 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 54 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 55 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 56 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 57 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 58 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 59 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 4 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 5 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 6 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 7 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 8 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 9 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 10 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 11 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 12 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 13 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 14 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 15 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 16 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 17 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 18 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 19 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 20 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 21 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 22 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 23 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 24 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 25 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 26 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 27 | 168.39 | 181 | 156 | 0.999 | -0.2144437 | -0.63 | 0.52868577 |
| 28 | 69.34 | 74 | 64 | 1 | -0.2094534 | -0.124 | 0.9013188 |
| 29 | | | | | | | |
| 30 | 197 | 211 | 183 | 0.999 | -0.2053994 | -0.563 | 0.57337155 |
| 31 | 192.15 | 205 | 179 | 1 | -0.1956643 | -0.536 | 0.59161889 |
| 32 | 192.15 | 205 | 179 | 1 | -0.1956643 | -0.536 | 0.59161889 |
| 33 | 192.15 | 205 | 179 | 1 | -0.1956643 | -0.536 | 0.59161889 |
| 34 | 192.15 | 205 | 179 | 1 | -0.1956643 | -0.536 | 0.59161889 |
| 35 | 192.15 | 205 | 179 | 1 | -0.1956643 | -0.536 | 0.59161889 |
| 36 | 192.15 | 205 | 179 | 1 | -0.1956643 | -0.536 | 0.59161889 |
| 37 | 192.15 | 205 | 179 | 1 | -0.1956643 | -0.536 | 0.59161889 |
| 38 | 192.15 | 205 | 179 | 1 | -0.1956643 | -0.536 | 0.59161889 |
| 39 | 192.15 | 205 | 179 | 1 | -0.1956643 | -0.536 | 0.59161889 |
| 40 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 41 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 42 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 43 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 44 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 45 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 46 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 47 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 48 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 49 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 50 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 51 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 52 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 53 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 54 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 55 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 56 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 57 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 58 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 59 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 |
| 60 | | | | | | | |

| | | | | | | | | |
|----|---------|------|------|-------|------------|--------|------------|--|
| 1 | | | | | | | | |
| 2 | | | | | | | | |
| 3 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 | |
| 4 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 | |
| 5 | 66.42 | 71 | 62 | 1 | -0.1955508 | -0.144 | 0.88527875 | |
| 6 | 2539.04 | 2705 | 2373 | 0.999 | -0.1889165 | -0.524 | 0.60007218 | |
| 7 | 326.79 | 347 | 306 | 0.999 | -0.181404 | -0.613 | 0.53988147 | |
| 8 | 326.79 | 347 | 306 | 0.999 | -0.181404 | -0.613 | 0.53988147 | |
| 9 | 326.79 | 347 | 306 | 0.999 | -0.181404 | -0.613 | 0.53988147 | |
| 10 | 326.79 | 347 | 306 | 0.999 | -0.181404 | -0.613 | 0.53988147 | |
| 11 | 326.79 | 347 | 306 | 0.999 | -0.181404 | -0.613 | 0.53988147 | |
| 12 | 326.79 | 347 | 306 | 0.999 | -0.181404 | -0.613 | 0.53988147 | |
| 13 | 326.79 | 347 | 306 | 0.999 | -0.181404 | -0.613 | 0.53988147 | |
| 14 | 326.79 | 347 | 306 | 0.999 | -0.181404 | -0.613 | 0.53988147 | |
| 15 | 326.79 | 347 | 306 | 0.999 | -0.181404 | -0.613 | 0.53988147 | |
| 16 | 326.79 | 347 | 306 | 0.999 | -0.181404 | -0.613 | 0.53988147 | |
| 17 | 326.79 | 347 | 306 | 0.999 | -0.181404 | -0.613 | 0.53988147 | |
| 18 | 326.79 | 347 | 306 | 0.999 | -0.181404 | -0.613 | 0.53988147 | |
| 19 | 326.79 | 347 | 306 | 0.999 | -0.181404 | -0.613 | 0.53988147 | |
| 20 | 326.79 | 347 | 306 | 0.999 | -0.181404 | -0.613 | 0.53988147 | |
| 21 | 326.79 | 347 | 306 | 0.999 | -0.181404 | -0.613 | 0.53988147 | |
| 22 | 326.79 | 347 | 306 | 0.999 | -0.181404 | -0.613 | 0.53988147 | |
| 23 | 326.79 | 347 | 306 | 0.999 | -0.181404 | -0.613 | 0.53988147 | |
| 24 | 326.79 | 347 | 306 | 0.999 | -0.181404 | -0.613 | 0.53988147 | |
| 25 | 326.79 | 347 | 306 | 0.999 | -0.181404 | -0.613 | 0.53988147 | |
| 26 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 27 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 28 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 29 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 30 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 31 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 32 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 33 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 34 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 35 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 36 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 37 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 38 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 39 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 40 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 41 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 42 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 43 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 44 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 45 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 46 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 47 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 48 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 49 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 50 | 220.39 | 234 | 207 | 1 | -0.1768778 | -0.157 | 0.87513213 | |
| 51 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 | |
| 52 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 | |
| 53 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 | |
| 54 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 | |
| 55 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 | |
| 56 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 | |
| 57 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 | |
| 58 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 | |
| 59 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 | |
| 60 | | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 4 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 5 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 6 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 7 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 8 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 9 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 10 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 11 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 12 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 13 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 14 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 15 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 16 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 17 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 18 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 19 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 20 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 21 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 22 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 23 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 24 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 25 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 26 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 27 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 28 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 29 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 30 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 31 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 32 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 33 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 34 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 35 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 36 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 37 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 38 | 204.01 | 216 | 192 | 0.999 | -0.169925 | -0.504 | 0.61408312 |
| 39 | 233.46 | 247 | 220 | 0.999 | -0.1670075 | -0.507 | 0.61220945 |
| 40 | 233.46 | 247 | 220 | 0.999 | -0.1670075 | -0.507 | 0.61220945 |
| 41 | 233.46 | 247 | 220 | 0.999 | -0.1670075 | -0.507 | 0.61220945 |
| 42 | 233.46 | 247 | 220 | 0.999 | -0.1670075 | -0.507 | 0.61220945 |
| 43 | 233.46 | 247 | 220 | 0.999 | -0.1670075 | -0.507 | 0.61220945 |
| 44 | 233.46 | 247 | 220 | 0.999 | -0.1670075 | -0.507 | 0.61220945 |
| 45 | 233.46 | 247 | 220 | 0.999 | -0.1670075 | -0.507 | 0.61220945 |
| 46 | 233.46 | 247 | 220 | 0.999 | -0.1670075 | -0.507 | 0.61220945 |
| 47 | 233.46 | 247 | 220 | 0.999 | -0.1670075 | -0.507 | 0.61220945 |
| 48 | 233.46 | 247 | 220 | 0.999 | -0.1670075 | -0.507 | 0.61220945 |
| 49 | 233.46 | 247 | 220 | 0.999 | -0.1670075 | -0.507 | 0.61220945 |
| 50 | 233.46 | 247 | 220 | 0.999 | -0.1670075 | -0.507 | 0.61220945 |
| 51 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 52 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 53 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 54 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 55 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 56 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 57 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 58 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 59 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 4 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 5 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 6 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 7 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 8 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 9 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 10 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 11 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 12 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 13 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 14 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 15 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 16 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 17 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 18 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 19 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 20 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 21 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 22 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 23 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 24 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 25 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 26 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 27 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 28 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 29 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 30 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 31 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 32 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 33 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 34 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 35 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 36 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 37 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 38 | 51.83 | 55 | 49 | 1 | -0.1666499 | -0.368 | 0.71321265 |
| 39 | 1733.99 | 1810 | 1658 | 0.999 | -0.1265457 | -0.455 | 0.64893761 |
| 40 | 116.02 | 121 | 111 | 1 | -0.1244474 | -0.354 | 0.72348885 |
| 41 | 116.02 | 121 | 111 | 1 | -0.1244474 | -0.354 | 0.72348885 |
| 42 | 116.02 | 121 | 111 | 1 | -0.1244474 | -0.354 | 0.72348885 |
| 43 | 109.35 | 114 | 105 | 1 | -0.1186445 | -0.316 | 0.75199545 |
| 44 | 109.35 | 114 | 105 | 1 | -0.1186445 | -0.316 | 0.75199545 |
| 45 | 109.35 | 114 | 105 | 1 | -0.1186445 | -0.316 | 0.75199545 |
| 46 | 109.35 | 114 | 105 | 1 | -0.1186445 | -0.316 | 0.75199545 |
| 47 | 109.35 | 114 | 105 | 1 | -0.1186445 | -0.316 | 0.75199545 |
| 48 | 122.05 | 127 | 117 | 1 | -0.11832 | -0.359 | 0.71963611 |
| 49 | 122.05 | 127 | 117 | 1 | -0.11832 | -0.359 | 0.71963611 |
| 50 | 122.05 | 127 | 117 | 1 | -0.11832 | -0.359 | 0.71963611 |
| 51 | 122.05 | 127 | 117 | 1 | -0.11832 | -0.359 | 0.71963611 |
| 52 | 122.05 | 127 | 117 | 1 | -0.11832 | -0.359 | 0.71963611 |
| 53 | 122.05 | 127 | 117 | 1 | -0.11832 | -0.359 | 0.71963611 |
| 54 | 122.05 | 127 | 117 | 1 | -0.11832 | -0.359 | 0.71963611 |
| 55 | 122.05 | 127 | 117 | 1 | -0.11832 | -0.359 | 0.71963611 |
| 56 | 122.05 | 127 | 117 | 1 | -0.11832 | -0.359 | 0.71963611 |
| 57 | 122.05 | 127 | 117 | 1 | -0.11832 | -0.359 | 0.71963611 |
| 58 | 122.05 | 127 | 117 | 1 | -0.11832 | -0.359 | 0.71963611 |
| 59 | 122.05 | 127 | 117 | 1 | -0.11832 | -0.359 | 0.71963611 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 23384.98 | 24342 | 22427 | 0.999 | -0.1182111 | -0.49 | 0.62417227 |
| 4 | 23384.98 | 24342 | 22427 | 0.999 | -0.1182111 | -0.49 | 0.62417227 |
| 5 | 23384.98 | 24342 | 22427 | 0.999 | -0.1182111 | -0.49 | 0.62417227 |
| 6 | 23384.98 | 24342 | 22427 | 0.999 | -0.1182111 | -0.49 | 0.62417227 |
| 7 | 23384.98 | 24342 | 22427 | 0.999 | -0.1182111 | -0.49 | 0.62417227 |
| 8 | 23384.98 | 24342 | 22427 | 0.999 | -0.1182111 | -0.49 | 0.62417227 |
| 9 | 23384.98 | 24342 | 22427 | 0.999 | -0.1182111 | -0.49 | 0.62417227 |
| 10 | 23384.98 | 24342 | 22427 | 0.999 | -0.1182111 | -0.49 | 0.62417227 |
| 11 | 23384.98 | 24342 | 22427 | 0.999 | -0.1182111 | -0.49 | 0.62417227 |
| 12 | 23384.98 | 24342 | 22427 | 0.999 | -0.1182111 | -0.49 | 0.62417227 |
| 13 | 23443.87 | 24394 | 22494 | 0.999 | -0.1169861 | -0.485 | 0.62792869 |
| 14 | 88.92 | 92 | 85 | 1 | -0.114171 | -0.28 | 0.77917697 |
| 15 | 88.92 | 92 | 85 | 1 | -0.114171 | -0.28 | 0.77917697 |
| 16 | 88.73 | 92 | 85 | 1 | -0.114171 | -0.261 | 0.79421214 |
| 17 | 88.73 | 92 | 85 | 1 | -0.114171 | -0.261 | 0.79421214 |
| 18 | 88.73 | 92 | 85 | 1 | -0.114171 | -0.261 | 0.79421214 |
| 19 | 88.73 | 92 | 85 | 1 | -0.114171 | -0.261 | 0.79421214 |
| 20 | 88.73 | 92 | 85 | 1 | -0.114171 | -0.261 | 0.79421214 |
| 21 | 88.73 | 92 | 85 | 1 | -0.114171 | -0.261 | 0.79421214 |
| 22 | 88.73 | 92 | 85 | 1 | -0.114171 | -0.261 | 0.79421214 |
| 23 | 88.73 | 92 | 85 | 1 | -0.114171 | -0.261 | 0.79421214 |
| 24 | 88.73 | 92 | 85 | 1 | -0.114171 | -0.261 | 0.79421214 |
| 25 | 343.45 | 357 | 330 | 1 | -0.113458 | -0.357 | 0.72111184 |
| 26 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 27 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 28 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 29 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 30 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 31 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 32 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 33 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 34 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 35 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 36 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 37 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 38 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 39 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 40 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 41 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 42 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 43 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 44 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 45 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 46 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 47 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 48 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 49 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 50 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 51 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 52 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 53 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 54 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 55 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 56 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 57 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 58 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 59 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 |
| 60 | | | | | | | |

| | | | | | | | | |
|----|--------|-----|-----|---|------------|--------|------------|--|
| 1 | | | | | | | | |
| 2 | | | | | | | | |
| 3 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 4 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 5 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 6 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 7 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 8 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 9 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 10 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 11 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 12 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 13 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 14 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 15 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 16 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 17 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 18 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 19 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 20 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 21 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 22 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 23 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 24 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 25 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 26 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 27 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 28 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 29 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 30 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 31 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 32 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 33 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 34 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 35 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 36 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 37 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 38 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 39 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 40 | 125.84 | 130 | 121 | 1 | -0.1035046 | -0.256 | 0.79780294 | |
| 41 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 | |
| 42 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 | |
| 43 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 | |
| 44 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 | |
| 45 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 | |
| 46 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 | |
| 47 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 | |
| 48 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 | |
| 49 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 | |
| 50 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 | |
| 51 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 | |
| 52 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 | |
| 53 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 | |
| 54 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 | |
| 55 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 | |
| 56 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 | |
| 57 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 | |
| 58 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 | |
| 59 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 | |
| 60 | | | | | | | | |

| | | | | | | | |
|----|---------|------|------|---|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 |
| 4 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 |
| 5 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 |
| 6 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 |
| 7 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 |
| 8 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 |
| 9 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 |
| 10 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 |
| 11 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 |
| 12 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 |
| 13 | 102.31 | 106 | 99 | 1 | -0.0985638 | -0.274 | 0.78389874 |
| 14 | 1041.03 | 1075 | 1007 | 1 | -0.094273 | -0.336 | 0.73654309 |
| 15 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 16 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 17 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 18 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 19 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 20 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 21 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 22 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 23 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 24 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 25 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 26 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 27 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 28 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 29 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 30 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 31 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 32 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 33 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 34 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 35 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 36 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 37 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 38 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 39 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 40 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 41 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 42 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 43 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 44 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 45 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 46 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 47 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 48 | 2813.12 | 2903 | 2724 | 1 | -0.0918179 | -0.332 | 0.73971749 |
| 49 | 110.69 | 114 | 107 | 1 | -0.091423 | -0.237 | 0.81250559 |
| 50 | 2842.26 | 2931 | 2753 | 1 | -0.0903884 | -0.33 | 0.74155968 |
| 51 | 2842.26 | 2931 | 2753 | 1 | -0.0903884 | -0.33 | 0.74155968 |
| 52 | 2842.26 | 2931 | 2753 | 1 | -0.0903884 | -0.33 | 0.74155968 |
| 53 | 2842.26 | 2931 | 2753 | 1 | -0.0903884 | -0.33 | 0.74155968 |
| 54 | 2842.26 | 2931 | 2753 | 1 | -0.0903884 | -0.33 | 0.74155968 |
| 55 | 2842.26 | 2931 | 2753 | 1 | -0.0903884 | -0.33 | 0.74155968 |
| 56 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 57 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 58 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 59 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|---|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 4 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 5 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 6 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 7 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 8 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 9 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 10 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 11 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 12 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 13 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 14 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 15 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 16 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 17 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 18 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 19 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 20 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 21 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 22 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 23 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 24 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 25 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 26 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 27 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 28 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 29 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 30 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 31 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 32 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 33 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 34 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 35 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 36 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 37 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 38 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 39 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 40 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 41 | 95.93 | 99 | 93 | 1 | -0.0901978 | -0.225 | 0.82178739 |
| 42 | 2819.23 | 2907 | 2731 | 1 | -0.0901018 | -0.327 | 0.7435407 |
| 43 | 2819.23 | 2907 | 2731 | 1 | -0.0901018 | -0.327 | 0.7435407 |
| 44 | 676.25 | 697 | 655 | 1 | -0.0896637 | -0.322 | 0.74747518 |
| 45 | 676.25 | 697 | 655 | 1 | -0.0896637 | -0.322 | 0.74747518 |
| 46 | 676.25 | 697 | 655 | 1 | -0.0896637 | -0.322 | 0.74747518 |
| 47 | 676.25 | 697 | 655 | 1 | -0.0896637 | -0.322 | 0.74747518 |
| 48 | 676.25 | 697 | 655 | 1 | -0.0896637 | -0.322 | 0.74747518 |
| 49 | 182.57 | 188 | 177 | 1 | -0.0869833 | -0.269 | 0.78810939 |
| 50 | 182.57 | 188 | 177 | 1 | -0.0869833 | -0.269 | 0.78810939 |
| 51 | 182.57 | 188 | 177 | 1 | -0.0869833 | -0.269 | 0.78810939 |
| 52 | 186.56 | 192 | 181 | 1 | -0.0851166 | -0.261 | 0.79376626 |
| 53 | 96.62 | 99 | 94 | 1 | -0.0747678 | -0.195 | 0.84528898 |
| 54 | 96.62 | 99 | 94 | 1 | -0.0747678 | -0.195 | 0.84528898 |
| 55 | 96.62 | 99 | 94 | 1 | -0.0747678 | -0.195 | 0.84528898 |
| 56 | 96.62 | 99 | 94 | 1 | -0.0747678 | -0.195 | 0.84528898 |
| 57 | 96.62 | 99 | 94 | 1 | -0.0747678 | -0.195 | 0.84528898 |
| 58 | 96.62 | 99 | 94 | 1 | -0.0747678 | -0.195 | 0.84528898 |
| 59 | 96.62 | 99 | 94 | 1 | -0.0747678 | -0.195 | 0.84528898 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|---|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 96.62 | 99 | 94 | 1 | -0.0747678 | -0.195 | 0.84528898 |
| 4 | 96.62 | 99 | 94 | 1 | -0.0747678 | -0.195 | 0.84528898 |
| 5 | 96.62 | 99 | 94 | 1 | -0.0747678 | -0.195 | 0.84528898 |
| 6 | 96.62 | 99 | 94 | 1 | -0.0747678 | -0.195 | 0.84528898 |
| 7 | 96.62 | 99 | 94 | 1 | -0.0747678 | -0.195 | 0.84528898 |
| 8 | 96.62 | 99 | 94 | 1 | -0.0747678 | -0.195 | 0.84528898 |
| 9 | 96.62 | 99 | 94 | 1 | -0.0747678 | -0.195 | 0.84528898 |
| 10 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 11 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 12 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 13 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 14 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 15 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 16 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 17 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 18 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 19 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 20 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 21 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 22 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 23 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 24 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 25 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 26 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 27 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 28 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 29 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 30 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 31 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 32 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 33 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 34 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 35 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 36 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 37 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 38 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 39 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 40 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 41 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 42 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 43 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 44 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 45 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 46 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 47 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 48 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 49 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 50 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 51 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 52 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 53 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 54 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 55 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 56 | 3830.32 | 3926 | 3735 | 1 | -0.0719519 | -0.256 | 0.79827963 |
| 57 | 177.95 | 182 | 174 | 1 | -0.0648511 | -0.255 | 0.79889255 |
| 58 | 177.65 | 182 | 174 | 1 | -0.0648511 | -0.212 | 0.83202546 |
| 59 | | | | | | | |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|------|------|---|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 771.21 | 787 | 755 | 1 | -0.059887 | -0.209 | 0.83434281 |
| 4 | 771.21 | 787 | 755 | 1 | -0.059887 | -0.209 | 0.83434281 |
| 5 | 771.21 | 787 | 755 | 1 | -0.059887 | -0.209 | 0.83434281 |
| 6 | 771.21 | 787 | 755 | 1 | -0.059887 | -0.209 | 0.83434281 |
| 7 | 771.21 | 787 | 755 | 1 | -0.059887 | -0.209 | 0.83434281 |
| 8 | 771.21 | 787 | 755 | 1 | -0.059887 | -0.209 | 0.83434281 |
| 9 | 771.21 | 787 | 755 | 1 | -0.059887 | -0.209 | 0.83434281 |
| 10 | 771.21 | 787 | 755 | 1 | -0.059887 | -0.209 | 0.83434281 |
| 11 | 771.21 | 787 | 755 | 1 | -0.059887 | -0.209 | 0.83434281 |
| 12 | 771.21 | 787 | 755 | 1 | -0.059887 | -0.209 | 0.83434281 |
| 13 | 771.21 | 787 | 755 | 1 | -0.059887 | -0.209 | 0.83434281 |
| 14 | 454.99 | 464 | 447 | 1 | -0.05385 | -0.185 | 0.8529207 |
| 15 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 16 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 17 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 18 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 19 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 20 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 21 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 22 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 23 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 24 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 25 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 26 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 27 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 28 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 29 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 30 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 31 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 32 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 33 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 34 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 35 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 36 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 37 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 38 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 39 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 40 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 41 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 42 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 43 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 44 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 45 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 46 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 47 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 48 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 49 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 50 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 51 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 52 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 53 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 54 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 55 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 56 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 57 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 58 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 59 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|---|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 4 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 5 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 6 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 7 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 8 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 9 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 10 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 11 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 12 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 13 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 14 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 15 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 16 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 17 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 18 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 19 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 20 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 21 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 22 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 23 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 24 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 25 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 26 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 27 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 28 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 29 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 30 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 31 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 32 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 33 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 34 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 35 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 36 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 37 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 38 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 39 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 40 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 41 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 42 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 43 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 44 | 4456 | 4533 | 4379 | 1 | -0.0498647 | -0.175 | 0.86112732 |
| 45 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 46 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 47 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 48 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 49 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 50 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 51 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 52 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 53 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 54 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 55 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 56 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 57 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 58 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 59 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|---|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 4 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 5 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 6 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 7 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 8 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 9 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 10 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 11 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 12 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 13 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 14 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 15 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 16 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 17 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 18 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 19 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 20 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 21 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 22 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 23 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 24 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 25 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 26 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 27 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 28 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 29 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 30 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 31 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 32 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 33 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 34 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 35 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 36 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 37 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 38 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 39 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 40 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 41 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 42 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 43 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 44 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 45 | 61.5 | 62 | 60 | 1 | -0.0473057 | -0.084 | 0.93269215 |
| 46 | 9468.94 | 9605 | 9333 | 1 | -0.0414447 | -0.16 | 0.87272051 |
| 47 | 9468.94 | 9605 | 9333 | 1 | -0.0414447 | -0.16 | 0.87272051 |
| 48 | 9477.23 | 9613 | 9341 | 1 | -0.0414097 | -0.16 | 0.8729265 |
| 49 | 9477.23 | 9613 | 9341 | 1 | -0.0414097 | -0.16 | 0.8729265 |
| 50 | 9477.23 | 9613 | 9341 | 1 | -0.0414097 | -0.16 | 0.8729265 |
| 51 | 387.8 | 391 | 384 | 1 | -0.0260623 | -0.086 | 0.9317648 |
| 52 | 387.8 | 391 | 384 | 1 | -0.0260623 | -0.086 | 0.9317648 |
| 53 | 387.8 | 391 | 384 | 1 | -0.0260623 | -0.086 | 0.9317648 |
| 54 | 387.8 | 391 | 384 | 1 | -0.0260623 | -0.086 | 0.9317648 |
| 55 | 387.8 | 391 | 384 | 1 | -0.0260623 | -0.086 | 0.9317648 |
| 56 | 387.8 | 391 | 384 | 1 | -0.0260623 | -0.086 | 0.9317648 |
| 57 | 387.8 | 391 | 384 | 1 | -0.0260623 | -0.086 | 0.9317648 |
| 58 | 387.8 | 391 | 384 | 1 | -0.0260623 | -0.086 | 0.9317648 |
| 59 | 387.8 | 391 | 384 | 1 | -0.0260623 | -0.086 | 0.9317648 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|---|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 563.55 | 569 | 559 | 1 | -0.0255804 | -0.096 | 0.92374405 |
| 4 | 565.2 | 570 | 560 | 1 | -0.0255351 | -0.098 | 0.92160242 |
| 5 | 565.2 | 570 | 560 | 1 | -0.0255351 | -0.098 | 0.92160242 |
| 6 | 565.2 | 570 | 560 | 1 | -0.0255351 | -0.098 | 0.92160242 |
| 7 | 565.2 | 570 | 560 | 1 | -0.0255351 | -0.098 | 0.92160242 |
| 8 | 565.2 | 570 | 560 | 1 | -0.0255351 | -0.098 | 0.92160242 |
| 9 | 565.2 | 570 | 560 | 1 | -0.0255351 | -0.098 | 0.92160242 |
| 10 | 565.2 | 570 | 560 | 1 | -0.0255351 | -0.098 | 0.92160242 |
| 11 | 567.35 | 572 | 562 | 1 | -0.025445 | -0.094 | 0.92520655 |
| 12 | 567.35 | 572 | 562 | 1 | -0.025445 | -0.094 | 0.92520655 |
| 13 | 567.35 | 572 | 562 | 1 | -0.025445 | -0.094 | 0.92520655 |
| 14 | 567.35 | 572 | 562 | 1 | -0.025445 | -0.094 | 0.92520655 |
| 15 | 567.35 | 572 | 562 | 1 | -0.025445 | -0.094 | 0.92520655 |
| 16 | 567.35 | 572 | 562 | 1 | -0.025445 | -0.094 | 0.92520655 |
| 17 | 567.35 | 572 | 562 | 1 | -0.025445 | -0.094 | 0.92520655 |
| 18 | 567.35 | 572 | 562 | 1 | -0.025445 | -0.094 | 0.92520655 |
| 19 | 567.35 | 572 | 562 | 1 | -0.025445 | -0.094 | 0.92520655 |
| 20 | 567.35 | 572 | 562 | 1 | -0.025445 | -0.094 | 0.92520655 |
| 21 | 567.35 | 572 | 562 | 1 | -0.025445 | -0.094 | 0.92520655 |
| 22 | 899.51 | 907 | 892 | 1 | -0.0240588 | -0.091 | 0.92787414 |
| 23 | 914.7 | 922 | 907 | 1 | -0.0236642 | -0.09 | 0.92849191 |
| 24 | 914.7 | 922 | 907 | 1 | -0.0236642 | -0.09 | 0.92849191 |
| 25 | 914.7 | 922 | 907 | 1 | -0.0236642 | -0.09 | 0.92849191 |
| 26 | 914.7 | 922 | 907 | 1 | -0.0236642 | -0.09 | 0.92849191 |
| 27 | 914.7 | 922 | 907 | 1 | -0.0236642 | -0.09 | 0.92849191 |
| 28 | 914.7 | 922 | 907 | 1 | -0.0236642 | -0.09 | 0.92849191 |
| 29 | 914.7 | 922 | 907 | 1 | -0.0236642 | -0.09 | 0.92849191 |
| 30 | 914.7 | 922 | 907 | 1 | -0.0236642 | -0.09 | 0.92849191 |
| 31 | 914.7 | 922 | 907 | 1 | -0.0236642 | -0.09 | 0.92849191 |
| 32 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 33 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 34 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 35 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 36 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 37 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 38 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 39 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 40 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 41 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 42 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 43 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 44 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 45 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 46 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 47 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 48 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 49 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 50 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 51 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 52 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 53 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 54 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 55 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 56 | 9590.49 | 9661 | 9519 | 1 | -0.0213625 | -0.089 | 0.92881018 |
| 57 | 9327.76 | 9389 | 9267 | 1 | -0.0188691 | -0.079 | 0.93684212 |
| 58 | 9327.76 | 9389 | 9267 | 1 | -0.0188691 | -0.079 | 0.93684212 |
| 59 | 9327.76 | 9389 | 9267 | 1 | -0.0188691 | -0.079 | 0.93684212 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|---|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 9330.28 | 9391 | 9270 | 1 | -0.0187095 | -0.078 | 0.93755891 |
| 4 | 9330.28 | 9391 | 9270 | 1 | -0.0187095 | -0.078 | 0.93755891 |
| 5 | 9330.28 | 9391 | 9270 | 1 | -0.0187095 | -0.078 | 0.93755891 |
| 6 | 243.3 | 245 | 242 | 1 | -0.0177747 | -0.047 | 0.96233375 |
| 7 | 287.67 | 289 | 286 | 1 | -0.0150543 | -0.025 | 0.98000584 |
| 8 | 324.32 | 326 | 323 | 1 | -0.0133378 | -0.048 | 0.96155246 |
| 9 | 324.32 | 326 | 323 | 1 | -0.0133378 | -0.048 | 0.96155246 |
| 10 | 242.53 | 243 | 241 | 1 | -0.0119232 | -0.033 | 0.97335829 |
| 11 | 242.53 | 243 | 241 | 1 | -0.0119232 | -0.033 | 0.97335829 |
| 12 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 13 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 14 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 15 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 16 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 17 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 18 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 19 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 20 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 21 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 22 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 23 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 24 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 25 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 26 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 27 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 28 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 29 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 30 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 31 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 32 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 33 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 34 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 35 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 36 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 37 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 38 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 39 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 40 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 41 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 42 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 43 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 44 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 45 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 46 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 47 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 48 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 49 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 50 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 51 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 52 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 53 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 54 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 55 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 56 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 57 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 58 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 59 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 |
| 60 | | | | | | | |

| | | | | | | | | |
|----|--------|-----|-----|---|------------|--------|------------|--|
| 1 | | | | | | | | |
| 2 | | | | | | | | |
| 3 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 | |
| 4 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 | |
| 5 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 | |
| 6 | 126.22 | 127 | 126 | 1 | -0.0114048 | -0.037 | 0.97014762 | |
| 7 | 133.31 | 134 | 133 | 1 | -0.0108068 | -0.003 | 0.99758817 | |
| 8 | 133.31 | 134 | 133 | 1 | -0.0108068 | -0.003 | 0.99758817 | |
| 9 | 133.31 | 134 | 133 | 1 | -0.0108068 | -0.003 | 0.99758817 | |
| 10 | 133.31 | 134 | 133 | 1 | -0.0108068 | -0.003 | 0.99758817 | |
| 11 | 133.31 | 134 | 133 | 1 | -0.0108068 | -0.003 | 0.99758817 | |
| 12 | 133.31 | 134 | 133 | 1 | -0.0108068 | -0.003 | 0.99758817 | |
| 13 | 133.31 | 134 | 133 | 1 | -0.0108068 | -0.003 | 0.99758817 | |
| 14 | 133.31 | 134 | 133 | 1 | -0.0108068 | -0.003 | 0.99758817 | |
| 15 | 153.44 | 154 | 153 | 1 | -0.0093987 | -0.031 | 0.97526153 | |
| 16 | 153.29 | 154 | 153 | 1 | -0.0093987 | -0.022 | 0.98223593 | |
| 17 | 493.69 | 495 | 493 | 1 | -0.0058409 | -0.009 | 0.99246682 | |
| 18 | 493.69 | 495 | 493 | 1 | -0.0058409 | -0.009 | 0.99246682 | |
| 19 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 20 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 21 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 22 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 23 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 24 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 25 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 26 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 27 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 28 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 29 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 30 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 31 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 32 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 33 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 34 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 35 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 36 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 37 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 38 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 39 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 40 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 41 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 42 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 43 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 44 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 45 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 46 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 47 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 48 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 49 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 50 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 51 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 52 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 53 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 54 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 55 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 56 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 57 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 58 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 59 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 | |
| 60 | | | | | | | | |

| | | | | | | | |
|----|---------|------|------|---|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 |
| 4 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 |
| 5 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 |
| 6 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 |
| 7 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 |
| 8 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 |
| 9 | 283.61 | 284 | 283 | 1 | -0.0050889 | -0.014 | 0.98870936 |
| 10 | 6646.44 | 6652 | 6641 | 1 | -0.0023877 | -0.011 | 0.99140382 |
| 11 | 6646.44 | 6652 | 6641 | 1 | -0.0023877 | -0.011 | 0.99140382 |
| 12 | 6646.44 | 6652 | 6641 | 1 | -0.0023877 | -0.011 | 0.99140382 |
| 13 | 6646.44 | 6652 | 6641 | 1 | -0.0023877 | -0.011 | 0.99140382 |
| 14 | 6646.44 | 6652 | 6641 | 1 | -0.0023877 | -0.011 | 0.99140382 |
| 15 | 6646.44 | 6652 | 6641 | 1 | -0.0023877 | -0.011 | 0.99140382 |
| 16 | 6646.44 | 6652 | 6641 | 1 | -0.0023877 | -0.011 | 0.99140382 |
| 17 | 6646.44 | 6652 | 6641 | 1 | -0.0023877 | -0.011 | 0.99140382 |
| 18 | 6646.44 | 6652 | 6641 | 1 | -0.0023877 | -0.011 | 0.99140382 |
| 19 | 6646.44 | 6652 | 6641 | 1 | -0.0023877 | -0.011 | 0.99140382 |
| 20 | 6646.44 | 6652 | 6641 | 1 | -0.0023877 | -0.011 | 0.99140382 |
| 21 | 6646.44 | 6652 | 6641 | 1 | -0.0023877 | -0.011 | 0.99140382 |
| 22 | 6714.73 | 6717 | 6712 | 1 | -0.0010743 | -0.005 | 0.99606538 |
| 23 | 6714.73 | 6717 | 6712 | 1 | -0.0010743 | -0.005 | 0.99606538 |
| 24 | 6754.36 | 6755 | 6754 | 1 | -0.0002136 | -0.001 | 0.99929018 |
| 25 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 26 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 27 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 28 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 29 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 30 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 31 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 32 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 33 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 34 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 35 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 36 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 37 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 38 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 39 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 40 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 41 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 42 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 43 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 44 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 45 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 46 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 47 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 48 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 49 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 50 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 51 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 52 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 53 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 54 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 55 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 56 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 57 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 58 | 167.97 | 168 | 168 | 1 | 0 | -0.02 | 0.98434459 |
| 59 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|---|---|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 4 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 5 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 6 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 7 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 8 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 9 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 10 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 11 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 12 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 13 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 14 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 15 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 16 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 17 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 18 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 19 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 20 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 21 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 22 | 153.13 | 153 | 153 | 1 | 0 | -0.012 | 0.99009238 |
| 23 | 309.19 | 309 | 309 | 1 | 0 | 0.01 | 0.99177196 |
| 24 | 164.94 | 165 | 165 | 1 | 0 | -0.004 | 0.99654392 |
| 25 | 164.94 | 165 | 165 | 1 | 0 | -0.004 | 0.99654392 |
| 26 | 164.94 | 165 | 165 | 1 | 0 | -0.004 | 0.99654392 |
| 27 | 164.94 | 165 | 165 | 1 | 0 | -0.004 | 0.99654392 |
| 28 | 164.94 | 165 | 165 | 1 | 0 | -0.004 | 0.99654392 |
| 29 | 164.94 | 165 | 165 | 1 | 0 | -0.004 | 0.99654392 |
| 30 | 164.94 | 165 | 165 | 1 | 0 | -0.004 | 0.99654392 |
| 31 | 164.94 | 165 | 165 | 1 | 0 | -0.004 | 0.99654392 |
| 32 | 164.94 | 165 | 165 | 1 | 0 | -0.004 | 0.99654392 |
| 33 | 164.94 | 165 | 165 | 1 | 0 | -0.004 | 0.99654392 |
| 34 | 164.94 | 165 | 165 | 1 | 0 | -0.004 | 0.99654392 |
| 35 | 164.94 | 165 | 165 | 1 | 0 | -0.004 | 0.99654392 |
| 36 | 164.94 | 165 | 165 | 1 | 0 | -0.004 | 0.99654392 |
| 37 | 164.94 | 165 | 165 | 1 | 0 | -0.004 | 0.99654392 |
| 38 | 164.94 | 165 | 165 | 1 | 0 | -0.004 | 0.99654392 |
| 39 | 164.94 | 165 | 165 | 1 | 0 | -0.004 | 0.99654392 |
| 40 | 164.94 | 165 | 165 | 1 | 0 | -0.004 | 0.99654392 |
| 41 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 |
| 42 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 |
| 43 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 |
| 44 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 |
| 45 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 |
| 46 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 |
| 47 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 |
| 48 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 |
| 49 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 |
| 50 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 |
| 51 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 |
| 52 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 |
| 53 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 |
| 54 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 |
| 55 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 |
| 56 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 |
| 57 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 |
| 58 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 |
| 59 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 |
| 60 | | | | | | | |

| | | | | | | | | |
|----|---------|------|------|---|------------|--------|------------|--|
| 1 | | | | | | | | |
| 2 | | | | | | | | |
| 3 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 4 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 5 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 6 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 7 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 8 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 9 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 10 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 11 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 12 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 13 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 14 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 15 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 16 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 17 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 18 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 19 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 20 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 21 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 22 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 23 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 24 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 25 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 26 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 27 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 28 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 29 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 30 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 31 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 32 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 33 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 34 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 35 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 36 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 37 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 38 | 57.16 | 57 | 57 | 1 | 0 | -0.003 | 0.99743997 | |
| 39 | 68.91 | 69 | 69 | 1 | 0 | 0.002 | 0.99831271 | |
| 40 | 1377.91 | 1378 | 1378 | 1 | 0 | 0.001 | 0.99896527 | |
| 41 | 1372.67 | 1372 | 1373 | 1 | 0.00105114 | 0.001 | 0.99909475 | |
| 42 | 1372.67 | 1372 | 1373 | 1 | 0.00105114 | 0.001 | 0.99909475 | |
| 43 | 1372.67 | 1372 | 1373 | 1 | 0.00105114 | 0.001 | 0.99909475 | |
| 44 | 1372.67 | 1372 | 1373 | 1 | 0.00105114 | 0.001 | 0.99909475 | |
| 45 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 | |
| 46 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 | |
| 47 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 | |
| 48 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 | |
| 49 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 | |
| 50 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 | |
| 51 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 | |
| 52 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 | |
| 53 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 | |
| 54 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 | |
| 55 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 | |
| 56 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 | |
| 57 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 | |
| 58 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 | |
| 59 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 | |
| 60 | | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|---|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 |
| 4 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 |
| 5 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 |
| 6 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 |
| 7 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 |
| 8 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 |
| 9 | 5121.43 | 5114 | 5129 | 1 | 0.00422541 | 0.014 | 0.98860733 |
| 10 | 655.89 | 655 | 657 | 1 | 0.00439846 | 0.02 | 0.98425623 |
| 11 | 13597.03 | 13572 | 13622 | 1 | 0.0053052 | 0.022 | 0.98275741 |
| 12 | 13597.03 | 13572 | 13622 | 1 | 0.0053052 | 0.022 | 0.98275741 |
| 13 | 13597.03 | 13572 | 13622 | 1 | 0.0053052 | 0.022 | 0.98275741 |
| 14 | 13597.03 | 13572 | 13622 | 1 | 0.0053052 | 0.022 | 0.98275741 |
| 15 | 13597.03 | 13572 | 13622 | 1 | 0.0053052 | 0.022 | 0.98275741 |
| 16 | 13597.03 | 13572 | 13622 | 1 | 0.0053052 | 0.022 | 0.98275741 |
| 17 | 13597.03 | 13572 | 13622 | 1 | 0.0053052 | 0.022 | 0.98275741 |
| 18 | 13597.03 | 13572 | 13622 | 1 | 0.0053052 | 0.022 | 0.98275741 |
| 19 | 13597.03 | 13572 | 13622 | 1 | 0.0053052 | 0.022 | 0.98275741 |
| 20 | 13597.03 | 13572 | 13622 | 1 | 0.0053052 | 0.022 | 0.98275741 |
| 21 | 13597.03 | 13572 | 13622 | 1 | 0.0053052 | 0.022 | 0.98275741 |
| 22 | 13597.03 | 13572 | 13622 | 1 | 0.0053052 | 0.022 | 0.98275741 |
| 23 | 12378.44 | 12349 | 12408 | 1 | 0.00687637 | 0.019 | 0.9846047 |
| 24 | 12378.44 | 12349 | 12408 | 1 | 0.00687637 | 0.019 | 0.9846047 |
| 25 | 12378.44 | 12349 | 12408 | 1 | 0.00687637 | 0.019 | 0.9846047 |
| 26 | 12378.44 | 12349 | 12408 | 1 | 0.00687637 | 0.019 | 0.9846047 |
| 27 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 28 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 29 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 30 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 31 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 32 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 33 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 34 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 35 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 36 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 37 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 38 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 39 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 40 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 41 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 42 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 43 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 44 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 45 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 46 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 47 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 48 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 49 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 50 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 51 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 52 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 53 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 54 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 55 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 56 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 57 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 58 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 59 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|---|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 4 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 5 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 6 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 7 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 8 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 9 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 10 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 11 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 12 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 13 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 14 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 15 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 16 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 17 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 18 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 19 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 20 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 21 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 22 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 23 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 24 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 25 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 26 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 27 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 28 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 29 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 30 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 31 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 32 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 33 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 34 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 35 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 36 | 12368.38 | 12338 | 12398 | 1 | 0.00699886 | 0.02 | 0.98415557 |
| 37 | | | | | | | |
| 38 | 192.38 | 192 | 193 | 1 | 0.00749454 | 0.011 | 0.99145863 |
| 39 | 192.38 | 192 | 193 | 1 | 0.00749454 | 0.011 | 0.99145863 |
| 40 | 192.38 | 192 | 193 | 1 | 0.00749454 | 0.011 | 0.99145863 |
| 41 | 192.38 | 192 | 193 | 1 | 0.00749454 | 0.011 | 0.99145863 |
| 42 | 192.38 | 192 | 193 | 1 | 0.00749454 | 0.011 | 0.99145863 |
| 43 | 192.38 | 192 | 193 | 1 | 0.00749454 | 0.011 | 0.99145863 |
| 44 | 192.38 | 192 | 193 | 1 | 0.00749454 | 0.011 | 0.99145863 |
| 45 | 192.38 | 192 | 193 | 1 | 0.00749454 | 0.011 | 0.99145863 |
| 46 | 192.38 | 192 | 193 | 1 | 0.00749454 | 0.011 | 0.99145863 |
| 47 | 192.38 | 192 | 193 | 1 | 0.00749454 | 0.011 | 0.99145863 |
| 48 | 192.38 | 192 | 193 | 1 | 0.00749454 | 0.011 | 0.99145863 |
| 49 | | | | | | | |
| 50 | 12403.15 | 12369 | 12437 | 1 | 0.00790966 | 0.022 | 0.98218512 |
| 51 | 12006.09 | 11972 | 12040 | 1 | 0.00817121 | 0.033 | 0.97360442 |
| 52 | 12006.09 | 11972 | 12040 | 1 | 0.00817121 | 0.033 | 0.97360442 |
| 53 | | | | | | | |
| 54 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 55 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 56 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 57 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 58 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 59 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----------|--------|--------|---|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 4 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 5 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 6 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 7 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 8 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 9 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 10 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 11 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 12 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 13 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 14 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 15 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 16 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 17 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 18 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 19 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 20 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 21 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 22 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 23 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 24 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 25 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 26 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 27 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 28 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 29 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 30 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 31 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 32 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 33 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 34 | 11999.97 | 11965 | 12035 | 1 | 0.00841574 | 0.034 | 0.97317471 |
| 35 | 135.32 | 135 | 136 | 1 | 0.01064724 | 0.045 | 0.96378541 |
| 36 | 255.17 | 254 | 256 | 1 | 0.01131531 | 0.031 | 0.97536035 |
| 37 | 102.42 | 102 | 103 | 1 | 0.01407519 | 0.032 | 0.97472456 |
| 38 | 102.42 | 102 | 103 | 1 | 0.01407519 | 0.032 | 0.97472456 |
| 39 | 102.42 | 102 | 103 | 1 | 0.01407519 | 0.032 | 0.97472456 |
| 40 | 102.42 | 102 | 103 | 1 | 0.01407519 | 0.032 | 0.97472456 |
| 41 | 102.42 | 102 | 103 | 1 | 0.01407519 | 0.032 | 0.97472456 |
| 42 | 102.42 | 102 | 103 | 1 | 0.01407519 | 0.032 | 0.97472456 |
| 43 | 102.42 | 102 | 103 | 1 | 0.01407519 | 0.032 | 0.97472456 |
| 44 | 102.42 | 102 | 103 | 1 | 0.01407519 | 0.032 | 0.97472456 |
| 45 | 102.42 | 102 | 103 | 1 | 0.01407519 | 0.032 | 0.97472456 |
| 46 | 102.42 | 102 | 103 | 1 | 0.01407519 | 0.032 | 0.97472456 |
| 47 | 102.42 | 102 | 103 | 1 | 0.01407519 | 0.032 | 0.97472456 |
| 48 | 102.42 | 102 | 103 | 1 | 0.01407519 | 0.032 | 0.97472456 |
| 49 | 102.42 | 102 | 103 | 1 | 0.01407519 | 0.032 | 0.97472456 |
| 50 | 102.42 | 102 | 103 | 1 | 0.01407519 | 0.032 | 0.97472456 |
| 51 | 102.42 | 102 | 103 | 1 | 0.01407519 | 0.032 | 0.97472456 |
| 52 | 101102.75 | 100591 | 101614 | 1 | 0.01459795 | 0.057 | 0.95461652 |
| 53 | 101102.75 | 100591 | 101614 | 1 | 0.01459795 | 0.057 | 0.95461652 |
| 54 | 101102.75 | 100591 | 101614 | 1 | 0.01459795 | 0.057 | 0.95461652 |
| 55 | 101102.75 | 100591 | 101614 | 1 | 0.01459795 | 0.057 | 0.95461652 |
| 56 | 101102.75 | 100591 | 101614 | 1 | 0.01459795 | 0.057 | 0.95461652 |
| 57 | 101102.75 | 100591 | 101614 | 1 | 0.01459795 | 0.057 | 0.95461652 |
| 58 | 101102.75 | 100591 | 101614 | 1 | 0.01459795 | 0.057 | 0.95461652 |
| 59 | 101102.75 | 100591 | 101614 | 1 | 0.01459795 | 0.057 | 0.95461652 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----------|--------|--------|---|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 104791.64 | 104071 | 105512 | 1 | 0.01983898 | 0.077 | 0.93839807 |
| 4 | 64.76 | 64 | 65 | 1 | 0.02236781 | 0.045 | 0.96402514 |
| 5 | 64.76 | 64 | 65 | 1 | 0.02236781 | 0.045 | 0.96402514 |
| 6 | 64.76 | 64 | 65 | 1 | 0.02236781 | 0.045 | 0.96402514 |
| 7 | 64.76 | 64 | 65 | 1 | 0.02236781 | 0.045 | 0.96402514 |
| 8 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 9 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 10 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 11 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 12 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 13 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 14 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 15 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 16 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 17 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 18 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 19 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 20 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 21 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 22 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 23 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 24 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 25 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 26 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 27 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 28 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 29 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 30 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 31 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 32 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 33 | 63.43 | 63 | 64 | 1 | 0.02272008 | 0.047 | 0.9626818 |
| 34 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 35 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 36 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 37 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 38 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 39 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 40 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 41 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 42 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 43 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 44 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 45 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 46 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 47 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 48 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 49 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 50 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 51 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 52 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 53 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 54 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 55 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 56 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 57 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 58 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 59 | 898.71 | 890 | 907 | 1 | 0.02729721 | 0.093 | 0.92575378 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|---|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 4 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 5 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 6 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 7 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 8 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 9 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 10 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 11 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 12 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 13 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 14 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 15 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 16 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 17 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 18 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 19 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 20 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 21 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 22 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 23 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 24 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 25 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 26 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 27 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 28 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 29 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 30 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 31 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 32 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 33 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 34 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 35 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 36 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 37 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 38 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 39 | 426.17 | 421 | 431 | 1 | 0.03386764 | 0.113 | 0.91022944 |
| 40 | 690.48 | 682 | 699 | 1 | 0.03552072 | 0.137 | 0.89139279 |
| 41 | 690.48 | 682 | 699 | 1 | 0.03552072 | 0.137 | 0.89139279 |
| 42 | 690.48 | 682 | 699 | 1 | 0.03552072 | 0.137 | 0.89139279 |
| 43 | 1233.17 | 1218 | 1249 | 1 | 0.03625934 | 0.09 | 0.92820804 |
| 44 | 311.48 | 307 | 315 | 1 | 0.03711317 | 0.1 | 0.92051986 |
| 45 | 311.48 | 307 | 315 | 1 | 0.03711317 | 0.1 | 0.92051986 |
| 46 | 311.48 | 307 | 315 | 1 | 0.03711317 | 0.1 | 0.92051986 |
| 47 | 426.32 | 421 | 432 | 1 | 0.03721108 | 0.116 | 0.90750036 |
| 48 | 426.32 | 421 | 432 | 1 | 0.03721108 | 0.116 | 0.90750036 |
| 49 | 301.91 | 298 | 306 | 1 | 0.03821932 | 0.096 | 0.92346825 |
| 50 | 301.91 | 298 | 306 | 1 | 0.03821932 | 0.096 | 0.92346825 |
| 51 | 301.91 | 298 | 306 | 1 | 0.03821932 | 0.096 | 0.92346825 |
| 52 | 301.91 | 298 | 306 | 1 | 0.03821932 | 0.096 | 0.92346825 |
| 53 | 301.91 | 298 | 306 | 1 | 0.03821932 | 0.096 | 0.92346825 |
| 54 | 301.91 | 298 | 306 | 1 | 0.03821932 | 0.096 | 0.92346825 |
| 55 | 64.76 | 64 | 66 | 1 | 0.04439412 | 0.127 | 0.89859678 |
| 56 | 10687.68 | 10506 | 10869 | 1 | 0.04900572 | 0.187 | 0.85154364 |
| 57 | 10687.68 | 10506 | 10869 | 1 | 0.04900572 | 0.187 | 0.85154364 |
| 58 | 10687.68 | 10506 | 10869 | 1 | 0.04900572 | 0.187 | 0.85154364 |
| 59 | 10687.68 | 10506 | 10869 | 1 | 0.04900572 | 0.187 | 0.85154364 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----------|--------|--------|---|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 10687.68 | 10506 | 10869 | 1 | 0.04900572 | 0.187 | 0.85154364 |
| 4 | 10687.68 | 10506 | 10869 | 1 | 0.04900572 | 0.187 | 0.85154364 |
| 5 | 10687.68 | 10506 | 10869 | 1 | 0.04900572 | 0.187 | 0.85154364 |
| 6 | 10687.68 | 10506 | 10869 | 1 | 0.04900572 | 0.187 | 0.85154364 |
| 7 | 1169.81 | 1147 | 1192 | 1 | 0.05551884 | 0.129 | 0.89740317 |
| 8 | | | | | | | |
| 9 | 297059.98 | 290668 | 303452 | 1 | 0.06209608 | 0.25 | 0.80278167 |
| 10 | 297059.98 | 290668 | 303452 | 1 | 0.06209608 | 0.25 | 0.80278167 |
| 11 | 297059.98 | 290668 | 303452 | 1 | 0.06209608 | 0.25 | 0.80278167 |
| 12 | 297059.98 | 290668 | 303452 | 1 | 0.06209608 | 0.25 | 0.80278167 |
| 13 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 14 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 15 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 16 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 17 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 18 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 19 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 20 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 21 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 22 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 23 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 24 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 25 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 26 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 27 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 28 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 29 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 30 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 31 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 32 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 33 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 34 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 35 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 36 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 37 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 38 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 39 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 40 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 41 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 42 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 43 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 44 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 45 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 46 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 47 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 48 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 49 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 50 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 51 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 52 | 104941.8 | 102484 | 107399 | 1 | 0.06758187 | 0.282 | 0.77831564 |
| 53 | | | | | | | |
| 54 | 277.05 | 271 | 284 | 1 | 0.06759808 | 0.177 | 0.85928993 |
| 55 | 277.32 | 271 | 284 | 1 | 0.06759808 | 0.168 | 0.86640625 |
| 56 | 191.44 | 187 | 196 | 1 | 0.06781538 | 0.201 | 0.8407443 |
| 57 | 191.44 | 187 | 196 | 1 | 0.06781538 | 0.201 | 0.8407443 |
| 58 | 191.44 | 187 | 196 | 1 | 0.06781538 | 0.201 | 0.8407443 |
| 59 | 191.44 | 187 | 196 | 1 | 0.06781538 | 0.201 | 0.8407443 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|--------|--------|---|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 4 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 5 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 6 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 7 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 8 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 9 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 10 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 11 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 12 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 13 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 14 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 15 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 16 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 17 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 18 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 19 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 20 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 21 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 22 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 23 | 276.71 | 270 | 283 | 1 | 0.06784265 | 0.176 | 0.86013823 |
| 24 | 113431.6 | 110592 | 116271 | 1 | 0.07224428 | 0.295 | 0.76780776 |
| 25 | 113431.6 | 110592 | 116271 | 1 | 0.07224428 | 0.295 | 0.76780776 |
| 26 | 113431.6 | 110592 | 116271 | 1 | 0.07224428 | 0.295 | 0.76780776 |
| 27 | 113431.6 | 110592 | 116271 | 1 | 0.07224428 | 0.295 | 0.76780776 |
| 28 | 113431.6 | 110592 | 116271 | 1 | 0.07224428 | 0.295 | 0.76780776 |
| 29 | 113431.6 | 110592 | 116271 | 1 | 0.07224428 | 0.295 | 0.76780776 |
| 30 | 113431.6 | 110592 | 116271 | 1 | 0.07224428 | 0.295 | 0.76780776 |
| 31 | 113431.6 | 110592 | 116271 | 1 | 0.07224428 | 0.295 | 0.76780776 |
| 32 | 113431.6 | 110592 | 116271 | 1 | 0.07224428 | 0.295 | 0.76780776 |
| 33 | 113431.6 | 110592 | 116271 | 1 | 0.07224428 | 0.295 | 0.76780776 |
| 34 | 113431.6 | 110592 | 116271 | 1 | 0.07224428 | 0.295 | 0.76780776 |
| 35 | 113431.6 | 110592 | 116271 | 1 | 0.07224428 | 0.295 | 0.76780776 |
| 36 | 113431.6 | 110592 | 116271 | 1 | 0.07224428 | 0.295 | 0.76780776 |
| 37 | 113431.6 | 110592 | 116271 | 1 | 0.07224428 | 0.295 | 0.76780776 |
| 38 | 113431.6 | 110592 | 116271 | 1 | 0.07224428 | 0.295 | 0.76780776 |
| 39 | 113431.6 | 110592 | 116271 | 1 | 0.07224428 | 0.295 | 0.76780776 |
| 40 | 108.6 | 106 | 112 | 1 | 0.07943447 | 0.232 | 0.81671774 |
| 41 | 108.6 | 106 | 112 | 1 | 0.07943447 | 0.232 | 0.81671774 |
| 42 | 108.6 | 106 | 112 | 1 | 0.07943447 | 0.232 | 0.81671774 |
| 43 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 44 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 45 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 46 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 47 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 48 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 49 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 50 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 51 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 52 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 53 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 54 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 55 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 56 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 57 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 58 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 59 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|---|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 4 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 5 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 6 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 7 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 8 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 9 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 10 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 11 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 12 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 13 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 14 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 15 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 16 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 17 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 18 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 19 | 6704.36 | 6501 | 6907 | 1 | 0.08739757 | 0.333 | 0.73887466 |
| 20 | 2339.63 | 2265 | 2414 | 1 | 0.09191463 | 0.342 | 0.73253296 |
| 21 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 22 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 23 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 24 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 25 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 26 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 27 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 28 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 29 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 30 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 31 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 32 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 33 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 34 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 35 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 36 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 37 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 38 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 39 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 40 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 41 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 42 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 43 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 44 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 45 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 46 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 47 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 48 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 49 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 50 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 51 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 52 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 53 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 54 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 55 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 56 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 57 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 58 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 59 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|------|-------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 4 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 5 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 6 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 7 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 8 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 9 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 10 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 11 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 12 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 13 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 14 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 15 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 16 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 17 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 18 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 19 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 20 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 21 | 4477.91 | 4335 | 4621 | 1 | 0.0921731 | 0.246 | 0.80583733 |
| 22 | 4486.82 | 4343 | 4631 | 1 | 0.0926318 | 0.247 | 0.8051075 |
| 23 | 2329.79 | 2253 | 2406 | 1 | 0.09478933 | 0.352 | 0.72478177 |
| 24 | 2329.79 | 2253 | 2406 | 1 | 0.09478933 | 0.352 | 0.72478177 |
| 25 | 2329.79 | 2253 | 2406 | 1 | 0.09478933 | 0.352 | 0.72478177 |
| 26 | 2329.79 | 2253 | 2406 | 1 | 0.09478933 | 0.352 | 0.72478177 |
| 27 | 2329.79 | 2253 | 2406 | 1 | 0.09478933 | 0.352 | 0.72478177 |
| 28 | 2329.79 | 2253 | 2406 | 1 | 0.09478933 | 0.352 | 0.72478177 |
| 29 | 2329.79 | 2253 | 2406 | 1 | 0.09478933 | 0.352 | 0.72478177 |
| 30 | 2329.79 | 2253 | 2406 | 1 | 0.09478933 | 0.352 | 0.72478177 |
| 31 | 2329.79 | 2253 | 2406 | 1 | 0.09478933 | 0.352 | 0.72478177 |
| 32 | 334.44 | 323 | 346 | 1 | 0.09923787 | 0.32 | 0.7490803 |
| 33 | 334.44 | 323 | 346 | 1 | 0.09923787 | 0.32 | 0.7490803 |
| 34 | 334.44 | 323 | 346 | 1 | 0.09923787 | 0.32 | 0.7490803 |
| 35 | 334.44 | 323 | 346 | 1 | 0.09923787 | 0.32 | 0.7490803 |
| 36 | 334.44 | 323 | 346 | 1 | 0.09923787 | 0.32 | 0.7490803 |
| 37 | 334.44 | 323 | 346 | 1 | 0.09923787 | 0.32 | 0.7490803 |
| 38 | 334.44 | 323 | 346 | 1 | 0.09923787 | 0.32 | 0.7490803 |
| 39 | 334.44 | 323 | 346 | 1 | 0.09923787 | 0.32 | 0.7490803 |
| 40 | 1403.77 | 1354 | 1454 | 1 | 0.10279953 | 0.361 | 0.71802608 |
| 41 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 42 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 43 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 44 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 45 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 46 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 47 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 48 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 49 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 50 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 51 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 52 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 53 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 54 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 55 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 56 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 57 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 58 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 59 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 4 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 5 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 6 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 7 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 8 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 9 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 10 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 11 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 12 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 13 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 14 | 10111.89 | 9751 | 10473 | 1.001 | 0.10305268 | 0.395 | 0.69267578 |
| 15 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 16 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 17 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 18 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 19 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 20 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 21 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 22 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 23 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 24 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 25 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 26 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 27 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 28 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 29 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 30 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 31 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 32 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 33 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 34 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 35 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 36 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 37 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 38 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 39 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 40 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 41 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 42 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 43 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 44 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 45 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 46 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 47 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 48 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 49 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 50 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 51 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 52 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 53 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 54 | 214.69 | 207 | 223 | 1 | 0.10741294 | 0.271 | 0.78662955 |
| 55 | 44428.58 | 42728 | 46130 | 1.001 | 0.1105235 | 0.478 | 0.63249088 |
| 56 | 1730.1 | 1660 | 1801 | 1.001 | 0.11761494 | 0.419 | 0.67523204 |
| 57 | 1730.1 | 1660 | 1801 | 1.001 | 0.11761494 | 0.419 | 0.67523204 |
| 58 | 1730.1 | 1660 | 1801 | 1.001 | 0.11761494 | 0.419 | 0.67523204 |
| 59 | 1730.1 | 1660 | 1801 | 1.001 | 0.11761494 | 0.419 | 0.67523204 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 3216.18 | 3080 | 3352 | 1.001 | 0.1220918 | 0.451 | 0.65179224 |
| 4 | 128.52 | 123 | 134 | 1 | 0.12357469 | 0.325 | 0.74501213 |
| 5 | 1179.03 | 1128 | 1230 | 1.001 | 0.12489125 | 0.445 | 0.65648997 |
| 6 | 1179.03 | 1128 | 1230 | 1.001 | 0.12489125 | 0.445 | 0.65648997 |
| 7 | 1179.03 | 1128 | 1230 | 1.001 | 0.12489125 | 0.445 | 0.65648997 |
| 8 | 1179.03 | 1128 | 1230 | 1.001 | 0.12489125 | 0.445 | 0.65648997 |
| 9 | 1179.03 | 1128 | 1230 | 1.001 | 0.12489125 | 0.445 | 0.65648997 |
| 10 | 1179.03 | 1128 | 1230 | 1.001 | 0.12489125 | 0.445 | 0.65648997 |
| 11 | 298.83 | 286 | 312 | 1 | 0.12553088 | 0.435 | 0.66325801 |
| 12 | 298.83 | 286 | 312 | 1 | 0.12553088 | 0.435 | 0.66325801 |
| 13 | 298.83 | 286 | 312 | 1 | 0.12553088 | 0.435 | 0.66325801 |
| 14 | 298.83 | 286 | 312 | 1 | 0.12553088 | 0.435 | 0.66325801 |
| 15 | 298.83 | 286 | 312 | 1 | 0.12553088 | 0.435 | 0.66325801 |
| 16 | 298.83 | 286 | 312 | 1 | 0.12553088 | 0.435 | 0.66325801 |
| 17 | 298.83 | 286 | 312 | 1 | 0.12553088 | 0.435 | 0.66325801 |
| 18 | 298.83 | 286 | 312 | 1 | 0.12553088 | 0.435 | 0.66325801 |
| 19 | 298.83 | 286 | 312 | 1 | 0.12553088 | 0.435 | 0.66325801 |
| 20 | 102.99 | 99 | 108 | 1 | 0.12553088 | 0.364 | 0.71579102 |
| 21 | 102.99 | 99 | 108 | 1 | 0.12553088 | 0.364 | 0.71579102 |
| 22 | 102.99 | 99 | 108 | 1 | 0.12553088 | 0.364 | 0.71579102 |
| 23 | 102.99 | 99 | 108 | 1 | 0.12553088 | 0.364 | 0.71579102 |
| 24 | 102.99 | 99 | 108 | 1 | 0.12553088 | 0.364 | 0.71579102 |
| 25 | 102.99 | 99 | 108 | 1 | 0.12553088 | 0.364 | 0.71579102 |
| 26 | 102.99 | 99 | 108 | 1 | 0.12553088 | 0.364 | 0.71579102 |
| 27 | 300.48 | 287 | 314 | 1.001 | 0.12971382 | 0.437 | 0.662293 |
| 28 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 29 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 30 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 31 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 32 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 33 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 34 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 35 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 36 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 37 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 38 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 39 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 40 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 41 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 42 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 43 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 44 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 45 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 46 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 47 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 48 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 49 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 50 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 51 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 52 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 53 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 54 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 55 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 56 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 57 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 58 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 59 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 4 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 5 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 6 | 298.21 | 285 | 312 | 1.001 | 0.13058411 | 0.447 | 0.65469903 |
| 7 | 52297.91 | 49827 | 54769 | 1.001 | 0.13643182 | 0.577 | 0.56423435 |
| 8 | 52297.91 | 49827 | 54769 | 1.001 | 0.13643182 | 0.577 | 0.56423435 |
| 9 | | | | | | | |
| 10 | 333.04 | 317 | 349 | 1.001 | 0.1387442 | 0.455 | 0.649012 |
| 11 | 333.04 | 317 | 349 | 1.001 | 0.1387442 | 0.455 | 0.649012 |
| 12 | 333.04 | 317 | 349 | 1.001 | 0.1387442 | 0.455 | 0.649012 |
| 13 | 333.04 | 317 | 349 | 1.001 | 0.1387442 | 0.455 | 0.649012 |
| 14 | 333.04 | 317 | 349 | 1.001 | 0.1387442 | 0.455 | 0.649012 |
| 15 | 333.04 | 317 | 349 | 1.001 | 0.1387442 | 0.455 | 0.649012 |
| 16 | 333.04 | 317 | 349 | 1.001 | 0.1387442 | 0.455 | 0.649012 |
| 17 | 333.04 | 317 | 349 | 1.001 | 0.1387442 | 0.455 | 0.649012 |
| 18 | 333.04 | 317 | 349 | 1.001 | 0.1387442 | 0.455 | 0.649012 |
| 19 | 333.04 | 317 | 349 | 1.001 | 0.1387442 | 0.455 | 0.649012 |
| 20 | | | | | | | |
| 21 | 72.37 | 69 | 76 | 1 | 0.13940306 | 0.36 | 0.71890701 |
| 22 | 72.37 | 69 | 76 | 1 | 0.13940306 | 0.36 | 0.71890701 |
| 23 | 72.37 | 69 | 76 | 1 | 0.13940306 | 0.36 | 0.71890701 |
| 24 | 72.37 | 69 | 76 | 1 | 0.13940306 | 0.36 | 0.71890701 |
| 25 | 72.37 | 69 | 76 | 1 | 0.13940306 | 0.36 | 0.71890701 |
| 26 | 72.37 | 69 | 76 | 1 | 0.13940306 | 0.36 | 0.71890701 |
| 27 | 72.37 | 69 | 76 | 1 | 0.13940306 | 0.36 | 0.71890701 |
| 28 | 72.37 | 69 | 76 | 1 | 0.13940306 | 0.36 | 0.71890701 |
| 29 | 72.37 | 69 | 76 | 1 | 0.13940306 | 0.36 | 0.71890701 |
| 30 | 72.37 | 69 | 76 | 1 | 0.13940306 | 0.36 | 0.71890701 |
| 31 | 72.37 | 69 | 76 | 1 | 0.13940306 | 0.36 | 0.71890701 |
| 32 | 72.37 | 69 | 76 | 1 | 0.13940306 | 0.36 | 0.71890701 |
| 33 | 72.37 | 69 | 76 | 1 | 0.13940306 | 0.36 | 0.71890701 |
| 34 | 72.37 | 69 | 76 | 1 | 0.13940306 | 0.36 | 0.71890701 |
| 35 | 72.37 | 69 | 76 | 1 | 0.13940306 | 0.36 | 0.71890701 |
| 36 | 72.37 | 69 | 76 | 1 | 0.13940306 | 0.36 | 0.71890701 |
| 37 | 72.37 | 69 | 76 | 1 | 0.13940306 | 0.36 | 0.71890701 |
| 38 | 72.37 | 69 | 76 | 1 | 0.13940306 | 0.36 | 0.71890701 |
| 39 | 72.37 | 69 | 76 | 1 | 0.13940306 | 0.36 | 0.71890701 |
| 40 | | | | | | | |
| 41 | 81.89 | 78 | 86 | 1 | 0.14086254 | 0.079 | 0.93685001 |
| 42 | 81.89 | 78 | 86 | 1 | 0.14086254 | 0.079 | 0.93685001 |
| 43 | 81.89 | 78 | 86 | 1 | 0.14086254 | 0.079 | 0.93685001 |
| 44 | 81.89 | 78 | 86 | 1 | 0.14086254 | 0.079 | 0.93685001 |
| 45 | 81.89 | 78 | 86 | 1 | 0.14086254 | 0.079 | 0.93685001 |
| 46 | 81.89 | 78 | 86 | 1 | 0.14086254 | 0.079 | 0.93685001 |
| 47 | 81.89 | 78 | 86 | 1 | 0.14086254 | 0.079 | 0.93685001 |
| 48 | 81.89 | 78 | 86 | 1 | 0.14086254 | 0.079 | 0.93685001 |
| 49 | 81.89 | 78 | 86 | 1 | 0.14086254 | 0.079 | 0.93685001 |
| 50 | 81.89 | 78 | 86 | 1 | 0.14086254 | 0.079 | 0.93685001 |
| 51 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 52 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 53 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 54 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 55 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 56 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 57 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 58 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 59 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|------|-------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 4 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 5 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 6 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 7 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 8 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 9 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 10 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 11 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 12 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 13 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 14 | 81.07 | 77 | 85 | 1 | 0.1426044 | 0.082 | 0.93448171 |
| 15 | 156.14 | 148 | 164 | 1 | 0.14809864 | 0.406 | 0.68495341 |
| 16 | 156.14 | 148 | 164 | 1 | 0.14809864 | 0.406 | 0.68495341 |
| 17 | | | | | | | |
| 18 | 7328.15 | 6933 | 7723 | 1.001 | 0.15568161 | 0.592 | 0.55378602 |
| 19 | 7328.15 | 6933 | 7723 | 1.001 | 0.15568161 | 0.592 | 0.55378602 |
| 20 | 7328.15 | 6933 | 7723 | 1.001 | 0.15568161 | 0.592 | 0.55378602 |
| 21 | 7328.15 | 6933 | 7723 | 1.001 | 0.15568161 | 0.592 | 0.55378602 |
| 22 | 7328.15 | 6933 | 7723 | 1.001 | 0.15568161 | 0.592 | 0.55378602 |
| 23 | 71.21 | 67 | 75 | 1 | 0.1627295 | 0.377 | 0.70593412 |
| 24 | | | | | | | |
| 25 | 10326.81 | 9741 | 10913 | 1.001 | 0.16390596 | 0.604 | 0.54561405 |
| 26 | 10326.81 | 9741 | 10913 | 1.001 | 0.16390596 | 0.604 | 0.54561405 |
| 27 | 10326.81 | 9741 | 10913 | 1.001 | 0.16390596 | 0.604 | 0.54561405 |
| 28 | 10326.81 | 9741 | 10913 | 1.001 | 0.16390596 | 0.604 | 0.54561405 |
| 29 | 10326.81 | 9741 | 10913 | 1.001 | 0.16390596 | 0.604 | 0.54561405 |
| 30 | 10326.81 | 9741 | 10913 | 1.001 | 0.16390596 | 0.604 | 0.54561405 |
| 31 | 10326.81 | 9741 | 10913 | 1.001 | 0.16390596 | 0.604 | 0.54561405 |
| 32 | 10326.81 | 9741 | 10913 | 1.001 | 0.16390596 | 0.604 | 0.54561405 |
| 33 | 10326.81 | 9741 | 10913 | 1.001 | 0.16390596 | 0.604 | 0.54561405 |
| 34 | 10326.81 | 9741 | 10913 | 1.001 | 0.16390596 | 0.604 | 0.54561405 |
| 35 | 10326.81 | 9741 | 10913 | 1.001 | 0.16390596 | 0.604 | 0.54561405 |
| 36 | 10326.81 | 9741 | 10913 | 1.001 | 0.16390596 | 0.604 | 0.54561405 |
| 37 | 10326.81 | 9741 | 10913 | 1.001 | 0.16390596 | 0.604 | 0.54561405 |
| 38 | 10326.81 | 9741 | 10913 | 1.001 | 0.16390596 | 0.604 | 0.54561405 |
| 39 | 10349.39 | 9762 | 10937 | 1.001 | 0.16396841 | 0.604 | 0.54602043 |
| 40 | | | | | | | |
| 41 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 42 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 43 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 44 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 45 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 46 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 47 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 48 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 49 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 50 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 51 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 52 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 53 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 54 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 55 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 56 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 57 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 58 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 59 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 4 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 5 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 6 | 6146.58 | 5778 | 6515 | 1.001 | 0.17319497 | 0.666 | 0.50553672 |
| 7 | 339.39 | 319 | 360 | 1.001 | 0.17444048 | 0.649 | 0.51662146 |
| 8 | 339.39 | 319 | 360 | 1.001 | 0.17444048 | 0.649 | 0.51662146 |
| 9 | 339.39 | 319 | 360 | 1.001 | 0.17444048 | 0.649 | 0.51662146 |
| 10 | 339.39 | 319 | 360 | 1.001 | 0.17444048 | 0.649 | 0.51662146 |
| 11 | 339.39 | 319 | 360 | 1.001 | 0.17444048 | 0.649 | 0.51662146 |
| 12 | 339.39 | 319 | 360 | 1.001 | 0.17444048 | 0.649 | 0.51662146 |
| 13 | 339.39 | 319 | 360 | 1.001 | 0.17444048 | 0.649 | 0.51662146 |
| 14 | 281.14 | 264 | 298 | 1.001 | 0.1747744 | 0.534 | 0.59319238 |
| 15 | 281.14 | 264 | 298 | 1.001 | 0.1747744 | 0.534 | 0.59319238 |
| 16 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 17 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 18 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 19 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 20 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 21 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 22 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 23 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 24 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 25 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 26 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 27 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 28 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 29 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 30 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 31 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 32 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 33 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 34 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 35 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 36 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 37 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 38 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 39 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 40 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 41 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 42 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 43 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 44 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 45 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 46 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 47 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 48 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 49 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 50 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 51 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 52 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 53 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 54 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 55 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 56 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 57 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 58 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 59 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 338.78 | 318 | 360 | 1.001 | 0.17897014 | 0.659 | 0.50981709 |
| 4 | 348.16 | 326 | 370 | 1.001 | 0.18265331 | 0.625 | 0.53224409 |
| 5 | 348.16 | 326 | 370 | 1.001 | 0.18265331 | 0.625 | 0.53224409 |
| 6 | 348.16 | 326 | 370 | 1.001 | 0.18265331 | 0.625 | 0.53224409 |
| 7 | 348.16 | 326 | 370 | 1.001 | 0.18265331 | 0.625 | 0.53224409 |
| 8 | 253.77 | 237 | 271 | 1.001 | 0.19340579 | 0.6 | 0.54872062 |
| 9 | 6459.69 | 6027 | 6892 | 1.001 | 0.19348264 | 0.75 | 0.4532886 |
| 10 | 6459.69 | 6027 | 6892 | 1.001 | 0.19348264 | 0.75 | 0.4532886 |
| 11 | 6459.69 | 6027 | 6892 | 1.001 | 0.19348264 | 0.75 | 0.4532886 |
| 12 | 6459.69 | 6027 | 6892 | 1.001 | 0.19348264 | 0.75 | 0.4532886 |
| 13 | 6459.69 | 6027 | 6892 | 1.001 | 0.19348264 | 0.75 | 0.4532886 |
| 14 | 6459.69 | 6027 | 6892 | 1.001 | 0.19348264 | 0.75 | 0.4532886 |
| 15 | 6459.69 | 6027 | 6892 | 1.001 | 0.19348264 | 0.75 | 0.4532886 |
| 16 | 6097.27 | 5675 | 6519 | 1.001 | 0.20003028 | 0.772 | 0.43985612 |
| 17 | 321.48 | 299 | 344 | 1.001 | 0.20226308 | 0.686 | 0.49279709 |
| 18 | 321.48 | 299 | 344 | 1.001 | 0.20226308 | 0.686 | 0.49279709 |
| 19 | 321.48 | 299 | 344 | 1.001 | 0.20226308 | 0.686 | 0.49279709 |
| 20 | 321.48 | 299 | 344 | 1.001 | 0.20226308 | 0.686 | 0.49279709 |
| 21 | 321.48 | 299 | 344 | 1.001 | 0.20226308 | 0.686 | 0.49279709 |
| 22 | 321.48 | 299 | 344 | 1.001 | 0.20226308 | 0.686 | 0.49279709 |
| 23 | 321.48 | 299 | 344 | 1.001 | 0.20226308 | 0.686 | 0.49279709 |
| 24 | 321.48 | 299 | 344 | 1.001 | 0.20226308 | 0.686 | 0.49279709 |
| 25 | 321.48 | 299 | 344 | 1.001 | 0.20226308 | 0.686 | 0.49279709 |
| 26 | 321.48 | 299 | 344 | 1.001 | 0.20226308 | 0.686 | 0.49279709 |
| 27 | 321.48 | 299 | 344 | 1.001 | 0.20226308 | 0.686 | 0.49279709 |
| 28 | 321.48 | 299 | 344 | 1.001 | 0.20226308 | 0.686 | 0.49279709 |
| 29 | 321.48 | 299 | 344 | 1.001 | 0.20226308 | 0.686 | 0.49279709 |
| 30 | 321.48 | 299 | 344 | 1.001 | 0.20226308 | 0.686 | 0.49279709 |
| 31 | 8828.39 | 8202 | 9455 | 1.001 | 0.20510171 | 0.788 | 0.43096626 |
| 32 | 8828.39 | 8202 | 9455 | 1.001 | 0.20510171 | 0.788 | 0.43096626 |
| 33 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 34 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 35 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 36 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 37 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 38 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 39 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 40 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 41 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 42 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 43 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 44 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 45 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 46 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 47 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 48 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 49 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 50 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 51 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 52 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 53 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 54 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 55 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 56 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 57 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 58 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 59 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 4 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 5 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 6 | 320.81 | 298 | 344 | 1.001 | 0.20709623 | 0.695 | 0.48723533 |
| 7 | 55.15 | 51 | 59 | 1 | 0.21021771 | 0.471 | 0.63787349 |
| 8 | 156.59 | 145 | 168 | 1.001 | 0.21240833 | 0.554 | 0.57976616 |
| 9 | 52.81 | 49 | 57 | 1 | 0.21818017 | 0.461 | 0.64493481 |
| 10 | 236.49 | 217 | 256 | 1.001 | 0.23844877 | 0.706 | 0.48005851 |
| 11 | 236.49 | 217 | 256 | 1.001 | 0.23844877 | 0.706 | 0.48005851 |
| 12 | 236.49 | 217 | 256 | 1.001 | 0.23844877 | 0.706 | 0.48005851 |
| 13 | 236.49 | 217 | 256 | 1.001 | 0.23844877 | 0.706 | 0.48005851 |
| 14 | 236.49 | 217 | 256 | 1.001 | 0.23844877 | 0.706 | 0.48005851 |
| 15 | 236.49 | 217 | 256 | 1.001 | 0.23844877 | 0.706 | 0.48005851 |
| 16 | 236.49 | 217 | 256 | 1.001 | 0.23844877 | 0.706 | 0.48005851 |
| 17 | 236.49 | 217 | 256 | 1.001 | 0.23844877 | 0.706 | 0.48005851 |
| 18 | 236.49 | 217 | 256 | 1.001 | 0.23844877 | 0.706 | 0.48005851 |
| 19 | 236.49 | 217 | 256 | 1.001 | 0.23844877 | 0.706 | 0.48005851 |
| 20 | 236.49 | 217 | 256 | 1.001 | 0.23844877 | 0.706 | 0.48005851 |
| 21 | 236.49 | 217 | 256 | 1.001 | 0.23844877 | 0.706 | 0.48005851 |
| 22 | 160.2 | 147 | 174 | 1.001 | 0.24327115 | 0.623 | 0.53310376 |
| 23 | 5602.86 | 5103 | 6102 | 1.001 | 0.25793654 | 1.016 | 0.30978276 |
| 24 | 223.27 | 203 | 243 | 1.001 | 0.25947659 | 0.91 | 0.36304605 |
| 25 | 223.27 | 203 | 243 | 1.001 | 0.25947659 | 0.91 | 0.36304605 |
| 26 | 223.27 | 203 | 243 | 1.001 | 0.25947659 | 0.91 | 0.36304605 |
| 27 | 581.23 | 528 | 634 | 1.001 | 0.26394491 | 0.982 | 0.32633394 |
| 28 | 581.23 | 528 | 634 | 1.001 | 0.26394491 | 0.982 | 0.32633394 |
| 29 | 581.23 | 528 | 634 | 1.001 | 0.26394491 | 0.982 | 0.32633394 |
| 30 | 581.23 | 528 | 634 | 1.001 | 0.26394491 | 0.982 | 0.32633394 |
| 31 | 581.23 | 528 | 634 | 1.001 | 0.26394491 | 0.982 | 0.32633394 |
| 32 | 581.23 | 528 | 634 | 1.001 | 0.26394491 | 0.982 | 0.32633394 |
| 33 | 581.23 | 528 | 634 | 1.001 | 0.26394491 | 0.982 | 0.32633394 |
| 34 | 581.23 | 528 | 634 | 1.001 | 0.26394491 | 0.982 | 0.32633394 |
| 35 | 581.23 | 528 | 634 | 1.001 | 0.26394491 | 0.982 | 0.32633394 |
| 36 | 581.23 | 528 | 634 | 1.001 | 0.26394491 | 0.982 | 0.32633394 |
| 37 | 581.23 | 528 | 634 | 1.001 | 0.26394491 | 0.982 | 0.32633394 |
| 38 | 581.23 | 528 | 634 | 1.001 | 0.26394491 | 0.982 | 0.32633394 |
| 39 | 581.23 | 528 | 634 | 1.001 | 0.26394491 | 0.982 | 0.32633394 |
| 40 | 487.58 | 443 | 532 | 1.001 | 0.26411955 | 0.75 | 0.45334014 |
| 41 | 157.14 | 142 | 172 | 1.001 | 0.27651764 | 0.81 | 0.41797895 |
| 42 | 157.14 | 142 | 172 | 1.001 | 0.27651764 | 0.81 | 0.41797895 |
| 43 | 157.14 | 142 | 172 | 1.001 | 0.27651764 | 0.81 | 0.41797895 |
| 44 | 651.94 | 589 | 716 | 1.001 | 0.28169195 | 1.071 | 0.28425623 |
| 45 | 651.94 | 589 | 716 | 1.001 | 0.28169195 | 1.071 | 0.28425623 |
| 46 | 651.94 | 589 | 716 | 1.001 | 0.28169195 | 1.071 | 0.28425623 |
| 47 | 218.97 | 197 | 241 | 1.001 | 0.29083752 | 0.969 | 0.33245343 |
| 48 | 2785.92 | 2506 | 3066 | 1.001 | 0.29097128 | 0.975 | 0.32963083 |
| 49 | 2785.92 | 2506 | 3066 | 1.001 | 0.29097128 | 0.975 | 0.32963083 |
| 50 | 2785.92 | 2506 | 3066 | 1.001 | 0.29097128 | 0.975 | 0.32963083 |
| 51 | 2785.92 | 2506 | 3066 | 1.001 | 0.29097128 | 0.975 | 0.32963083 |
| 52 | 2785.92 | 2506 | 3066 | 1.001 | 0.29097128 | 0.975 | 0.32963083 |
| 53 | 2785.92 | 2506 | 3066 | 1.001 | 0.29097128 | 0.975 | 0.32963083 |
| 54 | 2785.92 | 2506 | 3066 | 1.001 | 0.29097128 | 0.975 | 0.32963083 |
| 55 | 2785.92 | 2506 | 3066 | 1.001 | 0.29097128 | 0.975 | 0.32963083 |
| 56 | 2785.92 | 2506 | 3066 | 1.001 | 0.29097128 | 0.975 | 0.32963083 |
| 57 | 2785.92 | 2506 | 3066 | 1.001 | 0.29097128 | 0.975 | 0.32963083 |
| 58 | 2785.92 | 2506 | 3066 | 1.001 | 0.29097128 | 0.975 | 0.32963083 |
| 59 | 2785.92 | 2506 | 3066 | 1.001 | 0.29097128 | 0.975 | 0.32963083 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----------|--------|--------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 3282.22 | 2947 | 3618 | 1.001 | 0.29594535 | 1.093 | 0.27458295 |
| 4 | 3282.22 | 2947 | 3618 | 1.001 | 0.29594535 | 1.093 | 0.27458295 |
| 5 | 3282.22 | 2947 | 3618 | 1.001 | 0.29594535 | 1.093 | 0.27458295 |
| 6 | 3286.22 | 2950 | 3622 | 1.001 | 0.29607159 | 1.093 | 0.27441971 |
| 7 | 3286.22 | 2950 | 3622 | 1.001 | 0.29607159 | 1.093 | 0.27441971 |
| 8 | 3286.22 | 2950 | 3622 | 1.001 | 0.29607159 | 1.093 | 0.27441971 |
| 9 | 198.08 | 178 | 219 | 1.001 | 0.29905363 | 0.946 | 0.34430522 |
| 10 | 4349.45 | 3882 | 4816 | 1.001 | 0.31103527 | 1.15 | 0.25017723 |
| 11 | 4349.45 | 3882 | 4816 | 1.001 | 0.31103527 | 1.15 | 0.25017723 |
| 12 | 69.16 | 62 | 77 | 1.001 | 0.31259023 | 0.807 | 0.41980832 |
| 13 | 68.66 | 61 | 76 | 1.001 | 0.31719018 | 0.79 | 0.42972192 |
| 14 | 68.66 | 61 | 76 | 1.001 | 0.31719018 | 0.79 | 0.42972192 |
| 15 | 68.66 | 61 | 76 | 1.001 | 0.31719018 | 0.79 | 0.42972192 |
| 16 | 68.66 | 61 | 76 | 1.001 | 0.31719018 | 0.79 | 0.42972192 |
| 17 | 68.66 | 61 | 76 | 1.001 | 0.31719018 | 0.79 | 0.42972192 |
| 18 | 68.66 | 61 | 76 | 1.001 | 0.31719018 | 0.79 | 0.42972192 |
| 19 | 68.66 | 61 | 76 | 1.001 | 0.31719018 | 0.79 | 0.42972192 |
| 20 | 68.66 | 61 | 76 | 1.001 | 0.31719018 | 0.79 | 0.42972192 |
| 21 | 81.9 | 73 | 91 | 1.001 | 0.31797008 | 0.794 | 0.42711485 |
| 22 | 142731.01 | 126869 | 158593 | 1.001 | 0.3219895 | 0.851 | 0.394813 |
| 23 | 142731.01 | 126869 | 158593 | 1.001 | 0.3219895 | 0.851 | 0.394813 |
| 24 | 142731.01 | 126869 | 158593 | 1.001 | 0.3219895 | 0.851 | 0.394813 |
| 25 | 142731.01 | 126869 | 158593 | 1.001 | 0.3219895 | 0.851 | 0.394813 |
| 26 | 114.05 | 101 | 127 | 1.001 | 0.3304732 | 0.717 | 0.47345655 |
| 27 | 114.05 | 101 | 127 | 1.001 | 0.3304732 | 0.717 | 0.47345655 |
| 28 | 114.05 | 101 | 127 | 1.001 | 0.3304732 | 0.717 | 0.47345655 |
| 29 | 114.05 | 101 | 127 | 1.001 | 0.3304732 | 0.717 | 0.47345655 |
| 30 | 114.05 | 101 | 127 | 1.001 | 0.3304732 | 0.717 | 0.47345655 |
| 31 | 114.05 | 101 | 127 | 1.001 | 0.3304732 | 0.717 | 0.47345655 |
| 32 | 114.05 | 101 | 127 | 1.001 | 0.3304732 | 0.717 | 0.47345655 |
| 33 | 114.05 | 101 | 127 | 1.001 | 0.3304732 | 0.717 | 0.47345655 |
| 34 | 114.05 | 101 | 127 | 1.001 | 0.3304732 | 0.717 | 0.47345655 |
| 35 | 114.05 | 101 | 127 | 1.001 | 0.3304732 | 0.717 | 0.47345655 |
| 36 | 114.05 | 101 | 127 | 1.001 | 0.3304732 | 0.717 | 0.47345655 |
| 37 | 114.05 | 101 | 127 | 1.001 | 0.3304732 | 0.717 | 0.47345655 |
| 38 | 8886.21 | 7869 | 9903 | 1.001 | 0.33168533 | 1.106 | 0.26867058 |
| 39 | 8886.21 | 7869 | 9903 | 1.001 | 0.33168533 | 1.106 | 0.26867058 |
| 40 | 230.53 | 204 | 257 | 1.001 | 0.33319921 | 1.097 | 0.27269201 |
| 41 | 230.53 | 204 | 257 | 1.001 | 0.33319921 | 1.097 | 0.27269201 |
| 42 | 230.53 | 204 | 257 | 1.001 | 0.33319921 | 1.097 | 0.27269201 |
| 43 | 237.82 | 210 | 266 | 1.001 | 0.34103692 | 1.105 | 0.26908289 |
| 44 | 237.82 | 210 | 266 | 1.001 | 0.34103692 | 1.105 | 0.26908289 |
| 45 | 237.82 | 210 | 266 | 1.001 | 0.34103692 | 1.105 | 0.26908289 |
| 46 | 237.82 | 210 | 266 | 1.001 | 0.34103692 | 1.105 | 0.26908289 |
| 47 | 237.82 | 210 | 266 | 1.001 | 0.34103692 | 1.105 | 0.26908289 |
| 48 | 237.82 | 210 | 266 | 1.001 | 0.34103692 | 1.105 | 0.26908289 |
| 49 | 237.82 | 210 | 266 | 1.001 | 0.34103692 | 1.105 | 0.26908289 |
| 50 | 237.82 | 210 | 266 | 1.001 | 0.34103692 | 1.105 | 0.26908289 |
| 51 | 237.82 | 210 | 266 | 1.001 | 0.34103692 | 1.105 | 0.26908289 |
| 52 | 169.94 | 150 | 190 | 1.001 | 0.34103692 | 0.99 | 0.32201644 |
| 53 | 169.94 | 150 | 190 | 1.001 | 0.34103692 | 0.99 | 0.32201644 |
| 54 | 169.94 | 150 | 190 | 1.001 | 0.34103692 | 0.99 | 0.32201644 |
| 55 | 79.74 | 70 | 89 | 1.001 | 0.34645041 | 0.843 | 0.39933402 |
| 56 | 79.74 | 70 | 89 | 1.001 | 0.34645041 | 0.843 | 0.39933402 |
| 57 | 221.45 | 195 | 248 | 1.001 | 0.346866 | 1.142 | 0.25331815 |
| 58 | 221.45 | 195 | 248 | 1.001 | 0.346866 | 1.142 | 0.25331815 |
| 59 | 221.45 | 195 | 248 | 1.001 | 0.346866 | 1.142 | 0.25331815 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 221.45 | 195 | 248 | 1.001 | 0.346866 | 1.142 | 0.25331815 |
| 4 | 221.45 | 195 | 248 | 1.001 | 0.346866 | 1.142 | 0.25331815 |
| 5 | 221.45 | 195 | 248 | 1.001 | 0.346866 | 1.142 | 0.25331815 |
| 6 | 221.45 | 195 | 248 | 1.001 | 0.346866 | 1.142 | 0.25331815 |
| 7 | 221.45 | 195 | 248 | 1.001 | 0.346866 | 1.142 | 0.25331815 |
| 8 | 221.45 | 195 | 248 | 1.001 | 0.346866 | 1.142 | 0.25331815 |
| 9 | 221.45 | 195 | 248 | 1.001 | 0.346866 | 1.142 | 0.25331815 |
| 10 | 221.45 | 195 | 248 | 1.001 | 0.346866 | 1.142 | 0.25331815 |
| 11 | 112.25 | 99 | 126 | 1.001 | 0.3479233 | 0.723 | 0.46958971 |
| 12 | 112.25 | 99 | 126 | 1.001 | 0.3479233 | 0.723 | 0.46958971 |
| 13 | 112.25 | 99 | 126 | 1.001 | 0.3479233 | 0.723 | 0.46958971 |
| 14 | 112.25 | 99 | 126 | 1.001 | 0.3479233 | 0.723 | 0.46958971 |
| 15 | 1608.78 | 1406 | 1812 | 1.001 | 0.36598636 | 1.132 | 0.25764727 |
| 16 | 1608.78 | 1406 | 1812 | 1.001 | 0.36598636 | 1.132 | 0.25764727 |
| 17 | 1608.78 | 1406 | 1812 | 1.001 | 0.36598636 | 1.132 | 0.25764727 |
| 18 | 1608.78 | 1406 | 1812 | 1.001 | 0.36598636 | 1.132 | 0.25764727 |
| 19 | 1608.78 | 1406 | 1812 | 1.001 | 0.36598636 | 1.132 | 0.25764727 |
| 20 | 1608.78 | 1406 | 1812 | 1.001 | 0.36598636 | 1.132 | 0.25764727 |
| 21 | 1608.78 | 1406 | 1812 | 1.001 | 0.36598636 | 1.132 | 0.25764727 |
| 22 | 1608.78 | 1406 | 1812 | 1.001 | 0.36598636 | 1.132 | 0.25764727 |
| 23 | 1608.78 | 1406 | 1812 | 1.001 | 0.36598636 | 1.132 | 0.25764727 |
| 24 | 1608.78 | 1406 | 1812 | 1.001 | 0.36598636 | 1.132 | 0.25764727 |
| 25 | 1608.78 | 1406 | 1812 | 1.001 | 0.36598636 | 1.132 | 0.25764727 |
| 26 | 1608.78 | 1406 | 1812 | 1.001 | 0.36598636 | 1.132 | 0.25764727 |
| 27 | 1608.78 | 1406 | 1812 | 1.001 | 0.36598636 | 1.132 | 0.25764727 |
| 28 | 1608.78 | 1406 | 1812 | 1.001 | 0.36598636 | 1.132 | 0.25764727 |
| 29 | 1608.78 | 1406 | 1812 | 1.001 | 0.36598636 | 1.132 | 0.25764727 |
| 30 | 1608.78 | 1406 | 1812 | 1.001 | 0.36598636 | 1.132 | 0.25764727 |
| 31 | 54.03 | 47 | 61 | 1 | 0.37614849 | 0.647 | 0.51791658 |
| 32 | 54.03 | 47 | 61 | 1 | 0.37614849 | 0.647 | 0.51791658 |
| 33 | 54.03 | 47 | 61 | 1 | 0.37614849 | 0.647 | 0.51791658 |
| 34 | 54.03 | 47 | 61 | 1 | 0.37614849 | 0.647 | 0.51791658 |
| 35 | 54.03 | 47 | 61 | 1 | 0.37614849 | 0.647 | 0.51791658 |
| 36 | 54.03 | 47 | 61 | 1 | 0.37614849 | 0.647 | 0.51791658 |
| 37 | 54.03 | 47 | 61 | 1 | 0.37614849 | 0.647 | 0.51791658 |
| 38 | 54.03 | 47 | 61 | 1 | 0.37614849 | 0.647 | 0.51791658 |
| 39 | 54.03 | 47 | 61 | 1 | 0.37614849 | 0.647 | 0.51791658 |
| 40 | 54.03 | 47 | 61 | 1 | 0.37614849 | 0.647 | 0.51791658 |
| 41 | 54.03 | 47 | 61 | 1 | 0.37614849 | 0.647 | 0.51791658 |
| 42 | 54.03 | 47 | 61 | 1 | 0.37614849 | 0.647 | 0.51791658 |
| 43 | 54.03 | 47 | 61 | 1 | 0.37614849 | 0.647 | 0.51791658 |
| 44 | 54.03 | 47 | 61 | 1 | 0.37614849 | 0.647 | 0.51791658 |
| 45 | 54.03 | 47 | 61 | 1 | 0.37614849 | 0.647 | 0.51791658 |
| 46 | 54.03 | 47 | 61 | 1 | 0.37614849 | 0.647 | 0.51791658 |
| 47 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 48 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 49 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 50 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 51 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 52 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 53 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 54 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 55 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 56 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 57 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 58 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 59 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|-------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 4 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 5 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 6 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 7 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 8 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 9 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 10 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 11 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 12 | 91.51 | 80 | 104 | 1.001 | 0.37851162 | 0.908 | 0.36403319 |
| 13 | 83.91 | 73 | 95 | 1.001 | 0.38003105 | 0.793 | 0.42769265 |
| 14 | 83.91 | 73 | 95 | 1.001 | 0.38003105 | 0.793 | 0.42769265 |
| 15 | 83.91 | 73 | 95 | 1.001 | 0.38003105 | 0.793 | 0.42769265 |
| 16 | 83.91 | 73 | 95 | 1.001 | 0.38003105 | 0.793 | 0.42769265 |
| 17 | 83.91 | 73 | 95 | 1.001 | 0.38003105 | 0.793 | 0.42769265 |
| 18 | 83.91 | 73 | 95 | 1.001 | 0.38003105 | 0.793 | 0.42769265 |
| 19 | 72.27 | 63 | 82 | 1.001 | 0.38027208 | 0.89 | 0.37337613 |
| 20 | 122.03 | 106 | 138 | 1.001 | 0.380604 | 0.815 | 0.41490049 |
| 21 | 122.03 | 106 | 138 | 1.001 | 0.380604 | 0.815 | 0.41490049 |
| 22 | 122.03 | 106 | 138 | 1.001 | 0.380604 | 0.815 | 0.41490049 |
| 23 | 122.03 | 106 | 138 | 1.001 | 0.380604 | 0.815 | 0.41490049 |
| 24 | 122.03 | 106 | 138 | 1.001 | 0.380604 | 0.815 | 0.41490049 |
| 25 | 122.03 | 106 | 138 | 1.001 | 0.380604 | 0.815 | 0.41490049 |
| 26 | 122.03 | 106 | 138 | 1.001 | 0.380604 | 0.815 | 0.41490049 |
| 27 | 122.03 | 106 | 138 | 1.001 | 0.380604 | 0.815 | 0.41490049 |
| 28 | 259.73 | 225 | 295 | 1.001 | 0.39078995 | 1.2 | 0.23033198 |
| 29 | 3754.64 | 3243 | 4266 | 1.002 | 0.39555494 | 1.391 | 0.16417376 |
| 30 | 3754.64 | 3243 | 4266 | 1.002 | 0.39555494 | 1.391 | 0.16417376 |
| 31 | 3754.64 | 3243 | 4266 | 1.002 | 0.39555494 | 1.391 | 0.16417376 |
| 32 | 3754.64 | 3243 | 4266 | 1.002 | 0.39555494 | 1.391 | 0.16417376 |
| 33 | 3754.64 | 3243 | 4266 | 1.002 | 0.39555494 | 1.391 | 0.16417376 |
| 34 | 3754.64 | 3243 | 4266 | 1.002 | 0.39555494 | 1.391 | 0.16417376 |
| 35 | 3754.64 | 3243 | 4266 | 1.002 | 0.39555494 | 1.391 | 0.16417376 |
| 36 | 3754.64 | 3243 | 4266 | 1.002 | 0.39555494 | 1.391 | 0.16417376 |
| 37 | 3754.64 | 3243 | 4266 | 1.002 | 0.39555494 | 1.391 | 0.16417376 |
| 38 | 3754.64 | 3243 | 4266 | 1.002 | 0.39555494 | 1.391 | 0.16417376 |
| 39 | 3754.64 | 3243 | 4266 | 1.002 | 0.39555494 | 1.391 | 0.16417376 |
| 40 | 3754.64 | 3243 | 4266 | 1.002 | 0.39555494 | 1.391 | 0.16417376 |
| 41 | 3754.64 | 3243 | 4266 | 1.002 | 0.39555494 | 1.391 | 0.16417376 |
| 42 | 249.5 | 214 | 285 | 1.001 | 0.41335112 | 1.215 | 0.22435046 |
| 43 | 249.5 | 214 | 285 | 1.001 | 0.41335112 | 1.215 | 0.22435046 |
| 44 | 69.98 | 60 | 80 | 1.001 | 0.4150375 | 1.015 | 0.30994321 |
| 45 | 63.49 | 54 | 73 | 1 | 0.43493706 | 0.76 | 0.44723325 |
| 46 | 63.49 | 54 | 73 | 1 | 0.43493706 | 0.76 | 0.44723325 |
| 47 | 63.49 | 54 | 73 | 1 | 0.43493706 | 0.76 | 0.44723325 |
| 48 | 79.89 | 68 | 92 | 1.001 | 0.43609911 | 0.997 | 0.31868972 |
| 49 | 79.89 | 68 | 92 | 1.001 | 0.43609911 | 0.997 | 0.31868972 |
| 50 | 79.89 | 68 | 92 | 1.001 | 0.43609911 | 0.997 | 0.31868972 |
| 51 | 79.89 | 68 | 92 | 1.001 | 0.43609911 | 0.997 | 0.31868972 |
| 52 | 9348.17 | 7910 | 10787 | 1.002 | 0.44754409 | 1.79 | 0.07352049 |
| 53 | 67.43 | 57 | 78 | 1.001 | 0.4525122 | 1.045 | 0.29613926 |
| 54 | 67.43 | 57 | 78 | 1.001 | 0.4525122 | 1.045 | 0.29613926 |
| 55 | 67.43 | 57 | 78 | 1.001 | 0.4525122 | 1.045 | 0.29613926 |
| 56 | 67.43 | 57 | 78 | 1.001 | 0.4525122 | 1.045 | 0.29613926 |
| 57 | 67.43 | 57 | 78 | 1.001 | 0.4525122 | 1.045 | 0.29613926 |
| 58 | 67.43 | 57 | 78 | 1.001 | 0.4525122 | 1.045 | 0.29613926 |
| 59 | 67.43 | 57 | 78 | 1.001 | 0.4525122 | 1.045 | 0.29613926 |
| 60 | 67.43 | 57 | 78 | 1.001 | 0.4525122 | 1.045 | 0.29613926 |

| | | | | | | | |
|----|----------|-------|-------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 4 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 5 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 6 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 7 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 8 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 9 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 10 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 11 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 12 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 13 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 14 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 15 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 16 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 17 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 18 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 19 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 20 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 21 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 22 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 23 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 24 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 25 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 26 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 27 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 28 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 29 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 30 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 31 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 32 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 33 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 34 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 35 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 36 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 37 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 38 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 39 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 40 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 41 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 42 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 43 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 44 | 12891.99 | 10826 | 14958 | 1.002 | 0.466417 | 1.612 | 0.10685671 |
| 45 | 12991.21 | 10909 | 15073 | 1.002 | 0.46644773 | 1.612 | 0.1068821 |
| 46 | 347.85 | 292 | 404 | 1.002 | 0.46838692 | 1.537 | 0.12436711 |
| 47 | 347.85 | 292 | 404 | 1.002 | 0.46838692 | 1.537 | 0.12436711 |
| 48 | 347.85 | 292 | 404 | 1.002 | 0.46838692 | 1.537 | 0.12436711 |
| 49 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 50 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 51 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 52 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 53 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 54 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 55 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 56 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 57 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 58 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 59 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 4 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 5 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 6 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 7 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 8 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 9 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 10 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 11 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 12 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 13 | 65 | 54 | 76 | 1.001 | 0.49304001 | 0.947 | 0.34369062 |
| 14 | 55.67 | 46 | 65 | 1.001 | 0.49880586 | 1.08 | 0.28008841 |
| 15 | 631.99 | 522 | 742 | 1.001 | 0.50736938 | 1.305 | 0.19192189 |
| 16 | 148.38 | 122 | 174 | 1.002 | 0.51220616 | 1.588 | 0.11236333 |
| 17 | 51.3 | 42 | 60 | 1.001 | 0.51457317 | 1.215 | 0.22453308 |
| 18 | 3130.67 | 2575 | 3686 | 1.002 | 0.51748364 | 1.818 | 0.06903456 |
| 19 | 3130.67 | 2575 | 3686 | 1.002 | 0.51748364 | 1.818 | 0.06903456 |
| 20 | 53.33 | 44 | 63 | 1.001 | 0.5178483 | 1.101 | 0.27100359 |
| 21 | 53.33 | 44 | 63 | 1.001 | 0.5178483 | 1.101 | 0.27100359 |
| 22 | 2865.44 | 2350 | 3380 | 1.002 | 0.52436249 | 1.813 | 0.06981196 |
| 23 | 197.1 | 161 | 233 | 1.002 | 0.53326927 | 1.552 | 0.12064702 |
| 24 | 197.1 | 161 | 233 | 1.002 | 0.53326927 | 1.552 | 0.12064702 |
| 25 | 197.1 | 161 | 233 | 1.002 | 0.53326927 | 1.552 | 0.12064702 |
| 26 | 197.1 | 161 | 233 | 1.002 | 0.53326927 | 1.552 | 0.12064702 |
| 27 | 197.1 | 161 | 233 | 1.002 | 0.53326927 | 1.552 | 0.12064702 |
| 28 | 197.1 | 161 | 233 | 1.002 | 0.53326927 | 1.552 | 0.12064702 |
| 29 | 197.1 | 161 | 233 | 1.002 | 0.53326927 | 1.552 | 0.12064702 |
| 30 | 458.01 | 373 | 543 | 1.002 | 0.54177657 | 1.723 | 0.08487894 |
| 31 | 27927.58 | 22677 | 33178 | 1.001 | 0.54899713 | 1.459 | 0.14448767 |
| 32 | 27927.58 | 22677 | 33178 | 1.001 | 0.54899713 | 1.459 | 0.14448767 |
| 33 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 34 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 35 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 36 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 37 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 38 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 39 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 40 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 41 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 42 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 43 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 44 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 45 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 46 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 47 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 48 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 49 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 50 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 51 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 52 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 53 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 54 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 55 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 56 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 57 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 58 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 59 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 4 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 5 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 6 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 7 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 8 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 9 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 10 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 11 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 12 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 13 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 14 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 15 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 16 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 17 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 18 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 19 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 20 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 21 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 22 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 23 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 24 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 25 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 26 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 27 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 28 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 29 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 30 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 31 | 73.92 | 60 | 88 | 1.001 | 0.55254102 | 1.099 | 0.27171185 |
| 32 | 151.17 | 122 | 180 | 1.001 | 0.56111576 | 1.54 | 0.12348132 |
| 33 | 336.41 | 270 | 403 | 1.002 | 0.57782043 | 1.731 | 0.08345349 |
| 34 | 336.41 | 270 | 403 | 1.002 | 0.57782043 | 1.731 | 0.08345349 |
| 35 | 336.41 | 270 | 403 | 1.002 | 0.57782043 | 1.731 | 0.08345349 |
| 36 | 343.18 | 275 | 411 | 1.002 | 0.57970678 | 1.735 | 0.08276887 |
| 37 | 343.18 | 275 | 411 | 1.002 | 0.57970678 | 1.735 | 0.08276887 |
| 38 | 343.18 | 275 | 411 | 1.002 | 0.57970678 | 1.735 | 0.08276887 |
| 39 | 138.5 | 111 | 166 | 1.002 | 0.58062356 | 1.705 | 0.08827572 |
| 40 | 190.44 | 152 | 228 | 1.002 | 0.5849625 | 1.712 | 0.08682214 |
| 41 | 190.44 | 152 | 228 | 1.002 | 0.5849625 | 1.712 | 0.08682214 |
| 42 | 190.44 | 152 | 228 | 1.002 | 0.5849625 | 1.712 | 0.08682214 |
| 43 | 190.44 | 152 | 228 | 1.002 | 0.5849625 | 1.712 | 0.08682214 |
| 44 | 190.44 | 152 | 228 | 1.002 | 0.5849625 | 1.712 | 0.08682214 |
| 45 | 190.44 | 152 | 228 | 1.002 | 0.5849625 | 1.712 | 0.08682214 |
| 46 | 190.44 | 152 | 228 | 1.002 | 0.5849625 | 1.712 | 0.08682214 |
| 47 | 190.44 | 152 | 228 | 1.002 | 0.5849625 | 1.712 | 0.08682214 |
| 48 | 190.44 | 152 | 228 | 1.002 | 0.5849625 | 1.712 | 0.08682214 |
| 49 | 190.44 | 152 | 228 | 1.002 | 0.5849625 | 1.712 | 0.08682214 |
| 50 | 190.44 | 152 | 228 | 1.002 | 0.5849625 | 1.712 | 0.08682214 |
| 51 | 190.44 | 152 | 228 | 1.002 | 0.5849625 | 1.712 | 0.08682214 |
| 52 | 190.44 | 152 | 228 | 1.002 | 0.5849625 | 1.712 | 0.08682214 |
| 53 | 190.44 | 152 | 228 | 1.002 | 0.5849625 | 1.712 | 0.08682214 |
| 54 | 190.44 | 152 | 228 | 1.002 | 0.5849625 | 1.712 | 0.08682214 |
| 55 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 56 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 57 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 58 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 59 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 4 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 5 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 6 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 7 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 8 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 9 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 10 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 11 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 12 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 13 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 14 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 15 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 16 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 17 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 18 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 19 | 67.67 | 54 | 81 | 1.001 | 0.5849625 | 1.471 | 0.14133417 |
| 20 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 21 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 22 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 23 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 24 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 25 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 26 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 27 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 28 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 29 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 30 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 31 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 32 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 33 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 34 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 35 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 36 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 37 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 38 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 39 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 40 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 41 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 42 | 55.98 | 44 | 68 | 1.001 | 0.62803122 | 1.476 | 0.14006696 |
| 43 | 862.58 | 663 | 1062 | 1.003 | 0.67970299 | 2.254 | 0.02421726 |
| 44 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 45 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 46 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 47 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 48 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 49 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 50 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 51 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 52 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 53 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 54 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 55 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 56 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 57 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 58 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 59 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 4 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 5 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 6 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 7 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 8 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 9 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 10 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 11 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 12 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 13 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 14 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 15 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 16 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 17 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 18 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 19 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 20 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 21 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 22 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 23 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 24 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 25 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 26 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 27 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 28 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 29 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 30 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 31 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 32 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 33 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 34 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 35 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 36 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 37 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 38 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 39 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 40 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 41 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 42 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 43 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 44 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 45 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 46 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 47 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 48 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 49 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 50 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 51 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 52 | 861.57 | 662 | 1061 | 1.003 | 0.68052153 | 2.256 | 0.02408365 |
| 53 | 129.01 | 98 | 160 | 1.001 | 0.70721825 | 1.667 | 0.09559944 |
| 54 | 129.01 | 98 | 160 | 1.001 | 0.70721825 | 1.667 | 0.09559944 |
| 55 | 129.01 | 98 | 160 | 1.001 | 0.70721825 | 1.667 | 0.09559944 |
| 56 | 129.01 | 98 | 160 | 1.001 | 0.70721825 | 1.667 | 0.09559944 |
| 57 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 58 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 59 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 4 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 5 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 6 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 7 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 8 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 9 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 10 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 11 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 12 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 13 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 14 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 15 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 16 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 17 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 18 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 19 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 20 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 21 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 22 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 23 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 24 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 25 | 127.88 | 97 | 159 | 1.001 | 0.71297011 | 1.697 | 0.08968646 |
| 26 | 316.13 | 234 | 398 | 1.003 | 0.7662599 | 2.333 | 0.01962831 |
| 27 | 623.47 | 448 | 799 | 1.002 | 0.83469677 | 2.31 | 0.02089101 |
| 28 | 623.47 | 448 | 799 | 1.002 | 0.83469677 | 2.31 | 0.02089101 |
| 29 | 247.1 | 172 | 322 | 1.003 | 0.90465212 | 2.733 | 0.0062736 |
| 30 | 247.1 | 172 | 322 | 1.003 | 0.90465212 | 2.733 | 0.0062736 |
| 31 | 247.1 | 172 | 322 | 1.003 | 0.90465212 | 2.733 | 0.0062736 |
| 32 | 247.1 | 172 | 322 | 1.003 | 0.90465212 | 2.733 | 0.0062736 |
| 33 | 247.1 | 172 | 322 | 1.003 | 0.90465212 | 2.733 | 0.0062736 |
| 34 | 247.1 | 172 | 322 | 1.003 | 0.90465212 | 2.733 | 0.0062736 |
| 35 | 247.1 | 172 | 322 | 1.003 | 0.90465212 | 2.733 | 0.0062736 |
| 36 | 247.1 | 172 | 322 | 1.003 | 0.90465212 | 2.733 | 0.0062736 |
| 37 | 247.1 | 172 | 322 | 1.003 | 0.90465212 | 2.733 | 0.0062736 |
| 38 | 247.1 | 172 | 322 | 1.003 | 0.90465212 | 2.733 | 0.0062736 |
| 39 | 247.1 | 172 | 322 | 1.003 | 0.90465212 | 2.733 | 0.0062736 |
| 40 | 247.1 | 172 | 322 | 1.003 | 0.90465212 | 2.733 | 0.0062736 |
| 41 | 247.1 | 172 | 322 | 1.003 | 0.90465212 | 2.733 | 0.0062736 |
| 42 | 247.1 | 172 | 322 | 1.003 | 0.90465212 | 2.733 | 0.0062736 |
| 43 | 247.1 | 172 | 322 | 1.003 | 0.90465212 | 2.733 | 0.0062736 |
| 44 | 247.1 | 172 | 322 | 1.003 | 0.90465212 | 2.733 | 0.0062736 |
| 45 | 247.1 | 172 | 322 | 1.003 | 0.90465212 | 2.733 | 0.0062736 |
| 46 | 247.1 | 172 | 322 | 1.003 | 0.90465212 | 2.733 | 0.0062736 |
| 47 | 247.1 | 172 | 322 | 1.003 | 0.90465212 | 2.733 | 0.0062736 |
| 48 | 247.27 | 172 | 323 | 1.003 | 0.9091256 | 2.737 | 0.00620793 |
| 49 | 249.25 | 173 | 325 | 1.003 | 0.90966768 | 2.752 | 0.00592535 |
| 50 | 249.25 | 173 | 325 | 1.003 | 0.90966768 | 2.752 | 0.00592535 |
| 51 | 75.15 | 52 | 99 | 1.002 | 0.9289169 | 1.963 | 0.04960358 |
| 52 | 75.15 | 52 | 99 | 1.002 | 0.9289169 | 1.963 | 0.04960358 |
| 53 | 75.15 | 52 | 99 | 1.002 | 0.9289169 | 1.963 | 0.04960358 |
| 54 | 75.15 | 52 | 99 | 1.002 | 0.9289169 | 1.963 | 0.04960358 |
| 55 | 37670.73 | 25344 | 49997 | 1.003 | 0.98019729 | 2.724 | 0.00644433 |
| 56 | 59.03 | 36 | 82 | 1.002 | 1.187627 | 2.575 | 0.0100373 |
| 57 | 244.76 | 489 | 0 | 0.958 | #NUM! | -2.636 | NA |
| 58 | | | | | | | |
| 59 | | | | | | | |
| 60 | | | | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | | | |
|--------|-----|---|-------|-------|-----------|
| 178.44 | 357 | 0 | 0.873 | #NUM! | -3.119 NA |
| 178.44 | 357 | 0 | 0.873 | #NUM! | -3.119 NA |
| 178.44 | 357 | 0 | 0.873 | #NUM! | -3.119 NA |
| 178.44 | 357 | 0 | 0.873 | #NUM! | -3.119 NA |
| 178.44 | 357 | 0 | 0.873 | #NUM! | -3.119 NA |
| 178.44 | 357 | 0 | 0.873 | #NUM! | -3.119 NA |
| 178.44 | 357 | 0 | 0.873 | #NUM! | -3.119 NA |
| 178.44 | 357 | 0 | 0.873 | #NUM! | -3.119 NA |
| 178.44 | 357 | 0 | 0.873 | #NUM! | -3.119 NA |
| 53.48 | 107 | 0 | 0 | #NUM! | -5.87 NA |
| 53.48 | 107 | 0 | 0 | #NUM! | -5.87 NA |
| 51.89 | 104 | 0 | 0 | #NUM! | -5.91 NA |
| 51.89 | 104 | 0 | 0 | #NUM! | -5.91 NA |

Do not distribute

| | padj | dispGeneEst | dispFit | dispMAP | dispersion | betaConv | maxCooks |
|----|------------|-------------|---------|---------|------------|----------|----------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | | | | | | | |
| 4 | padj | dispGeneEst | dispFit | dispMAP | dispersion | betaConv | maxCooks |
| 5 | NA | 10 | 0.1354 | 1.1448 | 10 | TRUE | 32.7664 |
| 6 | NA | 5.9331 | 0.1753 | 1.0679 | 5.9331 | TRUE | 29.9634 |
| 7 | NA | 5.9331 | 0.1753 | 1.0679 | 5.9331 | TRUE | 29.9634 |
| 8 | NA | 5.9331 | 0.1753 | 1.0679 | 5.9331 | TRUE | 29.9634 |
| 9 | NA | 5.9331 | 0.1753 | 1.0679 | 5.9331 | TRUE | 29.9634 |
| 10 | NA | 5.9331 | 0.1753 | 1.0679 | 5.9331 | TRUE | 29.9634 |
| 11 | NA | 5.9331 | 0.1753 | 1.0679 | 5.9331 | TRUE | 29.9634 |
| 12 | NA | 5.9331 | 0.1753 | 1.0679 | 5.9331 | TRUE | 29.9634 |
| 13 | NA | 5.9331 | 0.1753 | 1.0679 | 5.9331 | TRUE | 29.9634 |
| 14 | NA | 5.9331 | 0.1753 | 1.0679 | 5.9331 | TRUE | 29.9634 |
| 15 | NA | 5.9331 | 0.1753 | 1.0679 | 5.9331 | TRUE | 29.9634 |
| 16 | NA | 5.9331 | 0.1753 | 1.0679 | 5.9331 | TRUE | 29.9634 |
| 17 | NA | 5.9331 | 0.1753 | 1.0679 | 5.9331 | TRUE | 29.9634 |
| 18 | 0.99796172 | 0.4018 | 0.1649 | 0.2377 | 0.2377 | TRUE | 3.19 |
| 19 | 0.99796172 | 0.4018 | 0.1649 | 0.2377 | 0.2377 | TRUE | 3.19 |
| 20 | 0.99796172 | 0.4018 | 0.1649 | 0.2377 | 0.2377 | TRUE | 3.19 |
| 21 | 0.99796172 | 0.4018 | 0.1649 | 0.2377 | 0.2377 | TRUE | 3.19 |
| 22 | 0.99796172 | 0.3943 | 0.096 | 0.1874 | 0.1874 | TRUE | 9.6964 |
| 23 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 24 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 25 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 26 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 27 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 28 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 29 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 30 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 31 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 32 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 33 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 34 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 35 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 36 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 37 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 38 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 39 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 40 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 41 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 42 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 43 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 44 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 45 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 46 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 47 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 48 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 49 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 50 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 51 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 52 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 53 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 54 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 55 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 56 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 57 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 58 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 59 | 0.99796172 | 0.4036 | 0.0979 | 0.1916 | 0.1916 | TRUE | 9.7776 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.1585 | 0.076 | 0.1024 | 0.1024 | TRUE | 0.9649 |
| 4 | 0.99796172 | 0.1585 | 0.076 | 0.1024 | 0.1024 | TRUE | 0.9649 |
| 5 | 0.99796172 | 0.1585 | 0.076 | 0.1024 | 0.1024 | TRUE | 0.9649 |
| 6 | 0.99796172 | 0.1585 | 0.076 | 0.1024 | 0.1024 | TRUE | 0.9649 |
| 7 | 0.99796172 | 0.1585 | 0.076 | 0.1024 | 0.1024 | TRUE | 0.9649 |
| 8 | 0.99796172 | 0.1585 | 0.076 | 0.1024 | 0.1024 | TRUE | 0.9649 |
| 9 | 0.99796172 | 0.1585 | 0.076 | 0.1024 | 0.1024 | TRUE | 0.9649 |
| 10 | 0.99796172 | 0.1585 | 0.076 | 0.1024 | 0.1024 | TRUE | 0.9649 |
| 11 | 0.99796172 | 0.1585 | 0.076 | 0.1024 | 0.1024 | TRUE | 0.9649 |
| 12 | 0.99796172 | 0.1585 | 0.076 | 0.1024 | 0.1024 | TRUE | 0.9649 |
| 13 | 0.99796172 | 0.1585 | 0.076 | 0.1024 | 0.1024 | TRUE | 0.9649 |
| 14 | 0.99796172 | 0.1585 | 0.076 | 0.1024 | 0.1024 | TRUE | 0.9649 |
| 15 | 0.99796172 | 0.1585 | 0.076 | 0.1024 | 0.1024 | TRUE | 0.9649 |
| 16 | 0.99796172 | 0.1585 | 0.076 | 0.1024 | 0.1024 | TRUE | 0.9649 |
| 17 | 0.99796172 | 0.1585 | 0.076 | 0.1024 | 0.1024 | TRUE | 0.9649 |
| 18 | 0.99796172 | 0.1585 | 0.076 | 0.1024 | 0.1024 | TRUE | 0.9649 |
| 19 | 0.99796172 | 0.1585 | 0.076 | 0.1024 | 0.1024 | TRUE | 0.9649 |
| 20 | 0.99796172 | 0.1661 | 0.0774 | 0.1056 | 0.1056 | TRUE | 0.8728 |
| 21 | 0.99796172 | 0.1661 | 0.0774 | 0.1056 | 0.1056 | TRUE | 0.8728 |
| 22 | 0.99796172 | 0.1661 | 0.0774 | 0.1056 | 0.1056 | TRUE | 0.8728 |
| 23 | 0.99796172 | 0.1661 | 0.0774 | 0.1056 | 0.1056 | TRUE | 0.8728 |
| 24 | 0.99796172 | 0.1663 | 0.0774 | 0.1057 | 0.1057 | TRUE | 0.8721 |
| 25 | 0.99796172 | 0.1663 | 0.0774 | 0.1057 | 0.1057 | TRUE | 0.8721 |
| 26 | 0.99796172 | 0.1663 | 0.0774 | 0.1057 | 0.1057 | TRUE | 0.8721 |
| 27 | 0.99796172 | 0.1663 | 0.0774 | 0.1057 | 0.1057 | TRUE | 0.8721 |
| 28 | 0.99796172 | 0.2291 | 0.142 | 0.1705 | 0.1705 | TRUE | 1.3856 |
| 29 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 30 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 31 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 32 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 33 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 34 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 35 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 36 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 37 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 38 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 39 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 40 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 41 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 42 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 43 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 44 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 45 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 46 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 47 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 48 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 49 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 50 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 51 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 52 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 53 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 54 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 55 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 56 | 0.99796172 | 0.2481 | 0.1451 | 0.1786 | 0.1786 | TRUE | 3.107 |
| 57 | 0.99796172 | 0.0681 | 0.0886 | 0.0815 | 0.0815 | TRUE | 0.164 |
| 58 | 0.99796172 | 0.1213 | 0.0646 | 0.0838 | 0.0838 | TRUE | 2.2184 |
| 59 | | | | | | | |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.1213 | 0.0646 | 0.0838 | 0.0838 | TRUE | 2.2184 |
| 4 | 0.99796172 | 0.1213 | 0.0646 | 0.0838 | 0.0838 | TRUE | 2.2184 |
| 5 | 0.99796172 | 0.1213 | 0.0646 | 0.0838 | 0.0838 | TRUE | 2.2184 |
| 6 | 0.99796172 | 0.1213 | 0.0646 | 0.0838 | 0.0838 | TRUE | 2.2184 |
| 7 | 0.99796172 | 0.1213 | 0.0646 | 0.0838 | 0.0838 | TRUE | 2.2184 |
| 8 | 0.99796172 | 0.1211 | 0.0647 | 0.0838 | 0.0838 | TRUE | 2.2127 |
| 9 | 0.99796172 | 0.1211 | 0.0647 | 0.0838 | 0.0838 | TRUE | 2.2127 |
| 10 | 0.99796172 | 0.1211 | 0.0647 | 0.0838 | 0.0838 | TRUE | 2.2127 |
| 11 | 0.99796172 | 0.1211 | 0.0647 | 0.0838 | 0.0838 | TRUE | 2.2127 |
| 12 | 0.99796172 | 0.1211 | 0.0647 | 0.0838 | 0.0838 | TRUE | 2.2127 |
| 13 | 0.99796172 | 0.1211 | 0.0647 | 0.0838 | 0.0838 | TRUE | 2.2127 |
| 14 | 0.99796172 | 0.1211 | 0.0647 | 0.0838 | 0.0838 | TRUE | 2.2127 |
| 15 | 0.99796172 | 0.1211 | 0.0647 | 0.0838 | 0.0838 | TRUE | 2.2127 |
| 16 | 0.99796172 | 0.1211 | 0.0647 | 0.0838 | 0.0838 | TRUE | 2.2127 |
| 17 | 0.99796172 | 0.1211 | 0.0647 | 0.0838 | 0.0838 | TRUE | 2.2127 |
| 18 | 0.99796172 | 0.1211 | 0.0647 | 0.0838 | 0.0838 | TRUE | 2.2127 |
| 19 | 0.99796172 | 0.1211 | 0.0647 | 0.0838 | 0.0838 | TRUE | 2.2127 |
| 20 | 0.99796172 | 0.1211 | 0.0647 | 0.0838 | 0.0838 | TRUE | 2.2127 |
| 21 | 0.99796172 | 0.1211 | 0.0647 | 0.0838 | 0.0838 | TRUE | 2.2127 |
| 22 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 23 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 24 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 25 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 26 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 27 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 28 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 29 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 30 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 31 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 32 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 33 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 34 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 35 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 36 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 37 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 38 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 39 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 40 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 41 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 42 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 43 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 44 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 45 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 46 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 47 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 48 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 49 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 50 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 51 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 52 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 53 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 54 | 0.99796172 | 0.1938 | 0.0733 | 0.1122 | 0.1122 | TRUE | 5.095 |
| 55 | 0.99796172 | 0.0756 | 0.106 | 0.0955 | 0.0955 | TRUE | 0.1354 |
| 56 | 0.99796172 | 0.0748 | 0.1062 | 0.0953 | 0.0953 | TRUE | 0.1332 |
| 57 | 0.99796172 | 0.0748 | 0.1062 | 0.0953 | 0.0953 | TRUE | 0.1332 |
| 58 | 0.99796172 | 0.0748 | 0.1062 | 0.0953 | 0.0953 | TRUE | 0.1332 |
| 59 | 0.99796172 | 0.0748 | 0.1062 | 0.0953 | 0.0953 | TRUE | 0.1332 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.1185 | 0.0834 | 0.0954 | 0.0954 | TRUE | 1.8884 |
| 4 | 0.99796172 | 0.1185 | 0.0834 | 0.0954 | 0.0954 | TRUE | 1.8884 |
| 5 | 0.99796172 | 0.1185 | 0.0834 | 0.0954 | 0.0954 | TRUE | 1.8884 |
| 6 | 0.99796172 | 0.1185 | 0.0834 | 0.0954 | 0.0954 | TRUE | 1.8884 |
| 7 | 0.99796172 | 0.1185 | 0.0834 | 0.0954 | 0.0954 | TRUE | 1.8884 |
| 8 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 9 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 10 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 11 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 12 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 13 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 14 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 15 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 16 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 17 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 18 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 19 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 20 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 21 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 22 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 23 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 24 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 25 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 26 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 27 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 28 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 29 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 30 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 31 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 32 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 33 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 34 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 35 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 36 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 37 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 38 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 39 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 40 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 41 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 42 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 43 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 44 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 45 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 46 | 0.99796172 | 0.8312 | 0.1584 | 0.3597 | 0.3597 | TRUE | 1.1668 |
| 47 | 0.99796172 | 0.7843 | 0.0688 | 0.2642 | 0.7843 | TRUE | 0.3437 |
| 48 | 0.99796172 | 0.7843 | 0.0688 | 0.2642 | 0.7843 | TRUE | 0.3437 |
| 49 | 0.99796172 | 0.7843 | 0.0688 | 0.2642 | 0.7843 | TRUE | 0.3437 |
| 50 | 0.99796172 | 0.7843 | 0.0688 | 0.2642 | 0.7843 | TRUE | 0.3437 |
| 51 | 0.99796172 | 0.7843 | 0.0688 | 0.2642 | 0.7843 | TRUE | 0.3437 |
| 52 | 0.99796172 | 0.7843 | 0.0688 | 0.2642 | 0.7843 | TRUE | 0.3437 |
| 53 | 0.99796172 | 0.7843 | 0.0688 | 0.2642 | 0.7843 | TRUE | 0.3437 |
| 54 | 0.99796172 | 0.7843 | 0.0688 | 0.2642 | 0.7843 | TRUE | 0.3437 |
| 55 | 0.99796172 | 0.058 | 0.1018 | 0.0866 | 0.0866 | TRUE | 0.9103 |
| 56 | 0.99796172 | 0.0595 | 0.102 | 0.0873 | 0.0873 | TRUE | 0.9425 |
| 57 | 0.99796172 | 0.0595 | 0.102 | 0.0873 | 0.0873 | TRUE | 0.9425 |
| 58 | 0.99796172 | 0.0595 | 0.102 | 0.0873 | 0.0873 | TRUE | 0.9425 |
| 59 | 0.99796172 | 0.0595 | 0.102 | 0.0873 | 0.0873 | TRUE | 0.9425 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.1402 | 0.1295 | 0.134 | 0.134 | TRUE | 0.3701 |
| 4 | 0.99796172 | 0.1402 | 0.1295 | 0.134 | 0.134 | TRUE | 0.3701 |
| 5 | 0.99796172 | 0.1402 | 0.1295 | 0.134 | 0.134 | TRUE | 0.3701 |
| 6 | 0.99796172 | 0.1402 | 0.1295 | 0.134 | 0.134 | TRUE | 0.3701 |
| 7 | 0.99796172 | 0.1402 | 0.1295 | 0.134 | 0.134 | TRUE | 0.3701 |
| 8 | 0.99796172 | 0.1402 | 0.1295 | 0.134 | 0.134 | TRUE | 0.3701 |
| 9 | 0.99796172 | 0.1402 | 0.1295 | 0.134 | 0.134 | TRUE | 0.3701 |
| 10 | 0.99796172 | 0.1402 | 0.1295 | 0.134 | 0.134 | TRUE | 0.3701 |
| 11 | 0.99796172 | 0.1402 | 0.1295 | 0.134 | 0.134 | TRUE | 0.3701 |
| 12 | 0.99796172 | 0.0553 | 0.1387 | 0.1114 | 0.1114 | TRUE | 0.4239 |
| 13 | 0.99796172 | 0.0553 | 0.1387 | 0.1114 | 0.1114 | TRUE | 0.4239 |
| 14 | 0.99796172 | 0.0553 | 0.1387 | 0.1114 | 0.1114 | TRUE | 0.4239 |
| 15 | 0.99796172 | 0.0553 | 0.1387 | 0.1114 | 0.1114 | TRUE | 0.4239 |
| 16 | 0.99796172 | 0.0553 | 0.1387 | 0.1114 | 0.1114 | TRUE | 0.4239 |
| 17 | 0.99796172 | 0.1779 | 0.1676 | 0.1709 | 0.1709 | TRUE | 0.2444 |
| 18 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 19 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 20 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 21 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 22 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 23 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 24 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 25 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 26 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 27 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 28 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 29 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 30 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 31 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 32 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 33 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 34 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 35 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 36 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 37 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 38 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 39 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 40 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 41 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 42 | 0.99796172 | 0.1756 | 0.1695 | 0.1712 | 0.1712 | TRUE | 0.2294 |
| 43 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 44 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 45 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 46 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 47 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 48 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 49 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 50 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 51 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 52 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 53 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 54 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 55 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 56 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 57 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 58 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 59 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 4 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 5 | 0.99796172 | 0.0475 | 0.1205 | 0.096 | 0.096 | TRUE | 0.2931 |
| 6 | 0.99796172 | 0.1709 | 0.1688 | 0.1695 | 0.1695 | TRUE | 0.2394 |
| 7 | 0.99796172 | 0.049 | 0.1101 | 0.0893 | 0.0893 | TRUE | 0.5532 |
| 8 | 0.99796172 | 0.049 | 0.1101 | 0.0893 | 0.0893 | TRUE | 0.5532 |
| 9 | 0.99796172 | 0.049 | 0.1101 | 0.0893 | 0.0893 | TRUE | 0.5532 |
| 10 | 0.99796172 | 0.049 | 0.1101 | 0.0893 | 0.0893 | TRUE | 0.5532 |
| 11 | 0.99796172 | 0.049 | 0.1101 | 0.0893 | 0.0893 | TRUE | 0.5532 |
| 12 | 0.99796172 | 0.049 | 0.1101 | 0.0893 | 0.0893 | TRUE | 0.5532 |
| 13 | 0.99796172 | 0.049 | 0.1101 | 0.0893 | 0.0893 | TRUE | 0.5532 |
| 14 | 0.99796172 | 0.049 | 0.1101 | 0.0893 | 0.0893 | TRUE | 0.5532 |
| 15 | 0.99796172 | 0.049 | 0.1101 | 0.0893 | 0.0893 | TRUE | 0.5532 |
| 16 | 0.99796172 | 0.049 | 0.1101 | 0.0893 | 0.0893 | TRUE | 0.5532 |
| 17 | 0.99796172 | 0.049 | 0.1101 | 0.0893 | 0.0893 | TRUE | 0.5532 |
| 18 | 0.99796172 | 0.049 | 0.1101 | 0.0893 | 0.0893 | TRUE | 0.5532 |
| 19 | 0.99796172 | 0.049 | 0.1101 | 0.0893 | 0.0893 | TRUE | 0.5532 |
| 20 | 0.99796172 | 0.049 | 0.1101 | 0.0893 | 0.0893 | TRUE | 0.5532 |
| 21 | 0.99796172 | 0.0268 | 0.0729 | 0.0556 | 0.0556 | TRUE | 0.3966 |
| 22 | 0.99796172 | 1.4464 | 0.1288 | 0.478 | 1.4464 | TRUE | 0.6288 |
| 23 | 0.99796172 | 1.4464 | 0.1288 | 0.478 | 1.4464 | TRUE | 0.6288 |
| 24 | 0.99796172 | 1.4464 | 0.1288 | 0.478 | 1.4464 | TRUE | 0.6288 |
| 25 | 0.99796172 | 1.4464 | 0.1288 | 0.478 | 1.4464 | TRUE | 0.6288 |
| 26 | 0.99796172 | 1.4464 | 0.1288 | 0.478 | 1.4464 | TRUE | 0.6288 |
| 27 | 0.99796172 | 1.4464 | 0.1288 | 0.478 | 1.4464 | TRUE | 0.6288 |
| 28 | 0.99796172 | 1.4464 | 0.1288 | 0.478 | 1.4464 | TRUE | 0.6288 |
| 29 | 0.99796172 | 1.4464 | 0.1288 | 0.478 | 1.4464 | TRUE | 0.6288 |
| 30 | 0.99796172 | 1.4464 | 0.1288 | 0.478 | 1.4464 | TRUE | 0.6288 |
| 31 | 0.99796172 | 1.4464 | 0.1288 | 0.478 | 1.4464 | TRUE | 0.6288 |
| 32 | 0.99796172 | 1.4464 | 0.1288 | 0.478 | 1.4464 | TRUE | 0.6288 |
| 33 | 0.99796172 | 1.4464 | 0.1288 | 0.478 | 1.4464 | TRUE | 0.6288 |
| 34 | 0.99796172 | 1.4464 | 0.1288 | 0.478 | 1.4464 | TRUE | 0.6288 |
| 35 | 0.99796172 | 1.4464 | 0.1288 | 0.478 | 1.4464 | TRUE | 0.6288 |
| 36 | 0.99796172 | 1.4464 | 0.1288 | 0.478 | 1.4464 | TRUE | 0.6288 |
| 37 | 0.99796172 | 1.4464 | 0.1288 | 0.478 | 1.4464 | TRUE | 0.6288 |
| 38 | 0.99796172 | 1.4464 | 0.1288 | 0.478 | 1.4464 | TRUE | 0.6288 |
| 39 | 0.99796172 | 1.4464 | 0.1288 | 0.478 | 1.4464 | TRUE | 0.6288 |
| 40 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 41 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 42 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 43 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 44 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 45 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 46 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 47 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 48 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 49 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 50 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 51 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 52 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 53 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 54 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 55 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 56 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 57 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 58 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 59 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 4 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 5 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 6 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 7 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 8 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 9 | 0.99796172 | 0.0272 | 0.0729 | 0.0557 | 0.0557 | TRUE | 0.3966 |
| 10 | 0.99796172 | 0.2377 | 0.1647 | 0.1877 | 0.1877 | TRUE | 1.1534 |
| 11 | 0.99796172 | 0.2377 | 0.1647 | 0.1877 | 0.1877 | TRUE | 1.1534 |
| 12 | 0.99796172 | 0.2377 | 0.1647 | 0.1877 | 0.1877 | TRUE | 1.1534 |
| 13 | 0.99796172 | 0.2377 | 0.1647 | 0.1877 | 0.1877 | TRUE | 1.1534 |
| 14 | 0.99796172 | 0.2377 | 0.1647 | 0.1877 | 0.1877 | TRUE | 1.1534 |
| 15 | 0.99796172 | 0.2377 | 0.1647 | 0.1877 | 0.1877 | TRUE | 1.1534 |
| 16 | 0.99796172 | 0.0288 | 0.0728 | 0.0563 | 0.0563 | TRUE | 0.4409 |
| 17 | 0.99796172 | 0.3451 | 0.1716 | 0.2276 | 0.2276 | TRUE | 7.016 |
| 18 | 0.99796172 | 0.3451 | 0.1716 | 0.2276 | 0.2276 | TRUE | 7.016 |
| 19 | 0.99796172 | 0.3451 | 0.1716 | 0.2276 | 0.2276 | TRUE | 7.016 |
| 20 | 0.99796172 | 0.3451 | 0.1716 | 0.2276 | 0.2276 | TRUE | 7.016 |
| 21 | 0.99796172 | 0.3451 | 0.1716 | 0.2276 | 0.2276 | TRUE | 7.016 |
| 22 | 0.99796172 | 0.3451 | 0.1716 | 0.2276 | 0.2276 | TRUE | 7.016 |
| 23 | 0.99796172 | 0.3451 | 0.1716 | 0.2276 | 0.2276 | TRUE | 7.016 |
| 24 | 0.99796172 | 0.3451 | 0.1716 | 0.2276 | 0.2276 | TRUE | 7.016 |
| 25 | 0.99796172 | 0.3451 | 0.1716 | 0.2276 | 0.2276 | TRUE | 7.016 |
| 26 | 0.99796172 | 0.3451 | 0.1716 | 0.2276 | 0.2276 | TRUE | 7.016 |
| 27 | 0.99796172 | 0.3451 | 0.1716 | 0.2276 | 0.2276 | TRUE | 7.016 |
| 28 | 0.99796172 | 0.3451 | 0.1716 | 0.2276 | 0.2276 | TRUE | 7.016 |
| 29 | 0.99796172 | 0.3451 | 0.1716 | 0.2276 | 0.2276 | TRUE | 7.016 |
| 30 | 0.99796172 | 0.3451 | 0.1716 | 0.2276 | 0.2276 | TRUE | 7.016 |
| 31 | 0.99796172 | 0.0442 | 0.101 | 0.0813 | 0.0813 | TRUE | 0.5065 |
| 32 | 0.99796172 | 0.2763 | 0.1463 | 0.1877 | 0.1877 | TRUE | 0.1875 |
| 33 | 0.99796172 | 0.2763 | 0.1463 | 0.1877 | 0.1877 | TRUE | 0.1875 |
| 34 | 0.99796172 | 0.2763 | 0.1463 | 0.1877 | 0.1877 | TRUE | 0.1875 |
| 35 | 0.99796172 | 0.2763 | 0.1463 | 0.1877 | 0.1877 | TRUE | 0.1875 |
| 36 | 0.99796172 | 0.2763 | 0.1463 | 0.1877 | 0.1877 | TRUE | 0.1875 |
| 37 | 0.99796172 | 0.2763 | 0.1463 | 0.1877 | 0.1877 | TRUE | 0.1875 |
| 38 | 0.99796172 | 0.2763 | 0.1463 | 0.1877 | 0.1877 | TRUE | 0.1875 |
| 39 | 0.99796172 | 0.0416 | 0.1018 | 0.0809 | 0.0809 | TRUE | 0.5051 |
| 40 | 0.99796172 | 0.0416 | 0.1018 | 0.0809 | 0.0809 | TRUE | 0.5051 |
| 41 | 0.99796172 | 0.0634 | 0.0861 | 0.0776 | 0.0776 | TRUE | 1.3263 |
| 42 | 0.99796172 | 0.0634 | 0.0861 | 0.0776 | 0.0776 | TRUE | 1.3263 |
| 43 | 0.99796172 | 0.0634 | 0.0861 | 0.0776 | 0.0776 | TRUE | 1.3263 |
| 44 | 0.99796172 | 0.0634 | 0.0861 | 0.0776 | 0.0776 | TRUE | 1.3263 |
| 45 | 0.99796172 | 0.0634 | 0.0861 | 0.0776 | 0.0776 | TRUE | 1.3263 |
| 46 | 0.99796172 | 1.4958 | 0.0718 | 0.4403 | 1.4958 | TRUE | 0.4815 |
| 47 | 0.99796172 | 1.4958 | 0.0718 | 0.4403 | 1.4958 | TRUE | 0.4815 |
| 48 | 0.99796172 | 1.4958 | 0.0718 | 0.4403 | 1.4958 | TRUE | 0.4815 |
| 49 | 0.99796172 | 1.4899 | 0.0719 | 0.439 | 1.4899 | TRUE | 0.4768 |
| 50 | 0.99796172 | 1.4899 | 0.0719 | 0.439 | 1.4899 | TRUE | 0.4768 |
| 51 | 0.99796172 | 1.4899 | 0.0719 | 0.439 | 1.4899 | TRUE | 0.4768 |
| 52 | 0.99796172 | 1.4899 | 0.0719 | 0.439 | 1.4899 | TRUE | 0.4768 |
| 53 | 0.99796172 | 1.4899 | 0.0719 | 0.439 | 1.4899 | TRUE | 0.4768 |
| 54 | 0.99796172 | 1.4899 | 0.0719 | 0.439 | 1.4899 | TRUE | 0.4768 |
| 55 | 0.99796172 | 1.4899 | 0.0719 | 0.439 | 1.4899 | TRUE | 0.4768 |
| 56 | 0.99796172 | 1.4899 | 0.0719 | 0.439 | 1.4899 | TRUE | 0.4768 |
| 57 | 0.99796172 | 1.4899 | 0.0719 | 0.439 | 1.4899 | TRUE | 0.4768 |
| 58 | 0.99796172 | 1.4899 | 0.0719 | 0.439 | 1.4899 | TRUE | 0.4768 |
| 59 | 0.99796172 | 1.4899 | 0.0719 | 0.439 | 1.4899 | TRUE | 0.4768 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.1949 | 0.0977 | 0.1292 | 0.1292 | TRUE | 0.334 |
| 4 | 0.99796172 | 0.1949 | 0.0977 | 0.1292 | 0.1292 | TRUE | 0.334 |
| 5 | 0.99796172 | 0.1949 | 0.0977 | 0.1292 | 0.1292 | TRUE | 0.334 |
| 6 | 0.99796172 | 0.1949 | 0.0977 | 0.1292 | 0.1292 | TRUE | 0.334 |
| 7 | 0.99796172 | 0.1949 | 0.0977 | 0.1292 | 0.1292 | TRUE | 0.334 |
| 8 | 0.99796172 | 0.1949 | 0.0977 | 0.1292 | 0.1292 | TRUE | 0.334 |
| 9 | 0.99796172 | 0.1949 | 0.0977 | 0.1292 | 0.1292 | TRUE | 0.334 |
| 10 | 0.99796172 | 0.1949 | 0.0977 | 0.1292 | 0.1292 | TRUE | 0.334 |
| 11 | 0.99796172 | 0.1949 | 0.0977 | 0.1292 | 0.1292 | TRUE | 0.334 |
| 12 | 0.99796172 | 0.1949 | 0.0977 | 0.1292 | 0.1292 | TRUE | 0.334 |
| 13 | 0.99796172 | 0.1949 | 0.0977 | 0.1292 | 0.1292 | TRUE | 0.334 |
| 14 | 0.99796172 | 0.1949 | 0.0977 | 0.1292 | 0.1292 | TRUE | 0.334 |
| 15 | 0.99796172 | 0.1949 | 0.0977 | 0.1292 | 0.1292 | TRUE | 0.334 |
| 16 | 0.99796172 | 0.1949 | 0.0977 | 0.1292 | 0.1292 | TRUE | 0.334 |
| 17 | 0.99796172 | 0.1949 | 0.0977 | 0.1292 | 0.1292 | TRUE | 0.334 |
| 18 | 0.99796172 | 0.1949 | 0.0977 | 0.1292 | 0.1292 | TRUE | 0.334 |
| 19 | 0.99796172 | 0.1949 | 0.0977 | 0.1292 | 0.1292 | TRUE | 0.334 |
| 20 | 0.99796172 | 0.0171 | 0.0636 | 0.0453 | 0.0453 | TRUE | 0.2273 |
| 21 | 0.99796172 | 0.0171 | 0.0636 | 0.0453 | 0.0453 | TRUE | 0.2273 |
| 22 | 0.99796172 | 0.0171 | 0.0636 | 0.0453 | 0.0453 | TRUE | 0.2273 |
| 23 | 0.99796172 | 0.0171 | 0.0636 | 0.0453 | 0.0453 | TRUE | 0.2273 |
| 24 | 0.99796172 | 0.0171 | 0.0636 | 0.0453 | 0.0453 | TRUE | 0.2273 |
| 25 | 0.99796172 | 0.0171 | 0.0636 | 0.0453 | 0.0453 | TRUE | 0.2273 |
| 26 | 0.99796172 | 0.0171 | 0.0636 | 0.0453 | 0.0453 | TRUE | 0.2273 |
| 27 | 0.99796172 | 0.0171 | 0.0636 | 0.0453 | 0.0453 | TRUE | 0.2273 |
| 28 | 0.99796172 | 0.0171 | 0.0636 | 0.0453 | 0.0453 | TRUE | 0.2273 |
| 29 | 0.99796172 | 0.0113 | 0.1108 | 0.0768 | 0.0768 | TRUE | 0.3753 |
| 30 | 0.99796172 | 0.0113 | 0.1108 | 0.0768 | 0.0768 | TRUE | 0.3753 |
| 31 | 0.99796172 | 0.0227 | 0.0636 | 0.0482 | 0.0482 | TRUE | 0.4924 |
| 32 | 0.99796172 | 0.0227 | 0.0636 | 0.0482 | 0.0482 | TRUE | 0.4924 |
| 33 | 0.99796172 | 0.0227 | 0.0636 | 0.0482 | 0.0482 | TRUE | 0.4924 |
| 34 | 0.99796172 | 0.0227 | 0.0636 | 0.0482 | 0.0482 | TRUE | 0.4924 |
| 35 | 0.99796172 | 0.0227 | 0.0636 | 0.0482 | 0.0482 | TRUE | 0.4924 |
| 36 | 0.99796172 | 0.0227 | 0.0636 | 0.0482 | 0.0482 | TRUE | 0.4924 |
| 37 | 0.99796172 | 0.0227 | 0.0636 | 0.0482 | 0.0482 | TRUE | 0.4924 |
| 38 | 0.99796172 | 0.0227 | 0.0636 | 0.0482 | 0.0482 | TRUE | 0.4924 |
| 39 | 0.99796172 | 0.0227 | 0.0636 | 0.0482 | 0.0482 | TRUE | 0.4924 |
| 40 | 0.99796172 | 0.0227 | 0.0636 | 0.0482 | 0.0482 | TRUE | 0.4924 |
| 41 | 0.99796172 | 0.0227 | 0.0636 | 0.0482 | 0.0482 | TRUE | 0.4924 |
| 42 | 0.99796172 | 0.0227 | 0.0636 | 0.0482 | 0.0482 | TRUE | 0.4924 |
| 43 | 0.99796172 | 0.0227 | 0.0636 | 0.0482 | 0.0482 | TRUE | 0.4924 |
| 44 | 0.99796172 | 0.0605 | 0.085 | 0.0755 | 0.0755 | TRUE | 1.3827 |
| 45 | 0.99796172 | 0.0605 | 0.085 | 0.0755 | 0.0755 | TRUE | 1.3827 |
| 46 | 0.99796172 | 0.0605 | 0.085 | 0.0755 | 0.0755 | TRUE | 1.3827 |
| 47 | 0.99796172 | 0.0605 | 0.085 | 0.0755 | 0.0755 | TRUE | 1.3827 |
| 48 | 0.99796172 | 0.0605 | 0.085 | 0.0755 | 0.0755 | TRUE | 1.3827 |
| 49 | 0.99796172 | 0.0605 | 0.085 | 0.0755 | 0.0755 | TRUE | 1.3827 |
| 50 | 0.99796172 | 0.0605 | 0.085 | 0.0755 | 0.0755 | TRUE | 1.3827 |
| 51 | 0.99796172 | 0.0605 | 0.085 | 0.0755 | 0.0755 | TRUE | 1.3827 |
| 52 | 0.99796172 | 0.0605 | 0.085 | 0.0755 | 0.0755 | TRUE | 1.3827 |
| 53 | 0.99796172 | 0.0605 | 0.085 | 0.0755 | 0.0755 | TRUE | 1.3827 |
| 54 | 0.99796172 | 0.0605 | 0.085 | 0.0755 | 0.0755 | TRUE | 1.3827 |
| 55 | 0.99796172 | 0.0605 | 0.085 | 0.0755 | 0.0755 | TRUE | 1.3827 |
| 56 | 0.99796172 | 0.0605 | 0.085 | 0.0755 | 0.0755 | TRUE | 1.3827 |
| 57 | 0.99796172 | 0.0605 | 0.085 | 0.0755 | 0.0755 | TRUE | 1.3827 |
| 58 | 0.99796172 | 0.0605 | 0.085 | 0.0755 | 0.0755 | TRUE | 1.3827 |
| 59 | 0.99796172 | 0.0605 | 0.085 | 0.0755 | 0.0755 | TRUE | 1.3827 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 1.2037 | 0.1409 | 0.4206 | 1.2037 | TRUE | 0.3573 |
| 4 | 0.99796172 | 1.2037 | 0.1409 | 0.4206 | 1.2037 | TRUE | 0.3573 |
| 5 | 0.99796172 | 1.2037 | 0.1409 | 0.4206 | 1.2037 | TRUE | 0.3573 |
| 6 | 0.99796172 | 0.1493 | 0.0649 | 0.0928 | 0.0928 | TRUE | 0.3897 |
| 7 | 0.99796172 | 0.0298 | 0.0787 | 0.0605 | 0.0605 | TRUE | 0.4691 |
| 8 | 0.99796172 | 0.0298 | 0.0787 | 0.0605 | 0.0605 | TRUE | 0.4691 |
| 9 | 0.99796172 | 0.0298 | 0.0787 | 0.0605 | 0.0605 | TRUE | 0.4691 |
| 10 | 0.99796172 | 0.0298 | 0.0787 | 0.0605 | 0.0605 | TRUE | 0.4691 |
| 11 | 0.99796172 | 0.0298 | 0.0787 | 0.0605 | 0.0605 | TRUE | 0.4691 |
| 12 | 0.99796172 | 0.0298 | 0.0787 | 0.0605 | 0.0605 | TRUE | 0.4691 |
| 13 | 0.99796172 | 0.0298 | 0.0787 | 0.0605 | 0.0605 | TRUE | 0.4691 |
| 14 | 0.99796172 | 0.0298 | 0.0787 | 0.0605 | 0.0605 | TRUE | 0.4691 |
| 15 | 0.99796172 | 0.0298 | 0.0787 | 0.0605 | 0.0605 | TRUE | 0.4691 |
| 16 | 0.99796172 | 0.0298 | 0.0787 | 0.0605 | 0.0605 | TRUE | 0.4691 |
| 17 | 0.99796172 | 0.0298 | 0.0787 | 0.0605 | 0.0605 | TRUE | 0.4691 |
| 18 | 0.99796172 | 0.0298 | 0.0787 | 0.0605 | 0.0605 | TRUE | 0.4691 |
| 19 | 0.99796172 | 0.0298 | 0.0787 | 0.0605 | 0.0605 | TRUE | 0.4691 |
| 20 | 0.99796172 | 0.0298 | 0.0787 | 0.0605 | 0.0605 | TRUE | 0.4691 |
| 21 | 0.99796172 | 0.0298 | 0.0787 | 0.0605 | 0.0605 | TRUE | 0.4691 |
| 22 | 0.99796172 | 0.0298 | 0.0787 | 0.0605 | 0.0605 | TRUE | 0.4691 |
| 23 | 0.99796172 | 0.0298 | 0.0787 | 0.0605 | 0.0605 | TRUE | 0.4691 |
| 24 | 0.99796172 | 0.0298 | 0.0787 | 0.0605 | 0.0605 | TRUE | 0.4691 |
| 25 | 0.99796172 | 0.0298 | 0.0787 | 0.0605 | 0.0605 | TRUE | 0.4691 |
| 26 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 27 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 28 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 29 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 30 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 31 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 32 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 33 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 34 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 35 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 36 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 37 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 38 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 39 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 40 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 41 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 42 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 43 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 44 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 45 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 46 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 47 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 48 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 49 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 50 | 0.99796172 | 0.9357 | 0.0864 | 0.3179 | 0.9357 | TRUE | 0.3363 |
| 51 | 0.99796172 | 0.0431 | 0.0883 | 0.072 | 0.072 | TRUE | 0.7209 |
| 52 | 0.99796172 | 0.0431 | 0.0883 | 0.072 | 0.072 | TRUE | 0.7209 |
| 53 | 0.99796172 | 0.0431 | 0.0883 | 0.072 | 0.072 | TRUE | 0.7209 |
| 54 | 0.99796172 | 0.0431 | 0.0883 | 0.072 | 0.072 | TRUE | 0.7209 |
| 55 | 0.99796172 | 0.0431 | 0.0883 | 0.072 | 0.072 | TRUE | 0.7209 |
| 56 | 0.99796172 | 0.0431 | 0.0883 | 0.072 | 0.072 | TRUE | 0.7209 |
| 57 | 0.99796172 | 0.0431 | 0.0883 | 0.072 | 0.072 | TRUE | 0.7209 |
| 58 | 0.99796172 | 0.0431 | 0.0883 | 0.072 | 0.072 | TRUE | 0.7209 |
| 59 | 0.99796172 | 0.0431 | 0.0883 | 0.072 | 0.072 | TRUE | 0.7209 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 4 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 5 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 6 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 7 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 8 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 9 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 10 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 11 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 12 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 13 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 14 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 15 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 16 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 17 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 18 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 19 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 20 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 21 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 22 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 23 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 24 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 25 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 26 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 27 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 28 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 29 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 30 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 31 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 32 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 33 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 34 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 35 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 36 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 37 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 38 | 0.99796172 | 0.0576 | 0.1629 | 0.1268 | 0.1268 | TRUE | 0.836 |
| 39 | 0.99796172 | 0.0384 | 0.0658 | 0.0554 | 0.0554 | TRUE | 0.296 |
| 40 | 0.99796172 | 0.0454 | 0.1075 | 0.0855 | 0.0855 | TRUE | 1.0762 |
| 41 | 0.99796172 | 0.0454 | 0.1075 | 0.0855 | 0.0855 | TRUE | 1.0762 |
| 42 | 0.99796172 | 0.0528 | 0.1103 | 0.0901 | 0.0901 | TRUE | 1.1846 |
| 43 | 0.99796172 | 0.0528 | 0.1103 | 0.0901 | 0.0901 | TRUE | 1.1846 |
| 44 | 0.99796172 | 0.0528 | 0.1103 | 0.0901 | 0.0901 | TRUE | 1.1846 |
| 45 | 0.99796172 | 0.0528 | 0.1103 | 0.0901 | 0.0901 | TRUE | 1.1846 |
| 46 | 0.99796172 | 0.0528 | 0.1103 | 0.0901 | 0.0901 | TRUE | 1.1846 |
| 47 | 0.99796172 | 0.0528 | 0.1103 | 0.0901 | 0.0901 | TRUE | 1.1846 |
| 48 | 0.99796172 | 0.0191 | 0.1053 | 0.0745 | 0.0745 | TRUE | 0.3429 |
| 49 | 0.99796172 | 0.0191 | 0.1053 | 0.0745 | 0.0745 | TRUE | 0.3429 |
| 50 | 0.99796172 | 0.0191 | 0.1053 | 0.0745 | 0.0745 | TRUE | 0.3429 |
| 51 | 0.99796172 | 0.0191 | 0.1053 | 0.0745 | 0.0745 | TRUE | 0.3429 |
| 52 | 0.99796172 | 0.0191 | 0.1053 | 0.0745 | 0.0745 | TRUE | 0.3429 |
| 53 | 0.99796172 | 0.0191 | 0.1053 | 0.0745 | 0.0745 | TRUE | 0.3429 |
| 54 | 0.99796172 | 0.0191 | 0.1053 | 0.0745 | 0.0745 | TRUE | 0.3429 |
| 55 | 0.99796172 | 0.0191 | 0.1053 | 0.0745 | 0.0745 | TRUE | 0.3429 |
| 56 | 0.99796172 | 0.0191 | 0.1053 | 0.0745 | 0.0745 | TRUE | 0.3429 |
| 57 | 0.99796172 | 0.0191 | 0.1053 | 0.0745 | 0.0745 | TRUE | 0.3429 |
| 58 | 0.99796172 | 0.0191 | 0.1053 | 0.0745 | 0.0745 | TRUE | 0.3429 |
| 59 | 0.99796172 | 0.0191 | 0.1053 | 0.0745 | 0.0745 | TRUE | 0.3429 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.0105 | 0.0631 | 0.0419 | 0.0419 | TRUE | 0.2152 |
| 4 | 0.99796172 | 0.0105 | 0.0631 | 0.0419 | 0.0419 | TRUE | 0.2152 |
| 5 | 0.99796172 | 0.0105 | 0.0631 | 0.0419 | 0.0419 | TRUE | 0.2152 |
| 6 | 0.99796172 | 0.0105 | 0.0631 | 0.0419 | 0.0419 | TRUE | 0.2152 |
| 7 | 0.99796172 | 0.0105 | 0.0631 | 0.0419 | 0.0419 | TRUE | 0.2152 |
| 8 | 0.99796172 | 0.0105 | 0.0631 | 0.0419 | 0.0419 | TRUE | 0.2152 |
| 9 | 0.99796172 | 0.0105 | 0.0631 | 0.0419 | 0.0419 | TRUE | 0.2152 |
| 10 | 0.99796172 | 0.0105 | 0.0631 | 0.0419 | 0.0419 | TRUE | 0.2152 |
| 11 | 0.99796172 | 0.0105 | 0.0631 | 0.0419 | 0.0419 | TRUE | 0.2152 |
| 12 | 0.99796172 | 0.0105 | 0.0631 | 0.0419 | 0.0419 | TRUE | 0.2152 |
| 13 | 0.99796172 | 0.0105 | 0.0631 | 0.042 | 0.042 | TRUE | 0.2164 |
| 14 | 0.99796172 | 0.066 | 0.1212 | 0.1023 | 0.1023 | TRUE | 0.8714 |
| 15 | 0.99796172 | 0.066 | 0.1212 | 0.1023 | 0.1023 | TRUE | 0.8714 |
| 16 | 0.99796172 | 0.1122 | 0.1213 | 0.1183 | 0.1183 | TRUE | 0.5918 |
| 17 | 0.99796172 | 0.1122 | 0.1213 | 0.1183 | 0.1183 | TRUE | 0.5918 |
| 18 | 0.99796172 | 0.1122 | 0.1213 | 0.1183 | 0.1183 | TRUE | 0.5918 |
| 19 | 0.99796172 | 0.1122 | 0.1213 | 0.1183 | 0.1183 | TRUE | 0.5918 |
| 20 | 0.99796172 | 0.1122 | 0.1213 | 0.1183 | 0.1183 | TRUE | 0.5918 |
| 21 | 0.99796172 | 0.1122 | 0.1213 | 0.1183 | 0.1183 | TRUE | 0.5918 |
| 22 | 0.99796172 | 0.1122 | 0.1213 | 0.1183 | 0.1183 | TRUE | 0.5918 |
| 23 | 0.99796172 | 0.1122 | 0.1213 | 0.1183 | 0.1183 | TRUE | 0.5918 |
| 24 | 0.99796172 | 0.0554 | 0.0779 | 0.0699 | 0.0699 | TRUE | 0.3326 |
| 25 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 26 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 27 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 28 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 29 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 30 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 31 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 32 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 33 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 34 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 35 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 36 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 37 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 38 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 39 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 40 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 41 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 42 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 43 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 44 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 45 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 46 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 47 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 48 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 49 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 50 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 51 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 52 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 53 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 54 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 55 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 56 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 57 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 58 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 59 | 0.99796172 | 0.1186 | 0.1041 | 0.1089 | 0.1089 | TRUE | 0.4345 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.0193 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.4754 |
| 4 | 0.99796172 | 0.0193 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.4754 |
| 5 | 0.99796172 | 0.0193 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.4754 |
| 6 | 0.99796172 | 0.0193 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.4754 |
| 7 | 0.99796172 | 0.0193 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.4754 |
| 8 | 0.99796172 | 0.0193 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.4754 |
| 9 | 0.99796172 | 0.0193 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.4754 |
| 10 | 0.99796172 | 0.0193 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.4754 |
| 11 | 0.99796172 | 0.0193 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.4754 |
| 12 | 0.99796172 | 0.0193 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.4754 |
| 13 | 0.99796172 | 0.0193 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.4754 |
| 14 | 0.99796172 | 0.0389 | 0.0678 | 0.0569 | 0.0569 | TRUE | 0.57 |
| 15 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 16 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 17 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 18 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 19 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 20 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 21 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 22 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 23 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 24 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 25 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 26 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 27 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 28 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 29 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 30 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 31 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 32 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 33 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 34 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 35 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 36 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 37 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 38 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 39 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 40 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 41 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 42 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 43 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 44 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 45 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 46 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 47 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 48 | 0.99796172 | 0.0381 | 0.0647 | 0.0546 | 0.0546 | TRUE | 0.7126 |
| 49 | 0.99796172 | 0.1448 | 0.1097 | 0.1212 | 0.1212 | TRUE | 0.6215 |
| 50 | 0.99796172 | 0.0371 | 0.0647 | 0.0542 | 0.0542 | TRUE | 0.6969 |
| 51 | 0.99796172 | 0.0371 | 0.0647 | 0.0542 | 0.0542 | TRUE | 0.6969 |
| 52 | 0.99796172 | 0.0371 | 0.0647 | 0.0542 | 0.0542 | TRUE | 0.6969 |
| 53 | 0.99796172 | 0.0371 | 0.0647 | 0.0542 | 0.0542 | TRUE | 0.6969 |
| 54 | 0.99796172 | 0.0371 | 0.0647 | 0.0542 | 0.0542 | TRUE | 0.6969 |
| 55 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 56 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 57 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 58 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 59 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 4 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 5 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 6 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 7 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 8 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 9 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 10 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 11 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 12 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 13 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 14 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 15 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 16 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 17 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 18 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 19 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 20 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 21 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 22 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 23 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 24 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 25 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 26 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 27 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 28 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 29 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 30 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 31 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 32 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 33 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 34 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 35 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 36 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 37 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 38 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 39 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 40 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 41 | 0.99796172 | 0.0258 | 0.1169 | 0.0847 | 0.0847 | TRUE | 0.5453 |
| 42 | 0.99796172 | 0.0379 | 0.0647 | 0.0545 | 0.0545 | TRUE | 0.7025 |
| 43 | 0.99796172 | 0.0379 | 0.0647 | 0.0545 | 0.0545 | TRUE | 0.7025 |
| 44 | 0.99796172 | 0.0339 | 0.0705 | 0.0567 | 0.0567 | TRUE | 0.7864 |
| 45 | 0.99796172 | 0.0339 | 0.0705 | 0.0567 | 0.0567 | TRUE | 0.7864 |
| 46 | 0.99796172 | 0.0339 | 0.0705 | 0.0567 | 0.0567 | TRUE | 0.7864 |
| 47 | 0.99796172 | 0.0339 | 0.0705 | 0.0567 | 0.0567 | TRUE | 0.7864 |
| 48 | 0.99796172 | 0.0339 | 0.0705 | 0.0567 | 0.0567 | TRUE | 0.7864 |
| 49 | 0.99796172 | 0.0193 | 0.0912 | 0.0647 | 0.0647 | TRUE | 0.4029 |
| 50 | 0.99796172 | 0.0193 | 0.0912 | 0.0647 | 0.0647 | TRUE | 0.4029 |
| 51 | 0.99796172 | 0.0193 | 0.0912 | 0.0647 | 0.0647 | TRUE | 0.4029 |
| 52 | 0.99796172 | 0.0199 | 0.0906 | 0.0645 | 0.0645 | TRUE | 0.4112 |
| 53 | 0.99796172 | 0.0136 | 0.1165 | 0.0805 | 0.0805 | TRUE | 0.2365 |
| 54 | 0.99796172 | 0.0136 | 0.1165 | 0.0805 | 0.0805 | TRUE | 0.2365 |
| 55 | 0.99796172 | 0.0136 | 0.1165 | 0.0805 | 0.0805 | TRUE | 0.2365 |
| 56 | 0.99796172 | 0.0136 | 0.1165 | 0.0805 | 0.0805 | TRUE | 0.2365 |
| 57 | 0.99796172 | 0.0136 | 0.1165 | 0.0805 | 0.0805 | TRUE | 0.2365 |
| 58 | 0.99796172 | 0.0136 | 0.1165 | 0.0805 | 0.0805 | TRUE | 0.2365 |
| 59 | 0.99796172 | 0.0136 | 0.1165 | 0.0805 | 0.0805 | TRUE | 0.2365 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.0156 | 0.072 | 0.05 | 0.05 | TRUE | 0.1884 |
| 4 | 0.99796172 | 0.0154 | 0.072 | 0.0499 | 0.0499 | TRUE | 0.1797 |
| 5 | 0.99796172 | 0.0154 | 0.072 | 0.0499 | 0.0499 | TRUE | 0.1797 |
| 6 | 0.99796172 | 0.0154 | 0.072 | 0.0499 | 0.0499 | TRUE | 0.1797 |
| 7 | 0.99796172 | 0.0154 | 0.072 | 0.0499 | 0.0499 | TRUE | 0.1797 |
| 8 | 0.99796172 | 0.0154 | 0.072 | 0.0499 | 0.0499 | TRUE | 0.1797 |
| 9 | 0.99796172 | 0.0154 | 0.072 | 0.0499 | 0.0499 | TRUE | 0.1797 |
| 10 | 0.99796172 | 0.0154 | 0.072 | 0.0499 | 0.0499 | TRUE | 0.1797 |
| 11 | 0.99796172 | 0.0155 | 0.072 | 0.0499 | 0.0499 | TRUE | 0.1833 |
| 12 | 0.99796172 | 0.0155 | 0.072 | 0.0499 | 0.0499 | TRUE | 0.1833 |
| 13 | 0.99796172 | 0.0155 | 0.072 | 0.0499 | 0.0499 | TRUE | 0.1833 |
| 14 | 0.99796172 | 0.0155 | 0.072 | 0.0499 | 0.0499 | TRUE | 0.1833 |
| 15 | 0.99796172 | 0.0155 | 0.072 | 0.0499 | 0.0499 | TRUE | 0.1833 |
| 16 | 0.99796172 | 0.0155 | 0.072 | 0.0499 | 0.0499 | TRUE | 0.1833 |
| 17 | 0.99796172 | 0.0155 | 0.072 | 0.0499 | 0.0499 | TRUE | 0.1833 |
| 18 | 0.99796172 | 0.0155 | 0.072 | 0.0499 | 0.0499 | TRUE | 0.1833 |
| 19 | 0.99796172 | 0.0155 | 0.072 | 0.0499 | 0.0499 | TRUE | 0.1833 |
| 20 | 0.99796172 | 0.0155 | 0.072 | 0.0499 | 0.0499 | TRUE | 0.1833 |
| 21 | 0.99796172 | 0.0199 | 0.0686 | 0.0496 | 0.0496 | TRUE | 0.2919 |
| 22 | 0.99796172 | 0.0207 | 0.0685 | 0.0498 | 0.0498 | TRUE | 0.2948 |
| 23 | 0.99796172 | 0.0207 | 0.0685 | 0.0498 | 0.0498 | TRUE | 0.2948 |
| 24 | 0.99796172 | 0.0207 | 0.0685 | 0.0498 | 0.0498 | TRUE | 0.2948 |
| 25 | 0.99796172 | 0.0207 | 0.0685 | 0.0498 | 0.0498 | TRUE | 0.2948 |
| 26 | 0.99796172 | 0.0207 | 0.0685 | 0.0498 | 0.0498 | TRUE | 0.2948 |
| 27 | 0.99796172 | 0.0207 | 0.0685 | 0.0498 | 0.0498 | TRUE | 0.2948 |
| 28 | 0.99796172 | 0.0207 | 0.0685 | 0.0498 | 0.0498 | TRUE | 0.2948 |
| 29 | 0.99796172 | 0.0207 | 0.0685 | 0.0498 | 0.0498 | TRUE | 0.2948 |
| 30 | 0.99796172 | 0.0207 | 0.0685 | 0.0498 | 0.0498 | TRUE | 0.2948 |
| 31 | 0.99796172 | 0.0207 | 0.0685 | 0.0498 | 0.0498 | TRUE | 0.2948 |
| 32 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 33 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 34 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 35 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 36 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 37 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 38 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 39 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 40 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 41 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 42 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 43 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 44 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 45 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 46 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 47 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 48 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 49 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 50 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 51 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 52 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 53 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 54 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 55 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 56 | 0.99796172 | 0.0096 | 0.0634 | 0.0412 | 0.0412 | TRUE | 0.216 |
| 57 | 0.99796172 | 0.0094 | 0.0634 | 0.0411 | 0.0411 | TRUE | 0.2084 |
| 58 | 0.99796172 | 0.0094 | 0.0634 | 0.0411 | 0.0411 | TRUE | 0.2084 |
| 59 | 0.99796172 | 0.0094 | 0.0634 | 0.0411 | 0.0411 | TRUE | 0.2084 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.0094 | 0.0634 | 0.0411 | 0.0411 | TRUE | 0.2087 |
| 4 | 0.99796172 | 0.0094 | 0.0634 | 0.0411 | 0.0411 | TRUE | 0.2087 |
| 5 | 0.99796172 | 0.0094 | 0.0634 | 0.0411 | 0.0411 | TRUE | 0.2087 |
| 6 | 0.99796172 | 0.1038 | 0.0842 | 0.0908 | 0.0908 | TRUE | 0.3848 |
| 7 | 0.99796172 | 0.0806 | 0.0809 | 0.0808 | 0.0808 | TRUE | 0.6606 |
| 8 | 0.99796172 | 0.0175 | 0.0788 | 0.0556 | 0.0556 | TRUE | 0.268 |
| 9 | 0.99796172 | 0.1042 | 0.0842 | 0.091 | 0.091 | TRUE | 0.4166 |
| 10 | 0.99796172 | 0.1042 | 0.0842 | 0.091 | 0.091 | TRUE | 0.4166 |
| 11 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 12 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 13 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 14 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 15 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 16 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 17 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 18 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 19 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 20 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 21 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 22 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 23 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 24 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 25 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 26 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 27 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 28 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 29 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 30 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 31 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 32 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 33 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 34 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 35 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 36 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 37 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 38 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 39 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 40 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 41 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 42 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 43 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 44 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 45 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 46 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 47 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 48 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 49 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 50 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 51 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 52 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 53 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 54 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 55 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 56 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 57 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 58 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 59 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 4 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 5 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 6 | 0.99796172 | 0.0525 | 0.1039 | 0.0859 | 0.0859 | TRUE | 1.0724 |
| 7 | 0.99803669 | 0.0446 | 0.1017 | 0.0815 | 0.0815 | TRUE | 0.7395 |
| 8 | 0.99803669 | 0.0446 | 0.1017 | 0.0815 | 0.0815 | TRUE | 0.7395 |
| 9 | 0.99803669 | 0.0446 | 0.1017 | 0.0815 | 0.0815 | TRUE | 0.7395 |
| 10 | 0.99803669 | 0.0446 | 0.1017 | 0.0815 | 0.0815 | TRUE | 0.7395 |
| 11 | 0.99803669 | 0.0446 | 0.1017 | 0.0815 | 0.0815 | TRUE | 0.7395 |
| 12 | 0.99803669 | 0.0446 | 0.1017 | 0.0815 | 0.0815 | TRUE | 0.7395 |
| 13 | 0.99803669 | 0.0446 | 0.1017 | 0.0815 | 0.0815 | TRUE | 0.7395 |
| 14 | 0.99803669 | 0.0446 | 0.1017 | 0.0815 | 0.0815 | TRUE | 0.7395 |
| 15 | 0.99796172 | 0.0074 | 0.0966 | 0.0638 | 0.0638 | TRUE | 0.1927 |
| 16 | 0.99796172 | 0.0076 | 0.0967 | 0.0639 | 0.0639 | TRUE | 0.1981 |
| 17 | 0.99803669 | 0.0729 | 0.0733 | 0.0731 | 0.0731 | TRUE | 0.9276 |
| 18 | 0.99803669 | 0.0729 | 0.0733 | 0.0731 | 0.0731 | TRUE | 0.9276 |
| 19 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 20 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 21 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 22 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 23 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 24 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 25 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 26 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 27 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 28 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 29 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 30 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 31 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 32 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 33 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 34 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 35 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 36 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 37 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 38 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 39 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 40 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 41 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 42 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 43 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 44 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 45 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 46 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 47 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 48 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 49 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 50 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 51 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 52 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 53 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 54 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 55 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 56 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 57 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 58 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 59 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 4 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 5 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 6 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 7 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 8 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 9 | 0.99796172 | 0.0796 | 0.0811 | 0.0806 | 0.0806 | TRUE | 0.5497 |
| 10 | 0.99796172 | 0.0065 | 0.0636 | 0.0398 | 0.0398 | TRUE | 0.1339 |
| 11 | 0.99796172 | 0.0065 | 0.0636 | 0.0398 | 0.0398 | TRUE | 0.1339 |
| 12 | 0.99796172 | 0.0065 | 0.0636 | 0.0398 | 0.0398 | TRUE | 0.1339 |
| 13 | 0.99796172 | 0.0065 | 0.0636 | 0.0398 | 0.0398 | TRUE | 0.1339 |
| 14 | 0.99796172 | 0.0065 | 0.0636 | 0.0398 | 0.0398 | TRUE | 0.1339 |
| 15 | 0.99796172 | 0.0065 | 0.0636 | 0.0398 | 0.0398 | TRUE | 0.1339 |
| 16 | 0.99796172 | 0.0065 | 0.0636 | 0.0398 | 0.0398 | TRUE | 0.1339 |
| 17 | 0.99796172 | 0.0065 | 0.0636 | 0.0398 | 0.0398 | TRUE | 0.1339 |
| 18 | 0.99796172 | 0.0065 | 0.0636 | 0.0398 | 0.0398 | TRUE | 0.1339 |
| 19 | 0.99796172 | 0.0065 | 0.0636 | 0.0398 | 0.0398 | TRUE | 0.1339 |
| 20 | 0.99796172 | 0.0065 | 0.0636 | 0.0398 | 0.0398 | TRUE | 0.1339 |
| 21 | 0.99796172 | 0.0065 | 0.0636 | 0.0398 | 0.0398 | TRUE | 0.1339 |
| 22 | 0.99803669 | 0.0066 | 0.0636 | 0.0399 | 0.0399 | TRUE | 0.135 |
| 23 | 0.99803669 | 0.0066 | 0.0636 | 0.0399 | 0.0399 | TRUE | 0.135 |
| 24 | 0.99929018 | 0.0064 | 0.0636 | 0.0398 | 0.0398 | TRUE | 0.1323 |
| 25 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 26 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 27 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 28 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 29 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 30 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 31 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 32 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 33 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 34 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 35 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 36 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 37 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 38 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 39 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 40 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 41 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 42 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 43 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 44 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 45 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 46 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 47 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 48 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 49 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 50 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 51 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 52 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 53 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 54 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 55 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 56 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 57 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 58 | 0.99796172 | 0.0323 | 0.0937 | 0.0715 | 0.0715 | TRUE | 0.6903 |
| 59 | 0.99796172 | 0.0071 | 0.0967 | 0.0638 | 0.0638 | TRUE | 0.1882 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 4 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 5 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 6 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 7 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 8 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 9 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 10 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 11 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 12 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 13 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 14 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 15 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 16 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 17 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 18 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 19 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 20 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 21 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 22 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 23 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 24 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 25 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 26 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 27 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 28 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 29 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 30 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 31 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 32 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 33 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 34 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 35 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 36 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 37 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 38 | 0.99803669 | 0.1171 | 0.1536 | 0.1416 | 0.1416 | TRUE | 0.4842 |
| 39 | 0.99868672 | 0.1466 | 0.1381 | 0.1409 | 0.1409 | TRUE | 1.4945 |
| 40 | 0.99916959 | 0.0318 | 0.0666 | 0.0533 | 0.0533 | TRUE | 0.5013 |
| 41 | 0.99916959 | 0.0319 | 0.0666 | 0.0533 | 0.0533 | TRUE | 0.5022 |
| 42 | 0.99916959 | 0.0319 | 0.0666 | 0.0533 | 0.0533 | TRUE | 0.5022 |
| 43 | 0.99916959 | 0.0319 | 0.0666 | 0.0533 | 0.0533 | TRUE | 0.5022 |
| 44 | 0.99916959 | 0.0319 | 0.0666 | 0.0533 | 0.0533 | TRUE | 0.5022 |
| 45 | 0.99796172 | 0.0323 | 0.0639 | 0.0539 | 0.0539 | TRUE | 0.643 |
| 46 | 0.99796172 | 0.0323 | 0.0639 | 0.0539 | 0.0539 | TRUE | 0.643 |
| 47 | 0.99796172 | 0.0323 | 0.0639 | 0.0539 | 0.0539 | TRUE | 0.643 |
| 48 | 0.99796172 | 0.0323 | 0.0639 | 0.0539 | 0.0539 | TRUE | 0.643 |
| 49 | 0.99796172 | 0.0323 | 0.0639 | 0.0539 | 0.0539 | TRUE | 0.643 |
| 50 | 0.99796172 | 0.0323 | 0.0639 | 0.0539 | 0.0539 | TRUE | 0.643 |
| 51 | 0.99796172 | 0.0323 | 0.0639 | 0.0539 | 0.0539 | TRUE | 0.643 |
| 52 | 0.99796172 | 0.0323 | 0.0639 | 0.0539 | 0.0539 | TRUE | 0.643 |
| 53 | 0.99796172 | 0.0323 | 0.0639 | 0.0539 | 0.0539 | TRUE | 0.643 |
| 54 | 0.99796172 | 0.0323 | 0.0639 | 0.0539 | 0.0539 | TRUE | 0.643 |
| 55 | 0.99796172 | 0.0323 | 0.0639 | 0.0539 | 0.0539 | TRUE | 0.643 |
| 56 | 0.99796172 | 0.0323 | 0.0639 | 0.0539 | 0.0539 | TRUE | 0.643 |
| 57 | 0.99796172 | 0.0323 | 0.0639 | 0.0539 | 0.0539 | TRUE | 0.643 |
| 58 | 0.99796172 | 0.0323 | 0.0639 | 0.0539 | 0.0539 | TRUE | 0.643 |
| 59 | 0.99796172 | 0.0323 | 0.0639 | 0.0539 | 0.0539 | TRUE | 0.643 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 4 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 5 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 6 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 7 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 8 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 9 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 10 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 11 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 12 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 13 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 14 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 15 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 16 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 17 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 18 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 19 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 20 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 21 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 22 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 23 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 24 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 25 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 26 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 27 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 28 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 29 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 30 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 31 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 32 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 33 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 34 | 0.99796172 | 0.0132 | 0.0633 | 0.0446 | 0.0446 | TRUE | 0.2273 |
| 35 | 0.99796172 | 0.0429 | 0.1012 | 0.0805 | 0.0805 | TRUE | 0.7913 |
| 36 | 0.99796172 | 0.0144 | 0.0832 | 0.0573 | 0.0573 | TRUE | 0.1868 |
| 37 | 0.99796172 | 0.0178 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.2788 |
| 38 | 0.99796172 | 0.0178 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.2788 |
| 39 | 0.99796172 | 0.0178 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.2788 |
| 40 | 0.99796172 | 0.0178 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.2788 |
| 41 | 0.99796172 | 0.0178 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.2788 |
| 42 | 0.99796172 | 0.0178 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.2788 |
| 43 | 0.99796172 | 0.0178 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.2788 |
| 44 | 0.99796172 | 0.0178 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.2788 |
| 45 | 0.99796172 | 0.0178 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.2788 |
| 46 | 0.99796172 | 0.0178 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.2788 |
| 47 | 0.99796172 | 0.0178 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.2788 |
| 48 | 0.99796172 | 0.0178 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.2788 |
| 49 | 0.99796172 | 0.0178 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.2788 |
| 50 | 0.99796172 | 0.0178 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.2788 |
| 51 | 0.99796172 | 0.0178 | 0.1135 | 0.0798 | 0.0798 | TRUE | 0.2788 |
| 52 | 0.99796172 | 0.02 | 0.0629 | 0.0474 | 0.0474 | TRUE | 0.5561 |
| 53 | 0.99796172 | 0.02 | 0.0629 | 0.0474 | 0.0474 | TRUE | 0.5561 |
| 54 | 0.99796172 | 0.02 | 0.0629 | 0.0474 | 0.0474 | TRUE | 0.5561 |
| 55 | 0.99796172 | 0.02 | 0.0629 | 0.0474 | 0.0474 | TRUE | 0.5561 |
| 56 | 0.99796172 | 0.02 | 0.0629 | 0.0474 | 0.0474 | TRUE | 0.5561 |
| 57 | 0.99796172 | 0.02 | 0.0629 | 0.0474 | 0.0474 | TRUE | 0.5561 |
| 58 | 0.99796172 | 0.02 | 0.0629 | 0.0474 | 0.0474 | TRUE | 0.5561 |
| 59 | 0.99796172 | 0.02 | 0.0629 | 0.0474 | 0.0474 | TRUE | 0.5561 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.02 | 0.0629 | 0.0474 | 0.0474 | TRUE | 0.5541 |
| 4 | 0.99796172 | 0.1357 | 0.1429 | 0.1405 | 0.1405 | TRUE | 2.663 |
| 5 | 0.99796172 | 0.1357 | 0.1429 | 0.1405 | 0.1405 | TRUE | 2.663 |
| 6 | 0.99796172 | 0.1357 | 0.1429 | 0.1405 | 0.1405 | TRUE | 2.663 |
| 7 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 8 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 9 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 10 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 11 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 12 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 13 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 14 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 15 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 16 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 17 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 18 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 19 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 20 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 21 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 22 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 23 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 24 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 25 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 26 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 27 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 28 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 29 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 30 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 31 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 32 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 33 | 0.99796172 | 0 | 0.1446 | 0.0966 | 0.0966 | TRUE | 0.1828 |
| 34 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 35 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 36 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 37 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 38 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 39 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 40 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 41 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 42 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 43 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 44 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 45 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 46 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 47 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 48 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 49 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 50 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 51 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 52 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 53 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 54 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 55 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 56 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 57 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 58 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 59 | 0.99796172 | 0.0344 | 0.0686 | 0.0556 | 0.0556 | TRUE | 0.6201 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 4 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 5 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 6 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 7 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 8 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 9 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 10 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 11 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 12 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 13 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 14 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 15 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 16 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 17 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 18 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 19 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 20 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 21 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 22 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 23 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 24 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 25 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 26 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 27 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 28 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 29 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 30 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 31 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 32 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 33 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 34 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 35 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 36 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 37 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 38 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 39 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2327 |
| 40 | 0.99796172 | 0.0181 | 0.0704 | 0.0499 | 0.0499 | TRUE | 0.256 |
| 41 | 0.99796172 | 0.0181 | 0.0704 | 0.0499 | 0.0499 | TRUE | 0.256 |
| 42 | 0.99796172 | 0.0181 | 0.0704 | 0.0499 | 0.0499 | TRUE | 0.256 |
| 43 | 0.99796172 | 0.2192 | 0.067 | 0.115 | 0.115 | TRUE | 0.19 |
| 44 | 0.99796172 | 0.1072 | 0.0795 | 0.0889 | 0.0889 | TRUE | 0.6072 |
| 45 | 0.99796172 | 0.1072 | 0.0795 | 0.0889 | 0.0889 | TRUE | 0.6072 |
| 46 | 0.99796172 | 0.1072 | 0.0795 | 0.0889 | 0.0889 | TRUE | 0.6072 |
| 47 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2382 |
| 48 | 0.99796172 | 0.0391 | 0.075 | 0.0618 | 0.0618 | TRUE | 0.2382 |
| 49 | 0.99796172 | 0.1306 | 0.08 | 0.0969 | 0.0969 | TRUE | 0.5889 |
| 50 | 0.99796172 | 0.1306 | 0.08 | 0.0969 | 0.0969 | TRUE | 0.5889 |
| 51 | 0.99796172 | 0.1306 | 0.08 | 0.0969 | 0.0969 | TRUE | 0.5889 |
| 52 | 0.99796172 | 0.1306 | 0.08 | 0.0969 | 0.0969 | TRUE | 0.5889 |
| 53 | 0.99796172 | 0.1306 | 0.08 | 0.0969 | 0.0969 | TRUE | 0.5889 |
| 54 | 0.99796172 | 0.1306 | 0.08 | 0.0969 | 0.0969 | TRUE | 0.5889 |
| 55 | 0.99796172 | 0 | 0.1429 | 0.0963 | 0.0963 | TRUE | 0.2014 |
| 56 | 0.99796172 | 0.0279 | 0.0633 | 0.0494 | 0.0494 | TRUE | 0.3863 |
| 57 | 0.99796172 | 0.0279 | 0.0633 | 0.0494 | 0.0494 | TRUE | 0.3863 |
| 58 | 0.99796172 | 0.0279 | 0.0633 | 0.0494 | 0.0494 | TRUE | 0.3863 |
| 59 | 0.99796172 | 0.0279 | 0.0633 | 0.0494 | 0.0494 | TRUE | 0.3863 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.0279 | 0.0633 | 0.0494 | 0.0494 | TRUE | 0.3863 |
| 4 | 0.99796172 | 0.0279 | 0.0633 | 0.0494 | 0.0494 | TRUE | 0.3863 |
| 5 | 0.99796172 | 0.0279 | 0.0633 | 0.0494 | 0.0494 | TRUE | 0.3863 |
| 6 | 0.99796172 | 0.0279 | 0.0633 | 0.0494 | 0.0494 | TRUE | 0.3863 |
| 7 | 0.99796172 | 0.2731 | 0.0673 | 0.1304 | 0.1304 | TRUE | 0.2014 |
| 8 | 0.99796172 | 0.0144 | 0.0629 | 0.0445 | 0.0445 | TRUE | 0.2332 |
| 9 | 0.99796172 | 0.0144 | 0.0629 | 0.0445 | 0.0445 | TRUE | 0.2332 |
| 10 | 0.99796172 | 0.0144 | 0.0629 | 0.0445 | 0.0445 | TRUE | 0.2332 |
| 11 | 0.99796172 | 0.0144 | 0.0629 | 0.0445 | 0.0445 | TRUE | 0.2332 |
| 12 | 0.99796172 | 0.0144 | 0.0629 | 0.0445 | 0.0445 | TRUE | 0.2332 |
| 13 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 14 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 15 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 16 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 17 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 18 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 19 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 20 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 21 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 22 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 23 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 24 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 25 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 26 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 27 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 28 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 29 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 30 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 31 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 32 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 33 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 34 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 35 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 36 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 37 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 38 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 39 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 40 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 41 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 42 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 43 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 44 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 45 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 46 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 47 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 48 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 49 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 50 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 51 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 52 | 0.99796172 | 0.01 | 0.0629 | 0.0415 | 0.0415 | TRUE | 0.2237 |
| 53 | 0.99796172 | 0.1275 | 0.0816 | 0.0969 | 0.0969 | TRUE | 0.5587 |
| 54 | 0.99796172 | 0.128 | 0.0815 | 0.0971 | 0.0971 | TRUE | 0.5664 |
| 55 | 0.99796172 | 0.0319 | 0.0899 | 0.0689 | 0.0689 | TRUE | 0.4622 |
| 56 | 0.99796172 | 0.0319 | 0.0899 | 0.0689 | 0.0689 | TRUE | 0.4622 |
| 57 | 0.99796172 | 0.0319 | 0.0899 | 0.0689 | 0.0689 | TRUE | 0.4622 |
| 58 | 0.99796172 | 0.0319 | 0.0899 | 0.0689 | 0.0689 | TRUE | 0.4622 |
| 59 | 0.99796172 | 0.0319 | 0.0899 | 0.0689 | 0.0689 | TRUE | 0.4622 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.1802 | 0.064 | 0.1015 | 0.1015 | TRUE | 0.6495 |
| 4 | 0.99796172 | 0.1802 | 0.064 | 0.1015 | 0.1015 | TRUE | 0.6495 |
| 5 | 0.99796172 | 0.1802 | 0.064 | 0.1015 | 0.1015 | TRUE | 0.6495 |
| 6 | 0.99796172 | 0.1802 | 0.064 | 0.1015 | 0.1015 | TRUE | 0.6495 |
| 7 | 0.99796172 | 0.1802 | 0.064 | 0.1015 | 0.1015 | TRUE | 0.6495 |
| 8 | 0.99796172 | 0.1802 | 0.064 | 0.1015 | 0.1015 | TRUE | 0.6495 |
| 9 | 0.99796172 | 0.1802 | 0.064 | 0.1015 | 0.1015 | TRUE | 0.6495 |
| 10 | 0.99796172 | 0.1802 | 0.064 | 0.1015 | 0.1015 | TRUE | 0.6495 |
| 11 | 0.99796172 | 0.1802 | 0.064 | 0.1015 | 0.1015 | TRUE | 0.6495 |
| 12 | 0.99796172 | 0.1802 | 0.064 | 0.1015 | 0.1015 | TRUE | 0.6495 |
| 13 | 0.99796172 | 0.1802 | 0.064 | 0.1015 | 0.1015 | TRUE | 0.6495 |
| 14 | 0.99796172 | 0.1802 | 0.064 | 0.1015 | 0.1015 | TRUE | 0.6495 |
| 15 | 0.99796172 | 0.1802 | 0.064 | 0.1015 | 0.1015 | TRUE | 0.6495 |
| 16 | 0.99796172 | 0.1802 | 0.064 | 0.1015 | 0.1015 | TRUE | 0.6495 |
| 17 | 0.99796172 | 0.1802 | 0.064 | 0.1015 | 0.1015 | TRUE | 0.6495 |
| 18 | 0.99796172 | 0.1802 | 0.064 | 0.1015 | 0.1015 | TRUE | 0.6495 |
| 19 | 0.99796172 | 0.1802 | 0.064 | 0.1015 | 0.1015 | TRUE | 0.6495 |
| 20 | 0.99796172 | 0.1802 | 0.064 | 0.1015 | 0.1015 | TRUE | 0.6495 |
| 21 | 0.99796172 | 0.1802 | 0.064 | 0.1015 | 0.1015 | TRUE | 0.6495 |
| 22 | 0.99796172 | 0.1797 | 0.064 | 0.1013 | 0.1013 | TRUE | 0.6595 |
| 23 | 0.99796172 | 0.0312 | 0.0651 | 0.052 | 0.052 | TRUE | 0.2496 |
| 24 | 0.99796172 | 0.0312 | 0.0651 | 0.052 | 0.052 | TRUE | 0.2496 |
| 25 | 0.99796172 | 0.0312 | 0.0651 | 0.052 | 0.052 | TRUE | 0.2496 |
| 26 | 0.99796172 | 0.0312 | 0.0651 | 0.052 | 0.052 | TRUE | 0.2496 |
| 27 | 0.99796172 | 0.0312 | 0.0651 | 0.052 | 0.052 | TRUE | 0.2496 |
| 28 | 0.99796172 | 0.0312 | 0.0651 | 0.052 | 0.052 | TRUE | 0.2496 |
| 29 | 0.99796172 | 0.0312 | 0.0651 | 0.052 | 0.052 | TRUE | 0.2496 |
| 30 | 0.99796172 | 0.0312 | 0.0651 | 0.052 | 0.052 | TRUE | 0.2496 |
| 31 | 0.99796172 | 0.0312 | 0.0651 | 0.052 | 0.052 | TRUE | 0.2496 |
| 32 | 0.99796172 | 0.0329 | 0.0783 | 0.0615 | 0.0615 | TRUE | 0.6625 |
| 33 | 0.99796172 | 0.0329 | 0.0783 | 0.0615 | 0.0615 | TRUE | 0.6625 |
| 34 | 0.99796172 | 0.0329 | 0.0783 | 0.0615 | 0.0615 | TRUE | 0.6625 |
| 35 | 0.99796172 | 0.0329 | 0.0783 | 0.0615 | 0.0615 | TRUE | 0.6625 |
| 36 | 0.99796172 | 0.0329 | 0.0783 | 0.0615 | 0.0615 | TRUE | 0.6625 |
| 37 | 0.99796172 | 0.0329 | 0.0783 | 0.0615 | 0.0615 | TRUE | 0.6625 |
| 38 | 0.99796172 | 0.0329 | 0.0783 | 0.0615 | 0.0615 | TRUE | 0.6625 |
| 39 | 0.99796172 | 0.0329 | 0.0783 | 0.0615 | 0.0615 | TRUE | 0.6625 |
| 40 | 0.99796172 | 0.0417 | 0.0665 | 0.0572 | 0.0572 | TRUE | 0.4532 |
| 41 | 0.99796172 | 0.0266 | 0.0634 | 0.0489 | 0.0489 | TRUE | 0.4709 |
| 42 | 0.99796172 | 0.0266 | 0.0634 | 0.0489 | 0.0489 | TRUE | 0.4709 |
| 43 | 0.99796172 | 0.0266 | 0.0634 | 0.0489 | 0.0489 | TRUE | 0.4709 |
| 44 | 0.99796172 | 0.0266 | 0.0634 | 0.0489 | 0.0489 | TRUE | 0.4709 |
| 45 | 0.99796172 | 0.0266 | 0.0634 | 0.0489 | 0.0489 | TRUE | 0.4709 |
| 46 | 0.99796172 | 0.0266 | 0.0634 | 0.0489 | 0.0489 | TRUE | 0.4709 |
| 47 | 0.99796172 | 0.0266 | 0.0634 | 0.0489 | 0.0489 | TRUE | 0.4709 |
| 48 | 0.99796172 | 0.0266 | 0.0634 | 0.0489 | 0.0489 | TRUE | 0.4709 |
| 49 | 0.99796172 | 0.0266 | 0.0634 | 0.0489 | 0.0489 | TRUE | 0.4709 |
| 50 | 0.99796172 | 0.0266 | 0.0634 | 0.0489 | 0.0489 | TRUE | 0.4709 |
| 51 | 0.99796172 | 0.0266 | 0.0634 | 0.0489 | 0.0489 | TRUE | 0.4709 |
| 52 | 0.99796172 | 0.0266 | 0.0634 | 0.0489 | 0.0489 | TRUE | 0.4709 |
| 53 | 0.99796172 | 0.0266 | 0.0634 | 0.0489 | 0.0489 | TRUE | 0.4709 |
| 54 | 0.99796172 | 0.0266 | 0.0634 | 0.0489 | 0.0489 | TRUE | 0.4709 |
| 55 | 0.99796172 | 0.0266 | 0.0634 | 0.0489 | 0.0489 | TRUE | 0.4709 |
| 56 | 0.99796172 | 0.0266 | 0.0634 | 0.0489 | 0.0489 | TRUE | 0.4709 |
| 57 | 0.99796172 | 0.0266 | 0.0634 | 0.0489 | 0.0489 | TRUE | 0.4709 |
| 58 | 0.99796172 | 0.0266 | 0.0634 | 0.0489 | 0.0489 | TRUE | 0.4709 |
| 59 | 0.99796172 | 0.0266 | 0.0634 | 0.0489 | 0.0489 | TRUE | 0.4709 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.0296 | 0.0645 | 0.0523 | 0.0523 | TRUE | 0.1731 |
| 4 | 0.99796172 | 0.0809 | 0.1032 | 0.0956 | 0.0956 | TRUE | 0.4046 |
| 5 | 0.99796172 | 0.0354 | 0.0672 | 0.0552 | 0.0552 | TRUE | 0.2307 |
| 6 | 0.99796172 | 0.0354 | 0.0672 | 0.0552 | 0.0552 | TRUE | 0.2307 |
| 7 | 0.99796172 | 0.0354 | 0.0672 | 0.0552 | 0.0552 | TRUE | 0.2307 |
| 8 | 0.99796172 | 0.0354 | 0.0672 | 0.0552 | 0.0552 | TRUE | 0.2307 |
| 9 | 0.99796172 | 0.0354 | 0.0672 | 0.0552 | 0.0552 | TRUE | 0.2307 |
| 10 | 0.99796172 | 0.0354 | 0.0672 | 0.0552 | 0.0552 | TRUE | 0.2307 |
| 11 | 0.99796172 | 0.0272 | 0.0802 | 0.0606 | 0.0606 | TRUE | 0.3502 |
| 12 | 0.99796172 | 0.0272 | 0.0802 | 0.0606 | 0.0606 | TRUE | 0.3502 |
| 13 | 0.99796172 | 0.0272 | 0.0802 | 0.0606 | 0.0606 | TRUE | 0.3502 |
| 14 | 0.99796172 | 0.0272 | 0.0802 | 0.0606 | 0.0606 | TRUE | 0.3502 |
| 15 | 0.99796172 | 0.0272 | 0.0802 | 0.0606 | 0.0606 | TRUE | 0.3502 |
| 16 | 0.99796172 | 0.0272 | 0.0802 | 0.0606 | 0.0606 | TRUE | 0.3502 |
| 17 | 0.99796172 | 0.0272 | 0.0802 | 0.0606 | 0.0606 | TRUE | 0.3502 |
| 18 | 0.99796172 | 0.0272 | 0.0802 | 0.0606 | 0.0606 | TRUE | 0.3502 |
| 19 | 0.99796172 | 0.0272 | 0.0802 | 0.0606 | 0.0606 | TRUE | 0.3502 |
| 20 | 0.99796172 | 0.0218 | 0.1132 | 0.081 | 0.081 | TRUE | 0.5211 |
| 21 | 0.99796172 | 0.0218 | 0.1132 | 0.081 | 0.081 | TRUE | 0.5211 |
| 22 | 0.99796172 | 0.0218 | 0.1132 | 0.081 | 0.081 | TRUE | 0.5211 |
| 23 | 0.99796172 | 0.0218 | 0.1132 | 0.081 | 0.081 | TRUE | 0.5211 |
| 24 | 0.99796172 | 0.0218 | 0.1132 | 0.081 | 0.081 | TRUE | 0.5211 |
| 25 | 0.99796172 | 0.0218 | 0.1132 | 0.081 | 0.081 | TRUE | 0.5211 |
| 26 | 0.99796172 | 0.0218 | 0.1132 | 0.081 | 0.081 | TRUE | 0.5211 |
| 27 | 0.99796172 | 0.0272 | 0.0801 | 0.0605 | 0.0605 | TRUE | 0.3524 |
| 28 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 29 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 30 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 31 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 32 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 33 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 34 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 35 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 36 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 37 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 38 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 39 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 40 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 41 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 42 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 43 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 44 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 45 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 46 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 47 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 48 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 49 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 50 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 51 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 52 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 53 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 54 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 55 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 56 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 57 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 58 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 59 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 4 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 5 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 6 | 0.99796172 | 0.0268 | 0.0802 | 0.0604 | 0.0604 | TRUE | 0.3474 |
| 7 | 0.99796172 | 0.0085 | 0.0629 | 0.0403 | 0.0403 | TRUE | 0.1069 |
| 8 | 0.99796172 | 0.0085 | 0.0629 | 0.0403 | 0.0403 | TRUE | 0.1069 |
| 9 | 0.99796172 | 0.038 | 0.0784 | 0.0636 | 0.0636 | TRUE | 0.4617 |
| 10 | 0.99796172 | 0.038 | 0.0784 | 0.0636 | 0.0636 | TRUE | 0.4617 |
| 11 | 0.99796172 | 0.038 | 0.0784 | 0.0636 | 0.0636 | TRUE | 0.4617 |
| 12 | 0.99796172 | 0.038 | 0.0784 | 0.0636 | 0.0636 | TRUE | 0.4617 |
| 13 | 0.99796172 | 0.038 | 0.0784 | 0.0636 | 0.0636 | TRUE | 0.4617 |
| 14 | 0.99796172 | 0.038 | 0.0784 | 0.0636 | 0.0636 | TRUE | 0.4617 |
| 15 | 0.99796172 | 0.038 | 0.0784 | 0.0636 | 0.0636 | TRUE | 0.4617 |
| 16 | 0.99796172 | 0.038 | 0.0784 | 0.0636 | 0.0636 | TRUE | 0.4617 |
| 17 | 0.99796172 | 0.038 | 0.0784 | 0.0636 | 0.0636 | TRUE | 0.4617 |
| 18 | 0.99796172 | 0.038 | 0.0784 | 0.0636 | 0.0636 | TRUE | 0.4617 |
| 19 | 0.99796172 | 0.038 | 0.0784 | 0.0636 | 0.0636 | TRUE | 0.4617 |
| 20 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 21 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 22 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 23 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 24 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 25 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 26 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 27 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 28 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 29 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 30 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 31 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 32 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 33 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 34 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 35 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 36 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 37 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 38 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 39 | 0.99796172 | 0.0081 | 0.1345 | 0.0905 | 0.0905 | TRUE | 0.2606 |
| 40 | 0.99796172 | 2.4515 | 0.1262 | 0.5752 | 2.4515 | TRUE | 0.6447 |
| 41 | 0.99796172 | 2.4515 | 0.1262 | 0.5752 | 2.4515 | TRUE | 0.6447 |
| 42 | 0.99796172 | 2.4515 | 0.1262 | 0.5752 | 2.4515 | TRUE | 0.6447 |
| 43 | 0.99796172 | 2.4515 | 0.1262 | 0.5752 | 2.4515 | TRUE | 0.6447 |
| 44 | 0.99796172 | 2.4515 | 0.1262 | 0.5752 | 2.4515 | TRUE | 0.6447 |
| 45 | 0.99796172 | 2.4515 | 0.1262 | 0.5752 | 2.4515 | TRUE | 0.6447 |
| 46 | 0.99796172 | 2.4515 | 0.1262 | 0.5752 | 2.4515 | TRUE | 0.6447 |
| 47 | 0.99796172 | 2.4515 | 0.1262 | 0.5752 | 2.4515 | TRUE | 0.6447 |
| 48 | 0.99796172 | 2.4515 | 0.1262 | 0.5752 | 2.4515 | TRUE | 0.6447 |
| 49 | 0.99796172 | 2.4515 | 0.1262 | 0.5752 | 2.4515 | TRUE | 0.6447 |
| 50 | 0.99796172 | 2.4515 | 0.1262 | 0.5752 | 2.4515 | TRUE | 0.6447 |
| 51 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 52 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 53 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 54 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 55 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 56 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 57 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 58 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 59 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 4 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 5 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 6 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 7 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 8 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 9 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 10 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 11 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 12 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 13 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 14 | 0.99796172 | 2.4595 | 0.1268 | 0.5782 | 2.4595 | TRUE | 0.631 |
| 15 | 0.99796172 | 0.0857 | 0.0961 | 0.0925 | 0.0925 | TRUE | 1.8099 |
| 16 | 0.99796172 | 0.0857 | 0.0961 | 0.0925 | 0.0925 | TRUE | 1.8099 |
| 17 | 0.99796172 | 0.0273 | 0.0636 | 0.0496 | 0.0496 | TRUE | 0.4101 |
| 18 | 0.99796172 | 0.0273 | 0.0636 | 0.0496 | 0.0496 | TRUE | 0.4101 |
| 19 | 0.99796172 | 0.0273 | 0.0636 | 0.0496 | 0.0496 | TRUE | 0.4101 |
| 20 | 0.99796172 | 0.0273 | 0.0636 | 0.0496 | 0.0496 | TRUE | 0.4101 |
| 21 | 0.99796172 | 0.0273 | 0.0636 | 0.0496 | 0.0496 | TRUE | 0.4101 |
| 22 | 0.99796172 | 0.0273 | 0.0636 | 0.0496 | 0.0496 | TRUE | 0.4101 |
| 23 | 0.99796172 | 0.0419 | 0.1357 | 0.1036 | 0.1036 | TRUE | 0.5118 |
| 24 | 0.99796172 | 0.036 | 0.0633 | 0.053 | 0.053 | TRUE | 0.4247 |
| 25 | 0.99796172 | 0.036 | 0.0633 | 0.053 | 0.053 | TRUE | 0.4247 |
| 26 | 0.99796172 | 0.036 | 0.0633 | 0.053 | 0.053 | TRUE | 0.4247 |
| 27 | 0.99796172 | 0.036 | 0.0633 | 0.053 | 0.053 | TRUE | 0.4247 |
| 28 | 0.99796172 | 0.036 | 0.0633 | 0.053 | 0.053 | TRUE | 0.4247 |
| 29 | 0.99796172 | 0.036 | 0.0633 | 0.053 | 0.053 | TRUE | 0.4247 |
| 30 | 0.99796172 | 0.036 | 0.0633 | 0.053 | 0.053 | TRUE | 0.4247 |
| 31 | 0.99796172 | 0.036 | 0.0633 | 0.053 | 0.053 | TRUE | 0.4247 |
| 32 | 0.99796172 | 0.036 | 0.0633 | 0.053 | 0.053 | TRUE | 0.4247 |
| 33 | 0.99796172 | 0.036 | 0.0633 | 0.053 | 0.053 | TRUE | 0.4247 |
| 34 | 0.99796172 | 0.036 | 0.0633 | 0.053 | 0.053 | TRUE | 0.4247 |
| 35 | 0.99796172 | 0.036 | 0.0633 | 0.053 | 0.053 | TRUE | 0.4247 |
| 36 | 0.99796172 | 0.036 | 0.0633 | 0.053 | 0.053 | TRUE | 0.4247 |
| 37 | 0.99796172 | 0.036 | 0.0633 | 0.053 | 0.053 | TRUE | 0.4247 |
| 38 | 0.99796172 | 0.036 | 0.0633 | 0.053 | 0.053 | TRUE | 0.4247 |
| 39 | 0.99796172 | 0.036 | 0.0633 | 0.053 | 0.053 | TRUE | 0.4216 |
| 40 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 41 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 42 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 43 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 44 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 45 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 46 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 47 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 48 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 49 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 50 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 51 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 52 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 53 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 54 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 55 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 56 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 57 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 58 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 59 | 0.99796172 | 0.0271 | 0.0637 | 0.0486 | 0.0486 | TRUE | 0.6251 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.0065 | 0.0782 | 0.0502 | 0.0502 | TRUE | 0.1807 |
| 4 | 0.99796172 | 0.0283 | 0.0777 | 0.0594 | 0.0594 | TRUE | 0.5387 |
| 5 | 0.99796172 | 0.0283 | 0.0777 | 0.0594 | 0.0594 | TRUE | 0.5387 |
| 6 | 0.99796172 | 0.0283 | 0.0777 | 0.0594 | 0.0594 | TRUE | 0.5387 |
| 7 | 0.99796172 | 0.0283 | 0.0777 | 0.0594 | 0.0594 | TRUE | 0.5387 |
| 8 | 0.99796172 | 0.048 | 0.0833 | 0.0706 | 0.0706 | TRUE | 0.4425 |
| 9 | 0.99796172 | 0.0252 | 0.0636 | 0.0478 | 0.0478 | TRUE | 0.6077 |
| 10 | 0.99796172 | 0.0252 | 0.0636 | 0.0478 | 0.0478 | TRUE | 0.6077 |
| 11 | 0.99796172 | 0.0252 | 0.0636 | 0.0478 | 0.0478 | TRUE | 0.6077 |
| 12 | 0.99796172 | 0.0252 | 0.0636 | 0.0478 | 0.0478 | TRUE | 0.6077 |
| 13 | 0.99796172 | 0.0252 | 0.0636 | 0.0478 | 0.0478 | TRUE | 0.6077 |
| 14 | 0.99796172 | 0.0252 | 0.0636 | 0.0478 | 0.0478 | TRUE | 0.6077 |
| 15 | 0.99796172 | 0.0252 | 0.0636 | 0.0478 | 0.0478 | TRUE | 0.6077 |
| 16 | 0.99796172 | 0.0259 | 0.0637 | 0.0481 | 0.0481 | TRUE | 0.6277 |
| 17 | 0.99796172 | 0.0305 | 0.079 | 0.0611 | 0.0611 | TRUE | 0.518 |
| 18 | 0.99796172 | 0.0305 | 0.079 | 0.0611 | 0.0611 | TRUE | 0.518 |
| 19 | 0.99796172 | 0.0305 | 0.079 | 0.0611 | 0.0611 | TRUE | 0.518 |
| 20 | 0.99796172 | 0.0305 | 0.079 | 0.0611 | 0.0611 | TRUE | 0.518 |
| 21 | 0.99796172 | 0.0305 | 0.079 | 0.0611 | 0.0611 | TRUE | 0.518 |
| 22 | 0.99796172 | 0.0305 | 0.079 | 0.0611 | 0.0611 | TRUE | 0.518 |
| 23 | 0.99796172 | 0.0305 | 0.079 | 0.0611 | 0.0611 | TRUE | 0.518 |
| 24 | 0.99796172 | 0.0305 | 0.079 | 0.0611 | 0.0611 | TRUE | 0.518 |
| 25 | 0.99796172 | 0.0305 | 0.079 | 0.0611 | 0.0611 | TRUE | 0.518 |
| 26 | 0.99796172 | 0.0305 | 0.079 | 0.0611 | 0.0611 | TRUE | 0.518 |
| 27 | 0.99796172 | 0.0305 | 0.079 | 0.0611 | 0.0611 | TRUE | 0.518 |
| 28 | 0.99796172 | 0.0305 | 0.079 | 0.0611 | 0.0611 | TRUE | 0.518 |
| 29 | 0.99796172 | 0.0305 | 0.079 | 0.0611 | 0.0611 | TRUE | 0.518 |
| 30 | 0.99796172 | 0.0248 | 0.0634 | 0.0487 | 0.0487 | TRUE | 0.4237 |
| 31 | 0.99796172 | 0.0248 | 0.0634 | 0.0487 | 0.0487 | TRUE | 0.4237 |
| 32 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 33 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 34 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 35 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 36 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 37 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 38 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 39 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 40 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 41 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 42 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 43 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 44 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 45 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 46 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 47 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 48 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 49 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 50 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 51 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 52 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 53 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 54 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 55 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 56 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 57 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 58 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 59 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 4 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 5 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 6 | 0.99796172 | 0.0308 | 0.079 | 0.0613 | 0.0613 | TRUE | 0.5265 |
| 7 | 0.99796172 | 0.0355 | 0.1569 | 0.1167 | 0.1167 | TRUE | 0.6572 |
| 8 | 0.99796172 | 0.0927 | 0.096 | 0.095 | 0.095 | TRUE | 1.2452 |
| 9 | 0.99796172 | 0.0425 | 0.161 | 0.1221 | 0.1221 | TRUE | 0.7749 |
| 10 | 0.99796172 | 0.071 | 0.0848 | 0.08 | 0.08 | TRUE | 0.2533 |
| 11 | 0.99796172 | 0.071 | 0.0848 | 0.08 | 0.08 | TRUE | 0.2533 |
| 12 | 0.99796172 | 0.071 | 0.0848 | 0.08 | 0.08 | TRUE | 0.2533 |
| 13 | 0.99796172 | 0.071 | 0.0848 | 0.08 | 0.08 | TRUE | 0.2533 |
| 14 | 0.99796172 | 0.071 | 0.0848 | 0.08 | 0.08 | TRUE | 0.2533 |
| 15 | 0.99796172 | 0.071 | 0.0848 | 0.08 | 0.08 | TRUE | 0.2533 |
| 16 | 0.99796172 | 0.071 | 0.0848 | 0.08 | 0.08 | TRUE | 0.2533 |
| 17 | 0.99796172 | 0.071 | 0.0848 | 0.08 | 0.08 | TRUE | 0.2533 |
| 18 | 0.99796172 | 0.071 | 0.0848 | 0.08 | 0.08 | TRUE | 0.2533 |
| 19 | 0.99796172 | 0.071 | 0.0848 | 0.08 | 0.08 | TRUE | 0.2533 |
| 20 | 0.99796172 | 0.071 | 0.0848 | 0.08 | 0.08 | TRUE | 0.2533 |
| 21 | 0.99796172 | 0.071 | 0.0848 | 0.08 | 0.08 | TRUE | 0.2533 |
| 22 | 0.99796172 | 0.1354 | 0.0952 | 0.1084 | 0.1084 | TRUE | 0.5894 |
| 23 | 0.99796172 | 0.0188 | 0.0638 | 0.0463 | 0.0463 | TRUE | 0.3773 |
| 24 | 0.99796172 | 0.0031 | 0.0861 | 0.0543 | 0.0543 | TRUE | 0.0864 |
| 25 | 0.99796172 | 0.0031 | 0.0861 | 0.0543 | 0.0543 | TRUE | 0.0864 |
| 26 | 0.99796172 | 0.0031 | 0.0861 | 0.0543 | 0.0543 | TRUE | 0.0864 |
| 27 | 0.99796172 | 0.0174 | 0.0718 | 0.0506 | 0.0506 | TRUE | 0.3515 |
| 28 | 0.99796172 | 0.0174 | 0.0718 | 0.0506 | 0.0506 | TRUE | 0.3515 |
| 29 | 0.99796172 | 0.0174 | 0.0718 | 0.0506 | 0.0506 | TRUE | 0.3515 |
| 30 | 0.99796172 | 0.0174 | 0.0718 | 0.0506 | 0.0506 | TRUE | 0.3515 |
| 31 | 0.99796172 | 0.0174 | 0.0718 | 0.0506 | 0.0506 | TRUE | 0.3515 |
| 32 | 0.99796172 | 0.0174 | 0.0718 | 0.0506 | 0.0506 | TRUE | 0.3515 |
| 33 | 0.99796172 | 0.0174 | 0.0718 | 0.0506 | 0.0506 | TRUE | 0.3515 |
| 34 | 0.99796172 | 0.0174 | 0.0718 | 0.0506 | 0.0506 | TRUE | 0.3515 |
| 35 | 0.99796172 | 0.0174 | 0.0718 | 0.0506 | 0.0506 | TRUE | 0.3515 |
| 36 | 0.99796172 | 0.0174 | 0.0718 | 0.0506 | 0.0506 | TRUE | 0.3515 |
| 37 | 0.99796172 | 0.0174 | 0.0718 | 0.0506 | 0.0506 | TRUE | 0.3515 |
| 38 | 0.99796172 | 0.0174 | 0.0718 | 0.0506 | 0.0506 | TRUE | 0.3515 |
| 39 | 0.99796172 | 0.0174 | 0.0718 | 0.0506 | 0.0506 | TRUE | 0.3515 |
| 40 | 0.99796172 | 0.1128 | 0.0735 | 0.0869 | 0.0869 | TRUE | 1.4026 |
| 41 | 0.99796172 | 0.0373 | 0.0958 | 0.0751 | 0.0751 | TRUE | 0.7971 |
| 42 | 0.99796172 | 0.0373 | 0.0958 | 0.0751 | 0.0751 | TRUE | 0.7971 |
| 43 | 0.99796172 | 0.0373 | 0.0958 | 0.0751 | 0.0751 | TRUE | 0.7971 |
| 44 | 0.99796172 | 0.0135 | 0.0708 | 0.0483 | 0.0483 | TRUE | 0.3424 |
| 45 | 0.99796172 | 0.0135 | 0.0708 | 0.0483 | 0.0483 | TRUE | 0.3424 |
| 46 | 0.99796172 | 0.0135 | 0.0708 | 0.0483 | 0.0483 | TRUE | 0.3424 |
| 47 | 0.99796172 | 0.0162 | 0.0865 | 0.0603 | 0.0603 | TRUE | 0.296 |
| 48 | 0.99796172 | 0.0581 | 0.0647 | 0.0639 | 0.0639 | TRUE | 1.2781 |
| 49 | 0.99796172 | 0.0581 | 0.0647 | 0.0639 | 0.0639 | TRUE | 1.2781 |
| 50 | 0.99796172 | 0.0581 | 0.0647 | 0.0639 | 0.0639 | TRUE | 1.2781 |
| 51 | 0.99796172 | 0.0581 | 0.0647 | 0.0639 | 0.0639 | TRUE | 1.2781 |
| 52 | 0.99796172 | 0.0581 | 0.0647 | 0.0639 | 0.0639 | TRUE | 1.2781 |
| 53 | 0.99796172 | 0.0581 | 0.0647 | 0.0639 | 0.0639 | TRUE | 1.2781 |
| 54 | 0.99796172 | 0.0581 | 0.0647 | 0.0639 | 0.0639 | TRUE | 1.2781 |
| 55 | 0.99796172 | 0.0581 | 0.0647 | 0.0639 | 0.0639 | TRUE | 1.2781 |
| 56 | 0.99796172 | 0.0581 | 0.0647 | 0.0639 | 0.0639 | TRUE | 1.2781 |
| 57 | 0.99796172 | 0.0581 | 0.0647 | 0.0639 | 0.0639 | TRUE | 1.2781 |
| 58 | 0.99796172 | 0.0581 | 0.0647 | 0.0639 | 0.0639 | TRUE | 1.2781 |
| 59 | 0.99796172 | 0.0581 | 0.0647 | 0.0639 | 0.0639 | TRUE | 1.2781 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.033 | 0.0644 | 0.0525 | 0.0525 | TRUE | 0.1969 |
| 4 | 0.99796172 | 0.033 | 0.0644 | 0.0525 | 0.0525 | TRUE | 0.1969 |
| 5 | 0.99796172 | 0.0332 | 0.0644 | 0.0526 | 0.0526 | TRUE | 0.1952 |
| 6 | 0.99796172 | 0.0332 | 0.0644 | 0.0526 | 0.0526 | TRUE | 0.1952 |
| 7 | 0.99796172 | 0.0316 | 0.089 | 0.0683 | 0.0683 | TRUE | 0.3234 |
| 8 | 0.99796172 | 0.0358 | 0.064 | 0.0524 | 0.0524 | TRUE | 0.7117 |
| 9 | 0.99796172 | 0.0358 | 0.064 | 0.0524 | 0.0524 | TRUE | 0.7117 |
| 10 | 0.99796172 | 0.0406 | 0.1378 | 0.1049 | 0.1049 | TRUE | 0.8973 |
| 11 | 0.99796172 | 0.0417 | 0.1384 | 0.1056 | 0.1056 | TRUE | 0.9298 |
| 12 | 0.99796172 | 0.0417 | 0.1384 | 0.1056 | 0.1056 | TRUE | 0.9298 |
| 13 | 0.99796172 | 0.0417 | 0.1384 | 0.1056 | 0.1056 | TRUE | 0.9298 |
| 14 | 0.99796172 | 0.0417 | 0.1384 | 0.1056 | 0.1056 | TRUE | 0.9298 |
| 15 | 0.99796172 | 0.0417 | 0.1384 | 0.1056 | 0.1056 | TRUE | 0.9298 |
| 16 | 0.99796172 | 0.0532 | 0.1262 | 0.1011 | 0.1011 | TRUE | 0.1735 |
| 17 | 0.99796172 | 0.1875 | 0.0629 | 0.1032 | 0.1032 | TRUE | 0.4253 |
| 18 | 0.99796172 | 0.1875 | 0.0629 | 0.1032 | 0.1032 | TRUE | 0.4253 |
| 19 | 0.99796172 | 0.1875 | 0.0629 | 0.1032 | 0.1032 | TRUE | 0.4253 |
| 20 | 0.99796172 | 0.1875 | 0.0629 | 0.1032 | 0.1032 | TRUE | 0.4253 |
| 21 | 0.99796172 | 0.2351 | 0.1083 | 0.1481 | 0.1481 | TRUE | 0.3329 |
| 22 | 0.99796172 | 0.2351 | 0.1083 | 0.1481 | 0.1481 | TRUE | 0.3329 |
| 23 | 0.99796172 | 0.2351 | 0.1083 | 0.1481 | 0.1481 | TRUE | 0.3329 |
| 24 | 0.99796172 | 0.2351 | 0.1083 | 0.1481 | 0.1481 | TRUE | 0.3329 |
| 25 | 0.99796172 | 0.2351 | 0.1083 | 0.1481 | 0.1481 | TRUE | 0.3329 |
| 26 | 0.99796172 | 0.2351 | 0.1083 | 0.1481 | 0.1481 | TRUE | 0.3329 |
| 27 | 0.99796172 | 0.2351 | 0.1083 | 0.1481 | 0.1481 | TRUE | 0.3329 |
| 28 | 0.99796172 | 0.2351 | 0.1083 | 0.1481 | 0.1481 | TRUE | 0.3329 |
| 29 | 0.99796172 | 0.2351 | 0.1083 | 0.1481 | 0.1481 | TRUE | 0.3329 |
| 30 | 0.99796172 | 0.2351 | 0.1083 | 0.1481 | 0.1481 | TRUE | 0.3329 |
| 31 | 0.99796172 | 0.2351 | 0.1083 | 0.1481 | 0.1481 | TRUE | 0.3329 |
| 32 | 0.99796172 | 0.2351 | 0.1083 | 0.1481 | 0.1481 | TRUE | 0.3329 |
| 33 | 0.99796172 | 0.2351 | 0.1083 | 0.1481 | 0.1481 | TRUE | 0.3329 |
| 34 | 0.99796172 | 0.2351 | 0.1083 | 0.1481 | 0.1481 | TRUE | 0.3329 |
| 35 | 0.99796172 | 0.2351 | 0.1083 | 0.1481 | 0.1481 | TRUE | 0.3329 |
| 36 | 0.99796172 | 0.2351 | 0.1083 | 0.1481 | 0.1481 | TRUE | 0.3329 |
| 37 | 0.99796172 | 0.0665 | 0.0634 | 0.0646 | 0.0646 | TRUE | 0.2512 |
| 38 | 0.99796172 | 0.0665 | 0.0634 | 0.0646 | 0.0646 | TRUE | 0.2512 |
| 39 | 0.99796172 | 0.0222 | 0.0853 | 0.062 | 0.062 | TRUE | 0.1748 |
| 40 | 0.99796172 | 0.0222 | 0.0853 | 0.062 | 0.062 | TRUE | 0.1748 |
| 41 | 0.99796172 | 0.0263 | 0.0846 | 0.0632 | 0.0632 | TRUE | 0.2498 |
| 42 | 0.99796172 | 0.0263 | 0.0846 | 0.0632 | 0.0632 | TRUE | 0.2498 |
| 43 | 0.99796172 | 0.0263 | 0.0846 | 0.0632 | 0.0632 | TRUE | 0.2498 |
| 44 | 0.99796172 | 0.0263 | 0.0846 | 0.0632 | 0.0632 | TRUE | 0.2498 |
| 45 | 0.99796172 | 0.0263 | 0.0846 | 0.0632 | 0.0632 | TRUE | 0.2498 |
| 46 | 0.99796172 | 0.0263 | 0.0846 | 0.0632 | 0.0632 | TRUE | 0.2498 |
| 47 | 0.99796172 | 0.0263 | 0.0846 | 0.0632 | 0.0632 | TRUE | 0.2498 |
| 48 | 0.99796172 | 0.0263 | 0.0846 | 0.0632 | 0.0632 | TRUE | 0.2498 |
| 49 | 0.99796172 | 0.0263 | 0.0846 | 0.0632 | 0.0632 | TRUE | 0.2498 |
| 50 | 0.99796172 | 0.0263 | 0.0846 | 0.0632 | 0.0632 | TRUE | 0.2498 |
| 51 | 0.99796172 | 0.0517 | 0.0934 | 0.0786 | 0.0786 | TRUE | 0.1983 |
| 52 | 0.99796172 | 0.0517 | 0.0934 | 0.0786 | 0.0786 | TRUE | 0.1983 |
| 53 | 0.99796172 | 0.0505 | 0.1279 | 0.1013 | 0.1013 | TRUE | 0.1939 |
| 54 | 0.99796172 | 0.0505 | 0.1279 | 0.1013 | 0.1013 | TRUE | 0.1939 |
| 55 | 0.99796172 | 0.019 | 0.0863 | 0.0613 | 0.0613 | TRUE | 0.2439 |
| 56 | 0.99796172 | 0.019 | 0.0863 | 0.0613 | 0.0613 | TRUE | 0.2439 |
| 57 | 0.99796172 | | | | | | |
| 58 | 0.99796172 | | | | | | |
| 59 | 0.99796172 | | | | | | |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.019 | 0.0863 | 0.0613 | 0.0613 | TRUE | 0.2439 |
| 4 | 0.99796172 | 0.019 | 0.0863 | 0.0613 | 0.0613 | TRUE | 0.2439 |
| 5 | 0.99796172 | 0.019 | 0.0863 | 0.0613 | 0.0613 | TRUE | 0.2439 |
| 6 | 0.99796172 | 0.019 | 0.0863 | 0.0613 | 0.0613 | TRUE | 0.2439 |
| 7 | 0.99796172 | 0.019 | 0.0863 | 0.0613 | 0.0613 | TRUE | 0.2439 |
| 8 | 0.99796172 | 0.019 | 0.0863 | 0.0613 | 0.0613 | TRUE | 0.2439 |
| 9 | 0.99796172 | 0.019 | 0.0863 | 0.0613 | 0.0613 | TRUE | 0.2439 |
| 10 | 0.99796172 | 0.019 | 0.0863 | 0.0613 | 0.0613 | TRUE | 0.2439 |
| 11 | 0.99796172 | 0.247 | 0.109 | 0.1521 | 0.1521 | TRUE | 0.3882 |
| 12 | 0.99796172 | 0.247 | 0.109 | 0.1521 | 0.1521 | TRUE | 0.3882 |
| 13 | 0.99796172 | 0.247 | 0.109 | 0.1521 | 0.1521 | TRUE | 0.3882 |
| 14 | 0.99796172 | 0.247 | 0.109 | 0.1521 | 0.1521 | TRUE | 0.3882 |
| 15 | 0.99796172 | 0.0917 | 0.0661 | 0.075 | 0.075 | TRUE | 0.516 |
| 16 | 0.99796172 | 0.0917 | 0.0661 | 0.075 | 0.075 | TRUE | 0.516 |
| 17 | 0.99796172 | 0.0917 | 0.0661 | 0.075 | 0.075 | TRUE | 0.516 |
| 18 | 0.99796172 | 0.0917 | 0.0661 | 0.075 | 0.075 | TRUE | 0.516 |
| 19 | 0.99796172 | 0.0917 | 0.0661 | 0.075 | 0.075 | TRUE | 0.516 |
| 20 | 0.99796172 | 0.0917 | 0.0661 | 0.075 | 0.075 | TRUE | 0.516 |
| 21 | 0.99796172 | 0.0917 | 0.0661 | 0.075 | 0.075 | TRUE | 0.516 |
| 22 | 0.99796172 | 0.0917 | 0.0661 | 0.075 | 0.075 | TRUE | 0.516 |
| 23 | 0.99796172 | 0.0917 | 0.0661 | 0.075 | 0.075 | TRUE | 0.516 |
| 24 | 0.99796172 | 0.0917 | 0.0661 | 0.075 | 0.075 | TRUE | 0.516 |
| 25 | 0.99796172 | 0.0917 | 0.0661 | 0.075 | 0.075 | TRUE | 0.516 |
| 26 | 0.99796172 | 0.0917 | 0.0661 | 0.075 | 0.075 | TRUE | 0.516 |
| 27 | 0.99796172 | 0.0917 | 0.0661 | 0.075 | 0.075 | TRUE | 0.516 |
| 28 | 0.99796172 | 0.0917 | 0.0661 | 0.075 | 0.075 | TRUE | 0.516 |
| 29 | 0.99796172 | 0.0917 | 0.0661 | 0.075 | 0.075 | TRUE | 0.516 |
| 30 | 0.99796172 | 0.0917 | 0.0661 | 0.075 | 0.075 | TRUE | 0.516 |
| 31 | 0.99796172 | 0.4456 | 0.1588 | 0.2432 | 0.2432 | TRUE | 0.5712 |
| 32 | 0.99796172 | 0.4456 | 0.1588 | 0.2432 | 0.2432 | TRUE | 0.5712 |
| 33 | 0.99796172 | 0.4456 | 0.1588 | 0.2432 | 0.2432 | TRUE | 0.5712 |
| 34 | 0.99796172 | 0.4456 | 0.1588 | 0.2432 | 0.2432 | TRUE | 0.5712 |
| 35 | 0.99796172 | 0.4456 | 0.1588 | 0.2432 | 0.2432 | TRUE | 0.5712 |
| 36 | 0.99796172 | 0.4456 | 0.1588 | 0.2432 | 0.2432 | TRUE | 0.5712 |
| 37 | 0.99796172 | 0.4456 | 0.1588 | 0.2432 | 0.2432 | TRUE | 0.5712 |
| 38 | 0.99796172 | 0.4456 | 0.1588 | 0.2432 | 0.2432 | TRUE | 0.5712 |
| 39 | 0.99796172 | 0.4456 | 0.1588 | 0.2432 | 0.2432 | TRUE | 0.5712 |
| 40 | 0.99796172 | 0.4456 | 0.1588 | 0.2432 | 0.2432 | TRUE | 0.5712 |
| 41 | 0.99796172 | 0.4456 | 0.1588 | 0.2432 | 0.2432 | TRUE | 0.5712 |
| 42 | 0.99796172 | 0.4456 | 0.1588 | 0.2432 | 0.2432 | TRUE | 0.5712 |
| 43 | 0.99796172 | 0.4456 | 0.1588 | 0.2432 | 0.2432 | TRUE | 0.5712 |
| 44 | 0.99796172 | 0.4456 | 0.1588 | 0.2432 | 0.2432 | TRUE | 0.5712 |
| 45 | 0.99796172 | 0.4456 | 0.1588 | 0.2432 | 0.2432 | TRUE | 0.5712 |
| 46 | 0.99796172 | 0.4456 | 0.1588 | 0.2432 | 0.2432 | TRUE | 0.5712 |
| 47 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 48 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 49 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 50 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 51 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 52 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 53 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 54 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 55 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 56 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 57 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 58 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 59 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 4 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 5 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 6 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 7 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 8 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 9 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 10 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 11 | 0.99796172 | 0.1015 | 0.1195 | 0.1136 | 0.1136 | TRUE | 1.3262 |
| 12 | 0.99796172 | 0.2102 | 0.1246 | 0.1517 | 0.1517 | TRUE | 0.7639 |
| 13 | 0.99796172 | 0.2102 | 0.1246 | 0.1517 | 0.1517 | TRUE | 0.7639 |
| 14 | 0.99796172 | 0.2102 | 0.1246 | 0.1517 | 0.1517 | TRUE | 0.7639 |
| 15 | 0.99796172 | 0.2102 | 0.1246 | 0.1517 | 0.1517 | TRUE | 0.7639 |
| 16 | 0.99796172 | 0.2102 | 0.1246 | 0.1517 | 0.1517 | TRUE | 0.7639 |
| 17 | 0.99796172 | 0.2102 | 0.1246 | 0.1517 | 0.1517 | TRUE | 0.7639 |
| 18 | 0.99796172 | 0.2102 | 0.1246 | 0.1517 | 0.1517 | TRUE | 0.7639 |
| 19 | 0.99796172 | 0.0623 | 0.1346 | 0.1103 | 0.1103 | TRUE | 1.2936 |
| 20 | 0.99796172 | 0.2517 | 0.1053 | 0.151 | 0.151 | TRUE | 0.3797 |
| 21 | 0.99796172 | 0.2517 | 0.1053 | 0.151 | 0.151 | TRUE | 0.3797 |
| 22 | 0.99796172 | 0.2517 | 0.1053 | 0.151 | 0.151 | TRUE | 0.3797 |
| 23 | 0.99796172 | 0.2517 | 0.1053 | 0.151 | 0.151 | TRUE | 0.3797 |
| 24 | 0.99796172 | 0.2517 | 0.1053 | 0.151 | 0.151 | TRUE | 0.3797 |
| 25 | 0.99796172 | 0.2517 | 0.1053 | 0.151 | 0.151 | TRUE | 0.3797 |
| 26 | 0.99796172 | 0.2517 | 0.1053 | 0.151 | 0.151 | TRUE | 0.3797 |
| 27 | 0.99796172 | 0.2517 | 0.1053 | 0.151 | 0.151 | TRUE | 0.3797 |
| 28 | 0.99796172 | 0.0571 | 0.0828 | 0.073 | 0.073 | TRUE | 1.1198 |
| 29 | 0.99796172 | 0.0512 | 0.0642 | 0.058 | 0.058 | TRUE | 0.6887 |
| 30 | 0.99796172 | 0.0512 | 0.0642 | 0.058 | 0.058 | TRUE | 0.6887 |
| 31 | 0.99796172 | 0.0512 | 0.0642 | 0.058 | 0.058 | TRUE | 0.6887 |
| 32 | 0.99796172 | 0.0512 | 0.0642 | 0.058 | 0.058 | TRUE | 0.6887 |
| 33 | 0.99796172 | 0.0512 | 0.0642 | 0.058 | 0.058 | TRUE | 0.6887 |
| 34 | 0.99796172 | 0.0512 | 0.0642 | 0.058 | 0.058 | TRUE | 0.6887 |
| 35 | 0.99796172 | 0.0512 | 0.0642 | 0.058 | 0.058 | TRUE | 0.6887 |
| 36 | 0.99796172 | 0.0512 | 0.0642 | 0.058 | 0.058 | TRUE | 0.6887 |
| 37 | 0.99796172 | 0.0512 | 0.0642 | 0.058 | 0.058 | TRUE | 0.6887 |
| 38 | 0.99796172 | 0.0512 | 0.0642 | 0.058 | 0.058 | TRUE | 0.6887 |
| 39 | 0.99796172 | 0.0512 | 0.0642 | 0.058 | 0.058 | TRUE | 0.6887 |
| 40 | 0.99796172 | 0.0512 | 0.0642 | 0.058 | 0.058 | TRUE | 0.6887 |
| 41 | 0.99796172 | 0.0633 | 0.0836 | 0.0759 | 0.0759 | TRUE | 0.8119 |
| 42 | 0.99796172 | 0.0633 | 0.0836 | 0.0759 | 0.0759 | TRUE | 0.8119 |
| 43 | 0.99796172 | 0.063 | 0.137 | 0.1124 | 0.1124 | TRUE | 0.7054 |
| 44 | 0.99796172 | 0.3796 | 0.1445 | 0.2152 | 0.2152 | TRUE | 3.7357 |
| 45 | 0.99796172 | 0.3796 | 0.1445 | 0.2152 | 0.2152 | TRUE | 3.7357 |
| 46 | 0.99796172 | 0.1042 | 0.1278 | 0.1199 | 0.1199 | TRUE | 1.3928 |
| 47 | 0.99796172 | 0.1042 | 0.1278 | 0.1199 | 0.1199 | TRUE | 1.3928 |
| 48 | 0.99796172 | 0.1042 | 0.1278 | 0.1199 | 0.1199 | TRUE | 1.3928 |
| 49 | 0.99796172 | 0.0179 | 0.0634 | 0.045 | 0.045 | TRUE | 0.3052 |
| 50 | 0.99796172 | 0.0755 | 0.1397 | 0.1185 | 0.1185 | TRUE | 0.5077 |
| 51 | 0.99796172 | 0.0755 | 0.1397 | 0.1185 | 0.1185 | TRUE | 0.5077 |
| 52 | 0.99796172 | 0.0755 | 0.1397 | 0.1185 | 0.1185 | TRUE | 0.5077 |
| 53 | 0.99796172 | 0.0755 | 0.1397 | 0.1185 | 0.1185 | TRUE | 0.5077 |
| 54 | 0.99796172 | 0.0755 | 0.1397 | 0.1185 | 0.1185 | TRUE | 0.5077 |
| 55 | 0.99796172 | 0.0755 | 0.1397 | 0.1185 | 0.1185 | TRUE | 0.5077 |
| 56 | 0.99796172 | 0.0755 | 0.1397 | 0.1185 | 0.1185 | TRUE | 0.5077 |
| 57 | 0.99796172 | 0.0755 | 0.1397 | 0.1185 | 0.1185 | TRUE | 0.5077 |
| 58 | 0.99796172 | 0.0755 | 0.1397 | 0.1185 | 0.1185 | TRUE | 0.5077 |
| 59 | 0.99796172 | 0.0755 | 0.1397 | 0.1185 | 0.1185 | TRUE | 0.5077 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.2604 | 0.1426 | 0.1785 | 0.1785 | TRUE | 3.2665 |
| 4 | 0.99796172 | 0.2604 | 0.1426 | 0.1785 | 0.1785 | TRUE | 3.2665 |
| 5 | 0.99796172 | 0.2604 | 0.1426 | 0.1785 | 0.1785 | TRUE | 3.2665 |
| 6 | 0.99796172 | 0.2604 | 0.1426 | 0.1785 | 0.1785 | TRUE | 3.2665 |
| 7 | 0.99796172 | 0.2604 | 0.1426 | 0.1785 | 0.1785 | TRUE | 3.2665 |
| 8 | 0.99796172 | 0.2604 | 0.1426 | 0.1785 | 0.1785 | TRUE | 3.2665 |
| 9 | 0.99796172 | 0.2604 | 0.1426 | 0.1785 | 0.1785 | TRUE | 3.2665 |
| 10 | 0.99796172 | 0.2604 | 0.1426 | 0.1785 | 0.1785 | TRUE | 3.2665 |
| 11 | 0.99796172 | 0.2604 | 0.1426 | 0.1785 | 0.1785 | TRUE | 3.2665 |
| 12 | 0.99796172 | 0.2604 | 0.1426 | 0.1785 | 0.1785 | TRUE | 3.2665 |
| 13 | 0.99796172 | 0.2604 | 0.1426 | 0.1785 | 0.1785 | TRUE | 3.2665 |
| 14 | 0.99796172 | 0.0871 | 0.156 | 0.1336 | 0.1336 | TRUE | 0.5158 |
| 15 | 0.99796172 | 0.1861 | 0.071 | 0.1079 | 0.1079 | TRUE | 0.3378 |
| 16 | 0.99796172 | 0.0156 | 0.0978 | 0.0683 | 0.0683 | TRUE | 0.3906 |
| 17 | 0.99796172 | 0.0124 | 0.1639 | 0.1142 | 0.1142 | TRUE | 0.4142 |
| 18 | 0.99796172 | 0.0464 | 0.0645 | 0.058 | 0.058 | TRUE | 0.5885 |
| 19 | 0.99796172 | 0.0464 | 0.0645 | 0.058 | 0.058 | TRUE | 0.5885 |
| 20 | 0.99796172 | 0.0873 | 0.1601 | 0.1365 | 0.1365 | TRUE | 1.0664 |
| 21 | 0.99796172 | 0.0873 | 0.1601 | 0.1365 | 0.1365 | TRUE | 1.0664 |
| 22 | 0.99796172 | 0.0504 | 0.0647 | 0.0598 | 0.0598 | TRUE | 0.6657 |
| 23 | 0.99796172 | 0.0569 | 0.0892 | 0.0782 | 0.0782 | TRUE | 0.7662 |
| 24 | 0.99796172 | 0.0569 | 0.0892 | 0.0782 | 0.0782 | TRUE | 0.7662 |
| 25 | 0.99796172 | 0.0569 | 0.0892 | 0.0782 | 0.0782 | TRUE | 0.7662 |
| 26 | 0.99796172 | 0.0569 | 0.0892 | 0.0782 | 0.0782 | TRUE | 0.7662 |
| 27 | 0.99796172 | 0.0569 | 0.0892 | 0.0782 | 0.0782 | TRUE | 0.7662 |
| 28 | 0.99796172 | 0.0569 | 0.0892 | 0.0782 | 0.0782 | TRUE | 0.7662 |
| 29 | 0.99796172 | 0.0569 | 0.0892 | 0.0782 | 0.0782 | TRUE | 0.7662 |
| 30 | 0.99796172 | 0.0614 | 0.0742 | 0.069 | 0.069 | TRUE | 0.589 |
| 31 | 0.99796172 | 0.1744 | 0.063 | 0.102 | 0.102 | TRUE | 0.5408 |
| 32 | 0.99796172 | 0.1744 | 0.063 | 0.102 | 0.102 | TRUE | 0.5408 |
| 33 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 34 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 35 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 36 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 37 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 38 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 39 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 40 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 41 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 42 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 43 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 44 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 45 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 46 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 47 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 48 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 49 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 50 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 51 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 52 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 53 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 54 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 55 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 56 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 57 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 58 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 59 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 4 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 5 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 6 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 7 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 8 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 9 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 10 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 11 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 12 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 13 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 14 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 15 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 16 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 17 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 18 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 19 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 20 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 21 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 22 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 23 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 24 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 25 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 26 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 27 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 28 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 29 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 30 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 31 | 0.99796172 | 0.2477 | 0.133 | 0.168 | 0.168 | TRUE | 3.2329 |
| 32 | 0.99796172 | 0.0739 | 0.0971 | 0.0892 | 0.0892 | TRUE | 0.3575 |
| 33 | 0.99796172 | 0.0745 | 0.0783 | 0.0766 | 0.0766 | TRUE | 0.3259 |
| 34 | 0.99796172 | 0.0745 | 0.0783 | 0.0766 | 0.0766 | TRUE | 0.3259 |
| 35 | 0.99796172 | 0.0769 | 0.078 | 0.0771 | 0.0771 | TRUE | 0.3403 |
| 36 | 0.99796172 | 0.0769 | 0.078 | 0.0771 | 0.0771 | TRUE | 0.3403 |
| 37 | 0.99796172 | 0.0274 | 0.1003 | 0.0747 | 0.0747 | TRUE | 0.4968 |
| 38 | 0.99796172 | 0.0537 | 0.0901 | 0.0775 | 0.0775 | TRUE | 0.8934 |
| 39 | 0.99796172 | 0.0537 | 0.0901 | 0.0775 | 0.0775 | TRUE | 0.8934 |
| 40 | 0.99796172 | 0.0537 | 0.0901 | 0.0775 | 0.0775 | TRUE | 0.8934 |
| 41 | 0.99796172 | 0.0537 | 0.0901 | 0.0775 | 0.0775 | TRUE | 0.8934 |
| 42 | 0.99796172 | 0.0537 | 0.0901 | 0.0775 | 0.0775 | TRUE | 0.8934 |
| 43 | 0.99796172 | 0.0537 | 0.0901 | 0.0775 | 0.0775 | TRUE | 0.8934 |
| 44 | 0.99796172 | 0.0537 | 0.0901 | 0.0775 | 0.0775 | TRUE | 0.8934 |
| 45 | 0.99796172 | 0.0537 | 0.0901 | 0.0775 | 0.0775 | TRUE | 0.8934 |
| 46 | 0.99796172 | 0.0537 | 0.0901 | 0.0775 | 0.0775 | TRUE | 0.8934 |
| 47 | 0.99796172 | 0.0537 | 0.0901 | 0.0775 | 0.0775 | TRUE | 0.8934 |
| 48 | 0.99796172 | 0.0537 | 0.0901 | 0.0775 | 0.0775 | TRUE | 0.8934 |
| 49 | 0.99796172 | 0.0537 | 0.0901 | 0.0775 | 0.0775 | TRUE | 0.8934 |
| 50 | 0.99796172 | 0.0537 | 0.0901 | 0.0775 | 0.0775 | TRUE | 0.8934 |
| 51 | 0.99796172 | 0.0537 | 0.0901 | 0.0775 | 0.0775 | TRUE | 0.8934 |
| 52 | 0.99796172 | 0.0537 | 0.0901 | 0.0775 | 0.0775 | TRUE | 0.8934 |
| 53 | 0.99796172 | 0.0537 | 0.0901 | 0.0775 | 0.0775 | TRUE | 0.8934 |
| 54 | 0.99796172 | 0.0537 | 0.0901 | 0.0775 | 0.0775 | TRUE | 0.8934 |
| 55 | 0.99796172 | 0.0331 | 0.1395 | 0.1026 | 0.1026 | TRUE | 0.2314 |
| 56 | 0.99796172 | 0.0331 | 0.1395 | 0.1026 | 0.1026 | TRUE | 0.2314 |
| 57 | 0.99796172 | 0.0331 | 0.1395 | 0.1026 | 0.1026 | TRUE | 0.2314 |
| 58 | 0.99796172 | 0.0331 | 0.1395 | 0.1026 | 0.1026 | TRUE | 0.2314 |
| 59 | 0.99796172 | 0.0331 | 0.1395 | 0.1026 | 0.1026 | TRUE | 0.2314 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 4 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 5 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 6 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 7 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 8 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 9 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 10 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 11 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 12 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 13 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 14 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 15 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 16 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 17 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 18 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 19 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 20 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 21 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 22 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 23 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 24 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 25 | 0.99796172 | 0.1515 | 0.1034 | 0.1189 | 0.1189 | TRUE | 0.4812 |
| 26 | 0.99796172 | 0.0634 | 0.0792 | 0.0739 | 0.0739 | TRUE | 0.5652 |
| 27 | 0.99796172 | 0.1333 | 0.0712 | 0.0919 | 0.0919 | TRUE | 1.2929 |
| 28 | 0.99796172 | 0.1333 | 0.0712 | 0.0919 | 0.0919 | TRUE | 1.2929 |
| 29 | 0.99796172 | 0.0601 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.2015 |
| 30 | 0.99796172 | 0.0601 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.2015 |
| 31 | 0.99796172 | 0.0601 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.2015 |
| 32 | 0.99796172 | 0.0601 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.2015 |
| 33 | 0.99796172 | 0.0601 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.2015 |
| 34 | 0.99796172 | 0.0601 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.2015 |
| 35 | 0.99796172 | 0.0601 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.2015 |
| 36 | 0.99796172 | 0.0601 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.2015 |
| 37 | 0.99796172 | 0.0601 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.2015 |
| 38 | 0.99796172 | 0.0601 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.2015 |
| 39 | 0.99796172 | 0.0601 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.2015 |
| 40 | 0.99796172 | 0.0601 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.2015 |
| 41 | 0.99796172 | 0.0601 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.2015 |
| 42 | 0.99796172 | 0.0601 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.2015 |
| 43 | 0.99796172 | 0.0601 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.2015 |
| 44 | 0.99796172 | 0.0601 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.2015 |
| 45 | 0.99796172 | 0.0601 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.2015 |
| 46 | 0.99796172 | 0.0601 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.2015 |
| 47 | 0.99796172 | 0.0601 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.2015 |
| 48 | 0.99796172 | 0.0604 | 0.0838 | 0.0754 | 0.0754 | TRUE | 1.206 |
| 49 | 0.99796172 | 0.0577 | 0.0836 | 0.0743 | 0.0743 | TRUE | 1.1646 |
| 50 | 0.99796172 | 0.0577 | 0.0836 | 0.0743 | 0.0743 | TRUE | 1.1646 |
| 51 | 0.99796172 | 0.0577 | 0.0836 | 0.0743 | 0.0743 | TRUE | 1.1646 |
| 52 | 0.99796172 | 0.17 | 0.1319 | 0.1443 | 0.1443 | TRUE | 0.8127 |
| 53 | 0.99796172 | 0.17 | 0.1319 | 0.1443 | 0.1443 | TRUE | 0.8127 |
| 54 | 0.99796172 | 0.17 | 0.1319 | 0.1443 | 0.1443 | TRUE | 0.8127 |
| 55 | 0.99796172 | 0.17 | 0.1319 | 0.1443 | 0.1443 | TRUE | 0.8127 |
| 56 | 0.99796172 | 0.172 | 0.063 | 0.0933 | 0.0933 | TRUE | 3.6096 |
| 57 | 0.99796172 | 0.0992 | 0.1507 | 0.1347 | 0.1347 | TRUE | 1.7485 |
| 58 | 0.99796172 | 0.0992 | 0.1507 | 0.1347 | 0.1347 | TRUE | 1.7485 |
| 59 | NA | 10 | 0.084 | 1.2226 | 10 | TRUE | 36.0827 |
| 60 | | | | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | | | | |
|----|--------|--------|--------|--------|------|---------|
| NA | 6.2015 | 0.0919 | 1.0138 | 6.2015 | TRUE | 35.2254 |
| NA | 6.2015 | 0.0919 | 1.0138 | 6.2015 | TRUE | 35.2254 |
| NA | 6.2015 | 0.0919 | 1.0138 | 6.2015 | TRUE | 35.2254 |
| NA | 6.2015 | 0.0919 | 1.0138 | 6.2015 | TRUE | 35.2254 |
| NA | 6.2015 | 0.0919 | 1.0138 | 6.2015 | TRUE | 35.2254 |
| NA | 6.2015 | 0.0919 | 1.0138 | 6.2015 | TRUE | 35.2254 |
| NA | 6.2015 | 0.0919 | 1.0138 | 6.2015 | TRUE | 35.2254 |
| NA | 6.2015 | 0.0919 | 1.0138 | 6.2015 | TRUE | 35.2254 |
| NA | 10 | 0.1598 | 1.2513 | 10 | TRUE | 31.4086 |
| NA | 10 | 0.1598 | 1.2513 | 10 | TRUE | 31.4086 |
| NA | 10 | 0.1628 | 1.2539 | 10 | TRUE | 31.2615 |
| NA | 10 | 0.1628 | 1.2539 | 10 | TRUE | 31.2615 |

Do not distribute

| | mean | 5% | 1% |
|----|------------|----|----|
| 1 | | | |
| 2 | | | |
| 3 | | | |
| 4 | 82.3333333 | 1 | 0 |
| 5 | | | |
| 6 | 53 | 1 | 1 |
| 7 | 53 | 1 | 0 |
| 8 | | | |
| 9 | 53 | 1 | 0 |
| 10 | 53 | 1 | 0 |
| 11 | 53 | 1 | 1 |
| 12 | | | |
| 13 | 53 | 1 | 1 |
| 14 | 53 | 1 | 1 |
| 15 | 53 | 1 | 1 |
| 16 | | | |
| 17 | 53 | 1 | 1 |
| 18 | 53.8333333 | 1 | 1 |
| 19 | 53.8333333 | 1 | 1 |
| 20 | | | |
| 21 | 53.8333333 | 1 | 1 |
| 22 | 164.166667 | 1 | 1 |
| 23 | 155.5 | 1 | 1 |
| 24 | 155.5 | 1 | 1 |
| 25 | | | |
| 26 | 155.5 | 1 | 1 |
| 27 | 155.5 | 1 | 1 |
| 28 | | | |
| 29 | 155.5 | 1 | 1 |
| 30 | 155.5 | 1 | 1 |
| 31 | 155.5 | 1 | 1 |
| 32 | 155.5 | 1 | 1 |
| 33 | | | |
| 34 | 155.5 | 1 | 0 |
| 35 | 155.5 | 1 | 0 |
| 36 | 155.5 | 1 | 0 |
| 37 | | | |
| 38 | 155.5 | 1 | 0 |
| 39 | 155.5 | 1 | 0 |
| 40 | 155.5 | 1 | 0 |
| 41 | | | |
| 42 | 155.5 | 1 | 0 |
| 43 | 155.5 | 1 | 0 |
| 44 | 155.5 | 1 | 0 |
| 45 | | | |
| 46 | 155.5 | 1 | 0 |
| 47 | 155.5 | 1 | 0 |
| 48 | 155.5 | 1 | 0 |
| 49 | | | |
| 50 | 155.5 | 1 | 0 |
| 51 | 155.5 | 1 | 0 |
| 52 | 155.5 | 1 | 0 |
| 53 | | | |
| 54 | 155.5 | 1 | 0 |
| 55 | 155.5 | 1 | 0 |
| 56 | 155.5 | 1 | 0 |
| 57 | | | |
| 58 | 155.5 | 1 | 0 |
| 59 | 155.5 | 1 | 0 |
| 60 | | | |

| | | | |
|----|-------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 155.5 | 1 | 0 |
| 4 | 155.5 | 1 | 0 |
| 5 | 155.5 | 1 | 0 |
| 6 | 155.5 | 1 | 0 |
| 7 | 155.5 | 1 | 0 |
| 8 | 155.5 | 1 | 0 |
| 9 | 155.5 | 1 | 0 |
| 10 | 155.5 | 1 | 0 |
| 11 | 155.5 | 1 | 0 |
| 12 | 155.5 | 1 | 0 |
| 13 | 155.5 | 1 | 0 |
| 14 | 155.5 | 1 | 0 |
| 15 | 155.5 | 1 | 0 |
| 16 | 155.5 | 1 | 0 |
| 17 | 155.5 | 1 | 0 |
| 18 | 155.5 | 1 | 0 |
| 19 | 155.5 | 1 | 0 |
| 20 | 155.5 | 1 | 0 |
| 21 | 155.5 | 1 | 0 |
| 22 | 155.5 | 1 | 0 |
| 23 | 155.5 | 1 | 0 |
| 24 | 155.5 | 1 | 0 |
| 25 | 155.5 | 1 | 0 |
| 26 | 155.5 | 1 | 0 |
| 27 | 159 | 1 | 0 |
| 28 | 158 | 1 | 0 |
| 29 | 158 | 1 | 0 |
| 30 | 158 | 1 | 0 |
| 31 | 158 | 1 | 0 |
| 32 | 158 | 1 | 0 |
| 33 | 158 | 1 | 0 |
| 34 | 158 | 1 | 0 |
| 35 | 158 | 1 | 0 |
| 36 | 158 | 1 | 0 |
| 37 | 158 | 1 | 0 |
| 38 | 158 | 1 | 0 |
| 39 | 158 | 1 | 0 |
| 40 | 158 | 1 | 0 |
| 41 | 158 | 1 | 0 |
| 42 | 158 | 1 | 0 |
| 43 | 158 | 1 | 0 |
| 44 | 158 | 1 | 0 |
| 45 | 158 | 1 | 0 |
| 46 | 158 | 1 | 0 |
| 47 | 158 | 1 | 0 |
| 48 | 158 | 1 | 0 |
| 49 | 158 | 1 | 0 |
| 50 | 158 | 1 | 0 |
| 51 | 158 | 1 | 0 |
| 52 | 158 | 1 | 0 |
| 53 | 158 | 1 | 0 |
| 54 | 158 | 1 | 0 |
| 55 | 158 | 1 | 0 |
| 56 | 158 | 1 | 0 |
| 57 | 158 | 1 | 0 |
| 58 | 158 | 1 | 0 |
| 59 | 158 | 1 | 0 |
| 60 | | | |

| | | | |
|----|-------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 158 | 1 | 0 |
| 4 | 158 | 1 | 0 |
| 5 | 158 | 1 | 0 |
| 6 | 158 | 1 | 0 |
| 7 | 158 | 1 | 0 |
| 8 | 158 | 1 | 0 |
| 9 | 158 | 1 | 0 |
| 10 | 158 | 1 | 0 |
| 11 | 158 | 1 | 0 |
| 12 | 158 | 1 | 0 |
| 13 | 158 | 1 | 0 |
| 14 | 158 | 1 | 0 |
| 15 | 158 | 1 | 0 |
| 16 | 158 | 1 | 0 |
| 17 | 158 | 1 | 0 |
| 18 | 158 | 1 | 0 |
| 19 | 158 | 1 | 0 |
| 20 | 158 | 1 | 0 |
| 21 | 158 | 1 | 0 |
| 22 | 158 | 1 | 0 |
| 23 | 158 | 1 | 0 |
| 24 | 413.5 | 1 | 1 |
| 25 | 413.5 | 1 | 1 |
| 26 | 413.5 | 1 | 1 |
| 27 | 413.5 | 1 | 1 |
| 28 | 413.5 | 1 | 1 |
| 29 | 413.5 | 1 | 1 |
| 30 | 413.5 | 1 | 1 |
| 31 | 413.5 | 1 | 1 |
| 32 | 413.5 | 1 | 1 |
| 33 | 413.5 | 1 | 1 |
| 34 | 413.5 | 1 | 1 |
| 35 | 413.5 | 1 | 1 |
| 36 | 413.5 | 1 | 1 |
| 37 | 413.5 | 1 | 1 |
| 38 | 413.5 | 1 | 1 |
| 39 | 413.5 | 1 | 1 |
| 40 | 413.5 | 1 | 1 |
| 41 | 413.5 | 1 | 1 |
| 42 | 413.5 | 1 | 1 |
| 43 | 413.5 | 1 | 1 |
| 44 | 413.5 | 1 | 1 |
| 45 | 413.5 | 1 | 0 |
| 46 | 413.5 | 1 | 1 |
| 47 | 413.5 | 1 | 1 |
| 48 | 413.5 | 1 | 1 |
| 49 | 413.5 | 1 | 1 |
| 50 | 413.5 | 1 | 1 |
| 51 | 413.5 | 1 | 1 |
| 52 | 413.5 | 1 | 1 |
| 53 | 413.5 | 1 | 1 |
| 54 | 413.5 | 1 | 1 |
| 55 | 413.5 | 1 | 1 |
| 56 | 413.5 | 1 | 1 |
| 57 | 413.5 | 1 | 1 |
| 58 | 413.5 | 1 | 1 |
| 59 | 413.5 | 1 | 1 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 413.5 | 1 | 1 |
| 4 | 413.5 | 1 | 1 |
| 5 | 413.5 | 1 | 1 |
| 6 | 413.5 | 1 | 1 |
| 7 | 413.5 | 1 | 1 |
| 8 | 413.5 | 1 | 1 |
| 9 | 413.5 | 1 | 1 |
| 10 | 413.5 | 1 | 1 |
| 11 | 413.5 | 1 | 1 |
| 12 | 413.5 | 1 | 1 |
| 13 | 413.5 | 1 | 1 |
| 14 | 413.5 | 1 | 1 |
| 15 | 413.5 | 1 | 1 |
| 16 | 413.5 | 1 | 1 |
| 17 | 413.5 | 1 | 1 |
| 18 | 413.5 | 1 | 1 |
| 19 | 413.5 | 1 | 1 |
| 20 | 373.666667 | 1 | 1 |
| 21 | 373.666667 | 1 | 1 |
| 22 | 373.666667 | 1 | 1 |
| 23 | 373.666667 | 1 | 1 |
| 24 | 373.5 | 1 | 1 |
| 25 | 373.5 | 1 | 1 |
| 26 | 373.5 | 1 | 1 |
| 27 | 373.5 | 1 | 1 |
| 28 | 69 | 1 | 1 |
| 29 | | | |
| 30 | 66.3333333 | 1 | 1 |
| 31 | 66.3333333 | 1 | 1 |
| 32 | 66.3333333 | 1 | 1 |
| 33 | 66.3333333 | 1 | 1 |
| 34 | 66.3333333 | 1 | 1 |
| 35 | 66.3333333 | 1 | 1 |
| 36 | 66.3333333 | 1 | 1 |
| 37 | 66.3333333 | 1 | 1 |
| 38 | 66.3333333 | 1 | 1 |
| 39 | 66.3333333 | 1 | 1 |
| 40 | 66.3333333 | 1 | 1 |
| 41 | 66.3333333 | 1 | 1 |
| 42 | 66.3333333 | 1 | 1 |
| 43 | 66.3333333 | 1 | 1 |
| 44 | 66.3333333 | 1 | 1 |
| 45 | 66.3333333 | 1 | 1 |
| 46 | 66.3333333 | 1 | 1 |
| 47 | 66.3333333 | 1 | 1 |
| 48 | 66.3333333 | 1 | 1 |
| 49 | 66.3333333 | 1 | 1 |
| 50 | 66.3333333 | 1 | 1 |
| 51 | 66.3333333 | 1 | 0 |
| 52 | 66.3333333 | 1 | 0 |
| 53 | 66.3333333 | 1 | 0 |
| 54 | 66.3333333 | 1 | 0 |
| 55 | 66.3333333 | 1 | 0 |
| 56 | 66.3333333 | 1 | 0 |
| 57 | 209.333333 | 1 | 0 |
| 58 | 3044.16667 | 1 | 0 |
| 59 | | | |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 3044.16667 | 1 | 0 |
| 4 | 3044.16667 | 1 | 0 |
| 5 | 3044.16667 | 1 | 0 |
| 6 | 3044.16667 | 1 | 0 |
| 7 | 3044.16667 | 1 | 0 |
| 8 | 3025.5 | 1 | 0 |
| 9 | 3025.5 | 1 | 0 |
| 10 | 3025.5 | 1 | 0 |
| 11 | 3025.5 | 1 | 0 |
| 12 | 3025.5 | 1 | 0 |
| 13 | 3025.5 | 1 | 0 |
| 14 | 3025.5 | 1 | 0 |
| 15 | 3025.5 | 1 | 0 |
| 16 | 3025.5 | 1 | 0 |
| 17 | 3025.5 | 1 | 0 |
| 18 | 3025.5 | 1 | 0 |
| 19 | 3025.5 | 1 | 0 |
| 20 | 3025.5 | 1 | 0 |
| 21 | 3025.5 | 1 | 0 |
| 22 | 526 | 1 | 0 |
| 23 | 526 | 1 | 0 |
| 24 | 526 | 1 | 0 |
| 25 | 526 | 1 | 0 |
| 26 | 526 | 1 | 0 |
| 27 | 526 | 1 | 0 |
| 28 | 526 | 1 | 0 |
| 29 | 526 | 1 | 0 |
| 30 | 526 | 1 | 0 |
| 31 | 526 | 1 | 0 |
| 32 | 526 | 1 | 0 |
| 33 | 526 | 1 | 0 |
| 34 | 526 | 1 | 0 |
| 35 | 526 | 1 | 0 |
| 36 | 526 | 1 | 0 |
| 37 | 526 | 1 | 0 |
| 38 | 526 | 1 | 0 |
| 39 | 526 | 1 | 0 |
| 40 | 526 | 1 | 0 |
| 41 | 526 | 1 | 0 |
| 42 | 526 | 1 | 0 |
| 43 | 526 | 1 | 0 |
| 44 | 526 | 1 | 0 |
| 45 | 526 | 1 | 0 |
| 46 | 526 | 1 | 0 |
| 47 | 526 | 1 | 0 |
| 48 | 526 | 1 | 0 |
| 49 | 526 | 1 | 0 |
| 50 | 526 | 1 | 0 |
| 51 | 526 | 1 | 0 |
| 52 | 526 | 1 | 0 |
| 53 | 526 | 1 | 0 |
| 54 | 526 | 1 | 0 |
| 55 | 125.666667 | 1 | 0 |
| 56 | 125.333333 | 1 | 0 |
| 57 | 125.333333 | 1 | 0 |
| 58 | 125.333333 | 1 | 0 |
| 59 | 125.333333 | 1 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 125.333333 | 1 | 0 |
| 4 | 125.333333 | 1 | 0 |
| 5 | 125.333333 | 1 | 0 |
| 6 | 125.333333 | 1 | 0 |
| 7 | 125.333333 | 1 | 0 |
| 8 | 92.5 | 1 | 0 |
| 9 | 92.5 | 1 | 0 |
| 10 | 92.5 | 1 | 0 |
| 11 | 92.5 | 1 | 0 |
| 12 | 92.5 | 1 | 0 |
| 13 | 92.5 | 1 | 0 |
| 14 | 92.5 | 1 | 0 |
| 15 | 92.5 | 1 | 0 |
| 16 | 92.5 | 1 | 0 |
| 17 | 92.5 | 1 | 0 |
| 18 | 92.5 | 1 | 0 |
| 19 | 92.5 | 1 | 0 |
| 20 | 92.5 | 1 | 0 |
| 21 | 92.5 | 1 | 0 |
| 22 | 92.5 | 1 | 0 |
| 23 | 92.5 | 1 | 0 |
| 24 | 92.5 | 1 | 0 |
| 25 | 92.5 | 1 | 0 |
| 26 | 92.5 | 1 | 0 |
| 27 | 92.5 | 1 | 0 |
| 28 | 92.5 | 1 | 0 |
| 29 | 92.5 | 1 | 0 |
| 30 | 92.5 | 1 | 0 |
| 31 | 92.5 | 1 | 0 |
| 32 | 92.5 | 1 | 0 |
| 33 | 92.5 | 1 | 0 |
| 34 | 92.5 | 1 | 0 |
| 35 | 92.5 | 1 | 0 |
| 36 | 92.5 | 1 | 0 |
| 37 | 92.5 | 1 | 0 |
| 38 | 92.5 | 1 | 0 |
| 39 | 92.833333 | 1 | 0 |
| 40 | 92.833333 | 1 | 0 |
| 41 | 103.5 | 1 | 0 |
| 42 | 103.5 | 1 | 0 |
| 43 | 103.5 | 1 | 0 |
| 44 | 103.5 | 1 | 0 |
| 45 | 103.5 | 1 | 0 |
| 46 | 103.5 | 1 | 0 |
| 47 | 103.5 | 1 | 0 |
| 48 | 103.5 | 1 | 0 |
| 49 | 103.5 | 1 | 0 |
| 50 | 103.5 | 1 | 0 |
| 51 | 103.5 | 1 | 0 |
| 52 | 103.5 | 1 | 0 |
| 53 | 103.5 | 1 | 0 |
| 54 | 103.5 | 1 | 0 |
| 55 | 103.5 | 1 | 0 |
| 56 | 103.5 | 1 | 0 |
| 57 | 103.5 | 0 | 0 |
| 58 | 103.5 | 0 | 0 |
| 59 | 103.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 103.5 | 0 | 0 |
| 4 | 103.5 | 0 | 0 |
| 5 | 103.5 | 0 | 0 |
| 6 | 103.5 | 0 | 0 |
| 7 | 103.5 | 0 | 0 |
| 8 | 103.5 | 0 | 0 |
| 9 | 103.5 | 0 | 0 |
| 10 | 103.5 | 0 | 0 |
| 11 | 103.5 | 0 | 0 |
| 12 | 103.5 | 0 | 0 |
| 13 | 103.5 | 0 | 0 |
| 14 | 103.5 | 0 | 0 |
| 15 | 103.5 | 0 | 0 |
| 16 | 103.5 | 0 | 0 |
| 17 | 103.5 | 0 | 0 |
| 18 | 103.5 | 0 | 0 |
| 19 | 103.5 | 0 | 0 |
| 20 | 103.5 | 0 | 0 |
| 21 | 103.5 | 0 | 0 |
| 22 | 103.5 | 0 | 0 |
| 23 | 103.5 | 0 | 0 |
| 24 | 103.5 | 0 | 0 |
| 25 | 103.5 | 0 | 0 |
| 26 | 103.5 | 0 | 0 |
| 27 | 103.5 | 0 | 0 |
| 28 | 103.5 | 0 | 0 |
| 29 | 103.5 | 0 | 0 |
| 30 | 103.5 | 0 | 0 |
| 31 | 103.5 | 0 | 0 |
| 32 | 103.5 | 0 | 0 |
| 33 | 103.5 | 0 | 0 |
| 34 | 103.5 | 0 | 0 |
| 35 | 267.166667 | 0 | 0 |
| 36 | 261.166667 | 0 | 0 |
| 37 | 261.166667 | 0 | 0 |
| 38 | 261.166667 | 0 | 0 |
| 39 | 261.166667 | 0 | 0 |
| 40 | 261.166667 | 0 | 0 |
| 41 | 261.166667 | 0 | 0 |
| 42 | 261.166667 | 0 | 0 |
| 43 | 261.166667 | 0 | 0 |
| 44 | 261.166667 | 0 | 0 |
| 45 | 261.166667 | 0 | 0 |
| 46 | 261.166667 | 0 | 0 |
| 47 | 261.166667 | 0 | 0 |
| 48 | 261.166667 | 0 | 0 |
| 49 | 261.166667 | 0 | 0 |
| 50 | 261.166667 | 0 | 0 |
| 51 | 261.166667 | 0 | 0 |
| 52 | 261.166667 | 0 | 0 |
| 53 | 261.166667 | 0 | 0 |
| 54 | 261.166667 | 0 | 0 |
| 55 | 261.166667 | 0 | 0 |
| 56 | 261.166667 | 0 | 0 |
| 57 | 261.166667 | 0 | 0 |
| 58 | 261.166667 | 0 | 0 |
| 59 | 261.166667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 261.166667 | 0 | 0 |
| 4 | 261.166667 | 0 | 0 |
| 5 | 261.166667 | 0 | 0 |
| 6 | 261.166667 | 0 | 0 |
| 7 | 261.166667 | 0 | 0 |
| 8 | 261.166667 | 0 | 0 |
| 9 | 261.166667 | 0 | 0 |
| 10 | 261.166667 | 0 | 0 |
| 11 | 261.166667 | 0 | 0 |
| 12 | 261.166667 | 0 | 0 |
| 13 | 261.166667 | 0 | 0 |
| 14 | 261.166667 | 0 | 0 |
| 15 | 261.166667 | 0 | 0 |
| 16 | 261.166667 | 0 | 0 |
| 17 | 261.166667 | 0 | 0 |
| 18 | 261.166667 | 0 | 0 |
| 19 | 261.166667 | 0 | 0 |
| 20 | 261.166667 | 0 | 0 |
| 21 | 261.166667 | 0 | 0 |
| 22 | 261.166667 | 0 | 0 |
| 23 | 261.166667 | 0 | 0 |
| 24 | 261.166667 | 0 | 0 |
| 25 | 261.166667 | 0 | 0 |
| 26 | 261.166667 | 0 | 0 |
| 27 | 261.166667 | 0 | 0 |
| 28 | 261.166667 | 0 | 0 |
| 29 | 261.166667 | 0 | 0 |
| 30 | 261.166667 | 0 | 0 |
| 31 | 261.166667 | 0 | 0 |
| 32 | 261.166667 | 0 | 0 |
| 33 | 261.166667 | 0 | 0 |
| 34 | 261.166667 | 0 | 0 |
| 35 | 261.166667 | 0 | 0 |
| 36 | 261.166667 | 0 | 0 |
| 37 | 261.166667 | 0 | 0 |
| 38 | 261.166667 | 0 | 0 |
| 39 | 261.166667 | 0 | 0 |
| 40 | 261.166667 | 0 | 0 |
| 41 | 261.166667 | 0 | 0 |
| 42 | 261.166667 | 0 | 0 |
| 43 | 261.166667 | 0 | 0 |
| 44 | 261.166667 | 0 | 0 |
| 45 | 261.166667 | 0 | 0 |
| 46 | 261.166667 | 0 | 0 |
| 47 | 261.166667 | 0 | 0 |
| 48 | 261.166667 | 0 | 0 |
| 49 | 261.166667 | 0 | 0 |
| 50 | 261.166667 | 0 | 0 |
| 51 | 261.166667 | 0 | 0 |
| 52 | 261.166667 | 0 | 0 |
| 53 | 261.166667 | 0 | 0 |
| 54 | 261.166667 | 0 | 0 |
| 55 | 261.166667 | 0 | 0 |
| 56 | 261.166667 | 0 | 0 |
| 57 | 261.166667 | 0 | 0 |
| 58 | 261.166667 | 0 | 0 |
| 59 | 261.166667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 261.166667 | 0 | 0 |
| 4 | 261.166667 | 0 | 0 |
| 5 | 261.166667 | 0 | 0 |
| 6 | 261.166667 | 0 | 0 |
| 7 | 261.166667 | 0 | 0 |
| 8 | 56.5 | 0 | 0 |
| 9 | 56.5 | 0 | 0 |
| 10 | 56.5 | 0 | 0 |
| 11 | 56.5 | 0 | 0 |
| 12 | 56.5 | 0 | 0 |
| 13 | 56.5 | 0 | 0 |
| 14 | 56.5 | 0 | 0 |
| 15 | 56.5 | 0 | 0 |
| 16 | 56.5 | 0 | 0 |
| 17 | 56.5 | 0 | 0 |
| 18 | 56.5 | 0 | 0 |
| 19 | 56.5 | 0 | 0 |
| 20 | 56.5 | 0 | 0 |
| 21 | 56.5 | 0 | 0 |
| 22 | 56.5 | 0 | 0 |
| 23 | 56.5 | 0 | 0 |
| 24 | 56.5 | 0 | 0 |
| 25 | 56.5 | 0 | 0 |
| 26 | 56.5 | 0 | 0 |
| 27 | 56.5 | 0 | 0 |
| 28 | 56.5 | 0 | 0 |
| 29 | 56.5 | 0 | 0 |
| 30 | 56.5 | 0 | 0 |
| 31 | 56.5 | 0 | 0 |
| 32 | 56.5 | 0 | 0 |
| 33 | 56.5 | 0 | 0 |
| 34 | 56.5 | 0 | 0 |
| 35 | 56.5 | 0 | 0 |
| 36 | 56.5 | 0 | 0 |
| 37 | 56.5 | 0 | 0 |
| 38 | 56.5 | 0 | 0 |
| 39 | 56.5 | 0 | 0 |
| 40 | 56.5 | 0 | 0 |
| 41 | 56.5 | 0 | 0 |
| 42 | 56.5 | 0 | 0 |
| 43 | 56.5 | 0 | 0 |
| 44 | 56.5 | 0 | 0 |
| 45 | 56.5 | 0 | 0 |
| 46 | 56.5 | 0 | 0 |
| 47 | 884.166667 | 0 | 0 |
| 48 | 884.166667 | 0 | 0 |
| 49 | 884.166667 | 0 | 0 |
| 50 | 884.166667 | 0 | 0 |
| 51 | 884.166667 | 0 | 0 |
| 52 | 884.166667 | 0 | 0 |
| 53 | 884.166667 | 0 | 0 |
| 54 | 884.166667 | 0 | 0 |
| 55 | 139.166667 | 0 | 0 |
| 56 | 138.166667 | 0 | 0 |
| 57 | 138.166667 | 0 | 0 |
| 58 | 138.166667 | 0 | 0 |
| 59 | 138.166667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 138.166667 | 0 | 0 |
| 4 | 138.166667 | 0 | 0 |
| 5 | 138.166667 | 0 | 0 |
| 6 | 138.166667 | 0 | 0 |
| 7 | 138.166667 | 0 | 0 |
| 8 | 138.166667 | 0 | 0 |
| 9 | 138.166667 | 0 | 0 |
| 10 | 138.166667 | 0 | 0 |
| 11 | 138.166667 | 0 | 0 |
| 12 | 138.166667 | 0 | 0 |
| 13 | 138.166667 | 0 | 0 |
| 14 | 138.166667 | 0 | 0 |
| 15 | 138.166667 | 0 | 0 |
| 16 | 138.166667 | 0 | 0 |
| 17 | 138.166667 | 0 | 0 |
| 18 | 138.166667 | 0 | 0 |
| 19 | 138.166667 | 0 | 0 |
| 20 | 138.166667 | 0 | 0 |
| 21 | 138.166667 | 0 | 0 |
| 22 | 138.166667 | 0 | 0 |
| 23 | 138.166667 | 0 | 0 |
| 24 | 138.166667 | 0 | 0 |
| 25 | 138.166667 | 0 | 0 |
| 26 | 138.166667 | 0 | 0 |
| 27 | 138.166667 | 0 | 0 |
| 28 | 138.166667 | 0 | 0 |
| 29 | 138.166667 | 0 | 0 |
| 30 | 138.166667 | 0 | 0 |
| 31 | 138.166667 | 0 | 0 |
| 32 | 138.166667 | 0 | 0 |
| 33 | 138.166667 | 0 | 0 |
| 34 | 138.166667 | 0 | 0 |
| 35 | 138.166667 | 0 | 0 |
| 36 | 138.166667 | 0 | 0 |
| 37 | 138.166667 | 0 | 0 |
| 38 | 138.166667 | 0 | 0 |
| 39 | 138.166667 | 0 | 0 |
| 40 | 138.166667 | 0 | 0 |
| 41 | 138.166667 | 0 | 0 |
| 42 | 138.166667 | 0 | 0 |
| 43 | 138.166667 | 0 | 0 |
| 44 | 138.166667 | 0 | 0 |
| 45 | 81.3333333 | 0 | 0 |
| 46 | 81.3333333 | 0 | 0 |
| 47 | 81.3333333 | 0 | 0 |
| 48 | 81.3333333 | 0 | 0 |
| 49 | 81.3333333 | 0 | 0 |
| 50 | 81.3333333 | 0 | 0 |
| 51 | 81.3333333 | 0 | 0 |
| 52 | 81.3333333 | 0 | 0 |
| 53 | 81.3333333 | 0 | 0 |
| 54 | 81.3333333 | 0 | 0 |
| 55 | 81.3333333 | 0 | 0 |
| 56 | 81.3333333 | 0 | 0 |
| 57 | 81.3333333 | 0 | 0 |
| 58 | 81.3333333 | 0 | 0 |
| 59 | 81.3333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 81.3333333 | 0 | 0 |
| 4 | 81.3333333 | 0 | 0 |
| 5 | 81.3333333 | 0 | 0 |
| 6 | 81.3333333 | 0 | 0 |
| 7 | 81.3333333 | 0 | 0 |
| 8 | 81.3333333 | 0 | 0 |
| 9 | 81.3333333 | 0 | 0 |
| 10 | 81.3333333 | 0 | 0 |
| 11 | 81.3333333 | 0 | 0 |
| 12 | 71.1666667 | 0 | 0 |
| 13 | 71.1666667 | 0 | 0 |
| 14 | 71.1666667 | 0 | 0 |
| 15 | 71.1666667 | 0 | 0 |
| 16 | 71.1666667 | 0 | 0 |
| 17 | 71.1666667 | 0 | 0 |
| 18 | 52.3333333 | 0 | 0 |
| 19 | 51.3333333 | 0 | 0 |
| 20 | 51.3333333 | 0 | 0 |
| 21 | 51.3333333 | 0 | 0 |
| 22 | 51.3333333 | 0 | 0 |
| 23 | 51.3333333 | 0 | 0 |
| 24 | 51.3333333 | 0 | 0 |
| 25 | 51.3333333 | 0 | 0 |
| 26 | 51.3333333 | 0 | 0 |
| 27 | 51.3333333 | 0 | 0 |
| 28 | 51.3333333 | 0 | 0 |
| 29 | 51.3333333 | 0 | 0 |
| 30 | 51.3333333 | 0 | 0 |
| 31 | 51.3333333 | 0 | 0 |
| 32 | 51.3333333 | 0 | 0 |
| 33 | 51.3333333 | 0 | 0 |
| 34 | 51.3333333 | 0 | 0 |
| 35 | 51.3333333 | 0 | 0 |
| 36 | 51.3333333 | 0 | 0 |
| 37 | 51.3333333 | 0 | 0 |
| 38 | 51.3333333 | 0 | 0 |
| 39 | 51.3333333 | 0 | 0 |
| 40 | 51.3333333 | 0 | 0 |
| 41 | 51.3333333 | 0 | 0 |
| 42 | 51.3333333 | 0 | 0 |
| 43 | 93.6666667 | 0 | 0 |
| 44 | 93.6666667 | 0 | 0 |
| 45 | 93.6666667 | 0 | 0 |
| 46 | 93.6666667 | 0 | 0 |
| 47 | 93.6666667 | 0 | 0 |
| 48 | 93.6666667 | 0 | 0 |
| 49 | 93.6666667 | 0 | 0 |
| 50 | 93.6666667 | 0 | 0 |
| 51 | 93.6666667 | 0 | 0 |
| 52 | 93.6666667 | 0 | 0 |
| 53 | 93.6666667 | 0 | 0 |
| 54 | 93.6666667 | 0 | 0 |
| 55 | 93.6666667 | 0 | 0 |
| 56 | 93.6666667 | 0 | 0 |
| 57 | 93.6666667 | 0 | 0 |
| 58 | 93.6666667 | 0 | 0 |
| 59 | 93.6666667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 93.666667 | 0 | 0 |
| 4 | 93.666667 | 0 | 0 |
| 5 | 93.666667 | 0 | 0 |
| 6 | 51.666667 | 0 | 0 |
| 7 | 114.333333 | 0 | 0 |
| 8 | 114.333333 | 0 | 0 |
| 9 | 114.333333 | 0 | 0 |
| 10 | 114.333333 | 0 | 0 |
| 11 | 114.333333 | 0 | 0 |
| 12 | 114.333333 | 0 | 0 |
| 13 | 114.333333 | 0 | 0 |
| 14 | 114.333333 | 0 | 0 |
| 15 | 114.333333 | 0 | 0 |
| 16 | 114.333333 | 0 | 0 |
| 17 | 114.333333 | 0 | 0 |
| 18 | 114.333333 | 0 | 0 |
| 19 | 114.333333 | 0 | 0 |
| 20 | 536.666667 | 0 | 0 |
| 21 | | | |
| 22 | 82 | 0 | 0 |
| 23 | 82 | 0 | 0 |
| 24 | 82 | 0 | 0 |
| 25 | 82 | 0 | 0 |
| 26 | 82 | 0 | 0 |
| 27 | 82 | 0 | 0 |
| 28 | 82 | 0 | 0 |
| 29 | 82 | 0 | 0 |
| 30 | 82 | 0 | 0 |
| 31 | 82 | 0 | 0 |
| 32 | 82 | 0 | 0 |
| 33 | 82 | 0 | 0 |
| 34 | 82 | 0 | 0 |
| 35 | 82 | 0 | 0 |
| 36 | 82 | 0 | 0 |
| 37 | 82 | 0 | 0 |
| 38 | 82 | 0 | 0 |
| 39 | 82 | 0 | 0 |
| 40 | 536.333333 | 0 | 0 |
| 41 | 536.333333 | 0 | 0 |
| 42 | 536.333333 | 0 | 0 |
| 43 | 536.333333 | 0 | 0 |
| 44 | 536.333333 | 0 | 0 |
| 45 | 536.333333 | 0 | 0 |
| 46 | 536.333333 | 0 | 0 |
| 47 | 536.333333 | 0 | 0 |
| 48 | 536.333333 | 0 | 0 |
| 49 | 536.333333 | 0 | 0 |
| 50 | 536.333333 | 0 | 0 |
| 51 | 536.333333 | 0 | 0 |
| 52 | 536.333333 | 0 | 0 |
| 53 | 536.333333 | 0 | 0 |
| 54 | 536.333333 | 0 | 0 |
| 55 | 536.333333 | 0 | 0 |
| 56 | 536.333333 | 0 | 0 |
| 57 | 536.333333 | 0 | 0 |
| 58 | 536.333333 | 0 | 0 |
| 59 | 536.333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 536.333333 | 0 | 0 |
| 4 | 536.333333 | 0 | 0 |
| 5 | 536.333333 | 0 | 0 |
| 6 | 536.333333 | 0 | 0 |
| 7 | 536.333333 | 0 | 0 |
| 8 | 536.333333 | 0 | 0 |
| 9 | 536.333333 | 0 | 0 |
| 10 | 53.5 | 0 | 0 |
| 11 | 53.5 | 0 | 0 |
| 12 | 53.5 | 0 | 0 |
| 13 | 53.5 | 0 | 0 |
| 14 | 53.5 | 0 | 0 |
| 15 | 53.5 | 0 | 0 |
| 16 | 542.666667 | 0 | 0 |
| 17 | 50 | 0 | 0 |
| 18 | 50 | 0 | 0 |
| 19 | 50 | 0 | 0 |
| 20 | 50 | 0 | 0 |
| 21 | 50 | 0 | 0 |
| 22 | 50 | 0 | 0 |
| 23 | 50 | 0 | 0 |
| 24 | 50 | 0 | 0 |
| 25 | 50 | 0 | 0 |
| 26 | 50 | 0 | 0 |
| 27 | 50 | 0 | 0 |
| 28 | 50 | 0 | 0 |
| 29 | 50 | 0 | 0 |
| 30 | 50 | 0 | 0 |
| 31 | 141.666667 | 0 | 0 |
| 32 | 63.666667 | 0 | 0 |
| 33 | 63.666667 | 0 | 0 |
| 34 | 63.666667 | 0 | 0 |
| 35 | 63.666667 | 0 | 0 |
| 36 | 63.666667 | 0 | 0 |
| 37 | 63.666667 | 0 | 0 |
| 38 | 63.666667 | 0 | 0 |
| 39 | 138.666667 | 0 | 0 |
| 40 | 138.666667 | 0 | 0 |
| 41 | 232.166667 | 0 | 0 |
| 42 | 232.166667 | 0 | 0 |
| 43 | 232.166667 | 0 | 0 |
| 44 | 232.166667 | 0 | 0 |
| 45 | 232.166667 | 0 | 0 |
| 46 | 232.166667 | 0 | 0 |
| 47 | 602.666667 | 0 | 0 |
| 48 | 602.666667 | 0 | 0 |
| 49 | 602.666667 | 0 | 0 |
| 50 | 602.666667 | 0 | 0 |
| 51 | 593.333333 | 0 | 0 |
| 52 | 593.333333 | 0 | 0 |
| 53 | 593.333333 | 0 | 0 |
| 54 | 593.333333 | 0 | 0 |
| 55 | 593.333333 | 0 | 0 |
| 56 | 593.333333 | 0 | 0 |
| 57 | 593.333333 | 0 | 0 |
| 58 | 593.333333 | 0 | 0 |
| 59 | 593.333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 593.333333 | 0 | 0 |
| 4 | 593.333333 | 0 | 0 |
| 5 | 593.333333 | 0 | 0 |
| 6 | 593.333333 | 0 | 0 |
| 7 | 593.333333 | 0 | 0 |
| 8 | 593.333333 | 0 | 0 |
| 9 | 593.333333 | 0 | 0 |
| 10 | 593.333333 | 0 | 0 |
| 11 | 5998 | 0 | 0 |
| 12 | 5998 | 0 | 0 |
| 13 | 5998 | 0 | 0 |
| 14 | 5998 | 0 | 0 |
| 15 | 95.5 | 0 | 0 |
| 16 | 95.5 | 0 | 0 |
| 17 | 95.5 | 0 | 0 |
| 18 | 95.5 | 0 | 0 |
| 19 | 95.5 | 0 | 0 |
| 20 | 409 | 0 | 0 |
| 21 | 409 | 0 | 0 |
| 22 | 409 | 0 | 0 |
| 23 | 409 | 0 | 0 |
| 24 | 409 | 0 | 0 |
| 25 | 409 | 0 | 0 |
| 26 | 409 | 0 | 0 |
| 27 | 409 | 0 | 0 |
| 28 | 409 | 0 | 0 |
| 29 | 409 | 0 | 0 |
| 30 | 409 | 0 | 0 |
| 31 | 409 | 0 | 0 |
| 32 | 409 | 0 | 0 |
| 33 | 409 | 0 | 0 |
| 34 | 409 | 0 | 0 |
| 35 | 409 | 0 | 0 |
| 36 | 409 | 0 | 0 |
| 37 | 409 | 0 | 0 |
| 38 | 409 | 0 | 0 |
| 39 | 409 | 0 | 0 |
| 40 | 409 | 0 | 0 |
| 41 | 409 | 0 | 0 |
| 42 | 409 | 0 | 0 |
| 43 | 409 | 0 | 0 |
| 44 | 409 | 0 | 0 |
| 45 | 409 | 0 | 0 |
| 46 | 409 | 0 | 0 |
| 47 | 409 | 0 | 0 |
| 48 | 409 | 0 | 0 |
| 49 | 409 | 0 | 0 |
| 50 | 409 | 0 | 0 |
| 51 | 409 | 0 | 0 |
| 52 | 409 | 0 | 0 |
| 53 | 409 | 0 | 0 |
| 54 | 409 | 0 | 0 |
| 55 | 409 | 0 | 0 |
| 56 | 409 | 0 | 0 |
| 57 | 409 | 0 | 0 |
| 58 | 409 | 0 | 0 |
| 59 | 409 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 409 | 0 | 0 |
| 4 | 409 | 0 | 0 |
| 5 | 409 | 0 | 0 |
| 6 | 409 | 0 | 0 |
| 7 | 409 | 0 | 0 |
| 8 | 409 | 0 | 0 |
| 9 | 409 | 0 | 0 |
| 10 | 409 | 0 | 0 |
| 11 | 409 | 0 | 0 |
| 12 | 409 | 0 | 0 |
| 13 | 409 | 0 | 0 |
| 14 | 409 | 0 | 0 |
| 15 | 409 | 0 | 0 |
| 16 | 409 | 0 | 0 |
| 17 | 409 | 0 | 0 |
| 18 | 409 | 0 | 0 |
| 19 | 409 | 0 | 0 |
| 20 | 409 | 0 | 0 |
| 21 | 409 | 0 | 0 |
| 22 | 409 | 0 | 0 |
| 23 | 409 | 0 | 0 |
| 24 | 409 | 0 | 0 |
| 25 | 409 | 0 | 0 |
| 26 | 409 | 0 | 0 |
| 27 | 409 | 0 | 0 |
| 28 | 409 | 0 | 0 |
| 29 | 409 | 0 | 0 |
| 30 | 409 | 0 | 0 |
| 31 | 410.166667 | 0 | 0 |
| 32 | 410.166667 | 0 | 0 |
| 33 | | | |
| 34 | 110 | 0 | 0 |
| 35 | 152.666667 | 0 | 0 |
| 36 | 152.666667 | 0 | 0 |
| 37 | 152.666667 | 0 | 0 |
| 38 | 152.666667 | 0 | 0 |
| 39 | 152.666667 | 0 | 0 |
| 40 | 152.666667 | 0 | 0 |
| 41 | 152.666667 | 0 | 0 |
| 42 | 152.666667 | 0 | 0 |
| 43 | 152.666667 | 0 | 0 |
| 44 | 152.666667 | 0 | 0 |
| 45 | 152.666667 | 0 | 0 |
| 46 | 152.666667 | 0 | 0 |
| 47 | 152.666667 | 0 | 0 |
| 48 | 152.666667 | 0 | 0 |
| 49 | 152.666667 | 0 | 0 |
| 50 | 152.666667 | 0 | 0 |
| 51 | 152.666667 | 0 | 0 |
| 52 | 152.666667 | 0 | 0 |
| 53 | 152.666667 | 0 | 0 |
| 54 | 152.666667 | 0 | 0 |
| 55 | 152.666667 | 0 | 0 |
| 56 | 152.666667 | 0 | 0 |
| 57 | 152.666667 | 0 | 0 |
| 58 | 152.666667 | 0 | 0 |
| 59 | 152.666667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 152.666667 | 0 | 0 |
| 4 | 152.666667 | 0 | 0 |
| 5 | 152.666667 | 0 | 0 |
| 6 | 152.666667 | 0 | 0 |
| 7 | 152.666667 | 0 | 0 |
| 8 | 152.666667 | 0 | 0 |
| 9 | 152.666667 | 0 | 0 |
| 10 | 152.666667 | 0 | 0 |
| 11 | 152.666667 | 0 | 0 |
| 12 | 152.666667 | 0 | 0 |
| 13 | 152.666667 | 0 | 0 |
| 14 | 152.666667 | 0 | 0 |
| 15 | 152.666667 | 0 | 0 |
| 16 | 152.666667 | 0 | 0 |
| 17 | 152.666667 | 0 | 0 |
| 18 | 152.666667 | 0 | 0 |
| 19 | 152.666667 | 0 | 0 |
| 20 | 6885.5 | 0 | 0 |
| 21 | 6885.5 | 0 | 0 |
| 22 | 6885.5 | 0 | 0 |
| 23 | 6885.5 | 0 | 0 |
| 24 | 6885.5 | 0 | 0 |
| 25 | 6885.5 | 0 | 0 |
| 26 | 6885.5 | 0 | 0 |
| 27 | 6885.5 | 0 | 0 |
| 28 | 6885.5 | 0 | 0 |
| 29 | 6885.5 | 0 | 0 |
| 30 | 111.666667 | 0 | 0 |
| 31 | 111.666667 | 0 | 0 |
| 32 | 7023.5 | 0 | 0 |
| 33 | 7023.5 | 0 | 0 |
| 34 | 7023.5 | 0 | 0 |
| 35 | 7023.5 | 0 | 0 |
| 36 | 7023.5 | 0 | 0 |
| 37 | 7023.5 | 0 | 0 |
| 38 | 7023.5 | 0 | 0 |
| 39 | 7023.5 | 0 | 0 |
| 40 | 7023.5 | 0 | 0 |
| 41 | 7023.5 | 0 | 0 |
| 42 | 7023.5 | 0 | 0 |
| 43 | 7023.5 | 0 | 0 |
| 44 | 241.333333 | 0 | 0 |
| 45 | 241.333333 | 0 | 0 |
| 46 | 241.333333 | 0 | 0 |
| 47 | 241.333333 | 0 | 0 |
| 48 | 241.333333 | 0 | 0 |
| 49 | 241.333333 | 0 | 0 |
| 50 | 241.333333 | 0 | 0 |
| 51 | 241.333333 | 0 | 0 |
| 52 | 241.333333 | 0 | 0 |
| 53 | 241.333333 | 0 | 0 |
| 54 | 241.333333 | 0 | 0 |
| 55 | 241.333333 | 0 | 0 |
| 56 | 241.333333 | 0 | 0 |
| 57 | 241.333333 | 0 | 0 |
| 58 | 241.333333 | 0 | 0 |
| 59 | 241.333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 241.333333 | 0 | 0 |
| 4 | 241.333333 | 0 | 0 |
| 5 | 241.333333 | 0 | 0 |
| 6 | 241.333333 | 0 | 0 |
| 7 | 241.333333 | 0 | 0 |
| 8 | 241.333333 | 0 | 0 |
| 9 | 241.333333 | 0 | 0 |
| 10 | 241.333333 | 0 | 0 |
| 11 | 241.333333 | 0 | 0 |
| 12 | 241.333333 | 0 | 0 |
| 13 | 241.333333 | 0 | 0 |
| 14 | 241.333333 | 0 | 0 |
| 15 | 241.333333 | 0 | 0 |
| 16 | 241.333333 | 0 | 0 |
| 17 | 241.333333 | 0 | 0 |
| 18 | 241.333333 | 0 | 0 |
| 19 | 241.333333 | 0 | 0 |
| 20 | 241.333333 | 0 | 0 |
| 21 | 241.333333 | 0 | 0 |
| 22 | 241.333333 | 0 | 0 |
| 23 | 241.333333 | 0 | 0 |
| 24 | 241.333333 | 0 | 0 |
| 25 | 241.333333 | 0 | 0 |
| 26 | 241.333333 | 0 | 0 |
| 27 | 241.333333 | 0 | 0 |
| 28 | 241.333333 | 0 | 0 |
| 29 | 241.333333 | 0 | 0 |
| 30 | 241.333333 | 0 | 0 |
| 31 | 241.333333 | 0 | 0 |
| 32 | 241.333333 | 0 | 0 |
| 33 | 241.333333 | 0 | 0 |
| 34 | 241.333333 | 0 | 0 |
| 35 | 241.333333 | 0 | 0 |
| 36 | 241.333333 | 0 | 0 |
| 37 | 241.333333 | 0 | 0 |
| 38 | 241.333333 | 0 | 0 |
| 39 | 111.333333 | 0 | 0 |
| 40 | 111.333333 | 0 | 0 |
| 41 | 1056.33333 | 0 | 0 |
| 42 | 1056.33333 | 0 | 0 |
| 43 | 1056.33333 | 0 | 0 |
| 44 | 3193.16667 | 0 | 0 |
| 45 | 3192.5 | 0 | 0 |
| 46 | 3192.5 | 0 | 0 |
| 47 | 3192.5 | 0 | 0 |
| 48 | 3192.5 | 0 | 0 |
| 49 | 3192.5 | 0 | 0 |
| 50 | 3192.5 | 0 | 0 |
| 51 | 3192.5 | 0 | 0 |
| 52 | 3192.5 | 0 | 0 |
| 53 | 3192.5 | 0 | 0 |
| 54 | 3192.5 | 0 | 0 |
| 55 | 3192.5 | 0 | 0 |
| 56 | 3192.5 | 0 | 0 |
| 57 | 3192.5 | 0 | 0 |
| 58 | 3192.5 | 0 | 0 |
| 59 | 3192.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|--------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 3192.5 | 0 | 0 |
| 4 | 3192.5 | 0 | 0 |
| 5 | 3192.5 | 0 | 0 |
| 6 | 3192.5 | 0 | 0 |
| 7 | 3192.5 | 0 | 0 |
| 8 | 3192.5 | 0 | 0 |
| 9 | 3192.5 | 0 | 0 |
| 10 | 3192.5 | 0 | 0 |
| 11 | 3192.5 | 0 | 0 |
| 12 | 3192.5 | 0 | 0 |
| 13 | 3192.5 | 0 | 0 |
| 14 | 3192.5 | 0 | 0 |
| 15 | 3192.5 | 0 | 0 |
| 16 | 3192.5 | 0 | 0 |
| 17 | 3192.5 | 0 | 0 |
| 18 | 3192.5 | 0 | 0 |
| 19 | 3192.5 | 0 | 0 |
| 20 | 3192.5 | 0 | 0 |
| 21 | 3192.5 | 0 | 0 |
| 22 | 3192.5 | 0 | 0 |
| 23 | 3192.5 | 0 | 0 |
| 24 | 3192.5 | 0 | 0 |
| 25 | 3192.5 | 0 | 0 |
| 26 | 3192.5 | 0 | 0 |
| 27 | 3192.5 | 0 | 0 |
| 28 | 3192.5 | 0 | 0 |
| 29 | 3192.5 | 0 | 0 |
| 30 | 3192.5 | 0 | 0 |
| 31 | 3192.5 | 0 | 0 |
| 32 | 3192.5 | 0 | 0 |
| 33 | 3192.5 | 0 | 0 |
| 34 | 3192.5 | 0 | 0 |
| 35 | 3192.5 | 0 | 0 |
| 36 | 3192.5 | 0 | 0 |
| 37 | 3192.5 | 0 | 0 |
| 38 | 3192.5 | 0 | 0 |
| 39 | 3192.5 | 0 | 0 |
| 40 | 3192.5 | 0 | 0 |
| 41 | 3192.5 | 0 | 0 |
| 42 | 3192.5 | 0 | 0 |
| 43 | 3192.5 | 0 | 0 |
| 44 | 3192.5 | 0 | 0 |
| 45 | 3192.5 | 0 | 0 |
| 46 | 3192.5 | 0 | 0 |
| 47 | 3192.5 | 0 | 0 |
| 48 | 3192.5 | 0 | 0 |
| 49 | 3192.5 | 0 | 0 |
| 50 | 3192.5 | 0 | 0 |
| 51 | 3192.5 | 0 | 0 |
| 52 | 3192.5 | 0 | 0 |
| 53 | 3192.5 | 0 | 0 |
| 54 | 3192.5 | 0 | 0 |
| 55 | 3192.5 | 0 | 0 |
| 56 | 3192.5 | 0 | 0 |
| 57 | 3192.5 | 0 | 0 |
| 58 | 3192.5 | 0 | 0 |
| 59 | 3192.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|--------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 3192.5 | 0 | 0 |
| 4 | 3192.5 | 0 | 0 |
| 5 | 3192.5 | 0 | 0 |
| 6 | 3192.5 | 0 | 0 |
| 7 | 3192.5 | 0 | 0 |
| 8 | 3192.5 | 0 | 0 |
| 9 | 3192.5 | 0 | 0 |
| 10 | 3192.5 | 0 | 0 |
| 11 | 3192.5 | 0 | 0 |
| 12 | 3192.5 | 0 | 0 |
| 13 | 3192.5 | 0 | 0 |
| 14 | 3192.5 | 0 | 0 |
| 15 | 3192.5 | 0 | 0 |
| 16 | 3192.5 | 0 | 0 |
| 17 | 3192.5 | 0 | 0 |
| 18 | 3192.5 | 0 | 0 |
| 19 | 3192.5 | 0 | 0 |
| 20 | 3192.5 | 0 | 0 |
| 21 | 3192.5 | 0 | 0 |
| 22 | 3192.5 | 0 | 0 |
| 23 | 3192.5 | 0 | 0 |
| 24 | 3192.5 | 0 | 0 |
| 25 | 3192.5 | 0 | 0 |
| 26 | 3192.5 | 0 | 0 |
| 27 | 3192.5 | 0 | 0 |
| 28 | 3192.5 | 0 | 0 |
| 29 | 3192.5 | 0 | 0 |
| 30 | 3192.5 | 0 | 0 |
| 31 | 3192.5 | 0 | 0 |
| 32 | 3192.5 | 0 | 0 |
| 33 | 3192.5 | 0 | 0 |
| 34 | 3192.5 | 0 | 0 |
| 35 | 3192.5 | 0 | 0 |
| 36 | 3192.5 | 0 | 0 |
| 37 | 3192.5 | 0 | 0 |
| 38 | 3192.5 | 0 | 0 |
| 39 | 3192.5 | 0 | 0 |
| 40 | 3192.5 | 0 | 0 |
| 41 | 3192.5 | 0 | 0 |
| 42 | 3192.5 | 0 | 0 |
| 43 | 3192.5 | 0 | 0 |
| 44 | 3192.5 | 0 | 0 |
| 45 | 3192.5 | 0 | 0 |
| 46 | 3192.5 | 0 | 0 |
| 47 | 3192.5 | 0 | 0 |
| 48 | 3192.5 | 0 | 0 |
| 49 | 3192.5 | 0 | 0 |
| 50 | 3192.5 | 0 | 0 |
| 51 | 3192.5 | 0 | 0 |
| 52 | 3192.5 | 0 | 0 |
| 53 | 3192.5 | 0 | 0 |
| 54 | 3192.5 | 0 | 0 |
| 55 | 3192.5 | 0 | 0 |
| 56 | 3192.5 | 0 | 0 |
| 57 | 3192.5 | 0 | 0 |
| 58 | 3192.5 | 0 | 0 |
| 59 | 3192.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|--------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 3192.5 | 0 | 0 |
| 4 | 3192.5 | 0 | 0 |
| 5 | 3192.5 | 0 | 0 |
| 6 | 3192.5 | 0 | 0 |
| 7 | 3192.5 | 0 | 0 |
| 8 | 3192.5 | 0 | 0 |
| 9 | 3192.5 | 0 | 0 |
| 10 | 3192.5 | 0 | 0 |
| 11 | 3192.5 | 0 | 0 |
| 12 | 3192.5 | 0 | 0 |
| 13 | 3192.5 | 0 | 0 |
| 14 | 3192.5 | 0 | 0 |
| 15 | 3192.5 | 0 | 0 |
| 16 | 3192.5 | 0 | 0 |
| 17 | 3192.5 | 0 | 0 |
| 18 | 3192.5 | 0 | 0 |
| 19 | 3192.5 | 0 | 0 |
| 20 | 3192.5 | 0 | 0 |
| 21 | 3192.5 | 0 | 0 |
| 22 | 3192.5 | 0 | 0 |
| 23 | 3192.5 | 0 | 0 |
| 24 | 3192.5 | 0 | 0 |
| 25 | 3192.5 | 0 | 0 |
| 26 | 3192.5 | 0 | 0 |
| 27 | 3192.5 | 0 | 0 |
| 28 | 3192.5 | 0 | 0 |
| 29 | 3192.5 | 0 | 0 |
| 30 | 3192.5 | 0 | 0 |
| 31 | 3192.5 | 0 | 0 |
| 32 | 3192.5 | 0 | 0 |
| 33 | 3192.5 | 0 | 0 |
| 34 | 3192.5 | 0 | 0 |
| 35 | 3192.5 | 0 | 0 |
| 36 | 3192.5 | 0 | 0 |
| 37 | 3192.5 | 0 | 0 |
| 38 | 3192.5 | 0 | 0 |
| 39 | 3192.5 | 0 | 0 |
| 40 | 3192.5 | 0 | 0 |
| 41 | 3192.5 | 0 | 0 |
| 42 | 3192.5 | 0 | 0 |
| 43 | 3192.5 | 0 | 0 |
| 44 | 3192.5 | 0 | 0 |
| 45 | 3192.5 | 0 | 0 |
| 46 | 3192.5 | 0 | 0 |
| 47 | 3192.5 | 0 | 0 |
| 48 | 3192.5 | 0 | 0 |
| 49 | 3192.5 | 0 | 0 |
| 50 | 3192.5 | 0 | 0 |
| 51 | 3192.5 | 0 | 0 |
| 52 | 3192.5 | 0 | 0 |
| 53 | 3192.5 | 0 | 0 |
| 54 | 3192.5 | 0 | 0 |
| 55 | 3192.5 | 0 | 0 |
| 56 | 3192.5 | 0 | 0 |
| 57 | 3192.5 | 0 | 0 |
| 58 | 3192.5 | 0 | 0 |
| 59 | 3192.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 3192.5 | 0 | 0 |
| 4 | 3192.5 | 0 | 0 |
| 5 | 3192.5 | 0 | 0 |
| 6 | 3192.5 | 0 | 0 |
| 7 | 3192.5 | 0 | 0 |
| 8 | 3192.5 | 0 | 0 |
| 9 | 3192.5 | 0 | 0 |
| 10 | 3192.5 | 0 | 0 |
| 11 | 3192.5 | 0 | 0 |
| 12 | 3192.5 | 0 | 0 |
| 13 | 3192.5 | 0 | 0 |
| 14 | 3192.5 | 0 | 0 |
| 15 | 3192.5 | 0 | 0 |
| 16 | 3192.5 | 0 | 0 |
| 17 | 3192.5 | 0 | 0 |
| 18 | 3192.5 | 0 | 0 |
| 19 | 3192.5 | 0 | 0 |
| 20 | 3192.5 | 0 | 0 |
| 21 | 3192.5 | 0 | 0 |
| 22 | 3192.5 | 0 | 0 |
| 23 | 3192.5 | 0 | 0 |
| 24 | 3192.5 | 0 | 0 |
| 25 | 3192.5 | 0 | 0 |
| 26 | 3192.5 | 0 | 0 |
| 27 | 3192.5 | 0 | 0 |
| 28 | 3192.5 | 0 | 0 |
| 29 | 3192.5 | 0 | 0 |
| 30 | 3192.5 | 0 | 0 |
| 31 | 3192.5 | 0 | 0 |
| 32 | 3192.5 | 0 | 0 |
| 33 | 3192.5 | 0 | 0 |
| 34 | 3192.5 | 0 | 0 |
| 35 | 3192.5 | 0 | 0 |
| 36 | 3295.16667 | 0 | 0 |
| 37 | 3295.16667 | 0 | 0 |
| 38 | 3295.16667 | 0 | 0 |
| 39 | 3295.16667 | 0 | 0 |
| 40 | 3295.16667 | 0 | 0 |
| 41 | 3295.16667 | 0 | 0 |
| 42 | 3295.16667 | 0 | 0 |
| 43 | 3295.16667 | 0 | 0 |
| 44 | 3295.16667 | 0 | 0 |
| 45 | 3295.16667 | 0 | 0 |
| 46 | 3295.16667 | 0 | 0 |
| 47 | 3210.66667 | 0 | 0 |
| 48 | 3210.66667 | 0 | 0 |
| 49 | 3210.66667 | 0 | 0 |
| 50 | 3210.66667 | 0 | 0 |
| 51 | 3210.66667 | 0 | 0 |
| 52 | 3210.66667 | 0 | 0 |
| 53 | 3210.66667 | 0 | 0 |
| 54 | 3210.66667 | 0 | 0 |
| 55 | 3210.66667 | 0 | 0 |
| 56 | 3210.66667 | 0 | 0 |
| 57 | 3210.66667 | 0 | 0 |
| 58 | 3210.66667 | 0 | 0 |
| 59 | 3210.66667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 3205 | 0 | 0 |
| 4 | 3205 | 0 | 0 |
| 5 | 3205 | 0 | 0 |
| 6 | 70.3333333 | 0 | 0 |
| 7 | 70.3333333 | 0 | 0 |
| 8 | 70.3333333 | 0 | 0 |
| 9 | 70.3333333 | 0 | 0 |
| 10 | 70.3333333 | 0 | 0 |
| 11 | 70.3333333 | 0 | 0 |
| 12 | 70.3333333 | 0 | 0 |
| 13 | 70.3333333 | 0 | 0 |
| 14 | 70.3333333 | 0 | 0 |
| 15 | 70.3333333 | 0 | 0 |
| 16 | 70.3333333 | 0 | 0 |
| 17 | 70.3333333 | 0 | 0 |
| 18 | 70.3333333 | 0 | 0 |
| 19 | 70.3333333 | 0 | 0 |
| 20 | 70.3333333 | 0 | 0 |
| 21 | 70.3333333 | 0 | 0 |
| 22 | 70.3333333 | 0 | 0 |
| 23 | 70.3333333 | 0 | 0 |
| 24 | 70.3333333 | 0 | 0 |
| 25 | 70.3333333 | 0 | 0 |
| 26 | 70.3333333 | 0 | 0 |
| 27 | 70.3333333 | 0 | 0 |
| 28 | 70.3333333 | 0 | 0 |
| 29 | 70.3333333 | 0 | 0 |
| 30 | 70.3333333 | 0 | 0 |
| 31 | 70.3333333 | 0 | 0 |
| 32 | 70.3333333 | 0 | 0 |
| 33 | 70.3333333 | 0 | 0 |
| 34 | 70.3333333 | 0 | 0 |
| 35 | 70.3333333 | 0 | 0 |
| 36 | 70.3333333 | 0 | 0 |
| 37 | 70.3333333 | 0 | 0 |
| 38 | 70.3333333 | 0 | 0 |
| 39 | 70.3333333 | 0 | 0 |
| 40 | 70.3333333 | 0 | 0 |
| 41 | 70.3333333 | 0 | 0 |
| 42 | 70.3333333 | 0 | 0 |
| 43 | 1035.5 | 0 | 0 |
| 44 | 1035.5 | 0 | 0 |
| 45 | 1035.5 | 0 | 0 |
| 46 | 1035.5 | 0 | 0 |
| 47 | 1035.5 | 0 | 0 |
| 48 | 1035.5 | 0 | 0 |
| 49 | 1035.5 | 0 | 0 |
| 50 | 1035.5 | 0 | 0 |
| 51 | 1035.5 | 0 | 0 |
| 52 | 1035.5 | 0 | 0 |
| 53 | 1035.5 | 0 | 0 |
| 54 | 1035.5 | 0 | 0 |
| 55 | 1035.5 | 0 | 0 |
| 56 | 1035.5 | 0 | 0 |
| 57 | 1035.5 | 0 | 0 |
| 58 | 1035.5 | 0 | 0 |
| 59 | 1035.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 1035.5 | 0 | 0 |
| 4 | 1035.5 | 0 | 0 |
| 5 | 1035.5 | 0 | 0 |
| 6 | 1035.5 | 0 | 0 |
| 7 | 1035.5 | 0 | 0 |
| 8 | 1035.5 | 0 | 0 |
| 9 | 1035.5 | 0 | 0 |
| 10 | 1035.5 | 0 | 0 |
| 11 | 1035.5 | 0 | 0 |
| 12 | 1035.5 | 0 | 0 |
| 13 | 1035.5 | 0 | 0 |
| 14 | 1035.5 | 0 | 0 |
| 15 | 1035.5 | 0 | 0 |
| 16 | 1035.5 | 0 | 0 |
| 17 | 1035.5 | 0 | 0 |
| 18 | 1035.5 | 0 | 0 |
| 19 | 1035.5 | 0 | 0 |
| 20 | 1035.5 | 0 | 0 |
| 21 | 1035.5 | 0 | 0 |
| 22 | 1035.5 | 0 | 0 |
| 23 | 1035.5 | 0 | 0 |
| 24 | 1035.5 | 0 | 0 |
| 25 | 1035.5 | 0 | 0 |
| 26 | 1035.5 | 0 | 0 |
| 27 | 1035.5 | 0 | 0 |
| 28 | 1035.5 | 0 | 0 |
| 29 | 1035.5 | 0 | 0 |
| 30 | 1035.5 | 0 | 0 |
| 31 | 1035.5 | 0 | 0 |
| 32 | 1035.5 | 0 | 0 |
| 33 | 1035.5 | 0 | 0 |
| 34 | 6454.5 | 0 | 0 |
| 35 | 6454.5 | 0 | 0 |
| 36 | 6454.5 | 0 | 0 |
| 37 | 6454.5 | 0 | 0 |
| 38 | 6454.5 | 0 | 0 |
| 39 | 6454.5 | 0 | 0 |
| 40 | 6454.5 | 0 | 0 |
| 41 | 6454.5 | 0 | 0 |
| 42 | 6454.5 | 0 | 0 |
| 43 | 6454.5 | 0 | 0 |
| 44 | 6454.5 | 0 | 0 |
| 45 | 6454.5 | 0 | 0 |
| 46 | 6454.5 | 0 | 0 |
| 47 | 6454.5 | 0 | 0 |
| 48 | 174.833333 | 0 | 0 |
| 49 | 174.833333 | 0 | 0 |
| 50 | 174.833333 | 0 | 0 |
| 51 | 174.833333 | 0 | 0 |
| 52 | 174.833333 | 0 | 0 |
| 53 | 174.833333 | 0 | 0 |
| 54 | 174.833333 | 0 | 0 |
| 55 | 174.833333 | 0 | 0 |
| 56 | 174.833333 | 0 | 0 |
| 57 | 174.833333 | 0 | 0 |
| 58 | 174.833333 | 0 | 0 |
| 59 | 174.833333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 174.833333 | 0 | 0 |
| 4 | 174.833333 | 0 | 0 |
| 5 | 174.833333 | 0 | 0 |
| 6 | 174.833333 | 0 | 0 |
| 7 | 174.833333 | 0 | 0 |
| 8 | 174.833333 | 0 | 0 |
| 9 | 174.833333 | 0 | 0 |
| 10 | 174.833333 | 0 | 0 |
| 11 | 174.833333 | 0 | 0 |
| 12 | 174.833333 | 0 | 0 |
| 13 | 174.833333 | 0 | 0 |
| 14 | 174.833333 | 0 | 0 |
| 15 | 174.833333 | 0 | 0 |
| 16 | 174.833333 | 0 | 0 |
| 17 | 174.833333 | 0 | 0 |
| 18 | 174.833333 | 0 | 0 |
| 19 | 174.833333 | 0 | 0 |
| 20 | 174.833333 | 0 | 0 |
| 21 | 174.833333 | 0 | 0 |
| 22 | 174.833333 | 0 | 0 |
| 23 | 174.833333 | 0 | 0 |
| 24 | 174.833333 | 0 | 0 |
| 25 | 174.833333 | 0 | 0 |
| 26 | 174.833333 | 0 | 0 |
| 27 | 174.833333 | 0 | 0 |
| 28 | 71.5 | 0 | 0 |
| 29 | 203 | 0 | 0 |
| 30 | 198 | 0 | 0 |
| 31 | 198 | 0 | 0 |
| 32 | 198 | 0 | 0 |
| 33 | 198 | 0 | 0 |
| 34 | 198 | 0 | 0 |
| 35 | 198 | 0 | 0 |
| 36 | 198 | 0 | 0 |
| 37 | 198 | 0 | 0 |
| 38 | 198 | 0 | 0 |
| 39 | 198 | 0 | 0 |
| 40 | 68 | 0 | 0 |
| 41 | 68 | 0 | 0 |
| 42 | 68 | 0 | 0 |
| 43 | 68 | 0 | 0 |
| 44 | 68 | 0 | 0 |
| 45 | 68 | 0 | 0 |
| 46 | 68 | 0 | 0 |
| 47 | 68 | 0 | 0 |
| 48 | 68 | 0 | 0 |
| 49 | 68 | 0 | 0 |
| 50 | 68 | 0 | 0 |
| 51 | 68 | 0 | 0 |
| 52 | 68 | 0 | 0 |
| 53 | 68 | 0 | 0 |
| 54 | 68 | 0 | 0 |
| 55 | 68 | 0 | 0 |
| 56 | 68 | 0 | 0 |
| 57 | 68 | 0 | 0 |
| 58 | 68 | 0 | 0 |
| 59 | 68 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 68 | 0 | 0 |
| 4 | 68 | 0 | 0 |
| 5 | 68 | 0 | 0 |
| 6 | 2574.66667 | 0 | 0 |
| 7 | 331.5 | 0 | 0 |
| 8 | 331.5 | 0 | 0 |
| 9 | 331.5 | 0 | 0 |
| 10 | 331.5 | 0 | 0 |
| 11 | 331.5 | 0 | 0 |
| 12 | 331.5 | 0 | 0 |
| 13 | 331.5 | 0 | 0 |
| 14 | 331.5 | 0 | 0 |
| 15 | 331.5 | 0 | 0 |
| 16 | 331.5 | 0 | 0 |
| 17 | 331.5 | 0 | 0 |
| 18 | 331.5 | 0 | 0 |
| 19 | 331.5 | 0 | 0 |
| 20 | 331.5 | 0 | 0 |
| 21 | 331.5 | 0 | 0 |
| 22 | 331.5 | 0 | 0 |
| 23 | 331.5 | 0 | 0 |
| 24 | 331.5 | 0 | 0 |
| 25 | 331.5 | 0 | 0 |
| 26 | 225.66667 | 0 | 0 |
| 27 | 225.66667 | 0 | 0 |
| 28 | 225.66667 | 0 | 0 |
| 29 | 225.66667 | 0 | 0 |
| 30 | 225.66667 | 0 | 0 |
| 31 | 225.66667 | 0 | 0 |
| 32 | 225.66667 | 0 | 0 |
| 33 | 225.66667 | 0 | 0 |
| 34 | 225.66667 | 0 | 0 |
| 35 | 225.66667 | 0 | 0 |
| 36 | 225.66667 | 0 | 0 |
| 37 | 225.66667 | 0 | 0 |
| 38 | 225.66667 | 0 | 0 |
| 39 | 225.66667 | 0 | 0 |
| 40 | 225.66667 | 0 | 0 |
| 41 | 225.66667 | 0 | 0 |
| 42 | 225.66667 | 0 | 0 |
| 43 | 225.66667 | 0 | 0 |
| 44 | 225.66667 | 0 | 0 |
| 45 | 225.66667 | 0 | 0 |
| 46 | 225.66667 | 0 | 0 |
| 47 | 225.66667 | 0 | 0 |
| 48 | 225.66667 | 0 | 0 |
| 49 | 225.66667 | 0 | 0 |
| 50 | 225.66667 | 0 | 0 |
| 51 | 210.833333 | 0 | 0 |
| 52 | 210.833333 | 0 | 0 |
| 53 | 210.833333 | 0 | 0 |
| 54 | 210.833333 | 0 | 0 |
| 55 | 210.833333 | 0 | 0 |
| 56 | 210.833333 | 0 | 0 |
| 57 | 210.833333 | 0 | 0 |
| 58 | 210.833333 | 0 | 0 |
| 59 | 210.833333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 210.833333 | 0 | 0 |
| 4 | 210.833333 | 0 | 0 |
| 5 | 210.833333 | 0 | 0 |
| 6 | 210.833333 | 0 | 0 |
| 7 | 210.833333 | 0 | 0 |
| 8 | 210.833333 | 0 | 0 |
| 9 | 210.833333 | 0 | 0 |
| 10 | 210.833333 | 0 | 0 |
| 11 | 210.833333 | 0 | 0 |
| 12 | 210.833333 | 0 | 0 |
| 13 | 210.833333 | 0 | 0 |
| 14 | 210.833333 | 0 | 0 |
| 15 | 210.833333 | 0 | 0 |
| 16 | 210.833333 | 0 | 0 |
| 17 | 210.833333 | 0 | 0 |
| 18 | 210.833333 | 0 | 0 |
| 19 | 210.833333 | 0 | 0 |
| 20 | 210.833333 | 0 | 0 |
| 21 | 210.833333 | 0 | 0 |
| 22 | 210.833333 | 0 | 0 |
| 23 | 210.833333 | 0 | 0 |
| 24 | 210.833333 | 0 | 0 |
| 25 | 210.833333 | 0 | 0 |
| 26 | 210.833333 | 0 | 0 |
| 27 | 210.833333 | 0 | 0 |
| 28 | 210.833333 | 0 | 0 |
| 29 | 210.833333 | 0 | 0 |
| 30 | 210.833333 | 0 | 0 |
| 31 | 210.833333 | 0 | 0 |
| 32 | 210.833333 | 0 | 0 |
| 33 | 210.833333 | 0 | 0 |
| 34 | 210.833333 | 0 | 0 |
| 35 | 210.833333 | 0 | 0 |
| 36 | 210.833333 | 0 | 0 |
| 37 | 210.833333 | 0 | 0 |
| 38 | 210.833333 | 0 | 0 |
| 39 | 241.333333 | 0 | 0 |
| 40 | 241.333333 | 0 | 0 |
| 41 | 241.333333 | 0 | 0 |
| 42 | 241.333333 | 0 | 0 |
| 43 | 241.333333 | 0 | 0 |
| 44 | 241.333333 | 0 | 0 |
| 45 | 241.333333 | 0 | 0 |
| 46 | 241.333333 | 0 | 0 |
| 47 | 241.333333 | 0 | 0 |
| 48 | 241.333333 | 0 | 0 |
| 49 | 241.333333 | 0 | 0 |
| 50 | 241.333333 | 0 | 0 |
| 51 | 53.5 | 0 | 0 |
| 52 | 53.5 | 0 | 0 |
| 53 | 53.5 | 0 | 0 |
| 54 | 53.5 | 0 | 0 |
| 55 | 53.5 | 0 | 0 |
| 56 | 53.5 | 0 | 0 |
| 57 | 53.5 | 0 | 0 |
| 58 | 53.5 | 0 | 0 |
| 59 | 53.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 53.5 | 0 | 0 |
| 4 | 53.5 | 0 | 0 |
| 5 | 53.5 | 0 | 0 |
| 6 | 53.5 | 0 | 0 |
| 7 | 53.5 | 0 | 0 |
| 8 | 53.5 | 0 | 0 |
| 9 | 53.5 | 0 | 0 |
| 10 | 53.5 | 0 | 0 |
| 11 | 53.5 | 0 | 0 |
| 12 | 53.5 | 0 | 0 |
| 13 | 53.5 | 0 | 0 |
| 14 | 53.5 | 0 | 0 |
| 15 | 53.5 | 0 | 0 |
| 16 | 53.5 | 0 | 0 |
| 17 | 53.5 | 0 | 0 |
| 18 | 53.5 | 0 | 0 |
| 19 | 53.5 | 0 | 0 |
| 20 | 53.5 | 0 | 0 |
| 21 | 53.5 | 0 | 0 |
| 22 | 53.5 | 0 | 0 |
| 23 | 53.5 | 0 | 0 |
| 24 | 53.5 | 0 | 0 |
| 25 | 53.5 | 0 | 0 |
| 26 | 53.5 | 0 | 0 |
| 27 | 53.5 | 0 | 0 |
| 28 | 53.5 | 0 | 0 |
| 29 | 53.5 | 0 | 0 |
| 30 | 53.5 | 0 | 0 |
| 31 | 53.5 | 0 | 0 |
| 32 | 53.5 | 0 | 0 |
| 33 | 53.5 | 0 | 0 |
| 34 | 53.5 | 0 | 0 |
| 35 | 53.5 | 0 | 0 |
| 36 | 53.5 | 0 | 0 |
| 37 | 53.5 | 0 | 0 |
| 38 | 53.5 | 0 | 0 |
| 39 | 1762.16667 | 0 | 0 |
| 40 | 120 | 0 | 0 |
| 41 | 120 | 0 | 0 |
| 42 | 120 | 0 | 0 |
| 43 | 113.166667 | 0 | 0 |
| 44 | 113.166667 | 0 | 0 |
| 45 | 113.166667 | 0 | 0 |
| 46 | 113.166667 | 0 | 0 |
| 47 | 113.166667 | 0 | 0 |
| 48 | 126.166667 | 0 | 0 |
| 49 | 126.166667 | 0 | 0 |
| 50 | 126.166667 | 0 | 0 |
| 51 | 126.166667 | 0 | 0 |
| 52 | 126.166667 | 0 | 0 |
| 53 | 126.166667 | 0 | 0 |
| 54 | 126.166667 | 0 | 0 |
| 55 | 126.166667 | 0 | 0 |
| 56 | 126.166667 | 0 | 0 |
| 57 | 126.166667 | 0 | 0 |
| 58 | 126.166667 | 0 | 0 |
| 59 | 126.166667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 126.166667 | 0 | 0 |
| 4 | 126.166667 | 0 | 0 |
| 5 | 126.166667 | 0 | 0 |
| 6 | 126.166667 | 0 | 0 |
| 7 | 126.166667 | 0 | 0 |
| 8 | 126.166667 | 0 | 0 |
| 9 | 126.166667 | 0 | 0 |
| 10 | 126.166667 | 0 | 0 |
| 11 | 126.166667 | 0 | 0 |
| 12 | 126.166667 | 0 | 0 |
| 13 | 126.166667 | 0 | 0 |
| 14 | 126.166667 | 0 | 0 |
| 15 | 126.166667 | 0 | 0 |
| 16 | 126.166667 | 0 | 0 |
| 17 | 126.166667 | 0 | 0 |
| 18 | 126.166667 | 0 | 0 |
| 19 | 126.166667 | 0 | 0 |
| 20 | 126.166667 | 0 | 0 |
| 21 | 126.166667 | 0 | 0 |
| 22 | 126.166667 | 0 | 0 |
| 23 | 126.166667 | 0 | 0 |
| 24 | 126.166667 | 0 | 0 |
| 25 | 126.166667 | 0 | 0 |
| 26 | 23854.6667 | 0 | 0 |
| 27 | 23854.6667 | 0 | 0 |
| 28 | 23854.6667 | 0 | 0 |
| 29 | 23854.6667 | 0 | 0 |
| 30 | 23854.6667 | 0 | 0 |
| 31 | 23854.6667 | 0 | 0 |
| 32 | 23854.6667 | 0 | 0 |
| 33 | 23854.6667 | 0 | 0 |
| 34 | 23854.6667 | 0 | 0 |
| 35 | 23854.6667 | 0 | 0 |
| 36 | 23854.6667 | 0 | 0 |
| 37 | 23854.6667 | 0 | 0 |
| 38 | 23854.6667 | 0 | 0 |
| 39 | 23854.6667 | 0 | 0 |
| 40 | 23854.6667 | 0 | 0 |
| 41 | 23854.6667 | 0 | 0 |
| 42 | 23854.6667 | 0 | 0 |
| 43 | 23854.6667 | 0 | 0 |
| 44 | 23854.6667 | 0 | 0 |
| 45 | 23854.6667 | 0 | 0 |
| 46 | 23854.6667 | 0 | 0 |
| 47 | 23854.6667 | 0 | 0 |
| 48 | 23854.6667 | 0 | 0 |
| 49 | 23854.6667 | 0 | 0 |
| 50 | 23854.6667 | 0 | 0 |
| 51 | 23854.6667 | 0 | 0 |
| 52 | 23854.6667 | 0 | 0 |
| 53 | 23854.6667 | 0 | 0 |
| 54 | 23854.6667 | 0 | 0 |
| 55 | 23854.6667 | 0 | 0 |
| 56 | 23854.6667 | 0 | 0 |
| 57 | 23854.6667 | 0 | 0 |
| 58 | 23854.6667 | 0 | 0 |
| 59 | 23854.6667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 23854.6667 | 0 | 0 |
| 4 | 23854.6667 | 0 | 0 |
| 5 | 23854.6667 | 0 | 0 |
| 6 | 23854.6667 | 0 | 0 |
| 7 | 23854.6667 | 0 | 0 |
| 8 | 23854.6667 | 0 | 0 |
| 9 | 23854.6667 | 0 | 0 |
| 10 | 23854.6667 | 0 | 0 |
| 11 | 23854.6667 | 0 | 0 |
| 12 | 23913.1667 | 0 | 0 |
| 13 | 23913.1667 | 0 | 0 |
| 14 | 91.1666667 | 0 | 0 |
| 15 | 91.1666667 | 0 | 0 |
| 16 | 91.5 | 0 | 0 |
| 17 | 91.5 | 0 | 0 |
| 18 | 91.5 | 0 | 0 |
| 19 | 91.5 | 0 | 0 |
| 20 | 91.5 | 0 | 0 |
| 21 | 91.5 | 0 | 0 |
| 22 | 91.5 | 0 | 0 |
| 23 | 91.5 | 0 | 0 |
| 24 | 346.833333 | 0 | 0 |
| 25 | 129.5 | 0 | 0 |
| 26 | 129.5 | 0 | 0 |
| 27 | 129.5 | 0 | 0 |
| 28 | 129.5 | 0 | 0 |
| 29 | 129.5 | 0 | 0 |
| 30 | 129.5 | 0 | 0 |
| 31 | 129.5 | 0 | 0 |
| 32 | 129.5 | 0 | 0 |
| 33 | 129.5 | 0 | 0 |
| 34 | 129.5 | 0 | 0 |
| 35 | 129.5 | 0 | 0 |
| 36 | 129.5 | 0 | 0 |
| 37 | 129.5 | 0 | 0 |
| 38 | 129.5 | 0 | 0 |
| 39 | 129.5 | 0 | 0 |
| 40 | 129.5 | 0 | 0 |
| 41 | 129.5 | 0 | 0 |
| 42 | 129.5 | 0 | 0 |
| 43 | 129.5 | 0 | 0 |
| 44 | 129.5 | 0 | 0 |
| 45 | 129.5 | 0 | 0 |
| 46 | 129.5 | 0 | 0 |
| 47 | 129.5 | 0 | 0 |
| 48 | 129.5 | 0 | 0 |
| 49 | 129.5 | 0 | 0 |
| 50 | 129.5 | 0 | 0 |
| 51 | 129.5 | 0 | 0 |
| 52 | 129.5 | 0 | 0 |
| 53 | 129.5 | 0 | 0 |
| 54 | 129.5 | 0 | 0 |
| 55 | 129.5 | 0 | 0 |
| 56 | 129.5 | 0 | 0 |
| 57 | 129.5 | 0 | 0 |
| 58 | 129.5 | 0 | 0 |
| 59 | 129.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|-------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 129.5 | 0 | 0 |
| 4 | 129.5 | 0 | 0 |
| 5 | 129.5 | 0 | 0 |
| 6 | 129.5 | 0 | 0 |
| 7 | 129.5 | 0 | 0 |
| 8 | 129.5 | 0 | 0 |
| 9 | 129.5 | 0 | 0 |
| 10 | 129.5 | 0 | 0 |
| 11 | 129.5 | 0 | 0 |
| 12 | 129.5 | 0 | 0 |
| 13 | 129.5 | 0 | 0 |
| 14 | 129.5 | 0 | 0 |
| 15 | 129.5 | 0 | 0 |
| 16 | 129.5 | 0 | 0 |
| 17 | 129.5 | 0 | 0 |
| 18 | 129.5 | 0 | 0 |
| 19 | 129.5 | 0 | 0 |
| 20 | 129.5 | 0 | 0 |
| 21 | 129.5 | 0 | 0 |
| 22 | 129.5 | 0 | 0 |
| 23 | 129.5 | 0 | 0 |
| 24 | 129.5 | 0 | 0 |
| 25 | 129.5 | 0 | 0 |
| 26 | 129.5 | 0 | 0 |
| 27 | 129.5 | 0 | 0 |
| 28 | 129.5 | 0 | 0 |
| 29 | 129.5 | 0 | 0 |
| 30 | 129.5 | 0 | 0 |
| 31 | 129.5 | 0 | 0 |
| 32 | 129.5 | 0 | 0 |
| 33 | 129.5 | 0 | 0 |
| 34 | 129.5 | 0 | 0 |
| 35 | 129.5 | 0 | 0 |
| 36 | 129.5 | 0 | 0 |
| 37 | 129.5 | 0 | 0 |
| 38 | 129.5 | 0 | 0 |
| 39 | 129.5 | 0 | 0 |
| 40 | 129.5 | 0 | 0 |
| 41 | 129.5 | 0 | 0 |
| 42 | 105.5 | 0 | 0 |
| 43 | 105.5 | 0 | 0 |
| 44 | 105.5 | 0 | 0 |
| 45 | 105.5 | 0 | 0 |
| 46 | 105.5 | 0 | 0 |
| 47 | 105.5 | 0 | 0 |
| 48 | 105.5 | 0 | 0 |
| 49 | 105.5 | 0 | 0 |
| 50 | 105.5 | 0 | 0 |
| 51 | 105.5 | 0 | 0 |
| 52 | 105.5 | 0 | 0 |
| 53 | 105.5 | 0 | 0 |
| 54 | 105.5 | 0 | 0 |
| 55 | 105.5 | 0 | 0 |
| 56 | 105.5 | 0 | 0 |
| 57 | 105.5 | 0 | 0 |
| 58 | 105.5 | 0 | 0 |
| 59 | 105.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 105.5 | 0 | 0 |
| 4 | 105.5 | 0 | 0 |
| 5 | 105.5 | 0 | 0 |
| 6 | 105.5 | 0 | 0 |
| 7 | 105.5 | 0 | 0 |
| 8 | 105.5 | 0 | 0 |
| 9 | 105.5 | 0 | 0 |
| 10 | 105.5 | 0 | 0 |
| 11 | 105.5 | 0 | 0 |
| 12 | 105.5 | 0 | 0 |
| 13 | 105.5 | 0 | 0 |
| 14 | 1052 | 0 | 0 |
| 15 | 2874.16667 | 0 | 0 |
| 16 | 2874.16667 | 0 | 0 |
| 17 | 2874.16667 | 0 | 0 |
| 18 | 2874.16667 | 0 | 0 |
| 19 | 2874.16667 | 0 | 0 |
| 20 | 2874.16667 | 0 | 0 |
| 21 | 2874.16667 | 0 | 0 |
| 22 | 2874.16667 | 0 | 0 |
| 23 | 2874.16667 | 0 | 0 |
| 24 | 2874.16667 | 0 | 0 |
| 25 | 2874.16667 | 0 | 0 |
| 26 | 2874.16667 | 0 | 0 |
| 27 | 2874.16667 | 0 | 0 |
| 28 | 2874.16667 | 0 | 0 |
| 29 | 2874.16667 | 0 | 0 |
| 30 | 2874.16667 | 0 | 0 |
| 31 | 2874.16667 | 0 | 0 |
| 32 | 2874.16667 | 0 | 0 |
| 33 | 2874.16667 | 0 | 0 |
| 34 | 2874.16667 | 0 | 0 |
| 35 | 2874.16667 | 0 | 0 |
| 36 | 2874.16667 | 0 | 0 |
| 37 | 2874.16667 | 0 | 0 |
| 38 | 2874.16667 | 0 | 0 |
| 39 | 2874.16667 | 0 | 0 |
| 40 | 2874.16667 | 0 | 0 |
| 41 | 2874.16667 | 0 | 0 |
| 42 | 2874.16667 | 0 | 0 |
| 43 | 2874.16667 | 0 | 0 |
| 44 | 2874.16667 | 0 | 0 |
| 45 | 2874.16667 | 0 | 0 |
| 46 | 2874.16667 | 0 | 0 |
| 47 | 2874.16667 | 0 | 0 |
| 48 | 2874.16667 | 0 | 0 |
| 49 | 111.666667 | 0 | 0 |
| 50 | 2903.33333 | 0 | 0 |
| 51 | 2903.33333 | 0 | 0 |
| 52 | 2903.33333 | 0 | 0 |
| 53 | 2903.33333 | 0 | 0 |
| 54 | 2903.33333 | 0 | 0 |
| 55 | 2903.33333 | 0 | 0 |
| 56 | 99 | 0 | 0 |
| 57 | 99 | 0 | 0 |
| 58 | 99 | 0 | 0 |
| 59 | 99 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 99 | 0 | 0 |
| 4 | 99 | 0 | 0 |
| 5 | 99 | 0 | 0 |
| 6 | 99 | 0 | 0 |
| 7 | 99 | 0 | 0 |
| 8 | 99 | 0 | 0 |
| 9 | 99 | 0 | 0 |
| 10 | 99 | 0 | 0 |
| 11 | 99 | 0 | 0 |
| 12 | 99 | 0 | 0 |
| 13 | 99 | 0 | 0 |
| 14 | 99 | 0 | 0 |
| 15 | 99 | 0 | 0 |
| 16 | 99 | 0 | 0 |
| 17 | 99 | 0 | 0 |
| 18 | 99 | 0 | 0 |
| 19 | 99 | 0 | 0 |
| 20 | 99 | 0 | 0 |
| 21 | 99 | 0 | 0 |
| 22 | 99 | 0 | 0 |
| 23 | 99 | 0 | 0 |
| 24 | 99 | 0 | 0 |
| 25 | 99 | 0 | 0 |
| 26 | 99 | 0 | 0 |
| 27 | 99 | 0 | 0 |
| 28 | 99 | 0 | 0 |
| 29 | 99 | 0 | 0 |
| 30 | 99 | 0 | 0 |
| 31 | 99 | 0 | 0 |
| 32 | 99 | 0 | 0 |
| 33 | 99 | 0 | 0 |
| 34 | 99 | 0 | 0 |
| 35 | 99 | 0 | 0 |
| 36 | 99 | 0 | 0 |
| 37 | 99 | 0 | 0 |
| 38 | 99 | 0 | 0 |
| 39 | 99 | 0 | 0 |
| 40 | 99 | 0 | 0 |
| 41 | 2880.33333 | 0 | 0 |
| 42 | 2880.33333 | 0 | 0 |
| 43 | 2880.33333 | 0 | 0 |
| 44 | 685.833333 | 0 | 0 |
| 45 | 685.833333 | 0 | 0 |
| 46 | 685.833333 | 0 | 0 |
| 47 | 685.833333 | 0 | 0 |
| 48 | 685.833333 | 0 | 0 |
| 49 | 188.166667 | 0 | 0 |
| 50 | 188.166667 | 0 | 0 |
| 51 | 188.166667 | 0 | 0 |
| 52 | 192.333333 | 0 | 0 |
| 53 | 99.5 | 0 | 0 |
| 54 | 99.5 | 0 | 0 |
| 55 | 99.5 | 0 | 0 |
| 56 | 99.5 | 0 | 0 |
| 57 | 99.5 | 0 | 0 |
| 58 | 99.5 | 0 | 0 |
| 59 | 99.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 99.5 | 0 | 0 |
| 4 | 99.5 | 0 | 0 |
| 5 | 99.5 | 0 | 0 |
| 6 | 99.5 | 0 | 0 |
| 7 | 99.5 | 0 | 0 |
| 8 | 99.5 | 0 | 0 |
| 9 | 99.5 | 0 | 0 |
| 10 | 99.5 | 0 | 0 |
| 11 | 99.5 | 0 | 0 |
| 12 | 99.5 | 0 | 0 |
| 13 | 99.5 | 0 | 0 |
| 14 | 99.5 | 0 | 0 |
| 15 | 99.5 | 0 | 0 |
| 16 | 99.5 | 0 | 0 |
| 17 | 99.5 | 0 | 0 |
| 18 | 99.5 | 0 | 0 |
| 19 | 99.5 | 0 | 0 |
| 20 | 99.5 | 0 | 0 |
| 21 | 99.5 | 0 | 0 |
| 22 | 99.5 | 0 | 0 |
| 23 | 99.5 | 0 | 0 |
| 24 | 99.5 | 0 | 0 |
| 25 | 99.5 | 0 | 0 |
| 26 | 99.5 | 0 | 0 |
| 27 | 99.5 | 0 | 0 |
| 28 | 99.5 | 0 | 0 |
| 29 | 99.5 | 0 | 0 |
| 30 | 99.5 | 0 | 0 |
| 31 | 99.5 | 0 | 0 |
| 32 | 99.5 | 0 | 0 |
| 33 | 99.5 | 0 | 0 |
| 34 | 99.5 | 0 | 0 |
| 35 | 99.5 | 0 | 0 |
| 36 | 99.5 | 0 | 0 |
| 37 | 99.5 | 0 | 0 |
| 38 | 99.5 | 0 | 0 |
| 39 | 99.5 | 0 | 0 |
| 40 | 99.5 | 0 | 0 |
| 41 | 99.5 | 0 | 0 |
| 42 | 99.5 | 0 | 0 |
| 43 | 99.5 | 0 | 0 |
| 44 | 99.5 | 0 | 0 |
| 45 | 99.5 | 0 | 0 |
| 46 | 99.5 | 0 | 0 |
| 47 | 99.5 | 0 | 0 |
| 48 | 99.5 | 0 | 0 |
| 49 | 99.5 | 0 | 0 |
| 50 | 99.5 | 0 | 0 |
| 51 | 99.5 | 0 | 0 |
| 52 | 99.5 | 0 | 0 |
| 53 | 99.5 | 0 | 0 |
| 54 | 99.5 | 0 | 0 |
| 55 | 99.5 | 0 | 0 |
| 56 | 99.5 | 0 | 0 |
| 57 | 99.5 | 0 | 0 |
| 58 | 99.5 | 0 | 0 |
| 59 | 99.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 99.5 | 0 | 0 |
| 4 | 99.5 | 0 | 0 |
| 5 | 99.5 | 0 | 0 |
| 6 | 99.5 | 0 | 0 |
| 7 | 99.5 | 0 | 0 |
| 8 | 99.5 | 0 | 0 |
| 9 | 99.5 | 0 | 0 |
| 10 | 3916.66667 | 0 | 0 |
| 11 | 3916.66667 | 0 | 0 |
| 12 | 3916.66667 | 0 | 0 |
| 13 | 3916.66667 | 0 | 0 |
| 14 | 3916.66667 | 0 | 0 |
| 15 | 3916.66667 | 0 | 0 |
| 16 | 3916.66667 | 0 | 0 |
| 17 | 3916.66667 | 0 | 0 |
| 18 | 3916.66667 | 0 | 0 |
| 19 | 3916.66667 | 0 | 0 |
| 20 | 3916.66667 | 0 | 0 |
| 21 | 3916.66667 | 0 | 0 |
| 22 | 3916.66667 | 0 | 0 |
| 23 | 3916.66667 | 0 | 0 |
| 24 | 3916.66667 | 0 | 0 |
| 25 | 3916.66667 | 0 | 0 |
| 26 | 3916.66667 | 0 | 0 |
| 27 | 3916.66667 | 0 | 0 |
| 28 | 3916.66667 | 0 | 0 |
| 29 | 3916.66667 | 0 | 0 |
| 30 | 3916.66667 | 0 | 0 |
| 31 | 3916.66667 | 0 | 0 |
| 32 | 3916.66667 | 0 | 0 |
| 33 | 3916.66667 | 0 | 0 |
| 34 | 3916.66667 | 0 | 0 |
| 35 | 3916.66667 | 0 | 0 |
| 36 | 3916.66667 | 0 | 0 |
| 37 | 3916.66667 | 0 | 0 |
| 38 | 3916.66667 | 0 | 0 |
| 39 | 3916.66667 | 0 | 0 |
| 40 | 3916.66667 | 0 | 0 |
| 41 | 3916.66667 | 0 | 0 |
| 42 | 3916.66667 | 0 | 0 |
| 43 | 3916.66667 | 0 | 0 |
| 44 | 3916.66667 | 0 | 0 |
| 45 | 3916.66667 | 0 | 0 |
| 46 | 3916.66667 | 0 | 0 |
| 47 | 3916.66667 | 0 | 0 |
| 48 | 3916.66667 | 0 | 0 |
| 49 | 3916.66667 | 0 | 0 |
| 50 | 3916.66667 | 0 | 0 |
| 51 | 3916.66667 | 0 | 0 |
| 52 | 3916.66667 | 0 | 0 |
| 53 | 3916.66667 | 0 | 0 |
| 54 | 3916.66667 | 0 | 0 |
| 55 | 3916.66667 | 0 | 0 |
| 56 | 3916.66667 | 0 | 0 |
| 57 | 181.833333 | 0 | 0 |
| 58 | 181.833333 | 0 | 0 |
| 59 | 183 | 0 | 0 |
| 60 | | | |

| | | | |
|----|-----|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 183 | 0 | 0 |
| 4 | 183 | 0 | 0 |
| 5 | 183 | 0 | 0 |
| 6 | 183 | 0 | 0 |
| 7 | 183 | 0 | 0 |
| 8 | 183 | 0 | 0 |
| 9 | 183 | 0 | 0 |
| 10 | 183 | 0 | 0 |
| 11 | 183 | 0 | 0 |
| 12 | 183 | 0 | 0 |
| 13 | 183 | 0 | 0 |
| 14 | 183 | 0 | 0 |
| 15 | 183 | 0 | 0 |
| 16 | 183 | 0 | 0 |
| 17 | 183 | 0 | 0 |
| 18 | 183 | 0 | 0 |
| 19 | 183 | 0 | 0 |
| 20 | 183 | 0 | 0 |
| 21 | 183 | 0 | 0 |
| 22 | 183 | 0 | 0 |
| 23 | 183 | 0 | 0 |
| 24 | 183 | 0 | 0 |
| 25 | 183 | 0 | 0 |
| 26 | 183 | 0 | 0 |
| 27 | 778 | 0 | 0 |
| 28 | 778 | 0 | 0 |
| 29 | 778 | 0 | 0 |
| 30 | 778 | 0 | 0 |
| 31 | 778 | 0 | 0 |
| 32 | 778 | 0 | 0 |
| 33 | 778 | 0 | 0 |
| 34 | 778 | 0 | 0 |
| 35 | 778 | 0 | 0 |
| 36 | 778 | 0 | 0 |
| 37 | 778 | 0 | 0 |
| 38 | 778 | 0 | 0 |
| 39 | 778 | 0 | 0 |
| 40 | 778 | 0 | 0 |
| 41 | 778 | 0 | 0 |
| 42 | 778 | 0 | 0 |
| 43 | 778 | 0 | 0 |
| 44 | 778 | 0 | 0 |
| 45 | 778 | 0 | 0 |
| 46 | 778 | 0 | 0 |
| 47 | 778 | 0 | 0 |
| 48 | 778 | 0 | 0 |
| 49 | 778 | 0 | 0 |
| 50 | 778 | 0 | 0 |
| 51 | 778 | 0 | 0 |
| 52 | 778 | 0 | 0 |
| 53 | 778 | 0 | 0 |
| 54 | 778 | 0 | 0 |
| 55 | 778 | 0 | 0 |
| 56 | 778 | 0 | 0 |
| 57 | 778 | 0 | 0 |
| 58 | 778 | 0 | 0 |
| 59 | 778 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 778 | 0 | 0 |
| 4 | 778 | 0 | 0 |
| 5 | 778 | 0 | 0 |
| 6 | 778 | 0 | 0 |
| 7 | 778 | 0 | 0 |
| 8 | 778 | 0 | 0 |
| 9 | 778 | 0 | 0 |
| 10 | 778 | 0 | 0 |
| 11 | 778 | 0 | 0 |
| 12 | 778 | 0 | 0 |
| 13 | 778 | 0 | 0 |
| 14 | 460.666667 | 0 | 0 |
| 15 | 4496.66667 | 0 | 0 |
| 16 | 4496.66667 | 0 | 0 |
| 17 | 4496.66667 | 0 | 0 |
| 18 | 4496.66667 | 0 | 0 |
| 19 | 4496.66667 | 0 | 0 |
| 20 | 4496.66667 | 0 | 0 |
| 21 | 4496.66667 | 0 | 0 |
| 22 | 4496.66667 | 0 | 0 |
| 23 | 4496.66667 | 0 | 0 |
| 24 | 4496.66667 | 0 | 0 |
| 25 | 4496.66667 | 0 | 0 |
| 26 | 4496.66667 | 0 | 0 |
| 27 | 4496.66667 | 0 | 0 |
| 28 | 4496.66667 | 0 | 0 |
| 29 | 4496.66667 | 0 | 0 |
| 30 | 4496.66667 | 0 | 0 |
| 31 | 4496.66667 | 0 | 0 |
| 32 | 4496.66667 | 0 | 0 |
| 33 | 4496.66667 | 0 | 0 |
| 34 | 4496.66667 | 0 | 0 |
| 35 | 4496.66667 | 0 | 0 |
| 36 | 4496.66667 | 0 | 0 |
| 37 | 4496.66667 | 0 | 0 |
| 38 | 4496.66667 | 0 | 0 |
| 39 | 4496.66667 | 0 | 0 |
| 40 | 4496.66667 | 0 | 0 |
| 41 | 4496.66667 | 0 | 0 |
| 42 | 4496.66667 | 0 | 0 |
| 43 | 4496.66667 | 0 | 0 |
| 44 | 4496.66667 | 0 | 0 |
| 45 | 4496.66667 | 0 | 0 |
| 46 | 4496.66667 | 0 | 0 |
| 47 | 4496.66667 | 0 | 0 |
| 48 | 4496.66667 | 0 | 0 |
| 49 | 4496.66667 | 0 | 0 |
| 50 | 4496.66667 | 0 | 0 |
| 51 | 4496.66667 | 0 | 0 |
| 52 | 4496.66667 | 0 | 0 |
| 53 | 4496.66667 | 0 | 0 |
| 54 | 4496.66667 | 0 | 0 |
| 55 | 4496.66667 | 0 | 0 |
| 56 | 4496.66667 | 0 | 0 |
| 57 | 4496.66667 | 0 | 0 |
| 58 | 4496.66667 | 0 | 0 |
| 59 | 4496.66667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 4496.66667 | 0 | 0 |
| 4 | 4496.66667 | 0 | 0 |
| 5 | 4496.66667 | 0 | 0 |
| 6 | 4496.66667 | 0 | 0 |
| 7 | 4496.66667 | 0 | 0 |
| 8 | 4496.66667 | 0 | 0 |
| 9 | 4496.66667 | 0 | 0 |
| 10 | 4496.66667 | 0 | 0 |
| 11 | 4496.66667 | 0 | 0 |
| 12 | 4496.66667 | 0 | 0 |
| 13 | 4496.66667 | 0 | 0 |
| 14 | 4496.66667 | 0 | 0 |
| 15 | 4496.66667 | 0 | 0 |
| 16 | 4496.66667 | 0 | 0 |
| 17 | 4496.66667 | 0 | 0 |
| 18 | 4496.66667 | 0 | 0 |
| 19 | 4496.66667 | 0 | 0 |
| 20 | 4496.66667 | 0 | 0 |
| 21 | 4496.66667 | 0 | 0 |
| 22 | 4496.66667 | 0 | 0 |
| 23 | 4496.66667 | 0 | 0 |
| 24 | 4496.66667 | 0 | 0 |
| 25 | 4496.66667 | 0 | 0 |
| 26 | 4496.66667 | 0 | 0 |
| 27 | 4496.66667 | 0 | 0 |
| 28 | 4496.66667 | 0 | 0 |
| 29 | 4496.66667 | 0 | 0 |
| 30 | 4496.66667 | 0 | 0 |
| 31 | 4496.66667 | 0 | 0 |
| 32 | 4496.66667 | 0 | 0 |
| 33 | 4496.66667 | 0 | 0 |
| 34 | 4496.66667 | 0 | 0 |
| 35 | 4496.66667 | 0 | 0 |
| 36 | 4496.66667 | 0 | 0 |
| 37 | 4496.66667 | 0 | 0 |
| 38 | 4496.66667 | 0 | 0 |
| 39 | 4496.66667 | 0 | 0 |
| 40 | 4496.66667 | 0 | 0 |
| 41 | 4496.66667 | 0 | 0 |
| 42 | 4496.66667 | 0 | 0 |
| 43 | 4496.66667 | 0 | 0 |
| 44 | 4496.66667 | 0 | 0 |
| 45 | 63.6666667 | 0 | 0 |
| 46 | 63.6666667 | 0 | 0 |
| 47 | 63.6666667 | 0 | 0 |
| 48 | 63.6666667 | 0 | 0 |
| 49 | 63.6666667 | 0 | 0 |
| 50 | 63.6666667 | 0 | 0 |
| 51 | 63.6666667 | 0 | 0 |
| 52 | 63.6666667 | 0 | 0 |
| 53 | 63.6666667 | 0 | 0 |
| 54 | 63.6666667 | 0 | 0 |
| 55 | 63.6666667 | 0 | 0 |
| 56 | 63.6666667 | 0 | 0 |
| 57 | 63.6666667 | 0 | 0 |
| 58 | 63.6666667 | 0 | 0 |
| 59 | 63.6666667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 63.6666667 | 0 | 0 |
| 4 | 63.6666667 | 0 | 0 |
| 5 | 63.6666667 | 0 | 0 |
| 6 | 63.6666667 | 0 | 0 |
| 7 | 63.6666667 | 0 | 0 |
| 8 | 63.6666667 | 0 | 0 |
| 9 | 63.6666667 | 0 | 0 |
| 10 | 63.6666667 | 0 | 0 |
| 11 | 63.6666667 | 0 | 0 |
| 12 | 63.6666667 | 0 | 0 |
| 13 | 63.6666667 | 0 | 0 |
| 14 | 63.6666667 | 0 | 0 |
| 15 | 63.6666667 | 0 | 0 |
| 16 | 63.6666667 | 0 | 0 |
| 17 | 63.6666667 | 0 | 0 |
| 18 | 63.6666667 | 0 | 0 |
| 19 | 63.6666667 | 0 | 0 |
| 20 | 63.6666667 | 0 | 0 |
| 21 | 63.6666667 | 0 | 0 |
| 22 | 63.6666667 | 0 | 0 |
| 23 | 63.6666667 | 0 | 0 |
| 24 | 63.6666667 | 0 | 0 |
| 25 | 63.6666667 | 0 | 0 |
| 26 | 63.6666667 | 0 | 0 |
| 27 | 63.6666667 | 0 | 0 |
| 28 | 63.6666667 | 0 | 0 |
| 29 | 63.6666667 | 0 | 0 |
| 30 | 63.6666667 | 0 | 0 |
| 31 | 63.6666667 | 0 | 0 |
| 32 | 63.6666667 | 0 | 0 |
| 33 | 63.6666667 | 0 | 0 |
| 34 | 63.6666667 | 0 | 0 |
| 35 | 63.6666667 | 0 | 0 |
| 36 | 63.6666667 | 0 | 0 |
| 37 | 63.6666667 | 0 | 0 |
| 38 | 63.6666667 | 0 | 0 |
| 39 | 63.6666667 | 0 | 0 |
| 40 | 63.6666667 | 0 | 0 |
| 41 | 63.6666667 | 0 | 0 |
| 42 | 63.6666667 | 0 | 0 |
| 43 | 63.6666667 | 0 | 0 |
| 44 | 63.6666667 | 0 | 0 |
| 45 | 63.6666667 | 0 | 0 |
| 46 | 63.6666667 | 0 | 0 |
| 47 | 63.6666667 | 0 | 0 |
| 48 | 63.6666667 | 0 | 0 |
| 49 | 63.6666667 | 0 | 0 |
| 50 | 63.6666667 | 0 | 0 |
| 51 | 63.6666667 | 0 | 0 |
| 52 | 63.6666667 | 0 | 0 |
| 53 | 63.6666667 | 0 | 0 |
| 54 | 63.6666667 | 0 | 0 |
| 55 | 63.6666667 | 0 | 0 |
| 56 | 63.6666667 | 0 | 0 |
| 57 | 63.6666667 | 0 | 0 |
| 58 | 63.6666667 | 0 | 0 |
| 59 | 63.6666667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 63.6666667 | 0 | 0 |
| 4 | 63.6666667 | 0 | 0 |
| 5 | 63.6666667 | 0 | 0 |
| 6 | 63.6666667 | 0 | 0 |
| 7 | 63.6666667 | 0 | 0 |
| 8 | 63.6666667 | 0 | 0 |
| 9 | 63.6666667 | 0 | 0 |
| 10 | 63.6666667 | 0 | 0 |
| 11 | 63.6666667 | 0 | 0 |
| 12 | 63.6666667 | 0 | 0 |
| 13 | 63.6666667 | 0 | 0 |
| 14 | 63.6666667 | 0 | 0 |
| 15 | 63.6666667 | 0 | 0 |
| 16 | 63.6666667 | 0 | 0 |
| 17 | 63.6666667 | 0 | 0 |
| 18 | 63.6666667 | 0 | 0 |
| 19 | 63.6666667 | 0 | 0 |
| 20 | 63.6666667 | 0 | 0 |
| 21 | 63.6666667 | 0 | 0 |
| 22 | 63.6666667 | 0 | 0 |
| 23 | 63.6666667 | 0 | 0 |
| 24 | 63.6666667 | 0 | 0 |
| 25 | 63.6666667 | 0 | 0 |
| 26 | 63.6666667 | 0 | 0 |
| 27 | 63.6666667 | 0 | 0 |
| 28 | 63.6666667 | 0 | 0 |
| 29 | 63.6666667 | 0 | 0 |
| 30 | 63.6666667 | 0 | 0 |
| 31 | 63.6666667 | 0 | 0 |
| 32 | 63.6666667 | 0 | 0 |
| 33 | 63.6666667 | 0 | 0 |
| 34 | 63.6666667 | 0 | 0 |
| 35 | 63.6666667 | 0 | 0 |
| 36 | 63.6666667 | 0 | 0 |
| 37 | 63.6666667 | 0 | 0 |
| 38 | 63.6666667 | 0 | 0 |
| 39 | 63.6666667 | 0 | 0 |
| 40 | 63.6666667 | 0 | 0 |
| 41 | 63.6666667 | 0 | 0 |
| 42 | 63.6666667 | 0 | 0 |
| 43 | 63.6666667 | 0 | 0 |
| 44 | 63.6666667 | 0 | 0 |
| 45 | 9590.5 | 0 | 0 |
| 46 | 9590.5 | 0 | 0 |
| 47 | 9590.5 | 0 | 0 |
| 48 | 9598.83333 | 0 | 0 |
| 49 | 9598.83333 | 0 | 0 |
| 50 | 9598.83333 | 0 | 0 |
| 51 | 395.666667 | 0 | 0 |
| 52 | 395.666667 | 0 | 0 |
| 53 | 395.666667 | 0 | 0 |
| 54 | 395.666667 | 0 | 0 |
| 55 | 395.666667 | 0 | 0 |
| 56 | 395.666667 | 0 | 0 |
| 57 | 395.666667 | 0 | 0 |
| 58 | 395.666667 | 0 | 0 |
| 59 | 395.666667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 572.666667 | 0 | 0 |
| 4 | 574.333333 | 0 | 0 |
| 5 | 574.333333 | 0 | 0 |
| 6 | 574.333333 | 0 | 0 |
| 7 | 574.333333 | 0 | 0 |
| 8 | 574.333333 | 0 | 0 |
| 9 | 574.333333 | 0 | 0 |
| 10 | 574.333333 | 0 | 0 |
| 11 | 576.5 | 0 | 0 |
| 12 | 576.5 | 0 | 0 |
| 13 | 576.5 | 0 | 0 |
| 14 | 576.5 | 0 | 0 |
| 15 | 576.5 | 0 | 0 |
| 16 | 576.5 | 0 | 0 |
| 17 | 576.5 | 0 | 0 |
| 18 | 576.5 | 0 | 0 |
| 19 | 576.5 | 0 | 0 |
| 20 | 576.5 | 0 | 0 |
| 21 | 576.5 | 0 | 0 |
| 22 | 911.166667 | 0 | 0 |
| 23 | 926.333333 | 0 | 0 |
| 24 | 926.333333 | 0 | 0 |
| 25 | 926.333333 | 0 | 0 |
| 26 | 926.333333 | 0 | 0 |
| 27 | 926.333333 | 0 | 0 |
| 28 | 926.333333 | 0 | 0 |
| 29 | 926.333333 | 0 | 0 |
| 30 | 926.333333 | 0 | 0 |
| 31 | 926.333333 | 0 | 0 |
| 32 | 9744.83333 | 0 | 0 |
| 33 | 9744.83333 | 0 | 0 |
| 34 | 9744.83333 | 0 | 0 |
| 35 | 9744.83333 | 0 | 0 |
| 36 | 9744.83333 | 0 | 0 |
| 37 | 9744.83333 | 0 | 0 |
| 38 | 9744.83333 | 0 | 0 |
| 39 | 9744.83333 | 0 | 0 |
| 40 | 9744.83333 | 0 | 0 |
| 41 | 9744.83333 | 0 | 0 |
| 42 | 9744.83333 | 0 | 0 |
| 43 | 9744.83333 | 0 | 0 |
| 44 | 9744.83333 | 0 | 0 |
| 45 | 9744.83333 | 0 | 0 |
| 46 | 9744.83333 | 0 | 0 |
| 47 | 9744.83333 | 0 | 0 |
| 48 | 9744.83333 | 0 | 0 |
| 49 | 9744.83333 | 0 | 0 |
| 50 | 9744.83333 | 0 | 0 |
| 51 | 9744.83333 | 0 | 0 |
| 52 | 9744.83333 | 0 | 0 |
| 53 | 9744.83333 | 0 | 0 |
| 54 | 9744.83333 | 0 | 0 |
| 55 | 9744.83333 | 0 | 0 |
| 56 | 9744.83333 | 0 | 0 |
| 57 | 9477.16667 | 0 | 0 |
| 58 | 9477.16667 | 0 | 0 |
| 59 | 9477.16667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 9477.16667 | 0 | 0 |
| 4 | 9477.16667 | 0 | 0 |
| 5 | 9477.16667 | 0 | 0 |
| 6 | 9477.16667 | 0 | 0 |
| 7 | 9477.16667 | 0 | 0 |
| 8 | 9477.16667 | 0 | 0 |
| 9 | 9477.16667 | 0 | 0 |
| 10 | 9477.16667 | 0 | 0 |
| 11 | 9477.16667 | 0 | 0 |
| 12 | 9477.16667 | 0 | 0 |
| 13 | 9477.16667 | 0 | 0 |
| 14 | 9477.16667 | 0 | 0 |
| 15 | 9477.16667 | 0 | 0 |
| 16 | 9477.16667 | 0 | 0 |
| 17 | 9477.16667 | 0 | 0 |
| 18 | 9477.16667 | 0 | 0 |
| 19 | 9477.16667 | 0 | 0 |
| 20 | 9477.16667 | 0 | 0 |
| 21 | 9477.16667 | 0 | 0 |
| 22 | 9477.16667 | 0 | 0 |
| 23 | 9477.16667 | 0 | 0 |
| 24 | 9477.16667 | 0 | 0 |
| 25 | 9477.16667 | 0 | 0 |
| 26 | 9477.16667 | 0 | 0 |
| 27 | 9477.16667 | 0 | 0 |
| 28 | 9477.16667 | 0 | 0 |
| 29 | 9477.16667 | 0 | 0 |
| 30 | 9477.16667 | 0 | 0 |
| 31 | 9477.16667 | 0 | 0 |
| 32 | 9477.16667 | 0 | 0 |
| 33 | 9477.16667 | 0 | 0 |
| 34 | 9477.16667 | 0 | 0 |
| 35 | 9477.16667 | 0 | 0 |
| 36 | 9477.16667 | 0 | 0 |
| 37 | 9477.16667 | 0 | 0 |
| 38 | 9477.16667 | 0 | 0 |
| 39 | 9477.16667 | 0 | 0 |
| 40 | 9477.16667 | 0 | 0 |
| 41 | 9477.16667 | 0 | 0 |
| 42 | 9477.16667 | 0 | 0 |
| 43 | 9477.16667 | 0 | 0 |
| 44 | 9477.16667 | 0 | 0 |
| 45 | 9477.16667 | 0 | 0 |
| 46 | 9477.16667 | 0 | 0 |
| 47 | 9477.16667 | 0 | 0 |
| 48 | 9477.16667 | 0 | 0 |
| 49 | 9477.16667 | 0 | 0 |
| 50 | 9477.16667 | 0 | 0 |
| 51 | 9477.16667 | 0 | 0 |
| 52 | 9477.16667 | 0 | 0 |
| 53 | 78.6666667 | 0 | 0 |
| 54 | 78.6666667 | 0 | 0 |
| 55 | 78.6666667 | 0 | 0 |
| 56 | 78.6666667 | 0 | 0 |
| 57 | 78.6666667 | 0 | 0 |
| 58 | 78.6666667 | 0 | 0 |
| 59 | 78.6666667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 9479.66667 | 0 | 0 |
| 4 | 9479.66667 | 0 | 0 |
| 5 | 9479.66667 | 0 | 0 |
| 6 | 244.833333 | 0 | 0 |
| 7 | 294 | 0 | 0 |
| 8 | 328.833333 | 0 | 0 |
| 9 | 328.833333 | 0 | 0 |
| 10 | 244 | 0 | 0 |
| 11 | 244 | 0 | 0 |
| 12 | 129.5 | 0 | 0 |
| 13 | 129.5 | 0 | 0 |
| 14 | 129.5 | 0 | 0 |
| 15 | 129.5 | 0 | 0 |
| 16 | 129.5 | 0 | 0 |
| 17 | 129.5 | 0 | 0 |
| 18 | 129.5 | 0 | 0 |
| 19 | 129.5 | 0 | 0 |
| 20 | 129.5 | 0 | 0 |
| 21 | 129.5 | 0 | 0 |
| 22 | 129.5 | 0 | 0 |
| 23 | 129.5 | 0 | 0 |
| 24 | 129.5 | 0 | 0 |
| 25 | 129.5 | 0 | 0 |
| 26 | 129.5 | 0 | 0 |
| 27 | 129.5 | 0 | 0 |
| 28 | 129.5 | 0 | 0 |
| 29 | 129.5 | 0 | 0 |
| 30 | 129.5 | 0 | 0 |
| 31 | 129.5 | 0 | 0 |
| 32 | 129.5 | 0 | 0 |
| 33 | 129.5 | 0 | 0 |
| 34 | 129.5 | 0 | 0 |
| 35 | 129.5 | 0 | 0 |
| 36 | 129.5 | 0 | 0 |
| 37 | 129.5 | 0 | 0 |
| 38 | 129.5 | 0 | 0 |
| 39 | 129.5 | 0 | 0 |
| 40 | 129.5 | 0 | 0 |
| 41 | 129.5 | 0 | 0 |
| 42 | 129.5 | 0 | 0 |
| 43 | 129.5 | 0 | 0 |
| 44 | 129.5 | 0 | 0 |
| 45 | 129.5 | 0 | 0 |
| 46 | 129.5 | 0 | 0 |
| 47 | 129.5 | 0 | 0 |
| 48 | 129.5 | 0 | 0 |
| 49 | 129.5 | 0 | 0 |
| 50 | 129.5 | 0 | 0 |
| 51 | 129.5 | 0 | 0 |
| 52 | 129.5 | 0 | 0 |
| 53 | 129.5 | 0 | 0 |
| 54 | 129.5 | 0 | 0 |
| 55 | 129.5 | 0 | 0 |
| 56 | 129.5 | 0 | 0 |
| 57 | 129.5 | 0 | 0 |
| 58 | 129.5 | 0 | 0 |
| 59 | 129.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 129.5 | 0 | 0 |
| 4 | 129.5 | 0 | 0 |
| 5 | 129.5 | 0 | 0 |
| 6 | 129.5 | 0 | 0 |
| 7 | 136.666667 | 0 | 0 |
| 8 | 136.666667 | 0 | 0 |
| 9 | 136.666667 | 0 | 0 |
| 10 | 136.666667 | 0 | 0 |
| 11 | 136.666667 | 0 | 0 |
| 12 | 136.666667 | 0 | 0 |
| 13 | 136.666667 | 0 | 0 |
| 14 | 136.666667 | 0 | 0 |
| 15 | 156.666667 | 0 | 0 |
| 16 | 156.5 | 0 | 0 |
| 17 | 502.166667 | 0 | 0 |
| 18 | 502.166667 | 0 | 0 |
| 19 | 502.166667 | 0 | 0 |
| 20 | 289.833333 | 0 | 0 |
| 21 | 289.833333 | 0 | 0 |
| 22 | 289.833333 | 0 | 0 |
| 23 | 289.833333 | 0 | 0 |
| 24 | 289.833333 | 0 | 0 |
| 25 | 289.833333 | 0 | 0 |
| 26 | 289.833333 | 0 | 0 |
| 27 | 289.833333 | 0 | 0 |
| 28 | 289.833333 | 0 | 0 |
| 29 | 289.833333 | 0 | 0 |
| 30 | 289.833333 | 0 | 0 |
| 31 | 289.833333 | 0 | 0 |
| 32 | 289.833333 | 0 | 0 |
| 33 | 289.833333 | 0 | 0 |
| 34 | 289.833333 | 0 | 0 |
| 35 | 289.833333 | 0 | 0 |
| 36 | 289.833333 | 0 | 0 |
| 37 | 289.833333 | 0 | 0 |
| 38 | 289.833333 | 0 | 0 |
| 39 | 289.833333 | 0 | 0 |
| 40 | 289.833333 | 0 | 0 |
| 41 | 289.833333 | 0 | 0 |
| 42 | 289.833333 | 0 | 0 |
| 43 | 289.833333 | 0 | 0 |
| 44 | 289.833333 | 0 | 0 |
| 45 | 289.833333 | 0 | 0 |
| 46 | 289.833333 | 0 | 0 |
| 47 | 289.833333 | 0 | 0 |
| 48 | 289.833333 | 0 | 0 |
| 49 | 289.833333 | 0 | 0 |
| 50 | 289.833333 | 0 | 0 |
| 51 | 289.833333 | 0 | 0 |
| 52 | 289.833333 | 0 | 0 |
| 53 | 289.833333 | 0 | 0 |
| 54 | 289.833333 | 0 | 0 |
| 55 | 289.833333 | 0 | 0 |
| 56 | 289.833333 | 0 | 0 |
| 57 | 289.833333 | 0 | 0 |
| 58 | 289.833333 | 0 | 0 |
| 59 | 289.833333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 289.833333 | 0 | 0 |
| 4 | 289.833333 | 0 | 0 |
| 5 | 289.833333 | 0 | 0 |
| 6 | 289.833333 | 0 | 0 |
| 7 | 289.833333 | 0 | 0 |
| 8 | 289.833333 | 0 | 0 |
| 9 | 289.833333 | 0 | 0 |
| 10 | 6755.5 | 0 | 0 |
| 11 | 6755.5 | 0 | 0 |
| 12 | 6755.5 | 0 | 0 |
| 13 | 6755.5 | 0 | 0 |
| 14 | 6755.5 | 0 | 0 |
| 15 | 6755.5 | 0 | 0 |
| 16 | 6755.5 | 0 | 0 |
| 17 | 6755.5 | 0 | 0 |
| 18 | 6755.5 | 0 | 0 |
| 19 | 6755.5 | 0 | 0 |
| 20 | 6755.5 | 0 | 0 |
| 21 | 6755.5 | 0 | 0 |
| 22 | 6824.33333 | 0 | 0 |
| 23 | 6824.33333 | 0 | 0 |
| 24 | 6865 | 0 | 0 |
| 25 | 173.166667 | 0 | 0 |
| 26 | 173.166667 | 0 | 0 |
| 27 | 173.166667 | 0 | 0 |
| 28 | 173.166667 | 0 | 0 |
| 29 | 173.166667 | 0 | 0 |
| 30 | 173.166667 | 0 | 0 |
| 31 | 173.166667 | 0 | 0 |
| 32 | 173.166667 | 0 | 0 |
| 33 | 173.166667 | 0 | 0 |
| 34 | 173.166667 | 0 | 0 |
| 35 | 173.166667 | 0 | 0 |
| 36 | 173.166667 | 0 | 0 |
| 37 | 173.166667 | 0 | 0 |
| 38 | 173.166667 | 0 | 0 |
| 39 | 173.166667 | 0 | 0 |
| 40 | 173.166667 | 0 | 0 |
| 41 | 173.166667 | 0 | 0 |
| 42 | 173.166667 | 0 | 0 |
| 43 | 173.166667 | 0 | 0 |
| 44 | 173.166667 | 0 | 0 |
| 45 | 173.166667 | 0 | 0 |
| 46 | 173.166667 | 0 | 0 |
| 47 | 173.166667 | 0 | 0 |
| 48 | 173.166667 | 0 | 0 |
| 49 | 173.166667 | 0 | 0 |
| 50 | 173.166667 | 0 | 0 |
| 51 | 173.166667 | 0 | 0 |
| 52 | 173.166667 | 0 | 0 |
| 53 | 173.166667 | 0 | 0 |
| 54 | 173.166667 | 0 | 0 |
| 55 | 173.166667 | 0 | 0 |
| 56 | 173.166667 | 0 | 0 |
| 57 | 173.166667 | 0 | 0 |
| 58 | 173.166667 | 0 | 0 |
| 59 | 156.333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 156.333333 | 0 | 0 |
| 4 | 156.333333 | 0 | 0 |
| 5 | 156.333333 | 0 | 0 |
| 6 | 156.333333 | 0 | 0 |
| 7 | 156.333333 | 0 | 0 |
| 8 | 156.333333 | 0 | 0 |
| 9 | 156.333333 | 0 | 0 |
| 10 | 156.333333 | 0 | 0 |
| 11 | 156.333333 | 0 | 0 |
| 12 | 156.333333 | 0 | 0 |
| 13 | 156.333333 | 0 | 0 |
| 14 | 156.333333 | 0 | 0 |
| 15 | 156.333333 | 0 | 0 |
| 16 | 156.333333 | 0 | 0 |
| 17 | 156.333333 | 0 | 0 |
| 18 | 156.333333 | 0 | 0 |
| 19 | 156.333333 | 0 | 0 |
| 20 | 156.333333 | 0 | 0 |
| 21 | 156.333333 | 0 | 0 |
| 22 | 156.333333 | 0 | 0 |
| 23 | 316 | 0 | 0 |
| 24 | 168.833333 | 0 | 0 |
| 25 | 168.833333 | 0 | 0 |
| 26 | 168.833333 | 0 | 0 |
| 27 | 168.833333 | 0 | 0 |
| 28 | 168.833333 | 0 | 0 |
| 29 | 168.833333 | 0 | 0 |
| 30 | 168.833333 | 0 | 0 |
| 31 | 168.833333 | 0 | 0 |
| 32 | 168.833333 | 0 | 0 |
| 33 | 168.833333 | 0 | 0 |
| 34 | 168.833333 | 0 | 0 |
| 35 | 168.833333 | 0 | 0 |
| 36 | 168.833333 | 0 | 0 |
| 37 | 168.833333 | 0 | 0 |
| 38 | 168.833333 | 0 | 0 |
| 39 | 168.833333 | 0 | 0 |
| 40 | 168.833333 | 0 | 0 |
| 41 | 58.8333333 | 0 | 0 |
| 42 | 58.8333333 | 0 | 0 |
| 43 | 58.8333333 | 0 | 0 |
| 44 | 58.8333333 | 0 | 0 |
| 45 | 58.8333333 | 0 | 0 |
| 46 | 58.8333333 | 0 | 0 |
| 47 | 58.8333333 | 0 | 0 |
| 48 | 58.8333333 | 0 | 0 |
| 49 | 58.8333333 | 0 | 0 |
| 50 | 58.8333333 | 0 | 0 |
| 51 | 58.8333333 | 0 | 0 |
| 52 | 58.8333333 | 0 | 0 |
| 53 | 58.8333333 | 0 | 0 |
| 54 | 58.8333333 | 0 | 0 |
| 55 | 58.8333333 | 0 | 0 |
| 56 | 58.8333333 | 0 | 0 |
| 57 | 58.8333333 | 0 | 0 |
| 58 | 58.8333333 | 0 | 0 |
| 59 | 58.8333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 58.8333333 | 0 | 0 |
| 4 | 58.8333333 | 0 | 0 |
| 5 | 58.8333333 | 0 | 0 |
| 6 | 58.8333333 | 0 | 0 |
| 7 | 58.8333333 | 0 | 0 |
| 8 | 58.8333333 | 0 | 0 |
| 9 | 58.8333333 | 0 | 0 |
| 10 | 58.8333333 | 0 | 0 |
| 11 | 58.8333333 | 0 | 0 |
| 12 | 58.8333333 | 0 | 0 |
| 13 | 58.8333333 | 0 | 0 |
| 14 | 58.8333333 | 0 | 0 |
| 15 | 58.8333333 | 0 | 0 |
| 16 | 58.8333333 | 0 | 0 |
| 17 | 58.8333333 | 0 | 0 |
| 18 | 58.8333333 | 0 | 0 |
| 19 | 58.8333333 | 0 | 0 |
| 20 | 58.8333333 | 0 | 0 |
| 21 | 58.8333333 | 0 | 0 |
| 22 | 58.8333333 | 0 | 0 |
| 23 | 58.8333333 | 0 | 0 |
| 24 | 58.8333333 | 0 | 0 |
| 25 | 58.8333333 | 0 | 0 |
| 26 | 58.8333333 | 0 | 0 |
| 27 | 58.8333333 | 0 | 0 |
| 28 | 58.8333333 | 0 | 0 |
| 29 | 58.8333333 | 0 | 0 |
| 30 | 58.8333333 | 0 | 0 |
| 31 | 58.8333333 | 0 | 0 |
| 32 | 58.8333333 | 0 | 0 |
| 33 | 58.8333333 | 0 | 0 |
| 34 | 58.8333333 | 0 | 0 |
| 35 | 58.8333333 | 0 | 0 |
| 36 | 58.8333333 | 0 | 0 |
| 37 | 58.8333333 | 0 | 0 |
| 38 | 58.8333333 | 0 | 0 |
| 39 | 70.8333333 | 0 | 0 |
| 40 | 1391.33333 | 0 | 0 |
| 41 | | | |
| 42 | 1386 | 0 | 0 |
| 43 | 1386 | 0 | 0 |
| 44 | 1386 | 0 | 0 |
| 45 | | | |
| 46 | 5189.66667 | 0 | 0 |
| 47 | 5189.66667 | 0 | 0 |
| 48 | 5189.66667 | 0 | 0 |
| 49 | 5189.66667 | 0 | 0 |
| 50 | 5189.66667 | 0 | 0 |
| 51 | 5189.66667 | 0 | 0 |
| 52 | 5189.66667 | 0 | 0 |
| 53 | 5189.66667 | 0 | 0 |
| 54 | 5189.66667 | 0 | 0 |
| 55 | 5189.66667 | 0 | 0 |
| 56 | 5189.66667 | 0 | 0 |
| 57 | 5189.66667 | 0 | 0 |
| 58 | 5189.66667 | 0 | 0 |
| 59 | 5189.66667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 5189.66667 | 0 | 0 |
| 4 | 5189.66667 | 0 | 0 |
| 5 | 5189.66667 | 0 | 0 |
| 6 | 5189.66667 | 0 | 0 |
| 7 | 5189.66667 | 0 | 0 |
| 8 | 5189.66667 | 0 | 0 |
| 9 | 5189.66667 | 0 | 0 |
| 10 | 668 | 0 | 0 |
| 11 | 13807.5 | 0 | 0 |
| 12 | 13807.5 | 0 | 0 |
| 13 | 13807.5 | 0 | 0 |
| 14 | 13807.5 | 0 | 0 |
| 15 | 13807.5 | 0 | 0 |
| 16 | 13807.5 | 0 | 0 |
| 17 | 13807.5 | 0 | 0 |
| 18 | 13807.5 | 0 | 0 |
| 19 | 13807.5 | 0 | 0 |
| 20 | 13807.5 | 0 | 0 |
| 21 | 13807.5 | 0 | 0 |
| 22 | 13807.5 | 0 | 0 |
| 23 | 12743 | 0 | 0 |
| 24 | 12743 | 0 | 0 |
| 25 | 12743 | 0 | 0 |
| 26 | 12743 | 0 | 0 |
| 27 | 12732.8333 | 0 | 0 |
| 28 | 12732.8333 | 0 | 0 |
| 29 | 12732.8333 | 0 | 0 |
| 30 | 12732.8333 | 0 | 0 |
| 31 | 12732.8333 | 0 | 0 |
| 32 | 12732.8333 | 0 | 0 |
| 33 | 12732.8333 | 0 | 0 |
| 34 | 12732.8333 | 0 | 0 |
| 35 | 12732.8333 | 0 | 0 |
| 36 | 12732.8333 | 0 | 0 |
| 37 | 12732.8333 | 0 | 0 |
| 38 | 12732.8333 | 0 | 0 |
| 39 | 12732.8333 | 0 | 0 |
| 40 | 12732.8333 | 0 | 0 |
| 41 | 12732.8333 | 0 | 0 |
| 42 | 12732.8333 | 0 | 0 |
| 43 | 12732.8333 | 0 | 0 |
| 44 | 12732.8333 | 0 | 0 |
| 45 | 12732.8333 | 0 | 0 |
| 46 | 12732.8333 | 0 | 0 |
| 47 | 12732.8333 | 0 | 0 |
| 48 | 12732.8333 | 0 | 0 |
| 49 | 12732.8333 | 0 | 0 |
| 50 | 12732.8333 | 0 | 0 |
| 51 | 12732.8333 | 0 | 0 |
| 52 | 12732.8333 | 0 | 0 |
| 53 | 12732.8333 | 0 | 0 |
| 54 | 12732.8333 | 0 | 0 |
| 55 | 12732.8333 | 0 | 0 |
| 56 | 12732.8333 | 0 | 0 |
| 57 | 12732.8333 | 0 | 0 |
| 58 | 12732.8333 | 0 | 0 |
| 59 | 12732.8333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 12732.8333 | 0 | 0 |
| 4 | 12732.8333 | 0 | 0 |
| 5 | 12732.8333 | 0 | 0 |
| 6 | 12732.8333 | 0 | 0 |
| 7 | 12732.8333 | 0 | 0 |
| 8 | 12732.8333 | 0 | 0 |
| 9 | 12732.8333 | 0 | 0 |
| 10 | 12732.8333 | 0 | 0 |
| 11 | 12732.8333 | 0 | 0 |
| 12 | 12732.8333 | 0 | 0 |
| 13 | 12732.8333 | 0 | 0 |
| 14 | 12732.8333 | 0 | 0 |
| 15 | 12732.8333 | 0 | 0 |
| 16 | 12732.8333 | 0 | 0 |
| 17 | 12732.8333 | 0 | 0 |
| 18 | 12732.8333 | 0 | 0 |
| 19 | 12732.8333 | 0 | 0 |
| 20 | 12732.8333 | 0 | 0 |
| 21 | 12732.8333 | 0 | 0 |
| 22 | 12732.8333 | 0 | 0 |
| 23 | 12732.8333 | 0 | 0 |
| 24 | 12732.8333 | 0 | 0 |
| 25 | 12732.8333 | 0 | 0 |
| 26 | 12732.8333 | 0 | 0 |
| 27 | 12732.8333 | 0 | 0 |
| 28 | 12732.8333 | 0 | 0 |
| 29 | 12732.8333 | 0 | 0 |
| 30 | 12732.8333 | 0 | 0 |
| 31 | 12732.8333 | 0 | 0 |
| 32 | 12732.8333 | 0 | 0 |
| 33 | 12732.8333 | 0 | 0 |
| 34 | 12732.8333 | 0 | 0 |
| 35 | 12732.8333 | 0 | 0 |
| 36 | 12732.8333 | 0 | 0 |
| 37 | 12732.8333 | 0 | 0 |
| 38 | 195 | 0 | 0 |
| 39 | 195 | 0 | 0 |
| 40 | 195 | 0 | 0 |
| 41 | 195 | 0 | 0 |
| 42 | 195 | 0 | 0 |
| 43 | 195 | 0 | 0 |
| 44 | 195 | 0 | 0 |
| 45 | 195 | 0 | 0 |
| 46 | 195 | 0 | 0 |
| 47 | 195 | 0 | 0 |
| 48 | 195 | 0 | 0 |
| 49 | 195 | 0 | 0 |
| 50 | 12768.1667 | 0 | 0 |
| 51 | 12190 | 0 | 0 |
| 52 | 12190 | 0 | 0 |
| 53 | 12183.6667 | 0 | 0 |
| 54 | 12183.6667 | 0 | 0 |
| 55 | 12183.6667 | 0 | 0 |
| 56 | 12183.6667 | 0 | 0 |
| 57 | 12183.6667 | 0 | 0 |
| 58 | 12183.6667 | 0 | 0 |
| 59 | 12183.6667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 12183.6667 | 0 | 0 |
| 4 | 12183.6667 | 0 | 0 |
| 5 | 12183.6667 | 0 | 0 |
| 6 | 12183.6667 | 0 | 0 |
| 7 | 12183.6667 | 0 | 0 |
| 8 | 12183.6667 | 0 | 0 |
| 9 | 12183.6667 | 0 | 0 |
| 10 | 12183.6667 | 0 | 0 |
| 11 | 12183.6667 | 0 | 0 |
| 12 | 12183.6667 | 0 | 0 |
| 13 | 12183.6667 | 0 | 0 |
| 14 | 12183.6667 | 0 | 0 |
| 15 | 12183.6667 | 0 | 0 |
| 16 | 12183.6667 | 0 | 0 |
| 17 | 12183.6667 | 0 | 0 |
| 18 | 12183.6667 | 0 | 0 |
| 19 | 12183.6667 | 0 | 0 |
| 20 | 12183.6667 | 0 | 0 |
| 21 | 12183.6667 | 0 | 0 |
| 22 | 12183.6667 | 0 | 0 |
| 23 | 12183.6667 | 0 | 0 |
| 24 | 12183.6667 | 0 | 0 |
| 25 | 12183.6667 | 0 | 0 |
| 26 | 12183.6667 | 0 | 0 |
| 27 | 12183.6667 | 0 | 0 |
| 28 | 12183.6667 | 0 | 0 |
| 29 | 12183.6667 | 0 | 0 |
| 30 | 12183.6667 | 0 | 0 |
| 31 | 12183.6667 | 0 | 0 |
| 32 | 12183.6667 | 0 | 0 |
| 33 | 12183.6667 | 0 | 0 |
| 34 | 12183.6667 | 0 | 0 |
| 35 | 12183.6667 | 0 | 0 |
| 36 | 12183.6667 | 0 | 0 |
| 37 | 12183.6667 | 0 | 0 |
| 38 | 12183.6667 | 0 | 0 |
| 39 | 12183.6667 | 0 | 0 |
| 40 | 12183.6667 | 0 | 0 |
| 41 | 12183.6667 | 0 | 0 |
| 42 | 12183.6667 | 0 | 0 |
| 43 | 12183.6667 | 0 | 0 |
| 44 | 12183.6667 | 0 | 0 |
| 45 | 12183.6667 | 0 | 0 |
| 46 | 12183.6667 | 0 | 0 |
| 47 | 12183.6667 | 0 | 0 |
| 48 | 12183.6667 | 0 | 0 |
| 49 | 12183.6667 | 0 | 0 |
| 50 | 12183.6667 | 0 | 0 |
| 51 | 12183.6667 | 0 | 0 |
| 52 | 12183.6667 | 0 | 0 |
| 53 | 12183.6667 | 0 | 0 |
| 54 | 12183.6667 | 0 | 0 |
| 55 | 12183.6667 | 0 | 0 |
| 56 | 12183.6667 | 0 | 0 |
| 57 | 12183.6667 | 0 | 0 |
| 58 | 12183.6667 | 0 | 0 |
| 59 | 12183.6667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 12183.6667 | 0 | 0 |
| 4 | 12183.6667 | 0 | 0 |
| 5 | 12183.6667 | 0 | 0 |
| 6 | 12183.6667 | 0 | 0 |
| 7 | 12183.6667 | 0 | 0 |
| 8 | 12183.6667 | 0 | 0 |
| 9 | 12183.6667 | 0 | 0 |
| 10 | 12183.6667 | 0 | 0 |
| 11 | 12183.6667 | 0 | 0 |
| 12 | 12183.6667 | 0 | 0 |
| 13 | 12183.6667 | 0 | 0 |
| 14 | 12183.6667 | 0 | 0 |
| 15 | 12183.6667 | 0 | 0 |
| 16 | 12183.6667 | 0 | 0 |
| 17 | 12183.6667 | 0 | 0 |
| 18 | 12183.6667 | 0 | 0 |
| 19 | 12183.6667 | 0 | 0 |
| 20 | 12183.6667 | 0 | 0 |
| 21 | 12183.6667 | 0 | 0 |
| 22 | 12183.6667 | 0 | 0 |
| 23 | 12183.6667 | 0 | 0 |
| 24 | 12183.6667 | 0 | 0 |
| 25 | 12183.6667 | 0 | 0 |
| 26 | 12183.6667 | 0 | 0 |
| 27 | 12183.6667 | 0 | 0 |
| 28 | 12183.6667 | 0 | 0 |
| 29 | 12183.6667 | 0 | 0 |
| 30 | 12183.6667 | 0 | 0 |
| 31 | 12183.6667 | 0 | 0 |
| 32 | 12183.6667 | 0 | 0 |
| 33 | 12183.6667 | 0 | 0 |
| 34 | 12183.6667 | 0 | 0 |
| 35 | 138.666667 | 0 | 0 |
| 36 | 258.833333 | 0 | 0 |
| 37 | 105.666667 | 0 | 0 |
| 38 | 105.666667 | 0 | 0 |
| 39 | 105.666667 | 0 | 0 |
| 40 | 105.666667 | 0 | 0 |
| 41 | 105.666667 | 0 | 0 |
| 42 | 105.666667 | 0 | 0 |
| 43 | 105.666667 | 0 | 0 |
| 44 | 105.666667 | 0 | 0 |
| 45 | 105.666667 | 0 | 0 |
| 46 | 105.666667 | 0 | 0 |
| 47 | 105.666667 | 0 | 0 |
| 48 | 105.666667 | 0 | 0 |
| 49 | 105.666667 | 0 | 0 |
| 50 | 105.666667 | 0 | 0 |
| 51 | 105.666667 | 0 | 0 |
| 52 | 102366.833 | 0 | 0 |
| 53 | 102366.833 | 0 | 0 |
| 54 | 102366.833 | 0 | 0 |
| 55 | 102366.833 | 0 | 0 |
| 56 | 102366.833 | 0 | 0 |
| 57 | 102366.833 | 0 | 0 |
| 58 | 102366.833 | 0 | 0 |
| 59 | 102366.833 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 102366.833 | 0 | 0 |
| 4 | 102366.833 | 0 | 0 |
| 5 | 102366.833 | 0 | 0 |
| 6 | 102366.833 | 0 | 0 |
| 7 | 102366.833 | 0 | 0 |
| 8 | 102366.833 | 0 | 0 |
| 9 | 102366.833 | 0 | 0 |
| 10 | 102366.833 | 0 | 0 |
| 11 | 102366.833 | 0 | 0 |
| 12 | 102366.833 | 0 | 0 |
| 13 | 102366.833 | 0 | 0 |
| 14 | 102366.833 | 0 | 0 |
| 15 | 102366.833 | 0 | 0 |
| 16 | 102366.833 | 0 | 0 |
| 17 | 102366.833 | 0 | 0 |
| 18 | 102366.833 | 0 | 0 |
| 19 | 102366.833 | 0 | 0 |
| 20 | 102366.833 | 0 | 0 |
| 21 | 102366.833 | 0 | 0 |
| 22 | 102366.833 | 0 | 0 |
| 23 | 102366.833 | 0 | 0 |
| 24 | 102366.833 | 0 | 0 |
| 25 | 102366.833 | 0 | 0 |
| 26 | 102366.833 | 0 | 0 |
| 27 | 102366.833 | 0 | 0 |
| 28 | 102366.833 | 0 | 0 |
| 29 | 102366.833 | 0 | 0 |
| 30 | 102366.833 | 0 | 0 |
| 31 | 102366.833 | 0 | 0 |
| 32 | 102366.833 | 0 | 0 |
| 33 | 102366.833 | 0 | 0 |
| 34 | 102366.833 | 0 | 0 |
| 35 | 102366.833 | 0 | 0 |
| 36 | 102366.833 | 0 | 0 |
| 37 | 102366.833 | 0 | 0 |
| 38 | 102366.833 | 0 | 0 |
| 39 | 102366.833 | 0 | 0 |
| 40 | 102366.833 | 0 | 0 |
| 41 | 102366.833 | 0 | 0 |
| 42 | 102366.833 | 0 | 0 |
| 43 | 102366.833 | 0 | 0 |
| 44 | 102366.833 | 0 | 0 |
| 45 | 102366.833 | 0 | 0 |
| 46 | 102366.833 | 0 | 0 |
| 47 | 102366.833 | 0 | 0 |
| 48 | 102366.833 | 0 | 0 |
| 49 | 102366.833 | 0 | 0 |
| 50 | 102366.833 | 0 | 0 |
| 51 | 102366.833 | 0 | 0 |
| 52 | 102366.833 | 0 | 0 |
| 53 | 102366.833 | 0 | 0 |
| 54 | 102366.833 | 0 | 0 |
| 55 | 102366.833 | 0 | 0 |
| 56 | 102366.833 | 0 | 0 |
| 57 | 102366.833 | 0 | 0 |
| 58 | 102366.833 | 0 | 0 |
| 59 | 102366.833 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 102366.833 | 0 | 0 |
| 4 | 102366.833 | 0 | 0 |
| 5 | 102366.833 | 0 | 0 |
| 6 | 102366.833 | 0 | 0 |
| 7 | 102366.833 | 0 | 0 |
| 8 | 102366.833 | 0 | 0 |
| 9 | 102366.833 | 0 | 0 |
| 10 | 102366.833 | 0 | 0 |
| 11 | 102366.833 | 0 | 0 |
| 12 | 102366.833 | 0 | 0 |
| 13 | 102366.833 | 0 | 0 |
| 14 | 102366.833 | 0 | 0 |
| 15 | 102366.833 | 0 | 0 |
| 16 | 102366.833 | 0 | 0 |
| 17 | 102366.833 | 0 | 0 |
| 18 | 102366.833 | 0 | 0 |
| 19 | 102366.833 | 0 | 0 |
| 20 | 102366.833 | 0 | 0 |
| 21 | 102366.833 | 0 | 0 |
| 22 | 102366.833 | 0 | 0 |
| 23 | 102366.833 | 0 | 0 |
| 24 | 102366.833 | 0 | 0 |
| 25 | 102366.833 | 0 | 0 |
| 26 | 102366.833 | 0 | 0 |
| 27 | 102366.833 | 0 | 0 |
| 28 | 102366.833 | 0 | 0 |
| 29 | 102366.833 | 0 | 0 |
| 30 | 102366.833 | 0 | 0 |
| 31 | 102366.833 | 0 | 0 |
| 32 | 102366.833 | 0 | 0 |
| 33 | 102366.833 | 0 | 0 |
| 34 | 102366.833 | 0 | 0 |
| 35 | 102366.833 | 0 | 0 |
| 36 | 102366.833 | 0 | 0 |
| 37 | 102366.833 | 0 | 0 |
| 38 | 102366.833 | 0 | 0 |
| 39 | 102366.833 | 0 | 0 |
| 40 | 102366.833 | 0 | 0 |
| 41 | 102366.833 | 0 | 0 |
| 42 | 102366.833 | 0 | 0 |
| 43 | 102366.833 | 0 | 0 |
| 44 | 102366.833 | 0 | 0 |
| 45 | 102366.833 | 0 | 0 |
| 46 | 102366.833 | 0 | 0 |
| 47 | 102366.833 | 0 | 0 |
| 48 | 102366.833 | 0 | 0 |
| 49 | 102366.833 | 0 | 0 |
| 50 | 102366.833 | 0 | 0 |
| 51 | 102366.833 | 0 | 0 |
| 52 | 102366.833 | 0 | 0 |
| 53 | 102366.833 | 0 | 0 |
| 54 | 102366.833 | 0 | 0 |
| 55 | 102366.833 | 0 | 0 |
| 56 | 102366.833 | 0 | 0 |
| 57 | 102366.833 | 0 | 0 |
| 58 | 102366.833 | 0 | 0 |
| 59 | 102366.833 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 102366.833 | 0 | 0 |
| 4 | 102366.833 | 0 | 0 |
| 5 | 102366.833 | 0 | 0 |
| 6 | 102366.833 | 0 | 0 |
| 7 | 102366.833 | 0 | 0 |
| 8 | 102366.833 | 0 | 0 |
| 9 | 102366.833 | 0 | 0 |
| 10 | 102366.833 | 0 | 0 |
| 11 | 102366.833 | 0 | 0 |
| 12 | 102366.833 | 0 | 0 |
| 13 | 102366.833 | 0 | 0 |
| 14 | 102366.833 | 0 | 0 |
| 15 | 102366.833 | 0 | 0 |
| 16 | 102366.833 | 0 | 0 |
| 17 | 102366.833 | 0 | 0 |
| 18 | 102366.833 | 0 | 0 |
| 19 | 102366.833 | 0 | 0 |
| 20 | 102366.833 | 0 | 0 |
| 21 | 102366.833 | 0 | 0 |
| 22 | 102366.833 | 0 | 0 |
| 23 | 102366.833 | 0 | 0 |
| 24 | 102366.833 | 0 | 0 |
| 25 | 102366.833 | 0 | 0 |
| 26 | 102366.833 | 0 | 0 |
| 27 | 102366.833 | 0 | 0 |
| 28 | 102366.833 | 0 | 0 |
| 29 | 102366.833 | 0 | 0 |
| 30 | 102366.833 | 0 | 0 |
| 31 | 102366.833 | 0 | 0 |
| 32 | 102366.833 | 0 | 0 |
| 33 | 102366.833 | 0 | 0 |
| 34 | 102366.833 | 0 | 0 |
| 35 | 102366.833 | 0 | 0 |
| 36 | 102366.833 | 0 | 0 |
| 37 | 102366.833 | 0 | 0 |
| 38 | 102366.833 | 0 | 0 |
| 39 | 102366.833 | 0 | 0 |
| 40 | 102366.833 | 0 | 0 |
| 41 | 102366.833 | 0 | 0 |
| 42 | 102366.833 | 0 | 0 |
| 43 | 102366.833 | 0 | 0 |
| 44 | 102366.833 | 0 | 0 |
| 45 | 102366.833 | 0 | 0 |
| 46 | 102366.833 | 0 | 0 |
| 47 | 102366.833 | 0 | 0 |
| 48 | 102366.833 | 0 | 0 |
| 49 | 102366.833 | 0 | 0 |
| 50 | 102366.833 | 0 | 0 |
| 51 | 102366.833 | 0 | 0 |
| 52 | 102366.833 | 0 | 0 |
| 53 | 102366.833 | 0 | 0 |
| 54 | 102366.833 | 0 | 0 |
| 55 | 102366.833 | 0 | 0 |
| 56 | 102366.833 | 0 | 0 |
| 57 | 102366.833 | 0 | 0 |
| 58 | 102366.833 | 0 | 0 |
| 59 | 102366.833 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 102366.833 | 0 | 0 |
| 4 | 102366.833 | 0 | 0 |
| 5 | 102366.833 | 0 | 0 |
| 6 | 102366.833 | 0 | 0 |
| 7 | 102366.833 | 0 | 0 |
| 8 | 102366.833 | 0 | 0 |
| 9 | 102366.833 | 0 | 0 |
| 10 | 102366.833 | 0 | 0 |
| 11 | 102366.833 | 0 | 0 |
| 12 | 102366.833 | 0 | 0 |
| 13 | 102366.833 | 0 | 0 |
| 14 | 102366.833 | 0 | 0 |
| 15 | 102366.833 | 0 | 0 |
| 16 | 102366.833 | 0 | 0 |
| 17 | 102366.833 | 0 | 0 |
| 18 | 102366.833 | 0 | 0 |
| 19 | 102366.833 | 0 | 0 |
| 20 | 102366.833 | 0 | 0 |
| 21 | 102366.833 | 0 | 0 |
| 22 | 102366.833 | 0 | 0 |
| 23 | 102366.833 | 0 | 0 |
| 24 | 102366.833 | 0 | 0 |
| 25 | 102366.833 | 0 | 0 |
| 26 | 102366.833 | 0 | 0 |
| 27 | 102366.833 | 0 | 0 |
| 28 | 102366.833 | 0 | 0 |
| 29 | 102366.833 | 0 | 0 |
| 30 | 102366.833 | 0 | 0 |
| 31 | 102366.833 | 0 | 0 |
| 32 | 102366.833 | 0 | 0 |
| 33 | 102366.833 | 0 | 0 |
| 34 | 102366.833 | 0 | 0 |
| 35 | 102366.833 | 0 | 0 |
| 36 | 102366.833 | 0 | 0 |
| 37 | 102366.833 | 0 | 0 |
| 38 | 102366.833 | 0 | 0 |
| 39 | 102366.833 | 0 | 0 |
| 40 | 102366.833 | 0 | 0 |
| 41 | 102366.833 | 0 | 0 |
| 42 | 102366.833 | 0 | 0 |
| 43 | 102366.833 | 0 | 0 |
| 44 | 102366.833 | 0 | 0 |
| 45 | 102366.833 | 0 | 0 |
| 46 | 102366.833 | 0 | 0 |
| 47 | 102366.833 | 0 | 0 |
| 48 | 102366.833 | 0 | 0 |
| 49 | 102400.833 | 0 | 0 |
| 50 | 102400.833 | 0 | 0 |
| 51 | 102400.833 | 0 | 0 |
| 52 | 102400.833 | 0 | 0 |
| 53 | 102400.833 | 0 | 0 |
| 54 | 102400.833 | 0 | 0 |
| 55 | 102400.833 | 0 | 0 |
| 56 | 103055.833 | 0 | 0 |
| 57 | 103055.833 | 0 | 0 |
| 58 | 103055.833 | 0 | 0 |
| 59 | 103055.833 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 106089.167 | 0 | 0 |
| 4 | | | |
| 5 | 66.5 | 0 | 0 |
| 6 | 66.5 | 0 | 0 |
| 7 | 66.5 | 0 | 0 |
| 8 | | | |
| 9 | 65.1666667 | 0 | 0 |
| 10 | 65.1666667 | 0 | 0 |
| 11 | 65.1666667 | 0 | 0 |
| 12 | 65.1666667 | 0 | 0 |
| 13 | 65.1666667 | 0 | 0 |
| 14 | 65.1666667 | 0 | 0 |
| 15 | 65.1666667 | 0 | 0 |
| 16 | 65.1666667 | 0 | 0 |
| 17 | 65.1666667 | 0 | 0 |
| 18 | 65.1666667 | 0 | 0 |
| 19 | 65.1666667 | 0 | 0 |
| 20 | 65.1666667 | 0 | 0 |
| 21 | 65.1666667 | 0 | 0 |
| 22 | 65.1666667 | 0 | 0 |
| 23 | 65.1666667 | 0 | 0 |
| 24 | 65.1666667 | 0 | 0 |
| 25 | 65.1666667 | 0 | 0 |
| 26 | 65.1666667 | 0 | 0 |
| 27 | 65.1666667 | 0 | 0 |
| 28 | 65.1666667 | 0 | 0 |
| 29 | 65.1666667 | 0 | 0 |
| 30 | 65.1666667 | 0 | 0 |
| 31 | 65.1666667 | 0 | 0 |
| 32 | 65.1666667 | 0 | 0 |
| 33 | 906.666667 | 0 | 0 |
| 34 | 906.666667 | 0 | 0 |
| 35 | 906.666667 | 0 | 0 |
| 36 | 906.666667 | 0 | 0 |
| 37 | 906.666667 | 0 | 0 |
| 38 | 906.666667 | 0 | 0 |
| 39 | 906.666667 | 0 | 0 |
| 40 | 906.666667 | 0 | 0 |
| 41 | 906.666667 | 0 | 0 |
| 42 | 906.666667 | 0 | 0 |
| 43 | 906.666667 | 0 | 0 |
| 44 | 906.666667 | 0 | 0 |
| 45 | 906.666667 | 0 | 0 |
| 46 | 906.666667 | 0 | 0 |
| 47 | 906.666667 | 0 | 0 |
| 48 | 906.666667 | 0 | 0 |
| 49 | 906.666667 | 0 | 0 |
| 50 | 906.666667 | 0 | 0 |
| 51 | 906.666667 | 0 | 0 |
| 52 | 906.666667 | 0 | 0 |
| 53 | 906.666667 | 0 | 0 |
| 54 | 906.666667 | 0 | 0 |
| 55 | 906.666667 | 0 | 0 |
| 56 | 906.666667 | 0 | 0 |
| 57 | 906.666667 | 0 | 0 |
| 58 | 906.666667 | 0 | 0 |
| 59 | 906.666667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 906.666667 | 0 | 0 |
| 4 | 906.666667 | 0 | 0 |
| 5 | 906.666667 | 0 | 0 |
| 6 | 906.666667 | 0 | 0 |
| 7 | 432.5 | 0 | 0 |
| 8 | 432.5 | 0 | 0 |
| 9 | 432.5 | 0 | 0 |
| 10 | 432.5 | 0 | 0 |
| 11 | 432.5 | 0 | 0 |
| 12 | 432.5 | 0 | 0 |
| 13 | 432.5 | 0 | 0 |
| 14 | 432.5 | 0 | 0 |
| 15 | 432.5 | 0 | 0 |
| 16 | 432.5 | 0 | 0 |
| 17 | 432.5 | 0 | 0 |
| 18 | 432.5 | 0 | 0 |
| 19 | 432.5 | 0 | 0 |
| 20 | 432.5 | 0 | 0 |
| 21 | 432.5 | 0 | 0 |
| 22 | 432.5 | 0 | 0 |
| 23 | 432.5 | 0 | 0 |
| 24 | 432.5 | 0 | 0 |
| 25 | 432.5 | 0 | 0 |
| 26 | 432.5 | 0 | 0 |
| 27 | 432.5 | 0 | 0 |
| 28 | 432.5 | 0 | 0 |
| 29 | 432.5 | 0 | 0 |
| 30 | 432.5 | 0 | 0 |
| 31 | 432.5 | 0 | 0 |
| 32 | 432.5 | 0 | 0 |
| 33 | 432.5 | 0 | 0 |
| 34 | 432.5 | 0 | 0 |
| 35 | 432.5 | 0 | 0 |
| 36 | 432.5 | 0 | 0 |
| 37 | 432.5 | 0 | 0 |
| 38 | 432.5 | 0 | 0 |
| 39 | 432.5 | 0 | 0 |
| 40 | 432.5 | 0 | 0 |
| 41 | 432.5 | 0 | 0 |
| 42 | 432.5 | 0 | 0 |
| 43 | 432.5 | 0 | 0 |
| 44 | 432.5 | 0 | 0 |
| 45 | 432.5 | 0 | 0 |
| 46 | 432.5 | 0 | 0 |
| 47 | 432.5 | 0 | 0 |
| 48 | 432.5 | 0 | 0 |
| 49 | 432.5 | 0 | 0 |
| 50 | 432.5 | 0 | 0 |
| 51 | 432.5 | 0 | 0 |
| 52 | 432.5 | 0 | 0 |
| 53 | 432.5 | 0 | 0 |
| 54 | 432.5 | 0 | 0 |
| 55 | 432.5 | 0 | 0 |
| 56 | 432.5 | 0 | 0 |
| 57 | 432.5 | 0 | 0 |
| 58 | 432.5 | 0 | 0 |
| 59 | 432.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 432.5 | 0 | 0 |
| 4 | 432.5 | 0 | 0 |
| 5 | 432.5 | 0 | 0 |
| 6 | 432.5 | 0 | 0 |
| 7 | 432.5 | 0 | 0 |
| 8 | 432.5 | 0 | 0 |
| 9 | 432.5 | 0 | 0 |
| 10 | 432.5 | 0 | 0 |
| 11 | 432.5 | 0 | 0 |
| 12 | 432.5 | 0 | 0 |
| 13 | 432.5 | 0 | 0 |
| 14 | 432.5 | 0 | 0 |
| 15 | 432.5 | 0 | 0 |
| 16 | 432.5 | 0 | 0 |
| 17 | 432.5 | 0 | 0 |
| 18 | 432.5 | 0 | 0 |
| 19 | 432.5 | 0 | 0 |
| 20 | 432.5 | 0 | 0 |
| 21 | 432.5 | 0 | 0 |
| 22 | 432.5 | 0 | 0 |
| 23 | 432.5 | 0 | 0 |
| 24 | 432.5 | 0 | 0 |
| 25 | 432.5 | 0 | 0 |
| 26 | 432.5 | 0 | 0 |
| 27 | 432.5 | 0 | 0 |
| 28 | 432.5 | 0 | 0 |
| 29 | 432.5 | 0 | 0 |
| 30 | 432.5 | 0 | 0 |
| 31 | 432.5 | 0 | 0 |
| 32 | 432.5 | 0 | 0 |
| 33 | 432.5 | 0 | 0 |
| 34 | 432.5 | 0 | 0 |
| 35 | 432.5 | 0 | 0 |
| 36 | 432.5 | 0 | 0 |
| 37 | 432.5 | 0 | 0 |
| 38 | 432.5 | 0 | 0 |
| 39 | 432.5 | 0 | 0 |
| 40 | 702 | 0 | 0 |
| 41 | 702 | 0 | 0 |
| 42 | 702 | 0 | 0 |
| 43 | 1244.5 | 0 | 0 |
| 44 | 318.5 | 0 | 0 |
| 45 | 318.5 | 0 | 0 |
| 46 | 318.5 | 0 | 0 |
| 47 | 432.666667 | 0 | 0 |
| 48 | 432.666667 | 0 | 0 |
| 49 | 308.666667 | 0 | 0 |
| 50 | 308.666667 | 0 | 0 |
| 51 | 308.666667 | 0 | 0 |
| 52 | 308.666667 | 0 | 0 |
| 53 | 308.666667 | 0 | 0 |
| 54 | 308.666667 | 0 | 0 |
| 55 | 66.5 | 0 | 0 |
| 56 | 10796.8333 | 0 | 0 |
| 57 | 10796.8333 | 0 | 0 |
| 58 | 10796.8333 | 0 | 0 |
| 59 | 10796.8333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 10796.8333 | 0 | 0 |
| 4 | 10796.8333 | 0 | 0 |
| 5 | 10796.8333 | 0 | 0 |
| 6 | 10796.8333 | 0 | 0 |
| 7 | 10796.8333 | 0 | 0 |
| 8 | 10796.8333 | 0 | 0 |
| 9 | 10796.8333 | 0 | 0 |
| 10 | 10796.8333 | 0 | 0 |
| 11 | 10796.8333 | 0 | 0 |
| 12 | 10796.8333 | 0 | 0 |
| 13 | 10796.8333 | 0 | 0 |
| 14 | 10796.8333 | 0 | 0 |
| 15 | 10796.8333 | 0 | 0 |
| 16 | 10796.8333 | 0 | 0 |
| 17 | 10796.8333 | 0 | 0 |
| 18 | 10796.8333 | 0 | 0 |
| 19 | 10796.8333 | 0 | 0 |
| 20 | 10796.8333 | 0 | 0 |
| 21 | 10796.8333 | 0 | 0 |
| 22 | 10796.8333 | 0 | 0 |
| 23 | 10796.8333 | 0 | 0 |
| 24 | 10796.8333 | 0 | 0 |
| 25 | 10796.8333 | 0 | 0 |
| 26 | 10796.8333 | 0 | 0 |
| 27 | 10796.8333 | 0 | 0 |
| 28 | 10796.8333 | 0 | 0 |
| 29 | 10796.8333 | 0 | 0 |
| 30 | 10796.8333 | 0 | 0 |
| 31 | 10796.8333 | 0 | 0 |
| 32 | 10796.8333 | 0 | 0 |
| 33 | 10796.8333 | 0 | 0 |
| 34 | 10796.8333 | 0 | 0 |
| 35 | 10796.8333 | 0 | 0 |
| 36 | 10796.8333 | 0 | 0 |
| 37 | 10796.8333 | 0 | 0 |
| 38 | 10796.8333 | 0 | 0 |
| 39 | 10796.8333 | 0 | 0 |
| 40 | 10796.8333 | 0 | 0 |
| 41 | 10796.8333 | 0 | 0 |
| 42 | 10796.8333 | 0 | 0 |
| 43 | 10796.8333 | 0 | 0 |
| 44 | 10796.8333 | 0 | 0 |
| 45 | 10796.8333 | 0 | 0 |
| 46 | 10796.8333 | 0 | 0 |
| 47 | 10796.8333 | 0 | 0 |
| 48 | 10796.8333 | 0 | 0 |
| 49 | 10796.8333 | 0 | 0 |
| 50 | 10796.8333 | 0 | 0 |
| 51 | 10796.8333 | 0 | 0 |
| 52 | 10796.8333 | 0 | 0 |
| 53 | 10796.8333 | 0 | 0 |
| 54 | 10796.8333 | 0 | 0 |
| 55 | 10796.8333 | 0 | 0 |
| 56 | 10796.8333 | 0 | 0 |
| 57 | 10796.8333 | 0 | 0 |
| 58 | 10796.8333 | 0 | 0 |
| 59 | 10796.8333 | 0 | 0 |
| 60 | | | |

1
2
3 10796.8333 0 0
4 10796.8333 0 0
5 10796.8333 0 0
6 10796.8333 0 0
7 10796.8333 0 0
8 10796.8333 0 0
9 10796.8333 0 0
10 10796.8333 0 0
11 10796.8333 0 0
12 10796.8333 0 0
13 10796.8333 0 0
14 10796.8333 0 0
15 10796.8333 0 0
16 10796.8333 0 0
17 10796.8333 0 0
18 10796.8333 0 0
19 10796.8333 0 0
20 10796.8333 0 0
21 10796.8333 0 0
22 10796.8333 0 0
23 10796.8333 0 0
24 10796.8333 0 0
25 10796.8333 0 0
26 10796.8333 0 0
27 10796.8333 0 0
28 10796.8333 0 0
29 10796.8333 0 0
30 10796.8333 0 0
31 10796.8333 0 0
32 10796.8333 0 0
33 10796.8333 0 0
34 10796.8333 0 0
35 10796.8333 0 0
36 10796.8333 0 0
37 10796.8333 0 0
38 10796.8333 0 0
39 10796.8333 0 0
40 10796.8333 0 0
41 10796.8333 0 0
42 10796.8333 0 0
43 10796.8333 0 0
44 10796.8333 0 0
45 10796.8333 0 0
46 10796.8333 0 0
47 10796.8333 0 0
48 10796.8333 0 0
49 10796.8333 0 0
50 10796.8333 0 0
51 10796.8333 0 0
52 10796.8333 0 0
53 10796.8333 0 0
54 10796.8333 0 0
55 10796.8333 0 0
56 10796.8333 0 0
57 10796.8333 0 0
58 10796.8333 0 0
59 10796.8333 0 0
60

Do not distribute

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 10796.8333 | 0 | 0 |
| 4 | 10796.8333 | 0 | 0 |
| 5 | 10796.8333 | 0 | 0 |
| 6 | 10796.8333 | 0 | 0 |
| 7 | 1180 | 0 | 0 |
| 8 | 301417.167 | 0 | 0 |
| 9 | 301417.167 | 0 | 0 |
| 10 | 301417.167 | 0 | 0 |
| 11 | 301417.167 | 0 | 0 |
| 12 | 301417.167 | 0 | 0 |
| 13 | 301417.167 | 0 | 0 |
| 14 | 106707.167 | 0 | 0 |
| 15 | 106707.167 | 0 | 0 |
| 16 | 106707.167 | 0 | 0 |
| 17 | 106707.167 | 0 | 0 |
| 18 | 106707.167 | 0 | 0 |
| 19 | 106707.167 | 0 | 0 |
| 20 | 106707.167 | 0 | 0 |
| 21 | 106707.167 | 0 | 0 |
| 22 | 106707.167 | 0 | 0 |
| 23 | 106707.167 | 0 | 0 |
| 24 | 106707.167 | 0 | 0 |
| 25 | 106707.167 | 0 | 0 |
| 26 | 106707.167 | 0 | 0 |
| 27 | 106707.167 | 0 | 0 |
| 28 | 106707.167 | 0 | 0 |
| 29 | 106707.167 | 0 | 0 |
| 30 | 106707.167 | 0 | 0 |
| 31 | 106707.167 | 0 | 0 |
| 32 | 106707.167 | 0 | 0 |
| 33 | 106707.167 | 0 | 0 |
| 34 | 106707.167 | 0 | 0 |
| 35 | 106707.167 | 0 | 0 |
| 36 | 106707.167 | 0 | 0 |
| 37 | 106707.167 | 0 | 0 |
| 38 | 106707.167 | 0 | 0 |
| 39 | 106707.167 | 0 | 0 |
| 40 | 106707.167 | 0 | 0 |
| 41 | 106707.167 | 0 | 0 |
| 42 | 106707.167 | 0 | 0 |
| 43 | 106707.167 | 0 | 0 |
| 44 | 106707.167 | 0 | 0 |
| 45 | 106707.167 | 0 | 0 |
| 46 | 106707.167 | 0 | 0 |
| 47 | 106707.167 | 0 | 0 |
| 48 | 106707.167 | 0 | 0 |
| 49 | 106707.167 | 0 | 0 |
| 50 | 106707.167 | 0 | 0 |
| 51 | 106707.167 | 0 | 0 |
| 52 | 106707.167 | 0 | 0 |
| 53 | 106707.167 | 0 | 0 |
| 54 | 282.666667 | 0 | 0 |
| 55 | 283 | 0 | 0 |
| 56 | 193 | 0 | 0 |
| 57 | 193 | 0 | 0 |
| 58 | 193 | 0 | 0 |
| 59 | 193 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 193 | 0 | 0 |
| 4 | 193 | 0 | 0 |
| 5 | 282.333333 | 0 | 0 |
| 6 | 282.333333 | 0 | 0 |
| 7 | 282.333333 | 0 | 0 |
| 8 | 282.333333 | 0 | 0 |
| 9 | 282.333333 | 0 | 0 |
| 10 | 282.333333 | 0 | 0 |
| 11 | 282.333333 | 0 | 0 |
| 12 | 282.333333 | 0 | 0 |
| 13 | 282.333333 | 0 | 0 |
| 14 | 282.333333 | 0 | 0 |
| 15 | 282.333333 | 0 | 0 |
| 16 | 282.333333 | 0 | 0 |
| 17 | 282.333333 | 0 | 0 |
| 18 | 282.333333 | 0 | 0 |
| 19 | 282.333333 | 0 | 0 |
| 20 | 282.333333 | 0 | 0 |
| 21 | 282.333333 | 0 | 0 |
| 22 | 282.333333 | 0 | 0 |
| 23 | 282.333333 | 0 | 0 |
| 24 | 282.333333 | 0 | 0 |
| 25 | 282.333333 | 0 | 0 |
| 26 | 282.333333 | 0 | 0 |
| 27 | 282.333333 | 0 | 0 |
| 28 | 282.333333 | 0 | 0 |
| 29 | 282.333333 | 0 | 0 |
| 30 | 282.333333 | 0 | 0 |
| 31 | 282.333333 | 0 | 0 |
| 32 | 282.333333 | 0 | 0 |
| 33 | 282.333333 | 0 | 0 |
| 34 | 282.333333 | 0 | 0 |
| 35 | 282.333333 | 0 | 0 |
| 36 | 282.333333 | 0 | 0 |
| 37 | 282.333333 | 0 | 0 |
| 38 | 282.333333 | 0 | 0 |
| 39 | 282.333333 | 0 | 0 |
| 40 | 282.333333 | 0 | 0 |
| 41 | 282.333333 | 0 | 0 |
| 42 | 282.333333 | 0 | 0 |
| 43 | 282.333333 | 0 | 0 |
| 44 | 282.333333 | 0 | 0 |
| 45 | 282.333333 | 0 | 0 |
| 46 | 282.333333 | 0 | 0 |
| 47 | 282.333333 | 0 | 0 |
| 48 | 282.333333 | 0 | 0 |
| 49 | 282.333333 | 0 | 0 |
| 50 | 282.333333 | 0 | 0 |
| 51 | 282.333333 | 0 | 0 |
| 52 | 282.333333 | 0 | 0 |
| 53 | 282.333333 | 0 | 0 |
| 54 | 282.333333 | 0 | 0 |
| 55 | 282.333333 | 0 | 0 |
| 56 | 282.333333 | 0 | 0 |
| 57 | 282.333333 | 0 | 0 |
| 58 | 282.333333 | 0 | 0 |
| 59 | 282.333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 282.333333 | 0 | 0 |
| 4 | 282.333333 | 0 | 0 |
| 5 | 282.333333 | 0 | 0 |
| 6 | 282.333333 | 0 | 0 |
| 7 | 282.333333 | 0 | 0 |
| 8 | 282.333333 | 0 | 0 |
| 9 | 282.333333 | 0 | 0 |
| 10 | 282.333333 | 0 | 0 |
| 11 | 282.333333 | 0 | 0 |
| 12 | 282.333333 | 0 | 0 |
| 13 | 282.333333 | 0 | 0 |
| 14 | 282.333333 | 0 | 0 |
| 15 | 282.333333 | 0 | 0 |
| 16 | 282.333333 | 0 | 0 |
| 17 | 282.333333 | 0 | 0 |
| 18 | 282.333333 | 0 | 0 |
| 19 | 282.333333 | 0 | 0 |
| 20 | 282.333333 | 0 | 0 |
| 21 | 282.333333 | 0 | 0 |
| 22 | 282.333333 | 0 | 0 |
| 23 | 282.333333 | 0 | 0 |
| 24 | 114984.5 | 0 | 0 |
| 25 | 114984.5 | 0 | 0 |
| 26 | 114984.5 | 0 | 0 |
| 27 | 114984.5 | 0 | 0 |
| 28 | 114984.5 | 0 | 0 |
| 29 | 114984.5 | 0 | 0 |
| 30 | 114984.5 | 0 | 0 |
| 31 | 114984.5 | 0 | 0 |
| 32 | 114984.5 | 0 | 0 |
| 33 | 114984.5 | 0 | 0 |
| 34 | 114984.5 | 0 | 0 |
| 35 | 114984.5 | 0 | 0 |
| 36 | 114984.5 | 0 | 0 |
| 37 | 114984.5 | 0 | 0 |
| 38 | 114984.5 | 0 | 0 |
| 39 | 114984.5 | 0 | 0 |
| 40 | 110.166667 | 0 | 0 |
| 41 | 110.166667 | 0 | 0 |
| 42 | 110.166667 | 0 | 0 |
| 43 | 6792.66667 | 0 | 0 |
| 44 | 6792.66667 | 0 | 0 |
| 45 | 6792.66667 | 0 | 0 |
| 46 | 6792.66667 | 0 | 0 |
| 47 | 6792.66667 | 0 | 0 |
| 48 | 6792.66667 | 0 | 0 |
| 49 | 6792.66667 | 0 | 0 |
| 50 | 6792.66667 | 0 | 0 |
| 51 | 6792.66667 | 0 | 0 |
| 52 | 6792.66667 | 0 | 0 |
| 53 | 6792.66667 | 0 | 0 |
| 54 | 6792.66667 | 0 | 0 |
| 55 | 6792.66667 | 0 | 0 |
| 56 | 6792.66667 | 0 | 0 |
| 57 | 6792.66667 | 0 | 0 |
| 58 | 6792.66667 | 0 | 0 |
| 59 | 6792.66667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 6792.66667 | 0 | 0 |
| 4 | 6792.66667 | 0 | 0 |
| 5 | 6792.66667 | 0 | 0 |
| 6 | 6792.66667 | 0 | 0 |
| 7 | 6792.66667 | 0 | 0 |
| 8 | 6792.66667 | 0 | 0 |
| 9 | 6792.66667 | 0 | 0 |
| 10 | 6792.66667 | 0 | 0 |
| 11 | 6792.66667 | 0 | 0 |
| 12 | 6792.66667 | 0 | 0 |
| 13 | 6792.66667 | 0 | 0 |
| 14 | 6792.66667 | 0 | 0 |
| 15 | 6792.66667 | 0 | 0 |
| 16 | 6792.66667 | 0 | 0 |
| 17 | 6792.66667 | 0 | 0 |
| 18 | 6792.66667 | 0 | 0 |
| 19 | 6792.66667 | 0 | 0 |
| 20 | 6792.66667 | 0 | 0 |
| 21 | 6792.66667 | 0 | 0 |
| 22 | 6792.66667 | 0 | 0 |
| 23 | 6792.66667 | 0 | 0 |
| 24 | 6792.66667 | 0 | 0 |
| 25 | 6792.66667 | 0 | 0 |
| 26 | 6792.66667 | 0 | 0 |
| 27 | 6792.66667 | 0 | 0 |
| 28 | 6792.66667 | 0 | 0 |
| 29 | 6792.66667 | 0 | 0 |
| 30 | 6792.66667 | 0 | 0 |
| 31 | 6792.66667 | 0 | 0 |
| 32 | 6792.66667 | 0 | 0 |
| 33 | 6792.66667 | 0 | 0 |
| 34 | 6792.66667 | 0 | 0 |
| 35 | 6792.66667 | 0 | 0 |
| 36 | 6792.66667 | 0 | 0 |
| 37 | 6792.66667 | 0 | 0 |
| 38 | 6792.66667 | 0 | 0 |
| 39 | 6792.66667 | 0 | 0 |
| 40 | 6792.66667 | 0 | 0 |
| 41 | 6792.66667 | 0 | 0 |
| 42 | 6792.66667 | 0 | 0 |
| 43 | 6792.66667 | 0 | 0 |
| 44 | 6792.66667 | 0 | 0 |
| 45 | 6792.66667 | 0 | 0 |
| 46 | 6792.66667 | 0 | 0 |
| 47 | 6792.66667 | 0 | 0 |
| 48 | 6792.66667 | 0 | 0 |
| 49 | 6792.66667 | 0 | 0 |
| 50 | 6792.66667 | 0 | 0 |
| 51 | 6792.66667 | 0 | 0 |
| 52 | 6792.66667 | 0 | 0 |
| 53 | 6792.66667 | 0 | 0 |
| 54 | 6792.66667 | 0 | 0 |
| 55 | 6792.66667 | 0 | 0 |
| 56 | 6792.66667 | 0 | 0 |
| 57 | 6792.66667 | 0 | 0 |
| 58 | 6792.66667 | 0 | 0 |
| 59 | 6792.66667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 6792.66667 | 0 | 0 |
| 4 | 6792.66667 | 0 | 0 |
| 5 | 6792.66667 | 0 | 0 |
| 6 | 6792.66667 | 0 | 0 |
| 7 | 6792.66667 | 0 | 0 |
| 8 | 6792.66667 | 0 | 0 |
| 9 | 6792.66667 | 0 | 0 |
| 10 | 6792.66667 | 0 | 0 |
| 11 | 6792.66667 | 0 | 0 |
| 12 | 6792.66667 | 0 | 0 |
| 13 | 6792.66667 | 0 | 0 |
| 14 | 6792.66667 | 0 | 0 |
| 15 | 6792.66667 | 0 | 0 |
| 16 | 6792.66667 | 0 | 0 |
| 17 | 6792.66667 | 0 | 0 |
| 18 | 6792.66667 | 0 | 0 |
| 19 | 6792.66667 | 0 | 0 |
| 20 | 2375.5 | 0 | 0 |
| 21 | 4552.83333 | 0 | 0 |
| 22 | 4552.83333 | 0 | 0 |
| 23 | 4552.83333 | 0 | 0 |
| 24 | 4552.83333 | 0 | 0 |
| 25 | 4552.83333 | 0 | 0 |
| 26 | 4552.83333 | 0 | 0 |
| 27 | 4552.83333 | 0 | 0 |
| 28 | 4552.83333 | 0 | 0 |
| 29 | 4552.83333 | 0 | 0 |
| 30 | 4552.83333 | 0 | 0 |
| 31 | 4552.83333 | 0 | 0 |
| 32 | 4552.83333 | 0 | 0 |
| 33 | 4552.83333 | 0 | 0 |
| 34 | 4552.83333 | 0 | 0 |
| 35 | 4552.83333 | 0 | 0 |
| 36 | 4552.83333 | 0 | 0 |
| 37 | 4552.83333 | 0 | 0 |
| 38 | 4552.83333 | 0 | 0 |
| 39 | 4552.83333 | 0 | 0 |
| 40 | 4552.83333 | 0 | 0 |
| 41 | 4552.83333 | 0 | 0 |
| 42 | 4552.83333 | 0 | 0 |
| 43 | 4552.83333 | 0 | 0 |
| 44 | 4552.83333 | 0 | 0 |
| 45 | 4552.83333 | 0 | 0 |
| 46 | 4552.83333 | 0 | 0 |
| 47 | 4552.83333 | 0 | 0 |
| 48 | 4552.83333 | 0 | 0 |
| 49 | 4552.83333 | 0 | 0 |
| 50 | 4552.83333 | 0 | 0 |
| 51 | 4552.83333 | 0 | 0 |
| 52 | 4552.83333 | 0 | 0 |
| 53 | 4552.83333 | 0 | 0 |
| 54 | 4552.83333 | 0 | 0 |
| 55 | 4552.83333 | 0 | 0 |
| 56 | 4552.83333 | 0 | 0 |
| 57 | 4552.83333 | 0 | 0 |
| 58 | 4552.83333 | 0 | 0 |
| 59 | 4552.83333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 4552.83333 | 0 | 0 |
| 4 | 4552.83333 | 0 | 0 |
| 5 | 4552.83333 | 0 | 0 |
| 6 | 4552.83333 | 0 | 0 |
| 7 | 4552.83333 | 0 | 0 |
| 8 | 4552.83333 | 0 | 0 |
| 9 | 4552.83333 | 0 | 0 |
| 10 | 4552.83333 | 0 | 0 |
| 11 | 4552.83333 | 0 | 0 |
| 12 | 4552.83333 | 0 | 0 |
| 13 | 4552.83333 | 0 | 0 |
| 14 | 4552.83333 | 0 | 0 |
| 15 | 4552.83333 | 0 | 0 |
| 16 | 4552.83333 | 0 | 0 |
| 17 | 4552.83333 | 0 | 0 |
| 18 | 4552.83333 | 0 | 0 |
| 19 | 4552.83333 | 0 | 0 |
| 20 | 4552.83333 | 0 | 0 |
| 21 | 4552.83333 | 0 | 0 |
| 22 | 4552.83333 | 0 | 0 |
| 23 | 4552.83333 | 0 | 0 |
| 24 | 4552.83333 | 0 | 0 |
| 25 | 4552.83333 | 0 | 0 |
| 26 | 4552.83333 | 0 | 0 |
| 27 | 4552.83333 | 0 | 0 |
| 28 | 4552.83333 | 0 | 0 |
| 29 | 4552.83333 | 0 | 0 |
| 30 | 4552.83333 | 0 | 0 |
| 31 | 4552.83333 | 0 | 0 |
| 32 | 4552.83333 | 0 | 0 |
| 33 | 4552.83333 | 0 | 0 |
| 34 | 4552.83333 | 0 | 0 |
| 35 | 4552.83333 | 0 | 0 |
| 36 | 4552.83333 | 0 | 0 |
| 37 | 4552.83333 | 0 | 0 |
| 38 | 4552.83333 | 0 | 0 |
| 39 | 4552.83333 | 0 | 0 |
| 40 | 4552.83333 | 0 | 0 |
| 41 | 4552.83333 | 0 | 0 |
| 42 | 4552.83333 | 0 | 0 |
| 43 | 4552.83333 | 0 | 0 |
| 44 | 4552.83333 | 0 | 0 |
| 45 | 4552.83333 | 0 | 0 |
| 46 | 4552.83333 | 0 | 0 |
| 47 | 4552.83333 | 0 | 0 |
| 48 | 4552.83333 | 0 | 0 |
| 49 | 4552.83333 | 0 | 0 |
| 50 | 4552.83333 | 0 | 0 |
| 51 | 4552.83333 | 0 | 0 |
| 52 | 4552.83333 | 0 | 0 |
| 53 | 4552.83333 | 0 | 0 |
| 54 | 4552.83333 | 0 | 0 |
| 55 | 4552.83333 | 0 | 0 |
| 56 | 4552.83333 | 0 | 0 |
| 57 | 4552.83333 | 0 | 0 |
| 58 | 4552.83333 | 0 | 0 |
| 59 | 4552.83333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 4552.83333 | 0 | 0 |
| 4 | 4552.83333 | 0 | 0 |
| 5 | 4552.83333 | 0 | 0 |
| 6 | 4552.83333 | 0 | 0 |
| 7 | 4552.83333 | 0 | 0 |
| 8 | 4552.83333 | 0 | 0 |
| 9 | 4552.83333 | 0 | 0 |
| 10 | 4552.83333 | 0 | 0 |
| 11 | 4552.83333 | 0 | 0 |
| 12 | 4552.83333 | 0 | 0 |
| 13 | 4552.83333 | 0 | 0 |
| 14 | 4552.83333 | 0 | 0 |
| 15 | 4552.83333 | 0 | 0 |
| 16 | 4552.83333 | 0 | 0 |
| 17 | 4552.83333 | 0 | 0 |
| 18 | 4552.83333 | 0 | 0 |
| 19 | 4552.83333 | 0 | 0 |
| 20 | 4552.83333 | 0 | 0 |
| 21 | 4552.83333 | 0 | 0 |
| 22 | 4561.83333 | 0 | 0 |
| 23 | 2365.33333 | 0 | 0 |
| 24 | 2365.33333 | 0 | 0 |
| 25 | 2365.33333 | 0 | 0 |
| 26 | 2365.33333 | 0 | 0 |
| 27 | 2365.33333 | 0 | 0 |
| 28 | 2365.33333 | 0 | 0 |
| 29 | 2365.33333 | 0 | 0 |
| 30 | 2365.33333 | 0 | 0 |
| 31 | 2365.33333 | 0 | 0 |
| 32 | 337.666667 | 0 | 0 |
| 33 | 337.666667 | 0 | 0 |
| 34 | 337.666667 | 0 | 0 |
| 35 | 337.666667 | 0 | 0 |
| 36 | 337.666667 | 0 | 0 |
| 37 | 337.666667 | 0 | 0 |
| 38 | 337.666667 | 0 | 0 |
| 39 | 337.666667 | 0 | 0 |
| 40 | 1412.83333 | 0 | 0 |
| 41 | 10238.3333 | 0 | 0 |
| 42 | 10238.3333 | 0 | 0 |
| 43 | 10238.3333 | 0 | 0 |
| 44 | 10238.3333 | 0 | 0 |
| 45 | 10238.3333 | 0 | 0 |
| 46 | 10238.3333 | 0 | 0 |
| 47 | 10238.3333 | 0 | 0 |
| 48 | 10238.3333 | 0 | 0 |
| 49 | 10238.3333 | 0 | 0 |
| 50 | 10238.3333 | 0 | 0 |
| 51 | 10238.3333 | 0 | 0 |
| 52 | 10238.3333 | 0 | 0 |
| 53 | 10238.3333 | 0 | 0 |
| 54 | 10238.3333 | 0 | 0 |
| 55 | 10238.3333 | 0 | 0 |
| 56 | 10238.3333 | 0 | 0 |
| 57 | 10238.3333 | 0 | 0 |
| 58 | 10238.3333 | 0 | 0 |
| 59 | 10238.3333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 10238.3333 | 0 | 0 |
| 4 | 10238.3333 | 0 | 0 |
| 5 | 10238.3333 | 0 | 0 |
| 6 | 10238.3333 | 0 | 0 |
| 7 | 10238.3333 | 0 | 0 |
| 8 | 10238.3333 | 0 | 0 |
| 9 | 10238.3333 | 0 | 0 |
| 10 | 10238.3333 | 0 | 0 |
| 11 | 10238.3333 | 0 | 0 |
| 12 | 10238.3333 | 0 | 0 |
| 13 | 10238.3333 | 0 | 0 |
| 14 | 10238.3333 | 0 | 0 |
| 15 | 217 | 0 | 0 |
| 16 | 217 | 0 | 0 |
| 17 | 217 | 0 | 0 |
| 18 | 217 | 0 | 0 |
| 19 | 217 | 0 | 0 |
| 20 | 217 | 0 | 0 |
| 21 | 217 | 0 | 0 |
| 22 | 217 | 0 | 0 |
| 23 | 217 | 0 | 0 |
| 24 | 217 | 0 | 0 |
| 25 | 217 | 0 | 0 |
| 26 | 217 | 0 | 0 |
| 27 | 217 | 0 | 0 |
| 28 | 217 | 0 | 0 |
| 29 | 217 | 0 | 0 |
| 30 | 217 | 0 | 0 |
| 31 | 217 | 0 | 0 |
| 32 | 217 | 0 | 0 |
| 33 | 217 | 0 | 0 |
| 34 | 217 | 0 | 0 |
| 35 | 217 | 0 | 0 |
| 36 | 217 | 0 | 0 |
| 37 | 217 | 0 | 0 |
| 38 | 217 | 0 | 0 |
| 39 | 217 | 0 | 0 |
| 40 | 217 | 0 | 0 |
| 41 | 217 | 0 | 0 |
| 42 | 217 | 0 | 0 |
| 43 | 217 | 0 | 0 |
| 44 | 217 | 0 | 0 |
| 45 | 217 | 0 | 0 |
| 46 | 217 | 0 | 0 |
| 47 | 217 | 0 | 0 |
| 48 | 217 | 0 | 0 |
| 49 | 217 | 0 | 0 |
| 50 | 217 | 0 | 0 |
| 51 | 217 | 0 | 0 |
| 52 | 217 | 0 | 0 |
| 53 | 217 | 0 | 0 |
| 54 | 217 | 0 | 0 |
| 55 | 45093.3333 | 0 | 0 |
| 56 | 1740.33333 | 0 | 0 |
| 57 | 1740.33333 | 0 | 0 |
| 58 | 1740.33333 | 0 | 0 |
| 59 | 1740.33333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 3246.16667 | 0 | 0 |
| 4 | 130 | 0 | 0 |
| 5 | 1186.83333 | 0 | 0 |
| 6 | 1186.83333 | 0 | 0 |
| 7 | 1186.83333 | 0 | 0 |
| 8 | 1186.83333 | 0 | 0 |
| 9 | 1186.83333 | 0 | 0 |
| 10 | 1186.83333 | 0 | 0 |
| 11 | 305.33333 | 0 | 0 |
| 12 | 305.33333 | 0 | 0 |
| 13 | 305.33333 | 0 | 0 |
| 14 | 305.33333 | 0 | 0 |
| 15 | 305.33333 | 0 | 0 |
| 16 | 305.33333 | 0 | 0 |
| 17 | 305.33333 | 0 | 0 |
| 18 | 305.33333 | 0 | 0 |
| 19 | 305.33333 | 0 | 0 |
| 20 | 104.83333 | 0 | 0 |
| 21 | 104.83333 | 0 | 0 |
| 22 | 104.83333 | 0 | 0 |
| 23 | 104.83333 | 0 | 0 |
| 24 | 104.83333 | 0 | 0 |
| 25 | 104.83333 | 0 | 0 |
| 26 | 104.83333 | 0 | 0 |
| 27 | 307 | 0 | 0 |
| 28 | 304.66667 | 0 | 0 |
| 29 | 304.66667 | 0 | 0 |
| 30 | 304.66667 | 0 | 0 |
| 31 | 304.66667 | 0 | 0 |
| 32 | 304.66667 | 0 | 0 |
| 33 | 304.66667 | 0 | 0 |
| 34 | 304.66667 | 0 | 0 |
| 35 | 304.66667 | 0 | 0 |
| 36 | 304.66667 | 0 | 0 |
| 37 | 304.66667 | 0 | 0 |
| 38 | 304.66667 | 0 | 0 |
| 39 | 304.66667 | 0 | 0 |
| 40 | 304.66667 | 0 | 0 |
| 41 | 304.66667 | 0 | 0 |
| 42 | 304.66667 | 0 | 0 |
| 43 | 304.66667 | 0 | 0 |
| 44 | 304.66667 | 0 | 0 |
| 45 | 304.66667 | 0 | 0 |
| 46 | 304.66667 | 0 | 0 |
| 47 | 304.66667 | 0 | 0 |
| 48 | 304.66667 | 0 | 0 |
| 49 | 304.66667 | 0 | 0 |
| 50 | 304.66667 | 0 | 0 |
| 51 | 304.66667 | 0 | 0 |
| 52 | 304.66667 | 0 | 0 |
| 53 | 304.66667 | 0 | 0 |
| 54 | 304.66667 | 0 | 0 |
| 55 | 304.66667 | 0 | 0 |
| 56 | 304.66667 | 0 | 0 |
| 57 | 304.66667 | 0 | 0 |
| 58 | 304.66667 | 0 | 0 |
| 59 | 304.66667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 304.666667 | 0 | 0 |
| 4 | 304.666667 | 0 | 0 |
| 5 | 304.666667 | 0 | 0 |
| 6 | 304.666667 | 0 | 0 |
| 7 | 52938.6667 | 0 | 0 |
| 8 | 52938.6667 | 0 | 0 |
| 9 | 340.166667 | 0 | 0 |
| 10 | 340.166667 | 0 | 0 |
| 11 | 340.166667 | 0 | 0 |
| 12 | 340.166667 | 0 | 0 |
| 13 | 340.166667 | 0 | 0 |
| 14 | 340.166667 | 0 | 0 |
| 15 | 340.166667 | 0 | 0 |
| 16 | 340.166667 | 0 | 0 |
| 17 | 340.166667 | 0 | 0 |
| 18 | 340.166667 | 0 | 0 |
| 19 | 340.166667 | 0 | 0 |
| 20 | 74 | 0 | 0 |
| 21 | 74 | 0 | 0 |
| 22 | 74 | 0 | 0 |
| 23 | 74 | 0 | 0 |
| 24 | 74 | 0 | 0 |
| 25 | 74 | 0 | 0 |
| 26 | 74 | 0 | 0 |
| 27 | 74 | 0 | 0 |
| 28 | 74 | 0 | 0 |
| 29 | 74 | 0 | 0 |
| 30 | 74 | 0 | 0 |
| 31 | 74 | 0 | 0 |
| 32 | 74 | 0 | 0 |
| 33 | 74 | 0 | 0 |
| 34 | 74 | 0 | 0 |
| 35 | 74 | 0 | 0 |
| 36 | 74 | 0 | 0 |
| 37 | 74 | 0 | 0 |
| 38 | 74 | 0 | 0 |
| 39 | 74 | 0 | 0 |
| 40 | 85.3333333 | 0 | 0 |
| 41 | 85.3333333 | 0 | 0 |
| 42 | 85.3333333 | 0 | 0 |
| 43 | 85.3333333 | 0 | 0 |
| 44 | 85.3333333 | 0 | 0 |
| 45 | 85.3333333 | 0 | 0 |
| 46 | 85.3333333 | 0 | 0 |
| 47 | 85.3333333 | 0 | 0 |
| 48 | 85.3333333 | 0 | 0 |
| 49 | 85.3333333 | 0 | 0 |
| 50 | 85.3333333 | 0 | 0 |
| 51 | 84.5 | 0 | 0 |
| 52 | 84.5 | 0 | 0 |
| 53 | 84.5 | 0 | 0 |
| 54 | 84.5 | 0 | 0 |
| 55 | 84.5 | 0 | 0 |
| 56 | 84.5 | 0 | 0 |
| 57 | 84.5 | 0 | 0 |
| 58 | 84.5 | 0 | 0 |
| 59 | 84.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 84.5 | 0 | 0 |
| 4 | 84.5 | 0 | 0 |
| 5 | 84.5 | 0 | 0 |
| 6 | 84.5 | 0 | 0 |
| 7 | 84.5 | 0 | 0 |
| 8 | 84.5 | 0 | 0 |
| 9 | 84.5 | 0 | 0 |
| 10 | 84.5 | 0 | 0 |
| 11 | 84.5 | 0 | 0 |
| 12 | 84.5 | 0 | 0 |
| 13 | 84.5 | 0 | 0 |
| 14 | 84.5 | 0 | 0 |
| 15 | 157 | 0 | 0 |
| 16 | 157 | 0 | 0 |
| 17 | | | |
| 18 | 7435.16667 | 0 | 0 |
| 19 | 7435.16667 | 0 | 0 |
| 20 | 7435.16667 | 0 | 0 |
| 21 | 7435.16667 | 0 | 0 |
| 22 | 7435.16667 | 0 | 0 |
| 23 | 72 | 0 | 0 |
| 24 | | | |
| 25 | 10412.1667 | 0 | 0 |
| 26 | 10412.1667 | 0 | 0 |
| 27 | 10412.1667 | 0 | 0 |
| 28 | 10412.1667 | 0 | 0 |
| 29 | 10412.1667 | 0 | 0 |
| 30 | 10412.1667 | 0 | 0 |
| 31 | 10412.1667 | 0 | 0 |
| 32 | 10412.1667 | 0 | 0 |
| 33 | 10412.1667 | 0 | 0 |
| 34 | 10412.1667 | 0 | 0 |
| 35 | 10412.1667 | 0 | 0 |
| 36 | 10412.1667 | 0 | 0 |
| 37 | 10412.1667 | 0 | 0 |
| 38 | 10412.1667 | 0 | 0 |
| 39 | 10435.1667 | 0 | 0 |
| 40 | | | |
| 41 | 6211 | 0 | 0 |
| 42 | 6211 | 0 | 0 |
| 43 | 6211 | 0 | 0 |
| 44 | 6211 | 0 | 0 |
| 45 | 6211 | 0 | 0 |
| 46 | 6211 | 0 | 0 |
| 47 | 6211 | 0 | 0 |
| 48 | 6211 | 0 | 0 |
| 49 | 6211 | 0 | 0 |
| 50 | 6211 | 0 | 0 |
| 51 | 6211 | 0 | 0 |
| 52 | 6211 | 0 | 0 |
| 53 | 6211 | 0 | 0 |
| 54 | 6211 | 0 | 0 |
| 55 | 6211 | 0 | 0 |
| 56 | 6211 | 0 | 0 |
| 57 | 6211 | 0 | 0 |
| 58 | 6211 | 0 | 0 |
| 59 | 6211 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 6211 | 0 | 0 |
| 4 | 6211 | 0 | 0 |
| 5 | 6211 | 0 | 0 |
| 6 | 6211 | 0 | 0 |
| 7 | 344.5 | 0 | 0 |
| 8 | 344.5 | 0 | 0 |
| 9 | 344.5 | 0 | 0 |
| 10 | 344.5 | 0 | 0 |
| 11 | 344.5 | 0 | 0 |
| 12 | 344.5 | 0 | 0 |
| 13 | 344.5 | 0 | 0 |
| 14 | 287.333333 | 0 | 0 |
| 15 | 287.333333 | 0 | 0 |
| 16 | 343.833333 | 0 | 0 |
| 17 | 343.833333 | 0 | 0 |
| 18 | 343.833333 | 0 | 0 |
| 19 | 343.833333 | 0 | 0 |
| 20 | 343.833333 | 0 | 0 |
| 21 | 343.833333 | 0 | 0 |
| 22 | 343.833333 | 0 | 0 |
| 23 | 343.833333 | 0 | 0 |
| 24 | 343.833333 | 0 | 0 |
| 25 | 343.833333 | 0 | 0 |
| 26 | 343.833333 | 0 | 0 |
| 27 | 343.833333 | 0 | 0 |
| 28 | 343.833333 | 0 | 0 |
| 29 | 343.833333 | 0 | 0 |
| 30 | 343.833333 | 0 | 0 |
| 31 | 343.833333 | 0 | 0 |
| 32 | 343.833333 | 0 | 0 |
| 33 | 343.833333 | 0 | 0 |
| 34 | 343.833333 | 0 | 0 |
| 35 | 343.833333 | 0 | 0 |
| 36 | 343.833333 | 0 | 0 |
| 37 | 343.833333 | 0 | 0 |
| 38 | 343.833333 | 0 | 0 |
| 39 | 343.833333 | 0 | 0 |
| 40 | 343.833333 | 0 | 0 |
| 41 | 343.833333 | 0 | 0 |
| 42 | 343.833333 | 0 | 0 |
| 43 | 343.833333 | 0 | 0 |
| 44 | 343.833333 | 0 | 0 |
| 45 | 343.833333 | 0 | 0 |
| 46 | 343.833333 | 0 | 0 |
| 47 | 343.833333 | 0 | 0 |
| 48 | 343.833333 | 0 | 0 |
| 49 | 343.833333 | 0 | 0 |
| 50 | 343.833333 | 0 | 0 |
| 51 | 343.833333 | 0 | 0 |
| 52 | 343.833333 | 0 | 0 |
| 53 | 343.833333 | 0 | 0 |
| 54 | 343.833333 | 0 | 0 |
| 55 | 343.833333 | 0 | 0 |
| 56 | 343.833333 | 0 | 0 |
| 57 | 343.833333 | 0 | 0 |
| 58 | 343.833333 | 0 | 0 |
| 59 | 343.833333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 343.833333 | 0 | 0 |
| 4 | 356.333333 | 0 | 0 |
| 5 | 356.333333 | 0 | 0 |
| 6 | 356.333333 | 0 | 0 |
| 7 | 356.333333 | 0 | 0 |
| 8 | 255.833333 | 0 | 0 |
| 9 | 6520.5 | 0 | 0 |
| 10 | 6520.5 | 0 | 0 |
| 11 | 6520.5 | 0 | 0 |
| 12 | 6520.5 | 0 | 0 |
| 13 | 6520.5 | 0 | 0 |
| 14 | 6520.5 | 0 | 0 |
| 15 | 6520.5 | 0 | 0 |
| 16 | 6153.5 | 0 | 0 |
| 17 | 328.666667 | 0 | 0 |
| 18 | 328.666667 | 0 | 0 |
| 19 | 328.666667 | 0 | 0 |
| 20 | 328.666667 | 0 | 0 |
| 21 | 328.666667 | 0 | 0 |
| 22 | 328.666667 | 0 | 0 |
| 23 | 328.666667 | 0 | 0 |
| 24 | 328.666667 | 0 | 0 |
| 25 | 328.666667 | 0 | 0 |
| 26 | 328.666667 | 0 | 0 |
| 27 | 328.666667 | 0 | 0 |
| 28 | 328.666667 | 0 | 0 |
| 29 | 328.666667 | 0 | 0 |
| 30 | 328.666667 | 0 | 0 |
| 31 | 8881.83333 | 0 | 0 |
| 32 | 8881.83333 | 0 | 0 |
| 33 | 328 | 0 | 0 |
| 34 | 328 | 0 | 0 |
| 35 | 328 | 0 | 0 |
| 36 | 328 | 0 | 0 |
| 37 | 328 | 0 | 0 |
| 38 | 328 | 0 | 0 |
| 39 | 328 | 0 | 0 |
| 40 | 328 | 0 | 0 |
| 41 | 328 | 0 | 0 |
| 42 | 328 | 0 | 0 |
| 43 | 328 | 0 | 0 |
| 44 | 328 | 0 | 0 |
| 45 | 328 | 0 | 0 |
| 46 | 328 | 0 | 0 |
| 47 | 328 | 0 | 0 |
| 48 | 328 | 0 | 0 |
| 49 | 328 | 0 | 0 |
| 50 | 328 | 0 | 0 |
| 51 | 328 | 0 | 0 |
| 52 | 328 | 0 | 0 |
| 53 | 328 | 0 | 0 |
| 54 | 328 | 0 | 0 |
| 55 | 328 | 0 | 0 |
| 56 | 328 | 0 | 0 |
| 57 | 328 | 0 | 0 |
| 58 | 328 | 0 | 0 |
| 59 | 328 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 328 | 0 | 0 |
| 4 | 328 | 0 | 0 |
| 5 | 328 | 0 | 0 |
| 6 | 328 | 0 | 0 |
| 7 | 56 | 0 | 0 |
| 8 | 157.166667 | 0 | 0 |
| 9 | 53.6666667 | 0 | 0 |
| 10 | 241.166667 | 0 | 0 |
| 11 | 241.166667 | 0 | 0 |
| 12 | 241.166667 | 0 | 0 |
| 13 | 241.166667 | 0 | 0 |
| 14 | 241.166667 | 0 | 0 |
| 15 | 241.166667 | 0 | 0 |
| 16 | 241.166667 | 0 | 0 |
| 17 | 241.166667 | 0 | 0 |
| 18 | 241.166667 | 0 | 0 |
| 19 | 241.166667 | 0 | 0 |
| 20 | 241.166667 | 0 | 0 |
| 21 | 241.166667 | 0 | 0 |
| 22 | 159.833333 | 0 | 0 |
| 23 | 5657 | 0 | 0 |
| 24 | 226.166667 | 0 | 0 |
| 25 | 226.166667 | 0 | 0 |
| 26 | 585 | 0 | 0 |
| 27 | 585 | 0 | 0 |
| 28 | 585 | 0 | 0 |
| 29 | 585 | 0 | 0 |
| 30 | 585 | 0 | 0 |
| 31 | 585 | 0 | 0 |
| 32 | 585 | 0 | 0 |
| 33 | 585 | 0 | 0 |
| 34 | 585 | 0 | 0 |
| 35 | 585 | 0 | 0 |
| 36 | 585 | 0 | 0 |
| 37 | 585 | 0 | 0 |
| 38 | 585 | 0 | 0 |
| 39 | 585 | 0 | 0 |
| 40 | 495.5 | 0 | 0 |
| 41 | 159 | 0 | 0 |
| 42 | 159 | 0 | 0 |
| 43 | 656.5 | 0 | 0 |
| 44 | 656.5 | 0 | 0 |
| 45 | 221 | 0 | 0 |
| 46 | 2826.33333 | 0 | 0 |
| 47 | 2826.33333 | 0 | 0 |
| 48 | 2826.33333 | 0 | 0 |
| 49 | 2826.33333 | 0 | 0 |
| 50 | 2826.33333 | 0 | 0 |
| 51 | 2826.33333 | 0 | 0 |
| 52 | 2826.33333 | 0 | 0 |
| 53 | 2826.33333 | 0 | 0 |
| 54 | 2826.33333 | 0 | 0 |
| 55 | 2826.33333 | 0 | 0 |
| 56 | 2826.33333 | 0 | 0 |
| 57 | 2826.33333 | 0 | 0 |
| 58 | 2826.33333 | 0 | 0 |
| 59 | 2826.33333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 203.333333 | 0 | 0 |
| 4 | 203.333333 | 0 | 0 |
| 5 | 203.333333 | 0 | 0 |
| 6 | 203.333333 | 0 | 0 |
| 7 | 203.333333 | 0 | 0 |
| 8 | 203.333333 | 0 | 0 |
| 9 | 203.333333 | 0 | 0 |
| 10 | 203.333333 | 0 | 0 |
| 11 | 203.333333 | 0 | 0 |
| 12 | 203.333333 | 0 | 0 |
| 13 | 203.333333 | 0 | 0 |
| 14 | 203.333333 | 0 | 0 |
| 15 | 203.333333 | 0 | 0 |
| 16 | 203.333333 | 0 | 0 |
| 17 | 203.333333 | 0 | 0 |
| 18 | 203.333333 | 0 | 0 |
| 19 | 203.333333 | 0 | 0 |
| 20 | 203.333333 | 0 | 0 |
| 21 | 203.333333 | 0 | 0 |
| 22 | 203.333333 | 0 | 0 |
| 23 | 203.333333 | 0 | 0 |
| 24 | 203.333333 | 0 | 0 |
| 25 | 203.333333 | 0 | 0 |
| 26 | 203.333333 | 0 | 0 |
| 27 | 203.333333 | 0 | 0 |
| 28 | 203.333333 | 0 | 0 |
| 29 | 203.333333 | 0 | 0 |
| 30 | 203.333333 | 0 | 0 |
| 31 | 203.333333 | 0 | 0 |
| 32 | 203.333333 | 0 | 0 |
| 33 | 203.333333 | 0 | 0 |
| 34 | 203.333333 | 0 | 0 |
| 35 | 203.333333 | 0 | 0 |
| 36 | 203.333333 | 0 | 0 |
| 37 | 203.333333 | 0 | 0 |
| 38 | 203.333333 | 0 | 0 |
| 39 | 203.333333 | 0 | 0 |
| 40 | 203.333333 | 0 | 0 |
| 41 | 203.333333 | 0 | 0 |
| 42 | 203.333333 | 0 | 0 |
| 43 | 203.333333 | 0 | 0 |
| 44 | 203.333333 | 0 | 0 |
| 45 | 203.333333 | 0 | 0 |
| 46 | 203.333333 | 0 | 0 |
| 47 | 203.333333 | 0 | 0 |
| 48 | 203.333333 | 0 | 0 |
| 49 | 203.333333 | 0 | 0 |
| 50 | 203.333333 | 0 | 0 |
| 51 | 203.333333 | 0 | 0 |
| 52 | 203.333333 | 0 | 0 |
| 53 | 203.333333 | 0 | 0 |
| 54 | 203.333333 | 0 | 0 |
| 55 | 203.333333 | 0 | 0 |
| 56 | 203.333333 | 0 | 0 |
| 57 | 203.333333 | 0 | 0 |
| 58 | 203.333333 | 0 | 0 |
| 59 | 161.166667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 3301.33333 | 0 | 0 |
| 4 | 3301.33333 | 0 | 0 |
| 5 | 3301.33333 | 0 | 0 |
| 6 | 3305.33333 | 0 | 0 |
| 7 | 3305.33333 | 0 | 0 |
| 8 | 200 | 0 | 0 |
| 9 | 4377 | 0 | 0 |
| 10 | 4377 | 0 | 0 |
| 11 | 4377 | 0 | 0 |
| 12 | 70.1666667 | 0 | 0 |
| 13 | 69.6666667 | 0 | 0 |
| 14 | 69.6666667 | 0 | 0 |
| 15 | 69.6666667 | 0 | 0 |
| 16 | 69.6666667 | 0 | 0 |
| 17 | 69.6666667 | 0 | 0 |
| 18 | 69.6666667 | 0 | 0 |
| 19 | 69.6666667 | 0 | 0 |
| 20 | 81.8333333 | 0 | 0 |
| 21 | 143646.333 | 0 | 0 |
| 22 | 143646.333 | 0 | 0 |
| 23 | 143646.333 | 0 | 0 |
| 24 | 143646.333 | 0 | 0 |
| 25 | 114.833333 | 0 | 0 |
| 26 | 114.833333 | 0 | 0 |
| 27 | 114.833333 | 0 | 0 |
| 28 | 114.833333 | 0 | 0 |
| 29 | 114.833333 | 0 | 0 |
| 30 | 114.833333 | 0 | 0 |
| 31 | 114.833333 | 0 | 0 |
| 32 | 114.833333 | 0 | 0 |
| 33 | 114.833333 | 0 | 0 |
| 34 | 114.833333 | 0 | 0 |
| 35 | 114.833333 | 0 | 0 |
| 36 | 114.833333 | 0 | 0 |
| 37 | 8847.83333 | 0 | 0 |
| 38 | 8847.83333 | 0 | 0 |
| 39 | 8847.83333 | 0 | 0 |
| 40 | 232.833333 | 0 | 0 |
| 41 | 232.833333 | 0 | 0 |
| 42 | 232.833333 | 0 | 0 |
| 43 | 240.166667 | 0 | 0 |
| 44 | 240.166667 | 0 | 0 |
| 45 | 240.166667 | 0 | 0 |
| 46 | 240.166667 | 0 | 0 |
| 47 | 240.166667 | 0 | 0 |
| 48 | 240.166667 | 0 | 0 |
| 49 | 240.166667 | 0 | 0 |
| 50 | 240.166667 | 0 | 0 |
| 51 | 240.166667 | 0 | 0 |
| 52 | 170.166667 | 0 | 0 |
| 53 | 170.166667 | 0 | 0 |
| 54 | 170.166667 | 0 | 0 |
| 55 | 79.6666667 | 0 | 0 |
| 56 | 79.6666667 | 0 | 0 |
| 57 | 223.833333 | 0 | 0 |
| 58 | 223.833333 | 0 | 0 |
| 59 | 223.833333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 223.833333 | 0 | 0 |
| 4 | 223.833333 | 0 | 0 |
| 5 | 223.833333 | 0 | 0 |
| 6 | 223.833333 | 0 | 0 |
| 7 | 223.833333 | 0 | 0 |
| 8 | 223.833333 | 0 | 0 |
| 9 | 223.833333 | 0 | 0 |
| 10 | 223.833333 | 0 | 0 |
| 11 | 113 | 0 | 0 |
| 12 | 113 | 0 | 0 |
| 13 | 113 | 0 | 0 |
| 14 | 113 | 0 | 0 |
| 15 | 1627.16667 | 0 | 0 |
| 16 | 1627.16667 | 0 | 0 |
| 17 | 1627.16667 | 0 | 0 |
| 18 | 1627.16667 | 0 | 0 |
| 19 | 1627.16667 | 0 | 0 |
| 20 | 1627.16667 | 0 | 0 |
| 21 | 1627.16667 | 0 | 0 |
| 22 | 1627.16667 | 0 | 0 |
| 23 | 1627.16667 | 0 | 0 |
| 24 | 1627.16667 | 0 | 0 |
| 25 | 1627.16667 | 0 | 0 |
| 26 | 1627.16667 | 0 | 0 |
| 27 | 1627.16667 | 0 | 0 |
| 28 | 1627.16667 | 0 | 0 |
| 29 | 1627.16667 | 0 | 0 |
| 30 | 1627.16667 | 0 | 0 |
| 31 | 54.3333333 | 0 | 0 |
| 32 | 54.3333333 | 0 | 0 |
| 33 | 54.3333333 | 0 | 0 |
| 34 | 54.3333333 | 0 | 0 |
| 35 | 54.3333333 | 0 | 0 |
| 36 | 54.3333333 | 0 | 0 |
| 37 | 54.3333333 | 0 | 0 |
| 38 | 54.3333333 | 0 | 0 |
| 39 | 54.3333333 | 0 | 0 |
| 40 | 54.3333333 | 0 | 0 |
| 41 | 54.3333333 | 0 | 0 |
| 42 | 54.3333333 | 0 | 0 |
| 43 | 54.3333333 | 0 | 0 |
| 44 | 54.3333333 | 0 | 0 |
| 45 | 54.3333333 | 0 | 0 |
| 46 | 54.3333333 | 0 | 0 |
| 47 | 91.1666667 | 0 | 0 |
| 48 | 91.1666667 | 0 | 0 |
| 49 | 91.1666667 | 0 | 0 |
| 50 | 91.1666667 | 0 | 0 |
| 51 | 91.1666667 | 0 | 0 |
| 52 | 91.1666667 | 0 | 0 |
| 53 | 91.1666667 | 0 | 0 |
| 54 | 91.1666667 | 0 | 0 |
| 55 | 91.1666667 | 0 | 0 |
| 56 | 91.1666667 | 0 | 0 |
| 57 | 91.1666667 | 0 | 0 |
| 58 | 91.1666667 | 0 | 0 |
| 59 | 91.1666667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|-------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 91.1666667 | 0 | 0 |
| 4 | 91.1666667 | 0 | 0 |
| 5 | 91.1666667 | 0 | 0 |
| 6 | 91.1666667 | 0 | 0 |
| 7 | 91.1666667 | 0 | 0 |
| 8 | 91.1666667 | 0 | 0 |
| 9 | 91.1666667 | 0 | 0 |
| 10 | 91.1666667 | 0 | 0 |
| 11 | 91.1666667 | 0 | 0 |
| 12 | 85.6666667 | 0 | 0 |
| 13 | 85.6666667 | 0 | 0 |
| 14 | 85.6666667 | 0 | 0 |
| 15 | 85.6666667 | 0 | 0 |
| 16 | 85.6666667 | 0 | 0 |
| 17 | 85.6666667 | 0 | 0 |
| 18 | 85.6666667 | 0 | 0 |
| 19 | 73.1666667 | 0 | 0 |
| 20 | 122.6666667 | 0 | 0 |
| 21 | 122.6666667 | 0 | 0 |
| 22 | 122.6666667 | 0 | 0 |
| 23 | 122.6666667 | 0 | 0 |
| 24 | 122.6666667 | 0 | 0 |
| 25 | 122.6666667 | 0 | 0 |
| 26 | 122.6666667 | 0 | 0 |
| 27 | 122.6666667 | 0 | 0 |
| 28 | 258.8333333 | 0 | 0 |
| 29 | 3784.66667 | 0 | 0 |
| 30 | 3784.66667 | 0 | 0 |
| 31 | 3784.66667 | 0 | 0 |
| 32 | 3784.66667 | 0 | 0 |
| 33 | 3784.66667 | 0 | 0 |
| 34 | 3784.66667 | 0 | 0 |
| 35 | 3784.66667 | 0 | 0 |
| 36 | 3784.66667 | 0 | 0 |
| 37 | 3784.66667 | 0 | 0 |
| 38 | 3784.66667 | 0 | 0 |
| 39 | 3784.66667 | 0 | 0 |
| 40 | 3784.66667 | 0 | 0 |
| 41 | 248.3333333 | 0 | 0 |
| 42 | 248.3333333 | 0 | 0 |
| 43 | 248.3333333 | 0 | 0 |
| 44 | 71.1666667 | 0 | 0 |
| 45 | 64.6666667 | 0 | 0 |
| 46 | 64.6666667 | 0 | 0 |
| 47 | 64.6666667 | 0 | 0 |
| 48 | 79.1666667 | 0 | 0 |
| 49 | 79.1666667 | 0 | 0 |
| 50 | 79.1666667 | 0 | 0 |
| 51 | 79.1666667 | 0 | 0 |
| 52 | 9424.333333 | 0 | 0 |
| 53 | | | |
| 54 | 68.5 | 0 | 0 |
| 55 | 68.5 | 0 | 0 |
| 56 | 68.5 | 0 | 0 |
| 57 | 68.5 | 0 | 0 |
| 58 | 68.5 | 0 | 0 |
| 59 | 68.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 68.5 | 0 | 0 |
| 4 | 68.5 | 0 | 0 |
| 5 | 68.5 | 0 | 0 |
| 6 | 68.5 | 0 | 0 |
| 7 | 68.5 | 0 | 0 |
| 8 | 68.5 | 0 | 0 |
| 9 | 68.5 | 0 | 0 |
| 10 | 68.5 | 0 | 0 |
| 11 | 68.5 | 0 | 0 |
| 12 | 68.5 | 0 | 0 |
| 13 | 68.5 | 0 | 0 |
| 14 | 68.5 | 0 | 0 |
| 15 | 68.5 | 0 | 0 |
| 16 | 68.5 | 0 | 0 |
| 17 | 68.5 | 0 | 0 |
| 18 | 68.5 | 0 | 0 |
| 19 | 68.5 | 0 | 0 |
| 20 | 68.5 | 0 | 0 |
| 21 | 68.5 | 0 | 0 |
| 22 | 8035.83333 | 0 | 0 |
| 23 | 8035.83333 | 0 | 0 |
| 24 | 8035.83333 | 0 | 0 |
| 25 | 8035.83333 | 0 | 0 |
| 26 | 8035.83333 | 0 | 0 |
| 27 | 8035.83333 | 0 | 0 |
| 28 | 8035.83333 | 0 | 0 |
| 29 | 8035.83333 | 0 | 0 |
| 30 | 8035.83333 | 0 | 0 |
| 31 | 8035.83333 | 0 | 0 |
| 32 | 8035.83333 | 0 | 0 |
| 33 | 8035.83333 | 0 | 0 |
| 34 | 8035.83333 | 0 | 0 |
| 35 | 8035.83333 | 0 | 0 |
| 36 | 8035.83333 | 0 | 0 |
| 37 | 8035.83333 | 0 | 0 |
| 38 | 8035.83333 | 0 | 0 |
| 39 | 8035.83333 | 0 | 0 |
| 40 | 8035.83333 | 0 | 0 |
| 41 | 8035.83333 | 0 | 0 |
| 42 | 8035.83333 | 0 | 0 |
| 43 | 8035.83333 | 0 | 0 |
| 44 | 8035.83333 | 0 | 0 |
| 45 | 8035.83333 | 0 | 0 |
| 46 | 8035.83333 | 0 | 0 |
| 47 | 8035.83333 | 0 | 0 |
| 48 | 8035.83333 | 0 | 0 |
| 49 | 8035.83333 | 0 | 0 |
| 50 | 8035.83333 | 0 | 0 |
| 51 | 8035.83333 | 0 | 0 |
| 52 | 8035.83333 | 0 | 0 |
| 53 | 8035.83333 | 0 | 0 |
| 54 | 8035.83333 | 0 | 0 |
| 55 | 8035.83333 | 0 | 0 |
| 56 | 8035.83333 | 0 | 0 |
| 57 | 8035.83333 | 0 | 0 |
| 58 | 8035.83333 | 0 | 0 |
| 59 | 8035.83333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 8035.83333 | 0 | 0 |
| 4 | 8035.83333 | 0 | 0 |
| 5 | 8035.83333 | 0 | 0 |
| 6 | 8035.83333 | 0 | 0 |
| 7 | 8035.83333 | 0 | 0 |
| 8 | 8035.83333 | 0 | 0 |
| 9 | 8035.83333 | 0 | 0 |
| 10 | 8035.83333 | 0 | 0 |
| 11 | 8035.83333 | 0 | 0 |
| 12 | 8035.83333 | 0 | 0 |
| 13 | 8035.83333 | 0 | 0 |
| 14 | 7625.33333 | 0 | 0 |
| 15 | 7625.33333 | 0 | 0 |
| 16 | 7625.33333 | 0 | 0 |
| 17 | 7625.33333 | 0 | 0 |
| 18 | 7625.33333 | 0 | 0 |
| 19 | 7625.33333 | 0 | 0 |
| 20 | 7625.33333 | 0 | 0 |
| 21 | 7625.33333 | 0 | 0 |
| 22 | 7625.33333 | 0 | 0 |
| 23 | 7625.33333 | 0 | 0 |
| 24 | 7625.33333 | 0 | 0 |
| 25 | 7625.33333 | 0 | 0 |
| 26 | 7625.33333 | 0 | 0 |
| 27 | 7625.33333 | 0 | 0 |
| 28 | 7625.33333 | 0 | 0 |
| 29 | 7625.33333 | 0 | 0 |
| 30 | 7625.33333 | 0 | 0 |
| 31 | 7625.33333 | 0 | 0 |
| 32 | 7625.33333 | 0 | 0 |
| 33 | 7625.33333 | 0 | 0 |
| 34 | 7625.33333 | 0 | 0 |
| 35 | 7625.33333 | 0 | 0 |
| 36 | 7625.33333 | 0 | 0 |
| 37 | 7625.33333 | 0 | 0 |
| 38 | 7625.33333 | 0 | 0 |
| 39 | 7625.33333 | 0 | 0 |
| 40 | 7625.33333 | 0 | 0 |
| 41 | 7625.33333 | 0 | 0 |
| 42 | 7625.33333 | 0 | 0 |
| 43 | 7625.33333 | 0 | 0 |
| 44 | 7625.33333 | 0 | 0 |
| 45 | 7625.33333 | 0 | 0 |
| 46 | 7625.33333 | 0 | 0 |
| 47 | 7625.33333 | 0 | 0 |
| 48 | 7625.33333 | 0 | 0 |
| 49 | 7625.33333 | 0 | 0 |
| 50 | 7625.33333 | 0 | 0 |
| 51 | 7625.33333 | 0 | 0 |
| 52 | 7625.33333 | 0 | 0 |
| 53 | 7625.33333 | 0 | 0 |
| 54 | 7625.33333 | 0 | 0 |
| 55 | 7625.33333 | 0 | 0 |
| 56 | 7625.33333 | 0 | 0 |
| 57 | 7625.33333 | 0 | 0 |
| 58 | 7625.33333 | 0 | 0 |
| 59 | 7625.33333 | 0 | 0 |
| 60 | | | |

Do not distribute

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 7625.33333 | 0 | 0 |
| 4 | 7625.33333 | 0 | 0 |
| 5 | 7625.33333 | 0 | 0 |
| 6 | 7625.33333 | 0 | 0 |
| 7 | 7625.33333 | 0 | 0 |
| 8 | 7625.33333 | 0 | 0 |
| 9 | 7625.33333 | 0 | 0 |
| 10 | 7625.33333 | 0 | 0 |
| 11 | 7625.33333 | 0 | 0 |
| 12 | 7625.33333 | 0 | 0 |
| 13 | 7625.33333 | 0 | 0 |
| 14 | 7625.33333 | 0 | 0 |
| 15 | 7625.33333 | 0 | 0 |
| 16 | 7625.33333 | 0 | 0 |
| 17 | 7625.33333 | 0 | 0 |
| 18 | 7625.33333 | 0 | 0 |
| 19 | 7625.33333 | 0 | 0 |
| 20 | 7625.33333 | 0 | 0 |
| 21 | 7625.33333 | 0 | 0 |
| 22 | 7625.33333 | 0 | 0 |
| 23 | 7625.33333 | 0 | 0 |
| 24 | 7625.33333 | 0 | 0 |
| 25 | 7625.33333 | 0 | 0 |
| 26 | 12894 | 0 | 0 |
| 27 | 12845.6667 | 0 | 0 |
| 28 | 12845.6667 | 0 | 0 |
| 29 | 12845.6667 | 0 | 0 |
| 30 | 12845.6667 | 0 | 0 |
| 31 | 12845.6667 | 0 | 0 |
| 32 | 12845.6667 | 0 | 0 |
| 33 | 12845.6667 | 0 | 0 |
| 34 | 12845.6667 | 0 | 0 |
| 35 | 12845.6667 | 0 | 0 |
| 36 | 12845.6667 | 0 | 0 |
| 37 | 12845.6667 | 0 | 0 |
| 38 | 12845.6667 | 0 | 0 |
| 39 | 12845.6667 | 0 | 0 |
| 40 | 12845.6667 | 0 | 0 |
| 41 | 12845.6667 | 0 | 0 |
| 42 | 12845.6667 | 0 | 0 |
| 43 | 12845.6667 | 0 | 0 |
| 44 | 12845.6667 | 0 | 0 |
| 45 | 12845.6667 | 0 | 0 |
| 46 | 12845.6667 | 0 | 0 |
| 47 | 12845.6667 | 0 | 0 |
| 48 | 12845.6667 | 0 | 0 |
| 49 | 12845.6667 | 0 | 0 |
| 50 | 12845.6667 | 0 | 0 |
| 51 | 12845.6667 | 0 | 0 |
| 52 | 12845.6667 | 0 | 0 |
| 53 | 12845.6667 | 0 | 0 |
| 54 | 12845.6667 | 0 | 0 |
| 55 | 12845.6667 | 0 | 0 |
| 56 | 12845.6667 | 0 | 0 |
| 57 | 12845.6667 | 0 | 0 |
| 58 | 12845.6667 | 0 | 0 |
| 59 | 12845.6667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 12845.6667 | 0 | 0 |
| 4 | 12845.6667 | 0 | 0 |
| 5 | 12845.6667 | 0 | 0 |
| 6 | 12845.6667 | 0 | 0 |
| 7 | 12845.6667 | 0 | 0 |
| 8 | 12845.6667 | 0 | 0 |
| 9 | 12845.6667 | 0 | 0 |
| 10 | 12845.6667 | 0 | 0 |
| 11 | 12845.6667 | 0 | 0 |
| 12 | 12845.6667 | 0 | 0 |
| 13 | 12845.6667 | 0 | 0 |
| 14 | 12845.6667 | 0 | 0 |
| 15 | 12845.6667 | 0 | 0 |
| 16 | 12845.6667 | 0 | 0 |
| 17 | 12845.6667 | 0 | 0 |
| 18 | 12845.6667 | 0 | 0 |
| 19 | 12845.6667 | 0 | 0 |
| 20 | 12845.6667 | 0 | 0 |
| 21 | 12845.6667 | 0 | 0 |
| 22 | 12845.6667 | 0 | 0 |
| 23 | 12845.6667 | 0 | 0 |
| 24 | 12845.6667 | 0 | 0 |
| 25 | 12845.6667 | 0 | 0 |
| 26 | 12845.6667 | 0 | 0 |
| 27 | 12845.6667 | 0 | 0 |
| 28 | 12845.6667 | 0 | 0 |
| 29 | 12845.6667 | 0 | 0 |
| 30 | 12845.6667 | 0 | 0 |
| 31 | 12845.6667 | 0 | 0 |
| 32 | 12845.6667 | 0 | 0 |
| 33 | 12845.6667 | 0 | 0 |
| 34 | 12845.6667 | 0 | 0 |
| 35 | 12845.6667 | 0 | 0 |
| 36 | 12845.6667 | 0 | 0 |
| 37 | 12845.6667 | 0 | 0 |
| 38 | 12845.6667 | 0 | 0 |
| 39 | 12845.6667 | 0 | 0 |
| 40 | 12845.6667 | 0 | 0 |
| 41 | 12845.6667 | 0 | 0 |
| 42 | 12845.6667 | 0 | 0 |
| 43 | 12845.6667 | 0 | 0 |
| 44 | 12845.6667 | 0 | 0 |
| 45 | 12845.6667 | 0 | 0 |
| 46 | 12845.6667 | 0 | 0 |
| 47 | 12845.6667 | 0 | 0 |
| 48 | 12845.6667 | 0 | 0 |
| 49 | 12845.6667 | 0 | 0 |
| 50 | 12845.6667 | 0 | 0 |
| 51 | 12845.6667 | 0 | 0 |
| 52 | 12845.6667 | 0 | 0 |
| 53 | 12845.6667 | 0 | 0 |
| 54 | 12845.6667 | 0 | 0 |
| 55 | 12845.6667 | 0 | 0 |
| 56 | 12845.6667 | 0 | 0 |
| 57 | 12845.6667 | 0 | 0 |
| 58 | 12845.6667 | 0 | 0 |
| 59 | 12845.6667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 12845.6667 | 0 | 0 |
| 4 | 12845.6667 | 0 | 0 |
| 5 | 12845.6667 | 0 | 0 |
| 6 | 12845.6667 | 0 | 0 |
| 7 | 12845.6667 | 0 | 0 |
| 8 | 12845.6667 | 0 | 0 |
| 9 | 12845.6667 | 0 | 0 |
| 10 | 12845.6667 | 0 | 0 |
| 11 | 12845.6667 | 0 | 0 |
| 12 | 12845.6667 | 0 | 0 |
| 13 | 12845.6667 | 0 | 0 |
| 14 | 12845.6667 | 0 | 0 |
| 15 | 12845.6667 | 0 | 0 |
| 16 | 12845.6667 | 0 | 0 |
| 17 | 12845.6667 | 0 | 0 |
| 18 | 12845.6667 | 0 | 0 |
| 19 | 12845.6667 | 0 | 0 |
| 20 | 12845.6667 | 0 | 0 |
| 21 | 12845.6667 | 0 | 0 |
| 22 | 12845.6667 | 0 | 0 |
| 23 | 12845.6667 | 0 | 0 |
| 24 | 12845.6667 | 0 | 0 |
| 25 | 12845.6667 | 0 | 0 |
| 26 | 12845.6667 | 0 | 0 |
| 27 | 12845.6667 | 0 | 0 |
| 28 | 12845.6667 | 0 | 0 |
| 29 | 12845.6667 | 0 | 0 |
| 30 | 12845.6667 | 0 | 0 |
| 31 | 12845.6667 | 0 | 0 |
| 32 | 12845.6667 | 0 | 0 |
| 33 | 12845.6667 | 0 | 0 |
| 34 | 12845.6667 | 0 | 0 |
| 35 | 12845.6667 | 0 | 0 |
| 36 | 12845.6667 | 0 | 0 |
| 37 | 12845.6667 | 0 | 0 |
| 38 | 12845.6667 | 0 | 0 |
| 39 | 12845.6667 | 0 | 0 |
| 40 | 12845.6667 | 0 | 0 |
| 41 | 12845.6667 | 0 | 0 |
| 42 | 12845.6667 | 0 | 0 |
| 43 | 12845.6667 | 0 | 0 |
| 44 | 12845.6667 | 0 | 0 |
| 45 | 12845.6667 | 0 | 0 |
| 46 | 12944.6667 | 0 | 0 |
| 47 | 347 | 0 | 0 |
| 48 | 347 | 0 | 0 |
| 49 | 347 | 0 | 0 |
| 50 | 347 | 0 | 0 |
| 51 | 65.1666667 | 0 | 0 |
| 52 | 65.1666667 | 0 | 0 |
| 53 | 65.1666667 | 0 | 0 |
| 54 | 65.1666667 | 0 | 0 |
| 55 | 65.1666667 | 0 | 0 |
| 56 | 65.1666667 | 0 | 0 |
| 57 | 65.1666667 | 0 | 0 |
| 58 | 65.1666667 | 0 | 0 |
| 59 | 65.1666667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 65.1666667 | 0 | 0 |
| 4 | 65.1666667 | 0 | 0 |
| 5 | 65.1666667 | 0 | 0 |
| 6 | 65.1666667 | 0 | 0 |
| 7 | 65.1666667 | 0 | 0 |
| 8 | 65.1666667 | 0 | 0 |
| 9 | 65.1666667 | 0 | 0 |
| 10 | 65.1666667 | 0 | 0 |
| 11 | 65.1666667 | 0 | 0 |
| 12 | 65.1666667 | 0 | 0 |
| 13 | 65.1666667 | 0 | 0 |
| 14 | 56.3333333 | 0 | 0 |
| 15 | 636.833333 | 0 | 0 |
| 16 | 150.166667 | 0 | 0 |
| 17 | 51.8333333 | 0 | 0 |
| 18 | 3136.16667 | 0 | 0 |
| 19 | 3136.16667 | 0 | 0 |
| 20 | | | |
| 21 | 54 | 0 | 0 |
| 22 | 54 | 0 | 0 |
| 23 | | | |
| 24 | 2868.66667 | 0 | 0 |
| 25 | 196.333333 | 0 | 0 |
| 26 | 196.333333 | 0 | 0 |
| 27 | 196.333333 | 0 | 0 |
| 28 | 196.333333 | 0 | 0 |
| 29 | 196.333333 | 0 | 0 |
| 30 | 196.333333 | 0 | 0 |
| 31 | 458.666667 | 0 | 0 |
| 32 | 28235.5 | 0 | 0 |
| 33 | 28235.5 | 0 | 0 |
| 34 | | | |
| 35 | 74.1666667 | 0 | 0 |
| 36 | 74.1666667 | 0 | 0 |
| 37 | 74.1666667 | 0 | 0 |
| 38 | 74.1666667 | 0 | 0 |
| 39 | 74.1666667 | 0 | 0 |
| 40 | 74.1666667 | 0 | 0 |
| 41 | 74.1666667 | 0 | 0 |
| 42 | 74.1666667 | 0 | 0 |
| 43 | 74.1666667 | 0 | 0 |
| 44 | 74.1666667 | 0 | 0 |
| 45 | 74.1666667 | 0 | 0 |
| 46 | 74.1666667 | 0 | 0 |
| 47 | 74.1666667 | 0 | 0 |
| 48 | 74.1666667 | 0 | 0 |
| 49 | 74.1666667 | 0 | 0 |
| 50 | 74.1666667 | 0 | 0 |
| 51 | 74.1666667 | 0 | 0 |
| 52 | 74.1666667 | 0 | 0 |
| 53 | 74.1666667 | 0 | 0 |
| 54 | 74.1666667 | 0 | 0 |
| 55 | 74.1666667 | 0 | 0 |
| 56 | 74.1666667 | 0 | 0 |
| 57 | 74.1666667 | 0 | 0 |
| 58 | 74.1666667 | 0 | 0 |
| 59 | 74.1666667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 74.1666667 | 0 | 0 |
| 4 | 74.1666667 | 0 | 0 |
| 5 | 74.1666667 | 0 | 0 |
| 6 | 74.1666667 | 0 | 0 |
| 7 | 74.1666667 | 0 | 0 |
| 8 | 74.1666667 | 0 | 0 |
| 9 | 74.1666667 | 0 | 0 |
| 10 | 74.1666667 | 0 | 0 |
| 11 | 74.1666667 | 0 | 0 |
| 12 | 74.1666667 | 0 | 0 |
| 13 | 74.1666667 | 0 | 0 |
| 14 | 74.1666667 | 0 | 0 |
| 15 | 74.1666667 | 0 | 0 |
| 16 | 74.1666667 | 0 | 0 |
| 17 | 74.1666667 | 0 | 0 |
| 18 | 74.1666667 | 0 | 0 |
| 19 | 74.1666667 | 0 | 0 |
| 20 | 74.1666667 | 0 | 0 |
| 21 | 74.1666667 | 0 | 0 |
| 22 | 74.1666667 | 0 | 0 |
| 23 | 74.1666667 | 0 | 0 |
| 24 | 74.1666667 | 0 | 0 |
| 25 | 74.1666667 | 0 | 0 |
| 26 | 74.1666667 | 0 | 0 |
| 27 | 74.1666667 | 0 | 0 |
| 28 | 74.1666667 | 0 | 0 |
| 29 | 74.1666667 | 0 | 0 |
| 30 | 74.1666667 | 0 | 0 |
| 31 | 74.1666667 | 0 | 0 |
| 32 | 153.5 | 0 | 0 |
| 33 | 335.333333 | 0 | 0 |
| 34 | 335.333333 | 0 | 0 |
| 35 | 342 | 0 | 0 |
| 36 | 342 | 0 | 0 |
| 37 | 138.833333 | 0 | 0 |
| 38 | 189.166667 | 0 | 0 |
| 39 | 189.166667 | 0 | 0 |
| 40 | 189.166667 | 0 | 0 |
| 41 | 189.166667 | 0 | 0 |
| 42 | 189.166667 | 0 | 0 |
| 43 | 189.166667 | 0 | 0 |
| 44 | 189.166667 | 0 | 0 |
| 45 | 189.166667 | 0 | 0 |
| 46 | 189.166667 | 0 | 0 |
| 47 | 189.166667 | 0 | 0 |
| 48 | 189.166667 | 0 | 0 |
| 49 | 189.166667 | 0 | 0 |
| 50 | 189.166667 | 0 | 0 |
| 51 | 189.166667 | 0 | 0 |
| 52 | 189.166667 | 0 | 0 |
| 53 | 189.166667 | 0 | 0 |
| 54 | 67.3333333 | 0 | 0 |
| 55 | 67.3333333 | 0 | 0 |
| 56 | 67.3333333 | 0 | 0 |
| 57 | 67.3333333 | 0 | 0 |
| 58 | 67.3333333 | 0 | 0 |
| 59 | 67.3333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 67.3333333 | 0 | 0 |
| 4 | 67.3333333 | 0 | 0 |
| 5 | 67.3333333 | 0 | 0 |
| 6 | 67.3333333 | 0 | 0 |
| 7 | 67.3333333 | 0 | 0 |
| 8 | 67.3333333 | 0 | 0 |
| 9 | 67.3333333 | 0 | 0 |
| 10 | 67.3333333 | 0 | 0 |
| 11 | 67.3333333 | 0 | 0 |
| 12 | 67.3333333 | 0 | 0 |
| 13 | 67.3333333 | 0 | 0 |
| 14 | 67.3333333 | 0 | 0 |
| 15 | 67.3333333 | 0 | 0 |
| 16 | 67.3333333 | 0 | 0 |
| 17 | 67.3333333 | 0 | 0 |
| 18 | 67.3333333 | 0 | 0 |
| 19 | 67.3333333 | 0 | 0 |
| 20 | 55.6666667 | 0 | 0 |
| 21 | 55.6666667 | 0 | 0 |
| 22 | 55.6666667 | 0 | 0 |
| 23 | 55.6666667 | 0 | 0 |
| 24 | 55.6666667 | 0 | 0 |
| 25 | 55.6666667 | 0 | 0 |
| 26 | 55.6666667 | 0 | 0 |
| 27 | 55.6666667 | 0 | 0 |
| 28 | 55.6666667 | 0 | 0 |
| 29 | 55.6666667 | 0 | 0 |
| 30 | 55.6666667 | 0 | 0 |
| 31 | 55.6666667 | 0 | 0 |
| 32 | 55.6666667 | 0 | 0 |
| 33 | 55.6666667 | 0 | 0 |
| 34 | 55.6666667 | 0 | 0 |
| 35 | 55.6666667 | 0 | 0 |
| 36 | 55.6666667 | 0 | 0 |
| 37 | 55.6666667 | 0 | 0 |
| 38 | 55.6666667 | 0 | 0 |
| 39 | 55.6666667 | 0 | 0 |
| 40 | 55.6666667 | 0 | 0 |
| 41 | 55.6666667 | 0 | 0 |
| 42 | 55.6666667 | 0 | 0 |
| 43 | 860.666667 | 0 | 0 |
| 44 | 859.666667 | 0 | 0 |
| 45 | 859.666667 | 0 | 0 |
| 46 | 859.666667 | 0 | 0 |
| 47 | 859.666667 | 0 | 0 |
| 48 | 859.666667 | 0 | 0 |
| 49 | 859.666667 | 0 | 0 |
| 50 | 859.666667 | 0 | 0 |
| 51 | 859.666667 | 0 | 0 |
| 52 | 859.666667 | 0 | 0 |
| 53 | 859.666667 | 0 | 0 |
| 54 | 859.666667 | 0 | 0 |
| 55 | 859.666667 | 0 | 0 |
| 56 | 859.666667 | 0 | 0 |
| 57 | 859.666667 | 0 | 0 |
| 58 | 859.666667 | 0 | 0 |
| 59 | 859.666667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 859.666667 | 0 | 0 |
| 4 | 859.666667 | 0 | 0 |
| 5 | 859.666667 | 0 | 0 |
| 6 | 859.666667 | 0 | 0 |
| 7 | 859.666667 | 0 | 0 |
| 8 | 859.666667 | 0 | 0 |
| 9 | 859.666667 | 0 | 0 |
| 10 | 859.666667 | 0 | 0 |
| 11 | 859.666667 | 0 | 0 |
| 12 | 859.666667 | 0 | 0 |
| 13 | 859.666667 | 0 | 0 |
| 14 | 859.666667 | 0 | 0 |
| 15 | 859.666667 | 0 | 0 |
| 16 | 859.666667 | 0 | 0 |
| 17 | 859.666667 | 0 | 0 |
| 18 | 859.666667 | 0 | 0 |
| 19 | 859.666667 | 0 | 0 |
| 20 | 859.666667 | 0 | 0 |
| 21 | 859.666667 | 0 | 0 |
| 22 | 859.666667 | 0 | 0 |
| 23 | 859.666667 | 0 | 0 |
| 24 | 859.666667 | 0 | 0 |
| 25 | 859.666667 | 0 | 0 |
| 26 | 859.666667 | 0 | 0 |
| 27 | 859.666667 | 0 | 0 |
| 28 | 859.666667 | 0 | 0 |
| 29 | 859.666667 | 0 | 0 |
| 30 | 859.666667 | 0 | 0 |
| 31 | 859.666667 | 0 | 0 |
| 32 | 859.666667 | 0 | 0 |
| 33 | 859.666667 | 0 | 0 |
| 34 | 859.666667 | 0 | 0 |
| 35 | 859.666667 | 0 | 0 |
| 36 | 859.666667 | 0 | 0 |
| 37 | 859.666667 | 0 | 0 |
| 38 | 859.666667 | 0 | 0 |
| 39 | 859.666667 | 0 | 0 |
| 40 | 859.666667 | 0 | 0 |
| 41 | 859.666667 | 0 | 0 |
| 42 | 859.666667 | 0 | 0 |
| 43 | 859.666667 | 0 | 0 |
| 44 | 859.666667 | 0 | 0 |
| 45 | 859.666667 | 0 | 0 |
| 46 | 859.666667 | 0 | 0 |
| 47 | 859.666667 | 0 | 0 |
| 48 | 859.666667 | 0 | 0 |
| 49 | 859.666667 | 0 | 0 |
| 50 | 859.666667 | 0 | 0 |
| 51 | 859.666667 | 0 | 0 |
| 52 | 859.666667 | 0 | 0 |
| 53 | 130.333333 | 0 | 0 |
| 54 | 130.333333 | 0 | 0 |
| 55 | 130.333333 | 0 | 0 |
| 56 | 130.333333 | 0 | 0 |
| 57 | 129.166667 | 0 | 0 |
| 58 | 129.166667 | 0 | 0 |
| 59 | 129.166667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 129.166667 | 0 | 0 |
| 4 | 129.166667 | 0 | 0 |
| 5 | 129.166667 | 0 | 0 |
| 6 | 129.166667 | 0 | 0 |
| 7 | 129.166667 | 0 | 0 |
| 8 | 129.166667 | 0 | 0 |
| 9 | 129.166667 | 0 | 0 |
| 10 | 129.166667 | 0 | 0 |
| 11 | 129.166667 | 0 | 0 |
| 12 | 129.166667 | 0 | 0 |
| 13 | 129.166667 | 0 | 0 |
| 14 | 129.166667 | 0 | 0 |
| 15 | 129.166667 | 0 | 0 |
| 16 | 129.166667 | 0 | 0 |
| 17 | 129.166667 | 0 | 0 |
| 18 | 129.166667 | 0 | 0 |
| 19 | 129.166667 | 0 | 0 |
| 20 | 129.166667 | 0 | 0 |
| 21 | 129.166667 | 0 | 0 |
| 22 | 129.166667 | 0 | 0 |
| 23 | 129.166667 | 0 | 0 |
| 24 | 129.166667 | 0 | 0 |
| 25 | 129.166667 | 0 | 0 |
| 26 | 314.333333 | 0 | 0 |
| 27 | 617 | 0 | 0 |
| 28 | 617 | 0 | 0 |
| 29 | 243.5 | 0 | 0 |
| 30 | 243.5 | 0 | 0 |
| 31 | 243.5 | 0 | 0 |
| 32 | 243.5 | 0 | 0 |
| 33 | 243.5 | 0 | 0 |
| 34 | 243.5 | 0 | 0 |
| 35 | 243.5 | 0 | 0 |
| 36 | 243.5 | 0 | 0 |
| 37 | 243.5 | 0 | 0 |
| 38 | 243.5 | 0 | 0 |
| 39 | 243.5 | 0 | 0 |
| 40 | 243.5 | 0 | 0 |
| 41 | 243.5 | 0 | 0 |
| 42 | 243.5 | 0 | 0 |
| 43 | 243.5 | 0 | 0 |
| 44 | 243.5 | 0 | 0 |
| 45 | 243.5 | 0 | 0 |
| 46 | 243.5 | 0 | 0 |
| 47 | 243.5 | 0 | 0 |
| 48 | 243.666667 | 0 | 0 |
| 49 | 245.666667 | 0 | 0 |
| 50 | 245.666667 | 0 | 0 |
| 51 | 245.666667 | 0 | 0 |
| 52 | 74.1666667 | 0 | 0 |
| 53 | 74.1666667 | 0 | 0 |
| 54 | 74.1666667 | 0 | 0 |
| 55 | 74.1666667 | 0 | 0 |
| 56 | 37424.6667 | 0 | 0 |
| 57 | 59.3333333 | 0 | 0 |
| 58 | 59.3333333 | 0 | 0 |
| 59 | 282.166667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 205.666667 | 0 | 0 |
| 4 | 205.666667 | 0 | 0 |
| 5 | 205.666667 | 0 | 0 |
| 6 | 205.666667 | 0 | 0 |
| 7 | 205.666667 | 0 | 0 |
| 8 | 205.666667 | 0 | 0 |
| 9 | 205.666667 | 0 | 0 |
| 10 | 205.666667 | 0 | 0 |
| 11 | 205.666667 | 0 | 0 |
| 12 | 205.666667 | 0 | 0 |
| 13 | 205.666667 | 0 | 0 |
| 14 | 205.666667 | 0 | 0 |
| 15 | 61.6666667 | 0 | 0 |
| 16 | 61.6666667 | 0 | 0 |
| 17 | 59.8333333 | 0 | 0 |
| 18 | 59.8333333 | 0 | 0 |
| 19 | | | |
| 20 | | | |
| 21 | | | |
| 22 | | | |
| 23 | | | |
| 24 | | | |
| 25 | | | |
| 26 | | | |
| 27 | | | |
| 28 | | | |
| 29 | | | |
| 30 | | | |
| 31 | | | |
| 32 | | | |
| 33 | | | |
| 34 | | | |
| 35 | | | |
| 36 | | | |
| 37 | | | |
| 38 | | | |
| 39 | | | |
| 40 | | | |
| 41 | | | |
| 42 | | | |
| 43 | | | |
| 44 | | | |
| 45 | | | |
| 46 | | | |
| 47 | | | |
| 48 | | | |
| 49 | | | |
| 50 | | | |
| 51 | | | |
| 52 | | | |
| 53 | | | |
| 54 | | | |
| 55 | | | |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| miRNA_Acc. | Target_Acc. | Expectation | UPE\$ | miRNA_start | miRNA_end |
|--------------|--------------------|-------------|-------|-------------|-----------|
| ugagguaguagg | Phvul.002G267400.1 | 2 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.002G267400.1 | 2 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.002G071800.1 | 2.5 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.002G071800.1 | 2.5 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.002G071800.1 | 2.5 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.002G071800.1 | 2.5 | -1 | 1 | 22 |
| agagguaguagg | Phvul.006G201700.1 | 2.5 | -1 | 1 | 24 |
| ugagguaguagg | Phvul.009G057800.1 | 2.5 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.009G057800.1 | 2.5 | -1 | 1 | 22 |
| agagguaguagg | Phvul.009G086800.1 | 2.5 | -1 | 1 | 24 |
| ugagguaguagg | Phvul.010G116400.1 | 2.5 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.010G116400.1 | 2.5 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.010G116400.1 | 2.5 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.010G116400.1 | 2.5 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.L009543.1 | 2.5 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.L009543.1 | 2.5 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.L009543.1 | 2.5 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.L009543.1 | 2.5 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.001G077200.2 | 3 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.001G077200.2 | 3 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.001G077200.2 | 3 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.001G077200.2 | 3 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.001G215300.1 | 3 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.001G215300.2 | 3 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.001G215300.1 | 3 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.001G215300.2 | 3 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.002G267400.1 | 3 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.002G267400.1 | 3 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.002G267400.1 | 3 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.002G267400.1 | 3 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.002G281100.1 | 3 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.002G281100.1 | 3 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.002G281100.1 | 3 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.002G281100.1 | 3 | -1 | 1 | 22 |
| agagguaguagg | Phvul.004G044900.1 | 3 | -1 | 1 | 24 |
| agagguaguagg | Phvul.006G158900.1 | 3 | -1 | 1 | 24 |
| ugagguaguagg | Phvul.008G071966.1 | 3 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.008G071966.1 | 3 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.008G071966.1 | 3 | -1 | 1 | 22 |
| ugagguaguagg | Phvul.008G071966.1 | 3 | -1 | 1 | 22 |
| agagguaguagg | Phvul.008G110200.1 | 3 | -1 | 1 | 24 |
| agagguaguagg | Phvul.008G110500.1 | 3 | -1 | 1 | 24 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagǵ Phvul.008G163350.4 | 3 | -1 | 1 | 22 |
| 4 | ugagguaguagǵ Phvul.008G163350.3 | 3 | -1 | 1 | 22 |
| 5 | ugagguaguagǵ Phvul.008G163350.3 | 3 | -1 | 1 | 22 |
| 6 | ugagguaguagǵ Phvul.008G163350.2 | 3 | -1 | 1 | 22 |
| 7 | ugagguaguagǵ Phvul.008G163350.1 | 3 | -1 | 1 | 22 |
| 8 | ugagguaguagǵ Phvul.008G163350.4 | 3 | -1 | 1 | 22 |
| 9 | ugagguaguagǵ Phvul.008G163350.4 | 3 | -1 | 1 | 22 |
| 10 | ugagguaguagǵ Phvul.008G163350.3 | 3 | -1 | 1 | 22 |
| 11 | ugagguaguagǵ Phvul.008G163350.2 | 3 | -1 | 1 | 22 |
| 12 | ugagguaguagǵ Phvul.008G163350.2 | 3 | -1 | 1 | 22 |
| 13 | ugagguaguagǵ Phvul.008G163350.1 | 3 | -1 | 1 | 22 |
| 14 | ugagguaguagǵ Phvul.008G163350.4 | 3 | -1 | 1 | 22 |
| 15 | ugagguaguagǵ Phvul.008G163350.3 | 3 | -1 | 1 | 22 |
| 16 | ugagguaguagǵ Phvul.008G163350.2 | 3 | -1 | 1 | 22 |
| 17 | ugagguaguagǵ Phvul.008G163350.2 | 3 | -1 | 1 | 22 |
| 18 | ugagguaguagǵ Phvul.008G163350.1 | 3 | -1 | 1 | 22 |
| 19 | ugagguaguagǵ Phvul.008G163350.4 | 3 | -1 | 1 | 22 |
| 20 | ugagguaguagǵ Phvul.008G163350.3 | 3 | -1 | 1 | 22 |
| 21 | ugagguaguagǵ Phvul.008G163350.3 | 3 | -1 | 1 | 22 |
| 22 | ugagguaguagǵ Phvul.008G163350.2 | 3 | -1 | 1 | 22 |
| 23 | ugagguaguagǵ Phvul.008G163350.1 | 3 | -1 | 1 | 22 |
| 24 | ugagguaguagǵ Phvul.009G057800.1 | 3 | -1 | 1 | 22 |
| 25 | ugagguaguagǵ Phvul.009G057800.1 | 3 | -1 | 1 | 22 |
| 26 | ugagguaguagǵ Phvul.009G057800.1 | 3 | -1 | 1 | 22 |
| 27 | ugagguaguagǵ Phvul.009G057800.1 | 3 | -1 | 1 | 22 |
| 28 | ugagguaguagǵ Phvul.009G057800.1 | 3 | -1 | 1 | 22 |
| 29 | ugagguaguagǵ Phvul.009G057800.1 | 3 | -1 | 1 | 22 |
| 30 | ugagguaguagǵ Phvul.010G058700.1 | 3 | -1 | 1 | 22 |
| 31 | ugagguaguagǵ Phvul.010G058700.1 | 3 | -1 | 1 | 22 |
| 32 | ugagguaguagǵ Phvul.001G022400.1 | 3.5 | -1 | 1 | 22 |
| 33 | ugagguaguagǵ Phvul.001G022400.1 | 3.5 | -1 | 1 | 22 |
| 34 | ugagguaguagǵ Phvul.001G022400.1 | 3.5 | -1 | 1 | 22 |
| 35 | ugagguaguagǵ Phvul.001G077200.2 | 3.5 | -1 | 1 | 22 |
| 36 | ugagguaguagǵ Phvul.001G077200.2 | 3.5 | -1 | 1 | 22 |
| 37 | ugagguaguagǵ Phvul.001G077200.2 | 3.5 | -1 | 1 | 22 |
| 38 | ugagguaguagǵ Phvul.001G077700.1 | 3.5 | -1 | 1 | 22 |
| 39 | ugagguaguagǵ Phvul.001G077700.1 | 3.5 | -1 | 1 | 22 |
| 40 | ugagguaguagǵ Phvul.001G077700.1 | 3.5 | -1 | 1 | 22 |
| 41 | ugagguaguagǵ Phvul.001G086466.1 | 3.5 | -1 | 1 | 22 |
| 42 | ugagguaguagǵ Phvul.001G086466.1 | 3.5 | -1 | 1 | 22 |
| 43 | ugagguaguagǵ Phvul.001G086466.1 | 3.5 | -1 | 1 | 22 |
| 44 | ugagguaguagǵ Phvul.001G086466.1 | 3.5 | -1 | 1 | 22 |
| 45 | ugagguaguagǵ Phvul.001G086466.1 | 3.5 | -1 | 1 | 22 |
| 46 | ugagguaguagǵ Phvul.001G089600.1 | 3.5 | -1 | 1 | 22 |
| 47 | ugagguaguagǵ Phvul.001G089600.1 | 3.5 | -1 | 1 | 22 |
| 48 | ugagguaguagǵ Phvul.001G089600.1 | 3.5 | -1 | 1 | 22 |
| 49 | ugagguaguagǵ Phvul.001G089600.1 | 3.5 | -1 | 1 | 22 |
| 50 | ugagguaguagǵ Phvul.001G089600.1 | 3.5 | -1 | 1 | 22 |
| 51 | ugagguaguagǵ Phvul.001G091100.1 | 3.5 | -1 | 1 | 22 |
| 52 | ugagguaguagǵ Phvul.001G091100.1 | 3.5 | -1 | 1 | 22 |
| 53 | ugagguaguagǵ Phvul.001G091100.1 | 3.5 | -1 | 1 | 22 |
| 54 | ugagguaguagǵ Phvul.001G091100.1 | 3.5 | -1 | 1 | 22 |
| 55 | ugagguaguagǵ Phvul.001G091100.1 | 3.5 | -1 | 1 | 22 |
| 56 | agagguaguagǵ Phvul.001G121000.1 | 3.5 | -1 | 1 | 24 |
| 57 | agagguaguagǵ Phvul.001G121000.2 | 3.5 | -1 | 1 | 24 |
| 58 | agagguaguagǵ Phvul.001G121000.2 | 3.5 | -1 | 1 | 24 |
| 59 | ugagguaguagǵ Phvul.001G131150.1 | 3.5 | -1 | 1 | 22 |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagξ Phvul.001G131150.2 | 3.5 | -1 | 1 | 22 |
| 4 | ugagguaguagξ Phvul.001G131150.1 | 3.5 | -1 | 1 | 22 |
| 5 | ugagguaguagξ Phvul.001G131150.2 | 3.5 | -1 | 1 | 22 |
| 6 | ugagguaguagξ Phvul.001G131150.2 | 3.5 | -1 | 1 | 22 |
| 7 | ugagguaguagξ Phvul.001G131150.1 | 3.5 | -1 | 1 | 22 |
| 8 | ugagguaguagξ Phvul.001G131150.2 | 3.5 | -1 | 1 | 22 |
| 9 | ugagguaguagξ Phvul.001G131150.2 | 3.5 | -1 | 1 | 22 |
| 10 | ugagguaguagξ Phvul.001G131150.1 | 3.5 | -1 | 1 | 22 |
| 11 | ugagguaguagξ Phvul.001G131150.2 | 3.5 | -1 | 1 | 22 |
| 12 | ugagguaguagξ Phvul.001G141000.1 | 3.5 | -1 | 1 | 22 |
| 13 | ugagguaguagξ Phvul.001G141000.1 | 3.5 | -1 | 1 | 22 |
| 14 | ugagguaguagξ Phvul.001G141000.1 | 3.5 | -1 | 1 | 22 |
| 15 | ugagguaguagξ Phvul.001G141000.1 | 3.5 | -1 | 1 | 22 |
| 16 | ugagguaguagξ Phvul.001G141000.1 | 3.5 | -1 | 1 | 22 |
| 17 | ugagguaguagξ Phvul.001G141000.1 | 3.5 | -1 | 1 | 22 |
| 18 | agagguaguagξ Phvul.001G179700.1 | 3.5 | -1 | 1 | 24 |
| 19 | ugagguaguagξ Phvul.001G179700.1 | 3.5 | -1 | 1 | 22 |
| 20 | ugagguaguagξ Phvul.001G179700.1 | 3.5 | -1 | 1 | 22 |
| 21 | ugagguaguagξ Phvul.001G179700.1 | 3.5 | -1 | 1 | 22 |
| 22 | ugagguaguagξ Phvul.001G179700.1 | 3.5 | -1 | 1 | 22 |
| 23 | ugagguaguagξ Phvul.001G179700.1 | 3.5 | -1 | 1 | 22 |
| 24 | ugagguaguagξ Phvul.002G042000.2 | 3.5 | -1 | 1 | 22 |
| 25 | ugagguaguagξ Phvul.002G042000.8 | 3.5 | -1 | 1 | 22 |
| 26 | ugagguaguagξ Phvul.002G042000.8 | 3.5 | -1 | 1 | 22 |
| 27 | ugagguaguagξ Phvul.002G042000.7 | 3.5 | -1 | 1 | 22 |
| 28 | ugagguaguagξ Phvul.002G042000.6 | 3.5 | -1 | 1 | 22 |
| 29 | ugagguaguagξ Phvul.002G042000.5 | 3.5 | -1 | 1 | 22 |
| 30 | ugagguaguagξ Phvul.002G042000.5 | 3.5 | -1 | 1 | 22 |
| 31 | ugagguaguagξ Phvul.002G042000.3 | 3.5 | -1 | 1 | 22 |
| 32 | ugagguaguagξ Phvul.002G042000.4 | 3.5 | -1 | 1 | 22 |
| 33 | ugagguaguagξ Phvul.002G042000.4 | 3.5 | -1 | 1 | 22 |
| 34 | ugagguaguagξ Phvul.002G042000.1 | 3.5 | -1 | 1 | 22 |
| 35 | ugagguaguagξ Phvul.002G042000.2 | 3.5 | -1 | 1 | 22 |
| 36 | ugagguaguagξ Phvul.002G042000.8 | 3.5 | -1 | 1 | 22 |
| 37 | ugagguaguagξ Phvul.002G042000.8 | 3.5 | -1 | 1 | 22 |
| 38 | ugagguaguagξ Phvul.002G042000.7 | 3.5 | -1 | 1 | 22 |
| 39 | ugagguaguagξ Phvul.002G042000.6 | 3.5 | -1 | 1 | 22 |
| 40 | ugagguaguagξ Phvul.002G042000.5 | 3.5 | -1 | 1 | 22 |
| 41 | ugagguaguagξ Phvul.002G042000.5 | 3.5 | -1 | 1 | 22 |
| 42 | ugagguaguagξ Phvul.002G042000.3 | 3.5 | -1 | 1 | 22 |
| 43 | ugagguaguagξ Phvul.002G042000.4 | 3.5 | -1 | 1 | 22 |
| 44 | ugagguaguagξ Phvul.002G042000.4 | 3.5 | -1 | 1 | 22 |
| 45 | ugagguaguagξ Phvul.002G042000.1 | 3.5 | -1 | 1 | 22 |
| 46 | ugagguaguagξ Phvul.002G068200.1 | 3.5 | -1 | 1 | 22 |
| 47 | ugagguaguagξ Phvul.002G068200.1 | 3.5 | -1 | 1 | 22 |
| 48 | ugagguaguagξ Phvul.002G071800.1 | 3.5 | -1 | 1 | 22 |
| 49 | ugagguaguagξ Phvul.002G071800.1 | 3.5 | -1 | 1 | 22 |
| 50 | ugagguaguagξ Phvul.002G071800.1 | 3.5 | -1 | 1 | 22 |
| 51 | ugagguaguagξ Phvul.002G076600.1 | 3.5 | -1 | 1 | 22 |
| 52 | ugagguaguagξ Phvul.002G076600.1 | 3.5 | -1 | 1 | 22 |
| 53 | ugagguaguagξ Phvul.002G076600.1 | 3.5 | -1 | 1 | 22 |
| 54 | ugagguaguagξ Phvul.002G076600.1 | 3.5 | -1 | 1 | 22 |
| 55 | ugagguaguagξ Phvul.002G076600.1 | 3.5 | -1 | 1 | 22 |
| 56 | agagguaguagξ Phvul.002G185150.2 | 3.5 | -1 | 1 | 24 |
| 57 | agagguaguagξ Phvul.002G185150.1 | 3.5 | -1 | 1 | 24 |
| 58 | agagguaguagξ Phvul.002G185150.1 | 3.5 | -1 | 1 | 24 |
| 59 | agagguaguagξ Phvul.002G185150.3 | 3.5 | -1 | 1 | 24 |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | agagguaguagǵ Phvul.002G304500.1 | 3.5 | -1 | 1 | 24 |
| 4 | ugagguaguagǵ Phvul.003G103100.2 | 3.5 | -1 | 1 | 22 |
| 5 | ugagguaguagǵ Phvul.003G103100.2 | 3.5 | -1 | 1 | 22 |
| 6 | ugagguaguagǵ Phvul.003G103100.2 | 3.5 | -1 | 1 | 22 |
| 7 | agagguaguagǵ Phvul.004G044800.1 | 3.5 | -1 | 1 | 24 |
| 8 | agagguaguagǵ Phvul.004G106000.1 | 3.5 | -1 | 1 | 24 |
| 9 | ugagguaguagǵ Phvul.004G133400.1 | 3.5 | -1 | 1 | 22 |
| 10 | ugagguaguagǵ Phvul.004G133400.1 | 3.5 | -1 | 1 | 22 |
| 11 | ugagguaguagǵ Phvul.004G133400.1 | 3.5 | -1 | 1 | 22 |
| 12 | ugagguaguagǵ Phvul.004G176700.1 | 3.5 | -1 | 1 | 22 |
| 13 | ugagguaguagǵ Phvul.004G176700.1 | 3.5 | -1 | 1 | 22 |
| 14 | ugagguaguagǵ Phvul.004G176700.1 | 3.5 | -1 | 1 | 22 |
| 15 | ugagguaguagǵ Phvul.004G176700.1 | 3.5 | -1 | 1 | 22 |
| 16 | ugagguaguagǵ Phvul.004G176700.1 | 3.5 | -1 | 1 | 22 |
| 17 | ugagguaguagǵ Phvul.004G176700.1 | 3.5 | -1 | 1 | 22 |
| 18 | agagguaguagǵ Phvul.005G087300.1 | 3.5 | -1 | 1 | 24 |
| 19 | ugagguaguagǵ Phvul.005G116100.2 | 3.5 | -1 | 1 | 22 |
| 20 | ugagguaguagǵ Phvul.005G116100.1 | 3.5 | -1 | 1 | 22 |
| 21 | ugagguaguagǵ Phvul.005G116100.2 | 3.5 | -1 | 1 | 22 |
| 22 | ugagguaguagǵ Phvul.005G116100.2 | 3.5 | -1 | 1 | 22 |
| 23 | ugagguaguagǵ Phvul.005G116100.1 | 3.5 | -1 | 1 | 22 |
| 24 | ugagguaguagǵ Phvul.005G180200.1 | 3.5 | -1 | 1 | 22 |
| 25 | ugagguaguagǵ Phvul.005G180200.1 | 3.5 | -1 | 1 | 22 |
| 26 | ugagguaguagǵ Phvul.005G180200.1 | 3.5 | -1 | 1 | 22 |
| 27 | ugagguaguagǵ Phvul.006G019800.1 | 3.5 | -1 | 1 | 22 |
| 28 | ugagguaguagǵ Phvul.006G019800.1 | 3.5 | -1 | 1 | 22 |
| 29 | ugagguaguagǵ Phvul.006G019800.1 | 3.5 | -1 | 1 | 22 |
| 30 | ugagguaguagǵ Phvul.006G019800.1 | 3.5 | -1 | 1 | 22 |
| 31 | ugagguaguagǵ Phvul.006G019800.1 | 3.5 | -1 | 1 | 22 |
| 32 | ugagguaguagǵ Phvul.006G067700.1 | 3.5 | -1 | 1 | 22 |
| 33 | ugagguaguagǵ Phvul.006G067700.1 | 3.5 | -1 | 1 | 22 |
| 34 | ugagguaguagǵ Phvul.006G067700.1 | 3.5 | -1 | 1 | 22 |
| 35 | ugagguaguagǵ Phvul.006G067700.1 | 3.5 | -1 | 1 | 22 |
| 36 | ugagguaguagǵ Phvul.006G067700.1 | 3.5 | -1 | 1 | 22 |
| 37 | ugagguaguagǵ Phvul.006G067700.1 | 3.5 | -1 | 1 | 22 |
| 38 | agagguaguagǵ Phvul.006G106900.2 | 3.5 | -1 | 1 | 24 |
| 39 | agagguaguagǵ Phvul.006G106900.1 | 3.5 | -1 | 1 | 24 |
| 40 | agagguaguagǵ Phvul.006G137200.3 | 3.5 | -1 | 1 | 24 |
| 41 | agagguaguagǵ Phvul.006G137200.2 | 3.5 | -1 | 1 | 24 |
| 42 | ugagguaguagǵ Phvul.007G113800.1 | 3.5 | -1 | 1 | 22 |
| 43 | ugagguaguagǵ Phvul.007G113800.1 | 3.5 | -1 | 1 | 22 |
| 44 | ugagguaguagǵ Phvul.007G113800.1 | 3.5 | -1 | 1 | 22 |
| 45 | ugagguaguagǵ Phvul.007G211400.1 | 3.5 | -1 | 1 | 22 |
| 46 | ugagguaguagǵ Phvul.007G211400.1 | 3.5 | -1 | 1 | 22 |
| 47 | ugagguaguagǵ Phvul.007G211400.1 | 3.5 | -1 | 1 | 22 |
| 48 | ugagguaguagǵ Phvul.007G219400.1 | 3.5 | -1 | 1 | 22 |
| 49 | ugagguaguagǵ Phvul.007G219400.1 | 3.5 | -1 | 1 | 22 |
| 50 | ugagguaguagǵ Phvul.007G219400.1 | 3.5 | -1 | 1 | 22 |
| 51 | ugagguaguagǵ Phvul.008G071966.1 | 3.5 | -1 | 1 | 22 |
| 52 | ugagguaguagǵ Phvul.008G071966.1 | 3.5 | -1 | 1 | 22 |
| 53 | ugagguaguagǵ Phvul.008G107300.1 | 3.5 | -1 | 1 | 22 |
| 54 | ugagguaguagǵ Phvul.008G107300.1 | 3.5 | -1 | 1 | 22 |
| 55 | ugagguaguagǵ Phvul.008G107300.1 | 3.5 | -1 | 1 | 22 |
| 56 | ugagguaguagǵ Phvul.008G115900.1 | 3.5 | -1 | 1 | 22 |
| 57 | ugagguaguagǵ Phvul.008G115900.1 | 3.5 | -1 | 1 | 22 |
| 58 | ugagguaguagǵ Phvul.008G115900.1 | 3.5 | -1 | 1 | 22 |
| 59 | ugagguaguagǵ Phvul.008G257700.2 | 3.5 | -1 | 1 | 22 |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagc Phvul.008G257700.1 | 3.5 | -1 | 1 | 22 |
| 4 | ugagguaguagc Phvul.008G257700.2 | 3.5 | -1 | 1 | 22 |
| 5 | ugagguaguagc Phvul.008G257700.1 | 3.5 | -1 | 1 | 22 |
| 6 | ugagguaguagc Phvul.008G257700.1 | 3.5 | -1 | 1 | 22 |
| 7 | agagguaguagc Phvul.008G282700.1 | 3.5 | -1 | 1 | 24 |
| 8 | agagguaguagc Phvul.008G289600.1 | 3.5 | -1 | 1 | 24 |
| 9 | ugagguaguagc Phvul.009G127300.1 | 3.5 | -1 | 1 | 22 |
| 10 | ugagguaguagc Phvul.009G127300.1 | 3.5 | -1 | 1 | 22 |
| 11 | ugagguaguagc Phvul.009G127300.1 | 3.5 | -1 | 1 | 22 |
| 12 | ugagguaguagc Phvul.009G127300.1 | 3.5 | -1 | 1 | 22 |
| 13 | ugagguaguagc Phvul.009G127300.1 | 3.5 | -1 | 1 | 22 |
| 14 | ugagguaguagc Phvul.009G127300.1 | 3.5 | -1 | 1 | 22 |
| 15 | ugagguaguagc Phvul.009G160700.1 | 3.5 | -1 | 1 | 22 |
| 16 | ugagguaguagc Phvul.009G160700.1 | 3.5 | -1 | 1 | 22 |
| 17 | ugagguaguagc Phvul.009G160700.1 | 3.5 | -1 | 1 | 22 |
| 18 | ugagguaguagc Phvul.009G160700.1 | 3.5 | -1 | 1 | 22 |
| 19 | ugagguaguagc Phvul.009G160700.1 | 3.5 | -1 | 1 | 22 |
| 20 | ugagguaguagc Phvul.010G064700.1 | 3.5 | -1 | 1 | 22 |
| 21 | ugagguaguagc Phvul.010G064700.1 | 3.5 | -1 | 1 | 22 |
| 22 | ugagguaguagc Phvul.010G064700.1 | 3.5 | -1 | 1 | 22 |
| 23 | ugagguaguagc Phvul.010G064700.1 | 3.5 | -1 | 1 | 22 |
| 24 | ugagguaguagc Phvul.010G064700.1 | 3.5 | -1 | 1 | 22 |
| 25 | ugagguaguagc Phvul.010G064700.1 | 3.5 | -1 | 1 | 22 |
| 26 | ugagguaguagc Phvul.011G047100.1 | 3.5 | -1 | 1 | 22 |
| 27 | ugagguaguagc Phvul.011G047100.1 | 3.5 | -1 | 1 | 22 |
| 28 | ugagguaguagc Phvul.011G050300.1 | 3.5 | -1 | 1 | 22 |
| 29 | ugagguaguagc Phvul.011G050300.2 | 3.5 | -1 | 1 | 22 |
| 30 | ugagguaguagc Phvul.011G050300.2 | 3.5 | -1 | 1 | 22 |
| 31 | ugagguaguagc Phvul.011G050300.1 | 3.5 | -1 | 1 | 22 |
| 32 | ugagguaguagc Phvul.011G050300.2 | 3.5 | -1 | 1 | 22 |
| 33 | ugagguaguagc Phvul.011G050300.2 | 3.5 | -1 | 1 | 22 |
| 34 | ugagguaguagc Phvul.L007343.1 | 3.5 | -1 | 1 | 22 |
| 35 | ugagguaguagc Phvul.L007343.1 | 3.5 | -1 | 1 | 22 |
| 36 | ugagguaguagc Phvul.001G022700.1 | 4 | -1 | 1 | 22 |
| 37 | ugagguaguagc Phvul.001G022700.1 | 4 | -1 | 1 | 22 |
| 38 | ugagguaguagc Phvul.001G022700.1 | 4 | -1 | 1 | 22 |
| 39 | agagguaguagc Phvul.001G036800.1 | 4 | -1 | 1 | 24 |
| 40 | ugagguaguagc Phvul.001G100700.2 | 4 | -1 | 1 | 22 |
| 41 | ugagguaguagc Phvul.001G100700.2 | 4 | -1 | 1 | 22 |
| 42 | ugagguaguagc Phvul.001G100700.2 | 4 | -1 | 1 | 22 |
| 43 | ugagguaguagc Phvul.001G153600.2 | 4 | -1 | 1 | 22 |
| 44 | ugagguaguagc Phvul.001G153600.2 | 4 | -1 | 1 | 22 |
| 45 | ugagguaguagc Phvul.001G153600.2 | 4 | -1 | 1 | 22 |
| 46 | ugagguaguagc Phvul.001G153600.2 | 4 | -1 | 1 | 22 |
| 47 | ugagguaguagc Phvul.001G153600.2 | 4 | -1 | 1 | 22 |
| 48 | agagguaguagc Phvul.001G247000.1 | 4 | -1 | 1 | 24 |
| 49 | agagguaguagc Phvul.002G004100.1 | 4 | -1 | 1 | 24 |
| 50 | ugagguaguagc Phvul.002G013866.1 | 4 | -1 | 1 | 22 |
| 51 | ugagguaguagc Phvul.002G013866.1 | 4 | -1 | 1 | 22 |
| 52 | ugagguaguagc Phvul.002G013866.1 | 4 | -1 | 1 | 22 |
| 53 | agagguaguagc Phvul.002G212900.1 | 4 | -1 | 1 | 24 |
| 54 | ugagguaguagc Phvul.002G212900.1 | 4 | -1 | 1 | 22 |
| 55 | ugagguaguagc Phvul.002G253200.1 | 4 | -1 | 1 | 22 |
| 56 | ugagguaguagc Phvul.002G253200.1 | 4 | -1 | 1 | 22 |
| 57 | agagguaguagc Phvul.003G029000.2 | 4 | -1 | 1 | 24 |
| 58 | agagguaguagc Phvul.003G029000.2 | 4 | -1 | 1 | 24 |
| 59 | agagguaguagc Phvul.003G029000.1 | 4 | -1 | 1 | 24 |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagξ Phvul.003G087600.2 | 4 | -1 | 1 | 22 |
| 4 | ugagguaguagξ Phvul.003G087600.1 | 4 | -1 | 1 | 22 |
| 5 | ugagguaguagξ Phvul.003G087600.2 | 4 | -1 | 1 | 22 |
| 6 | ugagguaguagξ Phvul.003G087600.1 | 4 | -1 | 1 | 22 |
| 7 | ugagguaguagξ Phvul.003G087600.2 | 4 | -1 | 1 | 22 |
| 8 | ugagguaguagξ Phvul.003G087600.1 | 4 | -1 | 1 | 22 |
| 9 | ugagguaguagξ Phvul.003G087600.2 | 4 | -1 | 1 | 22 |
| 10 | ugagguaguagξ Phvul.003G087600.1 | 4 | -1 | 1 | 22 |
| 11 | ugagguaguagξ Phvul.003G087600.2 | 4 | -1 | 1 | 22 |
| 12 | ugagguaguagξ Phvul.003G087600.1 | 4 | -1 | 1 | 22 |
| 13 | ugagguaguagξ Phvul.003G087600.2 | 4 | -1 | 1 | 22 |
| 14 | ugagguaguagξ Phvul.003G104200.1 | 4 | -1 | 1 | 22 |
| 15 | ugagguaguagξ Phvul.003G104200.1 | 4 | -1 | 1 | 22 |
| 16 | ugagguaguagξ Phvul.003G141700.1 | 4 | -1 | 1 | 22 |
| 17 | ugagguaguagξ Phvul.003G141700.1 | 4 | -1 | 1 | 22 |
| 18 | ugagguaguagξ Phvul.003G231500.1 | 4 | -1 | 1 | 22 |
| 19 | ugagguaguagξ Phvul.003G231500.1 | 4 | -1 | 1 | 22 |
| 20 | ugagguaguagξ Phvul.003G231500.1 | 4 | -1 | 1 | 22 |
| 21 | ugagguaguagξ Phvul.003G231500.1 | 4 | -1 | 1 | 22 |
| 22 | ugagguaguagξ Phvul.003G231500.1 | 4 | -1 | 1 | 22 |
| 23 | ugagguaguagξ Phvul.003G231500.1 | 4 | -1 | 1 | 22 |
| 24 | agagguaguagξ Phvul.003G294601.1 | 4 | -1 | 1 | 24 |
| 25 | agagguaguagξ Phvul.003G294800.4 | 4 | -1 | 1 | 24 |
| 26 | agagguaguagξ Phvul.003G294800.3 | 4 | -1 | 1 | 24 |
| 27 | ugagguaguagξ Phvul.004G015500.1 | 4 | -1 | 1 | 22 |
| 28 | ugagguaguagξ Phvul.004G015500.1 | 4 | -1 | 1 | 22 |
| 29 | ugagguaguagξ Phvul.004G015500.1 | 4 | -1 | 1 | 22 |
| 30 | ugagguaguagξ Phvul.004G015500.1 | 4 | -1 | 1 | 22 |
| 31 | ugagguaguagξ Phvul.004G032100.1 | 4 | -1 | 1 | 24 |
| 32 | ugagguaguagξ Phvul.004G044900.1 | 4 | -1 | 1 | 22 |
| 33 | ugagguaguagξ Phvul.004G044900.1 | 4 | -1 | 1 | 22 |
| 34 | agagguaguagξ Phvul.004G163200.1 | 4 | -1 | 1 | 24 |
| 35 | agagguaguagξ Phvul.005G010700.2 | 4 | -1 | 1 | 24 |
| 36 | ugagguaguagξ Phvul.005G015800.2 | 4 | -1 | 1 | 22 |
| 37 | ugagguaguagξ Phvul.005G015800.1 | 4 | -1 | 1 | 22 |
| 38 | ugagguaguagξ Phvul.005G015800.2 | 4 | -1 | 1 | 22 |
| 39 | ugagguaguagξ Phvul.005G015800.1 | 4 | -1 | 1 | 22 |
| 40 | ugagguaguagξ Phvul.005G015800.2 | 4 | -1 | 1 | 22 |
| 41 | ugagguaguagξ Phvul.005G015800.1 | 4 | -1 | 1 | 22 |
| 42 | ugagguaguagξ Phvul.005G015800.2 | 4 | -1 | 1 | 22 |
| 43 | ugagguaguagξ Phvul.005G015800.1 | 4 | -1 | 1 | 22 |
| 44 | ugagguaguagξ Phvul.005G015800.2 | 4 | -1 | 1 | 22 |
| 45 | ugagguaguagξ Phvul.005G015800.1 | 4 | -1 | 1 | 22 |
| 46 | ugagguaguagξ Phvul.005G015800.2 | 4 | -1 | 1 | 22 |
| 47 | ugagguaguagξ Phvul.005G015800.1 | 4 | -1 | 1 | 22 |
| 48 | ugagguaguagξ Phvul.005G015800.2 | 4 | -1 | 1 | 22 |
| 49 | ugagguaguagξ Phvul.005G015800.1 | 4 | -1 | 1 | 22 |
| 50 | ugagguaguagξ Phvul.005G081600.1 | 4 | -1 | 1 | 22 |
| 51 | ugagguaguagξ Phvul.005G081600.1 | 4 | -1 | 1 | 22 |
| 52 | ugagguaguagξ Phvul.005G097200.3 | 4 | -1 | 1 | 22 |
| 53 | ugagguaguagξ Phvul.005G097200.6 | 4 | -1 | 1 | 22 |
| 54 | ugagguaguagξ Phvul.005G097200.5 | 4 | -1 | 1 | 22 |
| 55 | ugagguaguagξ Phvul.005G097200.3 | 4 | -1 | 1 | 22 |
| 56 | ugagguaguagξ Phvul.005G097200.6 | 4 | -1 | 1 | 22 |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagã Phvul.005G097200.5 | 4 | -1 | 1 | 22 |
| 4 | ugagguaguagã Phvul.006G062000.1 | 4 | -1 | 1 | 22 |
| 5 | ugagguaguagã Phvul.006G062000.1 | 4 | -1 | 1 | 22 |
| 6 | ugagguaguagã Phvul.006G130611.1 | 4 | -1 | 1 | 22 |
| 7 | ugagguaguagã Phvul.006G130611.1 | 4 | -1 | 1 | 22 |
| 8 | ugagguaguagã Phvul.006G130611.1 | 4 | -1 | 1 | 22 |
| 9 | ugagguaguagã Phvul.006G130611.1 | 4 | -1 | 1 | 22 |
| 10 | agagguaguagğ Phvul.006G192200.2 | 4 | -1 | 1 | 24 |
| 11 | agagguaguagğ Phvul.006G192200.1 | 4 | -1 | 1 | 24 |
| 12 | agagguaguagğ Phvul.006G192200.4 | 4 | -1 | 1 | 24 |
| 13 | agagguaguagğ Phvul.006G192200.4 | 4 | -1 | 1 | 24 |
| 14 | agagguaguagğ Phvul.006G192200.3 | 4 | -1 | 1 | 24 |
| 15 | agagguaguagğ Phvul.007G058400.1 | 4 | -1 | 1 | 24 |
| 16 | agagguaguagğ Phvul.007G058400.2 | 4 | -1 | 1 | 24 |
| 17 | agagguaguagğ Phvul.007G058400.2 | 4 | -1 | 1 | 24 |
| 18 | ugagguaguagã Phvul.007G064700.1 | 4 | -1 | 1 | 22 |
| 19 | ugagguaguagã Phvul.007G064700.1 | 4 | -1 | 1 | 22 |
| 20 | ugagguaguagã Phvul.007G064700.1 | 4 | -1 | 1 | 22 |
| 21 | agagguaguagğ Phvul.007G182300.2 | 4 | -1 | 1 | 24 |
| 22 | ugagguaguagã Phvul.007G198500.1 | 4 | -1 | 1 | 22 |
| 23 | ugagguaguagã Phvul.007G198500.1 | 4 | -1 | 1 | 22 |
| 24 | ugagguaguagã Phvul.007G233800.1 | 4 | -1 | 1 | 22 |
| 25 | ugagguaguagã Phvul.007G233800.1 | 4 | -1 | 1 | 22 |
| 26 | ugagguaguagã Phvul.007G233800.2 | 4 | -1 | 1 | 22 |
| 27 | ugagguaguagã Phvul.007G233800.1 | 4 | -1 | 1 | 22 |
| 28 | ugagguaguagã Phvul.007G233800.2 | 4 | -1 | 1 | 22 |
| 29 | ugagguaguagã Phvul.007G233800.2 | 4 | -1 | 1 | 22 |
| 30 | ugagguaguagã Phvul.008G008300.6 | 4 | -1 | 1 | 22 |
| 31 | ugagguaguagã Phvul.008G008300.3 | 4 | -1 | 1 | 22 |
| 32 | ugagguaguagã Phvul.008G008300.5 | 4 | -1 | 1 | 22 |
| 33 | ugagguaguagã Phvul.008G008300.5 | 4 | -1 | 1 | 22 |
| 34 | ugagguaguagã Phvul.008G008300.4 | 4 | -1 | 1 | 22 |
| 35 | ugagguaguagã Phvul.008G008300.2 | 4 | -1 | 1 | 22 |
| 36 | ugagguaguagã Phvul.008G008300.6 | 4 | -1 | 1 | 22 |
| 37 | ugagguaguagã Phvul.008G008300.6 | 4 | -1 | 1 | 22 |
| 38 | ugagguaguagã Phvul.008G008300.3 | 4 | -1 | 1 | 22 |
| 39 | ugagguaguagã Phvul.008G008300.5 | 4 | -1 | 1 | 22 |
| 40 | ugagguaguagã Phvul.008G008300.4 | 4 | -1 | 1 | 22 |
| 41 | ugagguaguagã Phvul.008G008300.4 | 4 | -1 | 1 | 22 |
| 42 | ugagguaguagã Phvul.008G008300.2 | 4 | -1 | 1 | 22 |
| 43 | ugagguaguagğ Phvul.008G009200.2 | 4 | -1 | 1 | 22 |
| 44 | ugagguaguagğ Phvul.008G009200.2 | 4 | -1 | 1 | 22 |
| 45 | ugagguaguagğ Phvul.008G009200.2 | 4 | -1 | 1 | 22 |
| 46 | ugagguaguagğ Phvul.008G009200.2 | 4 | -1 | 1 | 22 |
| 47 | ugagguaguagğ Phvul.008G009200.2 | 4 | -1 | 1 | 22 |
| 48 | ugagguaguagã Phvul.008G038300.1 | 4 | -1 | 1 | 22 |
| 49 | ugagguaguagã Phvul.008G038300.1 | 4 | -1 | 1 | 22 |
| 50 | ugagguaguagã Phvul.008G038300.1 | 4 | -1 | 1 | 22 |
| 51 | ugagguaguagã Phvul.008G093200.3 | 4 | -1 | 1 | 22 |
| 52 | ugagguaguagã Phvul.008G093200.2 | 4 | -1 | 1 | 22 |
| 53 | ugagguaguagã Phvul.008G093200.1 | 4 | -1 | 1 | 22 |
| 54 | ugagguaguagã Phvul.008G093200.1 | 4 | -1 | 1 | 22 |
| 55 | ugagguaguagã Phvul.008G093200.3 | 4 | -1 | 1 | 22 |
| 56 | ugagguaguagã Phvul.008G093200.2 | 4 | -1 | 1 | 22 |
| 57 | ugagguaguagã Phvul.008G093200.1 | 4 | -1 | 1 | 22 |
| 58 | ugagguaguagã Phvul.008G093200.1 | 4 | -1 | 1 | 22 |
| 59 | ugagguaguagã Phvul.008G108800.2 | 4 | -1 | 1 | 22 |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagc Phvul.008G108800.2 | 4 | -1 | 1 | 22 |
| 4 | ugagguaguagc Phvul.008G108800.2 | 4 | -1 | 1 | 22 |
| 5 | ugagguaguagc Phvul.008G108800.2 | 4 | -1 | 1 | 22 |
| 6 | ugagguaguagc Phvul.008G108800.2 | 4 | -1 | 1 | 22 |
| 7 | agagguaguagc Phvul.008G110000.1 | 4 | -1 | 1 | 24 |
| 8 | ugagguaguagc Phvul.008G110200.1 | 4 | -1 | 1 | 22 |
| 9 | ugagguaguagc Phvul.008G110200.1 | 4 | -1 | 1 | 22 |
| 10 | ugagguaguagc Phvul.008G110200.1 | 4 | -1 | 1 | 22 |
| 11 | agagguaguagc Phvul.008G110400.1 | 4 | -1 | 1 | 24 |
| 12 | ugagguaguagc Phvul.008G110500.1 | 4 | -1 | 1 | 22 |
| 13 | ugagguaguagc Phvul.008G110500.1 | 4 | -1 | 1 | 22 |
| 14 | ugagguaguagc Phvul.008G110500.1 | 4 | -1 | 1 | 22 |
| 15 | agagguaguagc Phvul.008G199500.1 | 4 | -1 | 1 | 24 |
| 16 | ugagguaguagc Phvul.008G290300.1 | 4 | -1 | 1 | 22 |
| 17 | ugagguaguagc Phvul.008G290300.1 | 4 | -1 | 1 | 22 |
| 18 | ugagguaguagc Phvul.008G290300.1 | 4 | -1 | 1 | 22 |
| 19 | ugagguaguagc Phvul.008G290300.1 | 4 | -1 | 1 | 22 |
| 20 | ugagguaguagc Phvul.008G290300.1 | 4 | -1 | 1 | 22 |
| 21 | ugagguaguagc Phvul.008G290300.1 | 4 | -1 | 1 | 22 |
| 22 | ugagguaguagc Phvul.009G026200.1 | 4 | -1 | 1 | 22 |
| 23 | ugagguaguagc Phvul.009G026200.1 | 4 | -1 | 1 | 22 |
| 24 | agagguaguagc Phvul.009G040800.3 | 4 | -1 | 1 | 24 |
| 25 | agagguaguagc Phvul.009G040800.1 | 4 | -1 | 1 | 24 |
| 26 | agagguaguagc Phvul.009G040800.1 | 4 | -1 | 1 | 24 |
| 27 | agagguaguagc Phvul.009G040800.2 | 4 | -1 | 1 | 24 |
| 28 | ugagguaguagc Phvul.009G121300.1 | 4 | -1 | 1 | 22 |
| 29 | ugagguaguagc Phvul.009G121300.2 | 4 | -1 | 1 | 22 |
| 30 | ugagguaguagc Phvul.009G121300.2 | 4 | -1 | 1 | 22 |
| 31 | ugagguaguagc Phvul.009G121300.1 | 4 | -1 | 1 | 22 |
| 32 | ugagguaguagc Phvul.009G121300.2 | 4 | -1 | 1 | 22 |
| 33 | ugagguaguagc Phvul.009G121300.1 | 4 | -1 | 1 | 22 |
| 34 | ugagguaguagc Phvul.009G121300.1 | 4 | -1 | 1 | 22 |
| 35 | ugagguaguagc Phvul.009G121300.2 | 4 | -1 | 1 | 22 |
| 36 | ugagguaguagc Phvul.009G121300.1 | 4 | -1 | 1 | 22 |
| 37 | ugagguaguagc Phvul.009G121300.2 | 4 | -1 | 1 | 22 |
| 38 | ugagguaguagc Phvul.009G121300.2 | 4 | -1 | 1 | 22 |
| 39 | ugagguaguagc Phvul.009G246900.4 | 4 | -1 | 1 | 22 |
| 40 | ugagguaguagc Phvul.009G246900.3 | 4 | -1 | 1 | 22 |
| 41 | ugagguaguagc Phvul.009G246900.1 | 4 | -1 | 1 | 22 |
| 42 | ugagguaguagc Phvul.009G246900.1 | 4 | -1 | 1 | 22 |
| 43 | ugagguaguagc Phvul.009G246900.2 | 4 | -1 | 1 | 22 |
| 44 | ugagguaguagc Phvul.009G246900.4 | 4 | -1 | 1 | 22 |
| 45 | ugagguaguagc Phvul.009G246900.3 | 4 | -1 | 1 | 22 |
| 46 | ugagguaguagc Phvul.009G246900.3 | 4 | -1 | 1 | 22 |
| 47 | ugagguaguagc Phvul.009G246900.1 | 4 | -1 | 1 | 22 |
| 48 | ugagguaguagc Phvul.009G246900.2 | 4 | -1 | 1 | 22 |
| 49 | ugagguaguagc Phvul.009G246900.2 | 4 | -1 | 1 | 22 |
| 50 | ugagguaguagc Phvul.010G048400.4 | 4 | -1 | 1 | 22 |
| 51 | ugagguaguagc Phvul.010G048400.3 | 4 | -1 | 1 | 22 |
| 52 | ugagguaguagc Phvul.010G048400.1 | 4 | -1 | 1 | 22 |
| 53 | ugagguaguagc Phvul.010G048400.2 | 4 | -1 | 1 | 22 |
| 54 | ugagguaguagc Phvul.010G048400.4 | 4 | -1 | 1 | 22 |
| 55 | ugagguaguagc Phvul.010G048400.4 | 4 | -1 | 1 | 22 |
| 56 | ugagguaguagc Phvul.010G048400.3 | 4 | -1 | 1 | 22 |
| 57 | ugagguaguagc Phvul.010G048400.1 | 4 | -1 | 1 | 22 |
| 58 | ugagguaguagc Phvul.010G048400.1 | 4 | -1 | 1 | 22 |
| 59 | ugagguaguagc Phvul.010G048400.2 | 4 | -1 | 1 | 22 |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagξ Phvul.010G048400.4 | 4 | -1 | 1 | 22 |
| 4 | ugagguaguagξ Phvul.010G048400.3 | 4 | -1 | 1 | 22 |
| 5 | ugagguaguagξ Phvul.010G048400.1 | 4 | -1 | 1 | 22 |
| 6 | ugagguaguagξ Phvul.010G048400.2 | 4 | -1 | 1 | 22 |
| 7 | ugagguaguagξ Phvul.010G048400.4 | 4 | -1 | 1 | 22 |
| 8 | ugagguaguagξ Phvul.010G048400.3 | 4 | -1 | 1 | 22 |
| 9 | ugagguaguagξ Phvul.010G048400.1 | 4 | -1 | 1 | 22 |
| 10 | ugagguaguagξ Phvul.010G048400.2 | 4 | -1 | 1 | 22 |
| 11 | ugagguaguagξ Phvul.010G116400.1 | 4 | -1 | 1 | 22 |
| 12 | ugagguaguagξ Phvul.010G116400.1 | 4 | -1 | 1 | 22 |
| 13 | ugagguaguagξ Phvul.010G116400.1 | 4 | -1 | 1 | 22 |
| 14 | ugagguaguagξ Phvul.010G116400.1 | 4 | -1 | 1 | 22 |
| 15 | ugagguaguagξ Phvul.011G013800.1 | 4 | -1 | 1 | 22 |
| 16 | ugagguaguagξ Phvul.011G013800.1 | 4 | -1 | 1 | 22 |
| 17 | ugagguaguagξ Phvul.011G013800.1 | 4 | -1 | 1 | 22 |
| 18 | ugagguaguagξ Phvul.011G013800.1 | 4 | -1 | 1 | 22 |
| 19 | ugagguaguagξ Phvul.011G123701.1 | 4 | -1 | 1 | 22 |
| 20 | ugagguaguagξ Phvul.011G123701.1 | 4 | -1 | 1 | 22 |
| 21 | ugagguaguagξ Phvul.011G123701.1 | 4 | -1 | 1 | 22 |
| 22 | ugagguaguagξ Phvul.011G123701.1 | 4 | -1 | 1 | 22 |
| 23 | ugagguaguagξ Phvul.011G123701.1 | 4 | -1 | 1 | 22 |
| 24 | ugagguaguagξ Phvul.011G160800.1 | 4 | -1 | 1 | 22 |
| 25 | ugagguaguagξ Phvul.011G160800.3 | 4 | -1 | 1 | 22 |
| 26 | ugagguaguagξ Phvul.011G160800.2 | 4 | -1 | 1 | 22 |
| 27 | ugagguaguagξ Phvul.011G160800.1 | 4 | -1 | 1 | 22 |
| 28 | ugagguaguagξ Phvul.011G160800.3 | 4 | -1 | 1 | 22 |
| 29 | ugagguaguagξ Phvul.011G160800.2 | 4 | -1 | 1 | 22 |
| 30 | ugagguaguagξ Phvul.011G173000.1 | 4 | -1 | 1 | 22 |
| 31 | ugagguaguagξ Phvul.011G173000.1 | 4 | -1 | 1 | 22 |
| 32 | ugagguaguagξ Phvul.011G173000.1 | 4 | -1 | 1 | 22 |
| 33 | ugagguaguagξ Phvul.011G173000.1 | 4 | -1 | 1 | 22 |
| 34 | agagguaguagξ Phvul.011G190200.3 | 4 | -1 | 1 | 24 |
| 35 | agagguaguagξ Phvul.011G190200.2 | 4 | -1 | 1 | 24 |
| 36 | ugagguaguagξ Phvul.001G098600.1 | 4.5 | -1 | 1 | 22 |
| 37 | ugagguaguagξ Phvul.001G098600.1 | 4.5 | -1 | 1 | 22 |
| 38 | ugagguaguagξ Phvul.001G102901.2 | 4.5 | -1 | 1 | 22 |
| 39 | ugagguaguagξ Phvul.001G102901.4 | 4.5 | -1 | 1 | 22 |
| 40 | ugagguaguagξ Phvul.001G102901.3 | 4.5 | -1 | 1 | 22 |
| 41 | ugagguaguagξ Phvul.001G102901.1 | 4.5 | -1 | 1 | 22 |
| 42 | ugagguaguagξ Phvul.001G102901.2 | 4.5 | -1 | 1 | 22 |
| 43 | ugagguaguagξ Phvul.001G102901.4 | 4.5 | -1 | 1 | 22 |
| 44 | ugagguaguagξ Phvul.001G102901.3 | 4.5 | -1 | 1 | 22 |
| 45 | ugagguaguagξ Phvul.001G102901.1 | 4.5 | -1 | 1 | 22 |
| 46 | ugagguaguagξ Phvul.001G102901.2 | 4.5 | -1 | 1 | 22 |
| 47 | ugagguaguagξ Phvul.001G102901.1 | 4.5 | -1 | 1 | 22 |
| 48 | ugagguaguagξ Phvul.001G102901.2 | 4.5 | -1 | 1 | 22 |
| 49 | ugagguaguagξ Phvul.001G102901.1 | 4.5 | -1 | 1 | 22 |
| 50 | ugagguaguagξ Phvul.001G102901.2 | 4.5 | -1 | 1 | 22 |
| 51 | ugagguaguagξ Phvul.001G102901.1 | 4.5 | -1 | 1 | 22 |
| 52 | ugagguaguagξ Phvul.001G102901.2 | 4.5 | -1 | 1 | 22 |
| 53 | ugagguaguagξ Phvul.001G102901.1 | 4.5 | -1 | 1 | 22 |
| 54 | ugagguaguagξ Phvul.001G102901.2 | 4.5 | -1 | 1 | 22 |
| 55 | ugagguaguagξ Phvul.001G102901.1 | 4.5 | -1 | 1 | 22 |
| 56 | ugagguaguagξ Phvul.001G102901.2 | 4.5 | -1 | 1 | 22 |
| 57 | ugagguaguagξ Phvul.001G102901.1 | 4.5 | -1 | 1 | 22 |
| 58 | ugagguaguagξ Phvul.001G102901.2 | 4.5 | -1 | 1 | 22 |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagξ Phvul.001G102901.4 | 4.5 | -1 | 1 | 22 |
| 4 | ugagguaguagξ Phvul.001G102901.3 | 4.5 | -1 | 1 | 22 |
| 5 | ugagguaguagξ Phvul.001G102901.3 | 4.5 | -1 | 1 | 22 |
| 6 | ugagguaguagξ Phvul.001G102901.1 | 4.5 | -1 | 1 | 22 |
| 7 | ugagguaguagξ Phvul.001G102901.2 | 4.5 | -1 | 1 | 22 |
| 8 | ugagguaguagξ Phvul.001G102901.4 | 4.5 | -1 | 1 | 22 |
| 9 | ugagguaguagξ Phvul.001G102901.4 | 4.5 | -1 | 1 | 22 |
| 10 | ugagguaguagξ Phvul.001G102901.3 | 4.5 | -1 | 1 | 22 |
| 11 | ugagguaguagξ Phvul.001G102901.1 | 4.5 | -1 | 1 | 22 |
| 12 | ugagguaguagξ Phvul.001G102901.1 | 4.5 | -1 | 1 | 22 |
| 13 | agagguaguagξ Phvul.001G147800.2 | 4.5 | -1 | 1 | 24 |
| 14 | ugagguaguagξ Phvul.001G173900.1 | 4.5 | -1 | 1 | 22 |
| 15 | ugagguaguagξ Phvul.001G173900.1 | 4.5 | -1 | 1 | 22 |
| 16 | ugagguaguagξ Phvul.001G173900.1 | 4.5 | -1 | 1 | 22 |
| 17 | ugagguaguagξ Phvul.001G173900.1 | 4.5 | -1 | 1 | 22 |
| 18 | ugagguaguagξ Phvul.001G173900.1 | 4.5 | -1 | 1 | 22 |
| 19 | ugagguaguagξ Phvul.001G179700.1 | 4.5 | -1 | 1 | 22 |
| 20 | ugagguaguagξ Phvul.001G179700.1 | 4.5 | -1 | 1 | 22 |
| 21 | ugagguaguagξ Phvul.001G179700.1 | 4.5 | -1 | 1 | 22 |
| 22 | ugagguaguagξ Phvul.001G200700.3 | 4.5 | -1 | 1 | 22 |
| 23 | ugagguaguagξ Phvul.001G200700.1 | 4.5 | -1 | 1 | 22 |
| 24 | ugagguaguagξ Phvul.001G200700.3 | 4.5 | -1 | 1 | 22 |
| 25 | ugagguaguagξ Phvul.001G200700.3 | 4.5 | -1 | 1 | 22 |
| 26 | ugagguaguagξ Phvul.001G200700.1 | 4.5 | -1 | 1 | 22 |
| 27 | ugagguaguagξ Phvul.001G200700.3 | 4.5 | -1 | 1 | 22 |
| 28 | ugagguaguagξ Phvul.001G200700.1 | 4.5 | -1 | 1 | 22 |
| 29 | ugagguaguagξ Phvul.001G200700.1 | 4.5 | -1 | 1 | 22 |
| 30 | ugagguaguagξ Phvul.001G200700.3 | 4.5 | -1 | 1 | 22 |
| 31 | ugagguaguagξ Phvul.001G200700.1 | 4.5 | -1 | 1 | 22 |
| 32 | ugagguaguagξ Phvul.001G200700.1 | 4.5 | -1 | 1 | 22 |
| 33 | agagguaguagξ Phvul.001G260300.1 | 4.5 | -1 | 1 | 24 |
| 34 | ugagguaguagξ Phvul.001G268700.1 | 4.5 | -1 | 1 | 22 |
| 35 | ugagguaguagξ Phvul.001G268700.1 | 4.5 | -1 | 1 | 22 |
| 36 | ugagguaguagξ Phvul.002G058900.1 | 4.5 | -1 | 1 | 22 |
| 37 | ugagguaguagξ Phvul.002G058900.1 | 4.5 | -1 | 1 | 22 |
| 38 | ugagguaguagξ Phvul.002G058900.1 | 4.5 | -1 | 1 | 22 |
| 39 | ugagguaguagξ Phvul.002G068200.1 | 4.5 | -1 | 1 | 22 |
| 40 | ugagguaguagξ Phvul.002G068200.1 | 4.5 | -1 | 1 | 22 |
| 41 | ugagguaguagξ Phvul.002G068200.1 | 4.5 | -1 | 1 | 22 |
| 42 | ugagguaguagξ Phvul.002G068200.1 | 4.5 | -1 | 1 | 22 |
| 43 | ugagguaguagξ Phvul.002G068200.1 | 4.5 | -1 | 1 | 22 |
| 44 | ugagguaguagξ Phvul.002G163400.1 | 4.5 | -1 | 1 | 22 |
| 45 | ugagguaguagξ Phvul.002G163400.1 | 4.5 | -1 | 1 | 22 |
| 46 | ugagguaguagξ Phvul.002G163400.1 | 4.5 | -1 | 1 | 22 |
| 47 | ugagguaguagξ Phvul.002G165300.1 | 4.5 | -1 | 1 | 22 |
| 48 | ugagguaguagξ Phvul.002G165300.1 | 4.5 | -1 | 1 | 22 |
| 49 | ugagguaguagξ Phvul.002G165300.1 | 4.5 | -1 | 1 | 22 |
| 50 | ugagguaguagξ Phvul.002G165300.1 | 4.5 | -1 | 1 | 22 |
| 51 | ugagguaguagξ Phvul.002G165300.1 | 4.5 | -1 | 1 | 22 |
| 52 | ugagguaguagξ Phvul.002G216700.3 | 4.5 | -1 | 1 | 22 |
| 53 | ugagguaguagξ Phvul.002G216700.2 | 4.5 | -1 | 1 | 22 |
| 54 | ugagguaguagξ Phvul.002G216700.2 | 4.5 | -1 | 1 | 22 |
| 55 | ugagguaguagξ Phvul.002G216700.3 | 4.5 | -1 | 1 | 22 |
| 56 | ugagguaguagξ Phvul.002G216700.2 | 4.5 | -1 | 1 | 22 |
| 57 | ugagguaguagξ Phvul.002G243300.1 | 4.5 | -1 | 1 | 22 |
| 58 | ugagguaguagξ Phvul.002G243300.1 | 4.5 | -1 | 1 | 22 |
| 59 | ugagguaguagξ Phvul.002G243300.1 | 4.5 | -1 | 1 | 22 |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagξ Phvul.002G253200.1 | 4.5 | -1 | 1 | 22 |
| 4 | ugagguaguagξ Phvul.002G253200.1 | 4.5 | -1 | 1 | 22 |
| 5 | ugagguaguagξ Phvul.002G253200.1 | 4.5 | -1 | 1 | 22 |
| 6 | ugagguaguagξ Phvul.002G253200.1 | 4.5 | -1 | 1 | 22 |
| 7 | ugagguaguagξ Phvul.002G253200.1 | 4.5 | -1 | 1 | 22 |
| 8 | ugagguaguagξ Phvul.002G283800.1 | 4.5 | -1 | 1 | 22 |
| 9 | ugagguaguagξ Phvul.002G283800.1 | 4.5 | -1 | 1 | 22 |
| 10 | ugagguaguagξ Phvul.002G283800.1 | 4.5 | -1 | 1 | 22 |
| 11 | ugagguaguagξ Phvul.002G283800.1 | 4.5 | -1 | 1 | 22 |
| 12 | ugagguaguagξ Phvul.002G283800.1 | 4.5 | -1 | 1 | 22 |
| 13 | ugagguaguagξ Phvul.002G283800.1 | 4.5 | -1 | 1 | 22 |
| 14 | ugagguaguagζ Phvul.002G290904.1 | 4.5 | -1 | 1 | 22 |
| 15 | ugagguaguagζ Phvul.002G290904.1 | 4.5 | -1 | 1 | 22 |
| 16 | ugagguaguagζ Phvul.002G309100.1 | 4.5 | -1 | 1 | 22 |
| 17 | ugagguaguagζ Phvul.002G309100.1 | 4.5 | -1 | 1 | 22 |
| 18 | ugagguaguagξ Phvul.002G320900.1 | 4.5 | -1 | 1 | 22 |
| 19 | ugagguaguagξ Phvul.002G320900.1 | 4.5 | -1 | 1 | 22 |
| 20 | ugagguaguagξ Phvul.002G320900.1 | 4.5 | -1 | 1 | 22 |
| 21 | ugagguaguagξ Phvul.002G320900.1 | 4.5 | -1 | 1 | 22 |
| 22 | ugagguaguagξ Phvul.002G320900.1 | 4.5 | -1 | 1 | 22 |
| 23 | ugagguaguagξ Phvul.002G320900.1 | 4.5 | -1 | 1 | 22 |
| 24 | ugagguaguagξ Phvul.002G329900.2 | 4.5 | -1 | 1 | 22 |
| 25 | ugagguaguagξ Phvul.002G329900.1 | 4.5 | -1 | 1 | 22 |
| 26 | ugagguaguagξ Phvul.002G329900.2 | 4.5 | -1 | 1 | 22 |
| 27 | ugagguaguagξ Phvul.002G329900.1 | 4.5 | -1 | 1 | 22 |
| 28 | ugagguaguagξ Phvul.002G329900.1 | 4.5 | -1 | 1 | 22 |
| 29 | ugagguaguagξ Phvul.002G329900.2 | 4.5 | -1 | 1 | 22 |
| 30 | ugagguaguagξ Phvul.002G329900.1 | 4.5 | -1 | 1 | 22 |
| 31 | ugagguaguagξ Phvul.002G329900.1 | 4.5 | -1 | 1 | 22 |
| 32 | ugagguaguagξ Phvul.002G329900.2 | 4.5 | -1 | 1 | 22 |
| 33 | ugagguaguagξ Phvul.002G329900.1 | 4.5 | -1 | 1 | 22 |
| 34 | ugagguaguagζ Phvul.003G032300.1 | 4.5 | -1 | 1 | 22 |
| 35 | ugagguaguagζ Phvul.003G032300.1 | 4.5 | -1 | 1 | 22 |
| 36 | ugagguaguagζ Phvul.003G057700.1 | 4.5 | -1 | 1 | 22 |
| 37 | ugagguaguagζ Phvul.003G057700.1 | 4.5 | -1 | 1 | 22 |
| 38 | ugagguaguagξ Phvul.003G078900.1 | 4.5 | -1 | 1 | 22 |
| 39 | ugagguaguagξ Phvul.003G078900.1 | 4.5 | -1 | 1 | 22 |
| 40 | ugagguaguagξ Phvul.003G078900.1 | 4.5 | -1 | 1 | 22 |
| 41 | ugagguaguagξ Phvul.003G078900.1 | 4.5 | -1 | 1 | 22 |
| 42 | ugagguaguagξ Phvul.003G078900.1 | 4.5 | -1 | 1 | 22 |
| 43 | ugagguaguagξ Phvul.003G078900.1 | 4.5 | -1 | 1 | 22 |
| 44 | ugagguaguagξ Phvul.003G078900.1 | 4.5 | -1 | 1 | 22 |
| 45 | ugagguaguagξ Phvul.003G137000.1 | 4.5 | -1 | 1 | 22 |
| 46 | ugagguaguagξ Phvul.003G137000.1 | 4.5 | -1 | 1 | 22 |
| 47 | ugagguaguagξ Phvul.003G137000.1 | 4.5 | -1 | 1 | 22 |
| 48 | ugagguaguagξ Phvul.003G137000.1 | 4.5 | -1 | 1 | 22 |
| 49 | ugagguaguagξ Phvul.003G137000.1 | 4.5 | -1 | 1 | 22 |
| 50 | ugagguaguagξ Phvul.003G137000.1 | 4.5 | -1 | 1 | 22 |
| 51 | ugagguaguagξ Phvul.003G247200.2 | 4.5 | -1 | 1 | 22 |
| 52 | ugagguaguagξ Phvul.003G247200.1 | 4.5 | -1 | 1 | 22 |
| 53 | ugagguaguagξ Phvul.003G247200.2 | 4.5 | -1 | 1 | 22 |
| 54 | ugagguaguagξ Phvul.003G247200.1 | 4.5 | -1 | 1 | 22 |
| 55 | ugagguaguagξ Phvul.003G247200.2 | 4.5 | -1 | 1 | 22 |
| 56 | ugagguaguagξ Phvul.003G247200.1 | 4.5 | -1 | 1 | 22 |
| 57 | ugagguaguagξ Phvul.003G247200.2 | 4.5 | -1 | 1 | 22 |
| 58 | ugagguaguagξ Phvul.003G247200.1 | 4.5 | -1 | 1 | 22 |
| 59 | ugagguaguagξ Phvul.003G247200.2 | 4.5 | -1 | 1 | 22 |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagξ Phvul.003G247200.1 | 4.5 | -1 | 1 | 22 |
| 4 | ugagguaguagξ Phvul.003G280100.2 | 4.5 | -1 | 1 | 22 |
| 5 | ugagguaguagξ Phvul.003G280100.2 | 4.5 | -1 | 1 | 22 |
| 6 | ugagguaguagξ Phvul.003G294601.1 | 4.5 | -1 | 1 | 22 |
| 7 | ugagguaguagξ Phvul.003G294601.1 | 4.5 | -1 | 1 | 22 |
| 8 | ugagguaguagξ Phvul.003G294601.1 | 4.5 | -1 | 1 | 22 |
| 9 | ugagguaguagξ Phvul.003G294601.1 | 4.5 | -1 | 1 | 22 |
| 10 | ugagguaguagξ Phvul.003G294601.1 | 4.5 | -1 | 1 | 22 |
| 11 | ugagguaguagξ Phvul.003G294601.1 | 4.5 | -1 | 1 | 22 |
| 12 | ugagguaguagξ Phvul.003G294800.4 | 4.5 | -1 | 1 | 22 |
| 13 | ugagguaguagξ Phvul.003G294800.4 | 4.5 | -1 | 1 | 22 |
| 14 | ugagguaguagξ Phvul.003G294800.3 | 4.5 | -1 | 1 | 22 |
| 15 | ugagguaguagξ Phvul.003G294800.4 | 4.5 | -1 | 1 | 22 |
| 16 | ugagguaguagξ Phvul.003G294800.3 | 4.5 | -1 | 1 | 22 |
| 17 | ugagguaguagξ Phvul.003G294800.3 | 4.5 | -1 | 1 | 22 |
| 18 | ugagguaguagξ Phvul.003G294800.4 | 4.5 | -1 | 1 | 22 |
| 19 | ugagguaguagξ Phvul.003G294800.3 | 4.5 | -1 | 1 | 22 |
| 20 | ugagguaguagξ Phvul.003G294800.4 | 4.5 | -1 | 1 | 22 |
| 21 | ugagguaguagξ Phvul.003G294800.4 | 4.5 | -1 | 1 | 22 |
| 22 | ugagguaguagξ Phvul.003G294800.3 | 4.5 | -1 | 1 | 22 |
| 23 | ugagguaguagξ Phvul.004G032100.1 | 4.5 | -1 | 1 | 22 |
| 24 | ugagguaguagξ Phvul.004G032100.1 | 4.5 | -1 | 1 | 22 |
| 25 | ugagguaguagξ Phvul.004G032100.1 | 4.5 | -1 | 1 | 22 |
| 26 | ugagguaguagξ Phvul.004G032100.1 | 4.5 | -1 | 1 | 22 |
| 27 | ugagguaguagξ Phvul.004G032100.1 | 4.5 | -1 | 1 | 22 |
| 28 | ugagguaguagξ Phvul.004G044800.1 | 4.5 | -1 | 1 | 22 |
| 29 | ugagguaguagξ Phvul.004G044800.1 | 4.5 | -1 | 1 | 22 |
| 30 | ugagguaguagξ Phvul.004G050550.1 | 4.5 | -1 | 1 | 22 |
| 31 | ugagguaguagξ Phvul.004G050550.1 | 4.5 | -1 | 1 | 22 |
| 32 | ugagguaguagξ Phvul.004G050550.1 | 4.5 | -1 | 1 | 22 |
| 33 | ugagguaguagξ Phvul.004G050550.1 | 4.5 | -1 | 1 | 22 |
| 34 | ugagguaguagξ Phvul.004G050550.1 | 4.5 | -1 | 1 | 22 |
| 35 | ugagguaguagξ Phvul.004G050550.1 | 4.5 | -1 | 1 | 22 |
| 36 | ugagguaguagξ Phvul.004G173101.1 | 4.5 | -1 | 1 | 22 |
| 37 | ugagguaguagξ Phvul.004G173101.1 | 4.5 | -1 | 1 | 22 |
| 38 | ugagguaguagξ Phvul.004G173101.1 | 4.5 | -1 | 1 | 22 |
| 39 | ugagguaguagξ Phvul.004G173101.1 | 4.5 | -1 | 1 | 22 |
| 40 | ugagguaguagξ Phvul.004G173101.1 | 4.5 | -1 | 1 | 22 |
| 41 | ugagguaguagξ Phvul.005G006400.1 | 4.5 | -1 | 1 | 22 |
| 42 | ugagguaguagξ Phvul.005G006400.1 | 4.5 | -1 | 1 | 22 |
| 43 | ugagguaguagξ Phvul.005G006400.1 | 4.5 | -1 | 1 | 22 |
| 44 | ugagguaguagξ Phvul.005G006400.1 | 4.5 | -1 | 1 | 22 |
| 45 | ugagguaguagξ Phvul.005G006400.1 | 4.5 | -1 | 1 | 22 |
| 46 | ugagguaguagξ Phvul.005G014300.2 | 4.5 | -1 | 1 | 24 |
| 47 | agagguaguagξ Phvul.005G056400.1 | 4.5 | -1 | 1 | 24 |
| 48 | agagguaguagξ Phvul.005G056400.1 | 4.5 | -1 | 1 | 24 |
| 49 | agagguaguagξ Phvul.005G095300.1 | 4.5 | -1 | 1 | 24 |
| 50 | agagguaguagξ Phvul.005G100300.1 | 4.5 | -1 | 1 | 24 |
| 51 | agagguaguagξ Phvul.005G100300.1 | 4.5 | -1 | 1 | 24 |
| 52 | ugagguaguagξ Phvul.005G116100.2 | 4.5 | -1 | 1 | 22 |
| 53 | ugagguaguagξ Phvul.005G116100.1 | 4.5 | -1 | 1 | 22 |
| 54 | ugagguaguagξ Phvul.005G116100.2 | 4.5 | -1 | 1 | 22 |
| 55 | ugagguaguagξ Phvul.005G116100.2 | 4.5 | -1 | 1 | 22 |
| 56 | ugagguaguagξ Phvul.005G116100.1 | 4.5 | -1 | 1 | 22 |
| 57 | ugagguaguagξ Phvul.005G116100.2 | 4.5 | -1 | 1 | 22 |
| 58 | ugagguaguagξ Phvul.005G116100.2 | 4.5 | -1 | 1 | 22 |
| 59 | ugagguaguagξ Phvul.005G116100.1 | 4.5 | -1 | 1 | 22 |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagξ Phvul.005G116100.2 | 4.5 | -1 | 1 | 22 |
| 4 | ugagguaguagξ Phvul.005G116100.1 | 4.5 | -1 | 1 | 22 |
| 5 | ugagguaguagξ Phvul.005G116100.1 | 4.5 | -1 | 1 | 22 |
| 6 | ugagguaguagξ Phvul.005G130100.1 | 4.5 | -1 | 1 | 22 |
| 7 | ugagguaguagξ Phvul.005G130100.1 | 4.5 | -1 | 1 | 22 |
| 8 | agagguaguagξ Phvul.006G105800.1 | 4.5 | -1 | 1 | 24 |
| 9 | ugagguaguagξ Phvul.006G113800.2 | 4.5 | -1 | 1 | 22 |
| 10 | ugagguaguagξ Phvul.006G113800.1 | 4.5 | -1 | 1 | 22 |
| 11 | ugagguaguagξ Phvul.006G113800.1 | 4.5 | -1 | 1 | 22 |
| 12 | ugagguaguagξ Phvul.006G113800.2 | 4.5 | -1 | 1 | 22 |
| 13 | ugagguaguagξ Phvul.006G113800.1 | 4.5 | -1 | 1 | 22 |
| 14 | ugagguaguagξ Phvul.006G113800.2 | 4.5 | -1 | 1 | 22 |
| 15 | ugagguaguagξ Phvul.006G113800.2 | 4.5 | -1 | 1 | 22 |
| 16 | ugagguaguagξ Phvul.006G113800.1 | 4.5 | -1 | 1 | 22 |
| 17 | ugagguaguagξ Phvul.006G113800.2 | 4.5 | -1 | 1 | 22 |
| 18 | ugagguaguagξ Phvul.006G113800.1 | 4.5 | -1 | 1 | 22 |
| 19 | ugagguaguagξ Phvul.006G113800.1 | 4.5 | -1 | 1 | 22 |
| 20 | ugagguaguagξ Phvul.006G121500.1 | 4.5 | -1 | 1 | 22 |
| 21 | ugagguaguagξ Phvul.006G121500.2 | 4.5 | -1 | 1 | 22 |
| 22 | ugagguaguagξ Phvul.006G121500.1 | 4.5 | -1 | 1 | 22 |
| 23 | ugagguaguagξ Phvul.006G121500.2 | 4.5 | -1 | 1 | 22 |
| 24 | ugagguaguagξ Phvul.006G121500.1 | 4.5 | -1 | 1 | 22 |
| 25 | ugagguaguagξ Phvul.006G121500.1 | 4.5 | -1 | 1 | 22 |
| 26 | ugagguaguagξ Phvul.006G121500.1 | 4.5 | -1 | 1 | 22 |
| 27 | ugagguaguagξ Phvul.006G121500.1 | 4.5 | -1 | 1 | 22 |
| 28 | ugagguaguagξ Phvul.006G121500.1 | 4.5 | -1 | 1 | 22 |
| 29 | ugagguaguagξ Phvul.006G121500.1 | 4.5 | -1 | 1 | 22 |
| 30 | ugagguaguagξ Phvul.006G121500.1 | 4.5 | -1 | 1 | 22 |
| 31 | agagguaguagξ Phvul.006G158900.1 | 4.5 | -1 | 1 | 24 |
| 32 | ugagguaguagξ Phvul.006G168154.1 | 4.5 | -1 | 1 | 22 |
| 33 | ugagguaguagξ Phvul.006G168154.2 | 4.5 | -1 | 1 | 22 |
| 34 | ugagguaguagξ Phvul.006G168154.1 | 4.5 | -1 | 1 | 22 |
| 35 | ugagguaguagξ Phvul.006G168154.2 | 4.5 | -1 | 1 | 22 |
| 36 | ugagguaguagξ Phvul.006G193700.1 | 4.5 | -1 | 1 | 22 |
| 37 | ugagguaguagξ Phvul.006G193700.1 | 4.5 | -1 | 1 | 22 |
| 38 | ugagguaguagξ Phvul.007G012500.1 | 4.5 | -1 | 1 | 22 |
| 39 | ugagguaguagξ Phvul.007G012500.1 | 4.5 | -1 | 1 | 22 |
| 40 | ugagguaguagξ Phvul.007G012500.1 | 4.5 | -1 | 1 | 22 |
| 41 | ugagguaguagξ Phvul.007G012500.1 | 4.5 | -1 | 1 | 22 |
| 42 | ugagguaguagξ Phvul.007G012500.1 | 4.5 | -1 | 1 | 22 |
| 43 | ugagguaguagξ Phvul.007G012500.1 | 4.5 | -1 | 1 | 22 |
| 44 | ugagguaguagξ Phvul.007G012500.1 | 4.5 | -1 | 1 | 22 |
| 45 | ugagguaguagξ Phvul.007G015000.1 | 4.5 | -1 | 1 | 22 |
| 46 | ugagguaguagξ Phvul.007G015000.1 | 4.5 | -1 | 1 | 22 |
| 47 | agagguaguagξ Phvul.007G034000.1 | 4.5 | -1 | 1 | 24 |
| 48 | ugagguaguagξ Phvul.007G051100.1 | 4.5 | -1 | 1 | 22 |
| 49 | ugagguaguagξ Phvul.007G051100.1 | 4.5 | -1 | 1 | 22 |
| 50 | ugagguaguagξ Phvul.007G051100.1 | 4.5 | -1 | 1 | 22 |
| 51 | ugagguaguagξ Phvul.007G051100.1 | 4.5 | -1 | 1 | 22 |
| 52 | ugagguaguagξ Phvul.007G051100.1 | 4.5 | -1 | 1 | 22 |
| 53 | ugagguaguagξ Phvul.007G051100.1 | 4.5 | -1 | 1 | 22 |
| 54 | ugagguaguagξ Phvul.007G056600.1 | 4.5 | -1 | 1 | 22 |
| 55 | ugagguaguagξ Phvul.007G056600.1 | 4.5 | -1 | 1 | 22 |
| 56 | ugagguaguagξ Phvul.007G056600.1 | 4.5 | -1 | 1 | 22 |
| 57 | ugagguaguagξ Phvul.007G056600.1 | 4.5 | -1 | 1 | 22 |
| 58 | ugagguaguagξ Phvul.007G056600.1 | 4.5 | -1 | 1 | 22 |
| 59 | ugagguaguagξ Phvul.007G056600.1 | 4.5 | -1 | 1 | 22 |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagξ Phvul.007G058400.1 | 4.5 | -1 | 1 | 22 |
| 4 | ugagguaguagξ Phvul.007G058400.2 | 4.5 | -1 | 1 | 22 |
| 5 | ugagguaguagξ Phvul.007G058400.2 | 4.5 | -1 | 1 | 22 |
| 6 | ugagguaguagξ Phvul.007G058400.1 | 4.5 | -1 | 1 | 22 |
| 7 | ugagguaguagξ Phvul.007G058400.2 | 4.5 | -1 | 1 | 22 |
| 8 | ugagguaguagξ Phvul.007G058400.1 | 4.5 | -1 | 1 | 22 |
| 9 | ugagguaguagξ Phvul.007G058400.2 | 4.5 | -1 | 1 | 22 |
| 10 | ugagguaguagξ Phvul.007G058400.2 | 4.5 | -1 | 1 | 22 |
| 11 | ugagguaguagξ Phvul.007G058400.1 | 4.5 | -1 | 1 | 22 |
| 12 | ugagguaguagξ Phvul.007G058400.2 | 4.5 | -1 | 1 | 22 |
| 13 | ugagguaguagξ Phvul.007G058400.2 | 4.5 | -1 | 1 | 22 |
| 14 | agagguaguagξ Phvul.007G064700.1 | 4.5 | -1 | 1 | 24 |
| 15 | ugagguaguagξ Phvul.007G064700.1 | 4.5 | -1 | 1 | 22 |
| 16 | ugagguaguagξ Phvul.007G064700.1 | 4.5 | -1 | 1 | 22 |
| 17 | ugagguaguagξ Phvul.007G064700.1 | 4.5 | -1 | 1 | 22 |
| 18 | ugagguaguagξ Phvul.007G064700.1 | 4.5 | -1 | 1 | 22 |
| 19 | ugagguaguagξ Phvul.007G064700.1 | 4.5 | -1 | 1 | 22 |
| 20 | ugagguaguagξ Phvul.007G073800.1 | 4.5 | -1 | 1 | 22 |
| 21 | ugagguaguagξ Phvul.007G073800.1 | 4.5 | -1 | 1 | 22 |
| 22 | ugagguaguagξ Phvul.007G073800.1 | 4.5 | -1 | 1 | 22 |
| 23 | ugagguaguagξ Phvul.007G073800.1 | 4.5 | -1 | 1 | 22 |
| 24 | ugagguaguagξ Phvul.007G073800.1 | 4.5 | -1 | 1 | 22 |
| 25 | ugagguaguagξ Phvul.007G073800.1 | 4.5 | -1 | 1 | 22 |
| 26 | ugagguaguagξ Phvul.007G099300.1 | 4.5 | -1 | 1 | 22 |
| 27 | ugagguaguagξ Phvul.007G099300.1 | 4.5 | -1 | 1 | 22 |
| 28 | ugagguaguagξ Phvul.007G099300.1 | 4.5 | -1 | 1 | 22 |
| 29 | ugagguaguagξ Phvul.007G099300.1 | 4.5 | -1 | 1 | 22 |
| 30 | ugagguaguagξ Phvul.007G099300.1 | 4.5 | -1 | 1 | 22 |
| 31 | ugagguaguagξ Phvul.007G107200.1 | 4.5 | -1 | 1 | 22 |
| 32 | ugagguaguagξ Phvul.007G107200.1 | 4.5 | -1 | 1 | 22 |
| 33 | ugagguaguagξ Phvul.007G107200.1 | 4.5 | -1 | 1 | 22 |
| 34 | ugagguaguagξ Phvul.007G107200.1 | 4.5 | -1 | 1 | 22 |
| 35 | ugagguaguagξ Phvul.007G107200.1 | 4.5 | -1 | 1 | 22 |
| 36 | ugagguaguagξ Phvul.007G182300.2 | 4.5 | -1 | 1 | 22 |
| 37 | ugagguaguagξ Phvul.007G182300.2 | 4.5 | -1 | 1 | 22 |
| 38 | ugagguaguagξ Phvul.007G182300.2 | 4.5 | -1 | 1 | 22 |
| 39 | ugagguaguagξ Phvul.007G182300.2 | 4.5 | -1 | 1 | 22 |
| 40 | ugagguaguagξ Phvul.007G182300.2 | 4.5 | -1 | 1 | 22 |
| 41 | ugagguaguagξ Phvul.007G182300.2 | 4.5 | -1 | 1 | 22 |
| 42 | ugagguaguagξ Phvul.007G189000.1 | 4.5 | -1 | 1 | 22 |
| 43 | ugagguaguagξ Phvul.007G189000.1 | 4.5 | -1 | 1 | 22 |
| 44 | ugagguaguagξ Phvul.007G204300.2 | 4.5 | -1 | 1 | 22 |
| 45 | ugagguaguagξ Phvul.007G204300.1 | 4.5 | -1 | 1 | 22 |
| 46 | ugagguaguagξ Phvul.007G204300.1 | 4.5 | -1 | 1 | 22 |
| 47 | ugagguaguagξ Phvul.007G204300.2 | 4.5 | -1 | 1 | 22 |
| 48 | ugagguaguagξ Phvul.007G204300.1 | 4.5 | -1 | 1 | 22 |
| 49 | ugagguaguagξ Phvul.007G204300.2 | 4.5 | -1 | 1 | 22 |
| 50 | ugagguaguagξ Phvul.007G204300.2 | 4.5 | -1 | 1 | 22 |
| 51 | ugagguaguagξ Phvul.007G204300.1 | 4.5 | -1 | 1 | 22 |
| 52 | ugagguaguagξ Phvul.007G204300.2 | 4.5 | -1 | 1 | 22 |
| 53 | ugagguaguagξ Phvul.007G204300.1 | 4.5 | -1 | 1 | 22 |
| 54 | ugagguaguagξ Phvul.007G204300.1 | 4.5 | -1 | 1 | 22 |
| 55 | agagguaguagξ Phvul.007G210400.1 | 4.5 | -1 | 1 | 24 |
| 56 | ugagguaguagξ Phvul.007G275700.1 | 4.5 | -1 | 1 | 22 |
| 57 | ugagguaguagξ Phvul.007G275700.1 | 4.5 | -1 | 1 | 22 |
| 58 | ugagguaguagξ Phvul.007G275700.1 | 4.5 | -1 | 1 | 22 |
| 59 | ugagguaguagξ Phvul.007G276200.1 | 4.5 | -1 | 1 | 22 |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagã Phvul.007G276200.1 | 4.5 | -1 | 1 | 22 |
| 4 | ugagguaguagã Phvul.007G276300.1 | 4.5 | -1 | 1 | 22 |
| 5 | ugagguaguagã Phvul.007G276300.1 | 4.5 | -1 | 1 | 22 |
| 6 | ugagguaguagã Phvul.007G276300.1 | 4.5 | -1 | 1 | 22 |
| 7 | ugagguaguagğ Phvul.008G003900.1 | 4.5 | -1 | 1 | 22 |
| 8 | ugagguaguagğ Phvul.008G003900.1 | 4.5 | -1 | 1 | 22 |
| 9 | ugagguaguagğ Phvul.008G003900.1 | 4.5 | -1 | 1 | 22 |
| 10 | ugagguaguagğ Phvul.008G003900.1 | 4.5 | -1 | 1 | 22 |
| 11 | ugagguaguagğ Phvul.008G003900.1 | 4.5 | -1 | 1 | 22 |
| 12 | agagguaguagğ Phvul.008G008300.6 | 4.5 | -1 | 1 | 24 |
| 13 | agagguaguagğ Phvul.008G008300.3 | 4.5 | -1 | 1 | 24 |
| 14 | agagguaguagğ Phvul.008G008300.5 | 4.5 | -1 | 1 | 24 |
| 15 | agagguaguagğ Phvul.008G008300.4 | 4.5 | -1 | 1 | 24 |
| 16 | agagguaguagğ Phvul.008G008300.2 | 4.5 | -1 | 1 | 24 |
| 17 | agagguaguagğ Phvul.008G012100.1 | 4.5 | -1 | 1 | 24 |
| 18 | agagguaguagğ Phvul.008G012100.2 | 4.5 | -1 | 1 | 24 |
| 19 | agagguaguagğ Phvul.008G048200.1 | 4.5 | -1 | 1 | 24 |
| 20 | ugagguaguagğ Phvul.008G069000.1 | 4.5 | -1 | 1 | 22 |
| 21 | ugagguaguagğ Phvul.008G069000.1 | 4.5 | -1 | 1 | 22 |
| 22 | ugagguaguagğ Phvul.008G069000.1 | 4.5 | -1 | 1 | 22 |
| 23 | ugagguaguagğ Phvul.008G069000.1 | 4.5 | -1 | 1 | 22 |
| 24 | ugagguaguagğ Phvul.008G069000.1 | 4.5 | -1 | 1 | 22 |
| 25 | ugagguaguagğ Phvul.008G069000.1 | 4.5 | -1 | 1 | 22 |
| 26 | ugagguaguagğ Phvul.008G071966.1 | 4.5 | -1 | 1 | 22 |
| 27 | ugagguaguagğ Phvul.008G071966.1 | 4.5 | -1 | 1 | 22 |
| 28 | ugagguaguagğ Phvul.008G071966.1 | 4.5 | -1 | 1 | 22 |
| 29 | ugagguaguagğ Phvul.008G071966.1 | 4.5 | -1 | 1 | 22 |
| 30 | ugagguaguagğ Phvul.008G071966.1 | 4.5 | -1 | 1 | 22 |
| 31 | ugagguaguagğ Phvul.008G071966.1 | 4.5 | -1 | 1 | 22 |
| 32 | ugagguaguagğ Phvul.008G071966.1 | 4.5 | -1 | 1 | 22 |
| 33 | ugagguaguagã Phvul.008G093200.3 | 4.5 | -1 | 1 | 22 |
| 34 | ugagguaguagã Phvul.008G093200.2 | 4.5 | -1 | 1 | 22 |
| 35 | ugagguaguagã Phvul.008G093200.1 | 4.5 | -1 | 1 | 22 |
| 36 | ugagguaguagã Phvul.008G093200.3 | 4.5 | -1 | 1 | 22 |
| 37 | ugagguaguagã Phvul.008G093200.2 | 4.5 | -1 | 1 | 22 |
| 38 | ugagguaguagã Phvul.008G093200.1 | 4.5 | -1 | 1 | 22 |
| 39 | ugagguaguagã Phvul.008G093200.1 | 4.5 | -1 | 1 | 22 |
| 40 | ugagguaguagã Phvul.008G110000.1 | 4.5 | -1 | 1 | 22 |
| 41 | ugagguaguagã Phvul.008G110000.1 | 4.5 | -1 | 1 | 22 |
| 42 | agagguaguagğ Phvul.008G110100.1 | 4.5 | -1 | 1 | 24 |
| 43 | ugagguaguagã Phvul.008G110400.1 | 4.5 | -1 | 1 | 22 |
| 44 | ugagguaguagã Phvul.008G110400.1 | 4.5 | -1 | 1 | 22 |
| 45 | ugagguaguagã Phvul.008G118900.1 | 4.5 | -1 | 1 | 22 |
| 46 | ugagguaguagã Phvul.008G118900.1 | 4.5 | -1 | 1 | 22 |
| 47 | ugagguaguagğ Phvul.008G157900.1 | 4.5 | -1 | 1 | 22 |
| 48 | ugagguaguagğ Phvul.008G157900.1 | 4.5 | -1 | 1 | 22 |
| 49 | ugagguaguagğ Phvul.008G157900.1 | 4.5 | -1 | 1 | 22 |
| 50 | ugagguaguagğ Phvul.008G157900.1 | 4.5 | -1 | 1 | 22 |
| 51 | ugagguaguagã Phvul.008G206400.5 | 4.5 | -1 | 1 | 22 |
| 52 | ugagguaguagã Phvul.008G206400.1 | 4.5 | -1 | 1 | 22 |
| 53 | ugagguaguagã Phvul.008G206400.5 | 4.5 | -1 | 1 | 22 |
| 54 | ugagguaguagã Phvul.008G206400.5 | 4.5 | -1 | 1 | 22 |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagã Phvul.008G206400.1 | 4.5 | -1 | 1 | 22 |
| 4 | ugagguaguagË Phvul.008G225900.1 | 4.5 | -1 | 1 | 22 |
| 5 | ugagguaguagË Phvul.008G225900.1 | 4.5 | -1 | 1 | 22 |
| 6 | ugagguaguagË Phvul.008G225900.1 | 4.5 | -1 | 1 | 22 |
| 7 | ugagguaguagË Phvul.008G225900.1 | 4.5 | -1 | 1 | 22 |
| 8 | ugagguaguagË Phvul.008G225900.1 | 4.5 | -1 | 1 | 22 |
| 9 | ugagguaguagË Phvul.008G227600.1 | 4.5 | -1 | 1 | 22 |
| 10 | ugagguaguagË Phvul.008G227600.1 | 4.5 | -1 | 1 | 22 |
| 11 | ugagguaguagË Phvul.008G227600.1 | 4.5 | -1 | 1 | 22 |
| 12 | ugagguaguagË Phvul.008G227600.1 | 4.5 | -1 | 1 | 22 |
| 13 | ugagguaguagË Phvul.008G227600.1 | 4.5 | -1 | 1 | 22 |
| 14 | ugagguaguagË Phvul.008G227600.1 | 4.5 | -1 | 1 | 22 |
| 15 | agagguaguagË Phvul.008G274900.1 | 4.5 | -1 | 1 | 24 |
| 16 | agagguaguagË Phvul.008G274900.2 | 4.5 | -1 | 1 | 24 |
| 17 | agagguaguagË Phvul.008G274900.3 | 4.5 | -1 | 1 | 24 |
| 18 | ugagguaguagã Phvul.008G282700.1 | 4.5 | -1 | 1 | 22 |
| 19 | ugagguaguagã Phvul.008G282700.1 | 4.5 | -1 | 1 | 22 |
| 20 | ugagguaguagã Phvul.008G282700.1 | 4.5 | -1 | 1 | 22 |
| 21 | agagguaguagË Phvul.009G106700.1 | 4.5 | -1 | 1 | 24 |
| 22 | ugagguaguagã Phvul.009G121300.1 | 4.5 | -1 | 1 | 22 |
| 23 | ugagguaguagã Phvul.009G121300.2 | 4.5 | -1 | 1 | 22 |
| 24 | ugagguaguagã Phvul.009G121300.1 | 4.5 | -1 | 1 | 22 |
| 25 | ugagguaguagã Phvul.009G121300.1 | 4.5 | -1 | 1 | 22 |
| 26 | ugagguaguagã Phvul.009G121300.2 | 4.5 | -1 | 1 | 22 |
| 27 | ugagguaguagã Phvul.009G121300.2 | 4.5 | -1 | 1 | 22 |
| 28 | ugagguaguagã Phvul.009G173100.1 | 4.5 | -1 | 1 | 22 |
| 29 | ugagguaguagã Phvul.009G173100.3 | 4.5 | -1 | 1 | 22 |
| 30 | ugagguaguagã Phvul.009G173100.3 | 4.5 | -1 | 1 | 22 |
| 31 | ugagguaguagã Phvul.009G173100.1 | 4.5 | -1 | 1 | 22 |
| 32 | ugagguaguagã Phvul.009G173100.3 | 4.5 | -1 | 1 | 22 |
| 33 | ugagguaguagã Phvul.009G232500.1 | 4.5 | -1 | 1 | 22 |
| 34 | ugagguaguagã Phvul.009G232500.1 | 4.5 | -1 | 1 | 22 |
| 35 | ugagguaguagã Phvul.009G232500.1 | 4.5 | -1 | 1 | 22 |
| 36 | ugagguaguagË Phvul.009G259000.1 | 4.5 | -1 | 1 | 22 |
| 37 | ugagguaguagË Phvul.009G259000.1 | 4.5 | -1 | 1 | 22 |
| 38 | ugagguaguagË Phvul.009G259000.1 | 4.5 | -1 | 1 | 22 |
| 39 | ugagguaguagË Phvul.009G259000.1 | 4.5 | -1 | 1 | 22 |
| 40 | ugagguaguagË Phvul.009G259000.1 | 4.5 | -1 | 1 | 22 |
| 41 | ugagguaguagË Phvul.010G032400.1 | 4.5 | -1 | 1 | 22 |
| 42 | ugagguaguagË Phvul.010G032400.1 | 4.5 | -1 | 1 | 22 |
| 43 | ugagguaguagË Phvul.010G032400.1 | 4.5 | -1 | 1 | 22 |
| 44 | ugagguaguagË Phvul.010G032400.1 | 4.5 | -1 | 1 | 22 |
| 45 | ugagguaguagË Phvul.010G032400.1 | 4.5 | -1 | 1 | 22 |
| 46 | ugagguaguagã Phvul.010G043700.5 | 4.5 | -1 | 1 | 22 |
| 47 | ugagguaguagã Phvul.010G043700.6 | 4.5 | -1 | 1 | 22 |
| 48 | ugagguaguagã Phvul.010G043700.4 | 4.5 | -1 | 1 | 22 |
| 49 | ugagguaguagã Phvul.010G043700.1 | 4.5 | -1 | 1 | 22 |
| 50 | ugagguaguagã Phvul.010G043700.3 | 4.5 | -1 | 1 | 22 |
| 51 | ugagguaguagã Phvul.010G043700.2 | 4.5 | -1 | 1 | 22 |
| 52 | ugagguaguagã Phvul.010G043700.9 | 4.5 | -1 | 1 | 22 |
| 53 | ugagguaguagã Phvul.010G043700.8 | 4.5 | -1 | 1 | 22 |
| 54 | ugagguaguagã Phvul.010G043700.7 | 4.5 | -1 | 1 | 22 |
| 55 | ugagguaguagã Phvul.010G043700.5 | 4.5 | -1 | 1 | 22 |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagε Phvul.010G043700.6 | 4.5 | -1 | 1 | 22 |
| 4 | ugagguaguagε Phvul.010G043700.4 | 4.5 | -1 | 1 | 22 |
| 5 | ugagguaguagε Phvul.010G043700.1 | 4.5 | -1 | 1 | 22 |
| 6 | ugagguaguagε Phvul.010G043700.3 | 4.5 | -1 | 1 | 22 |
| 7 | ugagguaguagε Phvul.010G043700.2 | 4.5 | -1 | 1 | 22 |
| 8 | ugagguaguagε Phvul.010G043700.9 | 4.5 | -1 | 1 | 22 |
| 9 | ugagguaguagε Phvul.010G043700.8 | 4.5 | -1 | 1 | 22 |
| 10 | ugagguaguagε Phvul.010G043700.7 | 4.5 | -1 | 1 | 22 |
| 11 | agagguaguagε Phvul.010G070600.1 | 4.5 | -1 | 1 | 24 |
| 12 | agagguaguagε Phvul.010G089200.1 | 4.5 | -1 | 1 | 24 |
| 13 | agagguaguagε Phvul.010G089200.2 | 4.5 | -1 | 1 | 24 |
| 14 | ugagguaguagε Phvul.010G089200.1 | 4.5 | -1 | 1 | 22 |
| 15 | ugagguaguagε Phvul.010G089200.2 | 4.5 | -1 | 1 | 22 |
| 16 | ugagguaguagε Phvul.010G089200.1 | 4.5 | -1 | 1 | 22 |
| 17 | ugagguaguagε Phvul.010G089200.2 | 4.5 | -1 | 1 | 22 |
| 18 | ugagguaguagε Phvul.010G089200.1 | 4.5 | -1 | 1 | 22 |
| 19 | ugagguaguagε Phvul.010G089200.2 | 4.5 | -1 | 1 | 22 |
| 20 | ugagguaguagε Phvul.010G135701.1 | 4.5 | -1 | 1 | 22 |
| 21 | ugagguaguagε Phvul.010G135701.1 | 4.5 | -1 | 1 | 22 |
| 22 | ugagguaguagε Phvul.010G135701.1 | 4.5 | -1 | 1 | 22 |
| 23 | ugagguaguagε Phvul.010G135701.1 | 4.5 | -1 | 1 | 22 |
| 24 | ugagguaguagε Phvul.011G013900.1 | 4.5 | -1 | 1 | 22 |
| 25 | ugagguaguagε Phvul.011G013900.1 | 4.5 | -1 | 1 | 22 |
| 26 | ugagguaguagε Phvul.011G013900.1 | 4.5 | -1 | 1 | 22 |
| 27 | ugagguaguagε Phvul.011G013900.1 | 4.5 | -1 | 1 | 22 |
| 28 | ugagguaguagε Phvul.011G013900.1 | 4.5 | -1 | 1 | 22 |
| 29 | ugagguaguagε Phvul.011G013900.1 | 4.5 | -1 | 1 | 22 |
| 30 | ugagguaguagε Phvul.011G050300.1 | 4.5 | -1 | 1 | 22 |
| 31 | ugagguaguagε Phvul.011G050300.2 | 4.5 | -1 | 1 | 22 |
| 32 | ugagguaguagε Phvul.011G050300.1 | 4.5 | -1 | 1 | 22 |
| 33 | ugagguaguagε Phvul.011G050300.2 | 4.5 | -1 | 1 | 22 |
| 34 | ugagguaguagε Phvul.011G061600.1 | 4.5 | -1 | 1 | 22 |
| 35 | ugagguaguagε Phvul.011G061600.1 | 4.5 | -1 | 1 | 22 |
| 36 | agagguaguagε Phvul.011G114700.1 | 4.5 | -1 | 1 | 24 |
| 37 | agagguaguagε Phvul.011G123000.1 | 4.5 | -1 | 1 | 24 |
| 38 | ugagguaguagε Phvul.011G123701.1 | 4.5 | -1 | 1 | 22 |
| 39 | ugagguaguagε Phvul.011G123701.1 | 4.5 | -1 | 1 | 22 |
| 40 | ugagguaguagε Phvul.011G160800.1 | 4.5 | -1 | 1 | 22 |
| 41 | ugagguaguagε Phvul.011G160800.3 | 4.5 | -1 | 1 | 22 |
| 42 | ugagguaguagε Phvul.011G160800.2 | 4.5 | -1 | 1 | 22 |
| 43 | ugagguaguagε Phvul.011G160800.1 | 4.5 | -1 | 1 | 22 |
| 44 | ugagguaguagε Phvul.011G160800.3 | 4.5 | -1 | 1 | 22 |
| 45 | ugagguaguagε Phvul.011G160800.2 | 4.5 | -1 | 1 | 22 |
| 46 | ugagguaguagε Phvul.011G160800.1 | 4.5 | -1 | 1 | 22 |
| 47 | ugagguaguagε Phvul.011G160800.3 | 4.5 | -1 | 1 | 22 |
| 48 | ugagguaguagε Phvul.011G160800.2 | 4.5 | -1 | 1 | 22 |
| 49 | ugagguaguagε Phvul.011G160800.1 | 4.5 | -1 | 1 | 22 |
| 50 | ugagguaguagε Phvul.011G160800.3 | 4.5 | -1 | 1 | 22 |
| 51 | ugagguaguagε Phvul.011G160800.2 | 4.5 | -1 | 1 | 22 |
| 52 | ugagguaguagε Phvul.011G160800.1 | 4.5 | -1 | 1 | 22 |
| 53 | ugagguaguagε Phvul.011G160800.3 | 4.5 | -1 | 1 | 22 |
| 54 | ugagguaguagε Phvul.011G160800.2 | 4.5 | -1 | 1 | 22 |
| 55 | ugagguaguagε Phvul.011G160800.1 | 4.5 | -1 | 1 | 22 |
| 56 | ugagguaguagε Phvul.011G160800.3 | 4.5 | -1 | 1 | 22 |
| 57 | ugagguaguagε Phvul.011G160800.2 | 4.5 | -1 | 1 | 22 |
| 58 | ugagguaguagε Phvul.011G160800.1 | 4.5 | -1 | 1 | 22 |
| 59 | ugagguaguagε Phvul.011G160800.3 | 4.5 | -1 | 1 | 22 |
| 60 | ugagguaguagε Phvul.011G160800.2 | 4.5 | -1 | 1 | 22 |

| | | | | | |
|----|---------------------------------|------|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagξ Phvul.011G160800.1 | 4.5 | -1 | 1 | 22 |
| 4 | ugagguaguagξ Phvul.011G160800.3 | 4.5 | -1 | 1 | 22 |
| 5 | ugagguaguagξ Phvul.011G160800.2 | 4.5 | -1 | 1 | 22 |
| 6 | ugagguaguagξ Phvul.011G160800.1 | 4.5 | -1 | 1 | 22 |
| 7 | ugagguaguagξ Phvul.011G160800.3 | 4.5 | -1 | 1 | 22 |
| 8 | ugagguaguagξ Phvul.011G160800.2 | 4.5 | -1 | 1 | 22 |
| 9 | ugagguaguagξ Phvul.011G202700.1 | 4.5 | -1 | 1 | 22 |
| 10 | ugagguaguagξ Phvul.011G202700.1 | 4.5 | -1 | 1 | 22 |
| 11 | ugagguaguagξ Phvul.011G202700.1 | 4.5 | -1 | 1 | 22 |
| 12 | ugagguaguagξ Phvul.011G202700.1 | 4.5 | -1 | 1 | 22 |
| 13 | ugagguaguagξ Phvul.011G202700.1 | 4.5 | -1 | 1 | 22 |
| 14 | ugagguaguagξ Phvul.L002051.1 | 4.5 | -1 | 1 | 22 |
| 15 | ugagguaguagξ Phvul.L002051.2 | 4.5 | -1 | 1 | 22 |
| 16 | ugagguaguagξ Phvul.L002051.1 | 4.5 | -1 | 1 | 22 |
| 17 | ugagguaguagξ Phvul.L002051.2 | 4.5 | -1 | 1 | 22 |
| 18 | ugagguaguagξ Phvul.L002051.1 | 4.5 | -1 | 1 | 22 |
| 19 | ugagguaguagξ Phvul.L002051.2 | 4.5 | -1 | 1 | 22 |
| 20 | ugagguaguagξ Phvul.L002051.1 | 4.5 | -1 | 1 | 22 |
| 21 | ugagguaguagξ Phvul.L002051.2 | 4.5 | -1 | 1 | 22 |
| 22 | ugagguaguagξ Phvul.L002051.1 | 4.5 | -1 | 1 | 22 |
| 23 | ugagguaguagξ Phvul.L002051.2 | 4.5 | -1 | 1 | 22 |
| 24 | ugagguaguagξ Phvul.L002051.1 | 4.5 | -1 | 1 | 22 |
| 25 | ugagguaguagξ Phvul.L002051.2 | 4.5 | -1 | 1 | 22 |
| 26 | agagguaguagξ Phvul.L002537.1 | 4.5 | -1 | 1 | 24 |
| 27 | ugagguaguagξ Phvul.L002537.1 | 4.5 | -1 | 1 | 22 |
| 28 | ugagguaguagξ Phvul.L002537.1 | 4.5 | -1 | 1 | 22 |
| 29 | ugagguaguagξ Phvul.L002537.1 | 4.5 | -1 | 1 | 22 |
| 30 | agagguaguagξ Phvul.L007343.1 | 4.5 | -1 | 1 | 24 |
| 31 | ugagguaguagξ Phvul.008G004400.1 | 4.75 | -1 | 1 | 22 |
| 32 | ugagguaguagξ Phvul.008G004400.1 | 4.75 | -1 | 1 | 22 |
| 33 | agagguaguagξ Phvul.001G020300.1 | 5 | -1 | 1 | 24 |
| 34 | agagguaguagξ Phvul.001G020350.1 | 5 | -1 | 1 | 24 |
| 35 | ugagguaguagξ Phvul.001G022700.1 | 5 | -1 | 1 | 22 |
| 36 | ugagguaguagξ Phvul.001G022700.1 | 5 | -1 | 1 | 22 |
| 37 | ugagguaguagξ Phvul.001G022700.1 | 5 | -1 | 1 | 22 |
| 38 | ugagguaguagξ Phvul.001G022700.1 | 5 | -1 | 1 | 22 |
| 39 | agagguaguagξ Phvul.001G036800.1 | 5 | -1 | 1 | 24 |
| 40 | ugagguaguagξ Phvul.001G057800.1 | 5 | -1 | 1 | 22 |
| 41 | ugagguaguagξ Phvul.001G057800.1 | 5 | -1 | 1 | 22 |
| 42 | ugagguaguagξ Phvul.001G077700.1 | 5 | -1 | 1 | 22 |
| 43 | ugagguaguagξ Phvul.001G077700.1 | 5 | -1 | 1 | 22 |
| 44 | ugagguaguagξ Phvul.001G097800.1 | 5 | -1 | 1 | 22 |
| 45 | ugagguaguagξ Phvul.001G097800.1 | 5 | -1 | 1 | 22 |
| 46 | ugagguaguagξ Phvul.001G109300.2 | 5 | -1 | 1 | 22 |
| 47 | ugagguaguagξ Phvul.001G109300.1 | 5 | -1 | 1 | 22 |
| 48 | ugagguaguagξ Phvul.001G109300.2 | 5 | -1 | 1 | 22 |
| 49 | ugagguaguagξ Phvul.001G109300.1 | 5 | -1 | 1 | 22 |
| 50 | ugagguaguagξ Phvul.001G114900.1 | 5 | -1 | 1 | 22 |
| 51 | ugagguaguagξ Phvul.001G114900.1 | 5 | -1 | 1 | 22 |
| 52 | ugagguaguagξ Phvul.001G114900.1 | 5 | -1 | 1 | 22 |
| 53 | ugagguaguagξ Phvul.001G114900.1 | 5 | -1 | 1 | 22 |
| 54 | ugagguaguagξ Phvul.001G114900.1 | 5 | -1 | 1 | 22 |
| 55 | ugagguaguagξ Phvul.001G114900.1 | 5 | -1 | 1 | 22 |
| 56 | ugagguaguagξ Phvul.001G114900.1 | 5 | -1 | 1 | 22 |
| 57 | ugagguaguagξ Phvul.001G114900.1 | 5 | -1 | 1 | 22 |
| 58 | ugagguaguagξ Phvul.001G114900.1 | 5 | -1 | 1 | 22 |
| 59 | ugagguaguagξ Phvul.001G114900.1 | 5 | -1 | 1 | 22 |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagc Phvul.001G123000.2 | 5 | -1 | 1 | 22 |
| 4 | ugagguaguagc Phvul.001G123000.2 | 5 | -1 | 1 | 22 |
| 5 | ugagguaguagc Phvul.001G123000.2 | 5 | -1 | 1 | 22 |
| 6 | ugagguaguagξ Phvul.001G134100.2 | 5 | -1 | 1 | 22 |
| 7 | ugagguaguagξ Phvul.001G134100.1 | 5 | -1 | 1 | 22 |
| 8 | ugagguaguagξ Phvul.001G134100.2 | 5 | -1 | 1 | 22 |
| 9 | ugagguaguagξ Phvul.001G134100.2 | 5 | -1 | 1 | 22 |
| 10 | ugagguaguagξ Phvul.001G134100.1 | 5 | -1 | 1 | 22 |
| 11 | ugagguaguagξ Phvul.001G134100.2 | 5 | -1 | 1 | 22 |
| 12 | ugagguaguagξ Phvul.001G134100.1 | 5 | -1 | 1 | 22 |
| 13 | ugagguaguagξ Phvul.001G134100.1 | 5 | -1 | 1 | 22 |
| 14 | ugagguaguagξ Phvul.001G134100.2 | 5 | -1 | 1 | 22 |
| 15 | ugagguaguagξ Phvul.001G134100.1 | 5 | -1 | 1 | 22 |
| 16 | agagguaguagξ Phvul.001G159300.1 | 5 | -1 | 1 | 24 |
| 17 | agagguaguagξ Phvul.001G159300.1 | 5 | -1 | 1 | 24 |
| 18 | ugagguaguagξ Phvul.001G163900.2 | 5 | -1 | 1 | 22 |
| 19 | ugagguaguagξ Phvul.001G163900.1 | 5 | -1 | 1 | 22 |
| 20 | ugagguaguagξ Phvul.001G163900.2 | 5 | -1 | 1 | 22 |
| 21 | ugagguaguagξ Phvul.001G163900.2 | 5 | -1 | 1 | 22 |
| 22 | ugagguaguagξ Phvul.001G163900.1 | 5 | -1 | 1 | 22 |
| 23 | ugagguaguagξ Phvul.001G163900.2 | 5 | -1 | 1 | 22 |
| 24 | ugagguaguagξ Phvul.001G163900.1 | 5 | -1 | 1 | 22 |
| 25 | ugagguaguagξ Phvul.001G163900.1 | 5 | -1 | 1 | 22 |
| 26 | ugagguaguagξ Phvul.001G163900.2 | 5 | -1 | 1 | 22 |
| 27 | ugagguaguagξ Phvul.001G163900.1 | 5 | -1 | 1 | 22 |
| 28 | agagguaguagξ Phvul.001G214300.2 | 5 | -1 | 1 | 24 |
| 29 | agagguaguagξ Phvul.001G214300.1 | 5 | -1 | 1 | 24 |
| 30 | agagguaguagξ Phvul.001G214300.1 | 5 | -1 | 1 | 24 |
| 31 | ugagguaguagξ Phvul.001G220900.1 | 5 | -1 | 1 | 22 |
| 32 | ugagguaguagξ Phvul.001G220900.1 | 5 | -1 | 1 | 22 |
| 33 | ugagguaguagξ Phvul.001G220900.1 | 5 | -1 | 1 | 22 |
| 34 | ugagguaguagξ Phvul.001G220900.1 | 5 | -1 | 1 | 22 |
| 35 | ugagguaguagξ Phvul.001G220900.1 | 5 | -1 | 1 | 22 |
| 36 | ugagguaguagξ Phvul.002G013866.1 | 5 | -1 | 1 | 22 |
| 37 | ugagguaguagξ Phvul.002G013866.1 | 5 | -1 | 1 | 22 |
| 38 | ugagguaguagξ Phvul.002G013866.1 | 5 | -1 | 1 | 22 |
| 39 | ugagguaguagξ Phvul.002G013866.1 | 5 | -1 | 1 | 22 |
| 40 | ugagguaguagξ Phvul.002G013866.1 | 5 | -1 | 1 | 22 |
| 41 | ugagguaguagξ Phvul.002G043500.1 | 5 | -1 | 1 | 22 |
| 42 | ugagguaguagξ Phvul.002G043500.1 | 5 | -1 | 1 | 22 |
| 43 | ugagguaguagξ Phvul.002G043500.1 | 5 | -1 | 1 | 22 |
| 44 | ugagguaguagξ Phvul.002G043500.1 | 5 | -1 | 1 | 22 |
| 45 | ugagguaguagξ Phvul.002G043500.1 | 5 | -1 | 1 | 22 |
| 46 | ugagguaguagξ Phvul.002G043500.1 | 5 | -1 | 1 | 22 |
| 47 | ugagguaguagc Phvul.002G058900.1 | 5 | -1 | 1 | 22 |
| 48 | ugagguaguagc Phvul.002G058900.1 | 5 | -1 | 1 | 22 |
| 49 | ugagguaguagξ Phvul.002G152900.1 | 5 | -1 | 1 | 22 |
| 50 | ugagguaguagξ Phvul.002G152900.1 | 5 | -1 | 1 | 22 |
| 51 | ugagguaguagξ Phvul.002G152900.1 | 5 | -1 | 1 | 22 |
| 52 | ugagguaguagξ Phvul.002G152900.1 | 5 | -1 | 1 | 22 |
| 53 | ugagguaguagξ Phvul.002G152900.1 | 5 | -1 | 1 | 22 |
| 54 | ugagguaguagξ Phvul.002G152900.1 | 5 | -1 | 1 | 22 |
| 55 | agagguaguagξ Phvul.002G153500.1 | 5 | -1 | 1 | 24 |
| 56 | ugagguaguagξ Phvul.002G243300.1 | 5 | -1 | 1 | 22 |
| 57 | ugagguaguagξ Phvul.002G243300.1 | 5 | -1 | 1 | 22 |
| 58 | ugagguaguagξ Phvul.002G243300.1 | 5 | -1 | 1 | 22 |
| 59 | ugagguaguagξ Phvul.002G243300.1 | 5 | -1 | 1 | 22 |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagξ Phvul.002G243300.1 | 5 | -1 | 1 | 22 |
| 4 | ugagguaguagζ Phvul.002G253100.1 | 5 | -1 | 1 | 22 |
| 5 | ugagguaguagζ Phvul.002G253100.1 | 5 | -1 | 1 | 22 |
| 6 | ugagguaguagζ Phvul.002G253100.1 | 5 | -1 | 1 | 22 |
| 7 | agagguaguagξ Phvul.002G262600.1 | 5 | -1 | 1 | 24 |
| 8 | ugagguaguagζ Phvul.002G290000.3 | 5 | -1 | 1 | 22 |
| 9 | ugagguaguagζ Phvul.002G290000.3 | 5 | -1 | 1 | 22 |
| 10 | ugagguaguagζ Phvul.002G290000.3 | 5 | -1 | 1 | 22 |
| 11 | ugagguaguagζ Phvul.003G022200.1 | 5 | -1 | 1 | 22 |
| 12 | ugagguaguagζ Phvul.003G022200.1 | 5 | -1 | 1 | 22 |
| 13 | ugagguaguagζ Phvul.003G022200.1 | 5 | -1 | 1 | 22 |
| 14 | ugagguaguagξ Phvul.003G035400.1 | 5 | -1 | 1 | 22 |
| 15 | ugagguaguagξ Phvul.003G035400.1 | 5 | -1 | 1 | 22 |
| 16 | ugagguaguagξ Phvul.003G035400.1 | 5 | -1 | 1 | 22 |
| 17 | ugagguaguagξ Phvul.003G035400.1 | 5 | -1 | 1 | 22 |
| 18 | ugagguaguagξ Phvul.003G035400.1 | 5 | -1 | 1 | 22 |
| 19 | ugagguaguagξ Phvul.003G050600.1 | 5 | -1 | 1 | 22 |
| 20 | ugagguaguagξ Phvul.003G050600.1 | 5 | -1 | 1 | 22 |
| 21 | ugagguaguagξ Phvul.003G050600.1 | 5 | -1 | 1 | 22 |
| 22 | ugagguaguagξ Phvul.003G050600.1 | 5 | -1 | 1 | 22 |
| 23 | ugagguaguagξ Phvul.003G050600.1 | 5 | -1 | 1 | 22 |
| 24 | ugagguaguagζ Phvul.003G088200.1 | 5 | -1 | 1 | 22 |
| 25 | ugagguaguagζ Phvul.003G088200.1 | 5 | -1 | 1 | 22 |
| 26 | ugagguaguagζ Phvul.003G088200.1 | 5 | -1 | 1 | 22 |
| 27 | ugagguaguagξ Phvul.003G104200.1 | 5 | -1 | 1 | 22 |
| 28 | ugagguaguagξ Phvul.003G104200.1 | 5 | -1 | 1 | 22 |
| 29 | ugagguaguagξ Phvul.003G104200.1 | 5 | -1 | 1 | 22 |
| 30 | ugagguaguagξ Phvul.003G104200.1 | 5 | -1 | 1 | 22 |
| 31 | ugagguaguagξ Phvul.003G104200.1 | 5 | -1 | 1 | 22 |
| 32 | agagguaguagξ Phvul.003G119100.3 | 5 | -1 | 1 | 24 |
| 33 | agagguaguagξ Phvul.003G119100.2 | 5 | -1 | 1 | 24 |
| 34 | agagguaguagξ Phvul.003G119100.2 | 5 | -1 | 1 | 24 |
| 35 | agagguaguagξ Phvul.003G119100.1 | 5 | -1 | 1 | 24 |
| 36 | agagguaguagξ Phvul.003G169700.1 | 5 | -1 | 1 | 24 |
| 37 | agagguaguagξ Phvul.003G169700.1 | 5 | -1 | 1 | 24 |
| 38 | agagguaguagξ Phvul.003G292000.1 | 5 | -1 | 1 | 24 |
| 39 | agagguaguagξ Phvul.004G058600.1 | 5 | -1 | 1 | 24 |
| 40 | ugagguaguagξ Phvul.004G121666.1 | 5 | -1 | 1 | 22 |
| 41 | ugagguaguagξ Phvul.004G121666.1 | 5 | -1 | 1 | 22 |
| 42 | ugagguaguagξ Phvul.004G121666.1 | 5 | -1 | 1 | 22 |
| 43 | ugagguaguagξ Phvul.004G121666.1 | 5 | -1 | 1 | 22 |
| 44 | ugagguaguagξ Phvul.004G121666.1 | 5 | -1 | 1 | 22 |
| 45 | ugagguaguagξ Phvul.004G121666.1 | 5 | -1 | 1 | 22 |
| 46 | ugagguaguagξ Phvul.004G133700.1 | 5 | -1 | 1 | 22 |
| 47 | ugagguaguagξ Phvul.004G133700.1 | 5 | -1 | 1 | 22 |
| 48 | ugagguaguagξ Phvul.004G133700.1 | 5 | -1 | 1 | 22 |
| 49 | ugagguaguagξ Phvul.004G133700.1 | 5 | -1 | 1 | 22 |
| 50 | ugagguaguagξ Phvul.004G133700.1 | 5 | -1 | 1 | 22 |
| 51 | ugagguaguagζ Phvul.004G176700.1 | 5 | -1 | 1 | 22 |
| 52 | ugagguaguagζ Phvul.004G176700.1 | 5 | -1 | 1 | 22 |
| 53 | ugagguaguagζ Phvul.004G176700.1 | 5 | -1 | 1 | 22 |
| 54 | ugagguaguagζ Phvul.005G056400.1 | 5 | -1 | 1 | 22 |
| 55 | ugagguaguagζ Phvul.005G056400.1 | 5 | -1 | 1 | 22 |
| 56 | agagguaguagξ Phvul.005G088800.1 | 5 | -1 | 1 | 24 |
| 57 | agagguaguagξ Phvul.005G088800.1 | 5 | -1 | 1 | 24 |
| 58 | agagguaguagξ Phvul.005G095600.1 | 5 | -1 | 1 | 24 |
| 59 | ugagguaguagξ Phvul.005G097200.3 | 5 | -1 | 1 | 22 |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagξ Phvul.005G097200.6 | 5 | -1 | 1 | 22 |
| 4 | ugagguaguagξ Phvul.005G097200.5 | 5 | -1 | 1 | 22 |
| 5 | ugagguaguagξ Phvul.005G097200.3 | 5 | -1 | 1 | 22 |
| 6 | ugagguaguagξ Phvul.005G097200.6 | 5 | -1 | 1 | 22 |
| 7 | ugagguaguagξ Phvul.005G097200.5 | 5 | -1 | 1 | 22 |
| 8 | ugagguaguagξ Phvul.005G097200.3 | 5 | -1 | 1 | 22 |
| 9 | ugagguaguagξ Phvul.005G097200.6 | 5 | -1 | 1 | 22 |
| 10 | ugagguaguagξ Phvul.005G097200.5 | 5 | -1 | 1 | 22 |
| 11 | ugagguaguagξ Phvul.005G097200.3 | 5 | -1 | 1 | 22 |
| 12 | ugagguaguagξ Phvul.005G097200.6 | 5 | -1 | 1 | 22 |
| 13 | ugagguaguagξ Phvul.005G097200.5 | 5 | -1 | 1 | 22 |
| 14 | ugagguaguagξ Phvul.005G097200.3 | 5 | -1 | 1 | 22 |
| 15 | ugagguaguagξ Phvul.005G097200.6 | 5 | -1 | 1 | 22 |
| 16 | ugagguaguagξ Phvul.005G097200.5 | 5 | -1 | 1 | 22 |
| 17 | ugagguaguagξ Phvul.005G097200.3 | 5 | -1 | 1 | 22 |
| 18 | ugagguaguagξ Phvul.005G101400.3 | 5 | -1 | 1 | 22 |
| 19 | ugagguaguagξ Phvul.005G101400.2 | 5 | -1 | 1 | 22 |
| 20 | ugagguaguagξ Phvul.005G101400.1 | 5 | -1 | 1 | 22 |
| 21 | ugagguaguagξ Phvul.005G101400.3 | 5 | -1 | 1 | 22 |
| 22 | ugagguaguagξ Phvul.005G101400.2 | 5 | -1 | 1 | 22 |
| 23 | ugagguaguagξ Phvul.005G101400.1 | 5 | -1 | 1 | 22 |
| 24 | ugagguaguagξ Phvul.005G130100.1 | 5 | -1 | 1 | 22 |
| 25 | ugagguaguagξ Phvul.005G130100.1 | 5 | -1 | 1 | 22 |
| 26 | ugagguaguagξ Phvul.005G130100.1 | 5 | -1 | 1 | 22 |
| 27 | ugagguaguagξ Phvul.005G130100.1 | 5 | -1 | 1 | 22 |
| 28 | ugagguaguagξ Phvul.005G130100.1 | 5 | -1 | 1 | 22 |
| 29 | ugagguaguagξ Phvul.005G130100.1 | 5 | -1 | 1 | 22 |
| 30 | ugagguaguagξ Phvul.005G173200.1 | 5 | -1 | 1 | 22 |
| 31 | ugagguaguagξ Phvul.005G173200.1 | 5 | -1 | 1 | 22 |
| 32 | ugagguaguagξ Phvul.005G173200.1 | 5 | -1 | 1 | 22 |
| 33 | ugagguaguagξ Phvul.005G173200.1 | 5 | -1 | 1 | 22 |
| 34 | ugagguaguagξ Phvul.005G173200.1 | 5 | -1 | 1 | 22 |
| 35 | ugagguaguagξ Phvul.006G143300.1 | 5 | -1 | 1 | 22 |
| 36 | ugagguaguagξ Phvul.006G143300.1 | 5 | -1 | 1 | 22 |
| 37 | ugagguaguagξ Phvul.006G143300.1 | 5 | -1 | 1 | 22 |
| 38 | ugagguaguagξ Phvul.006G143300.1 | 5 | -1 | 1 | 22 |
| 39 | ugagguaguagξ Phvul.006G143300.1 | 5 | -1 | 1 | 22 |
| 40 | ugagguaguagξ Phvul.006G143300.1 | 5 | -1 | 1 | 22 |
| 41 | ugagguaguagξ Phvul.006G168163.1 | 5 | -1 | 1 | 22 |
| 42 | ugagguaguagξ Phvul.006G168163.1 | 5 | -1 | 1 | 22 |
| 43 | ugagguaguagξ Phvul.007G035900.2 | 5 | -1 | 1 | 22 |
| 44 | ugagguaguagξ Phvul.007G035900.2 | 5 | -1 | 1 | 22 |
| 45 | ugagguaguagξ Phvul.007G035900.2 | 5 | -1 | 1 | 22 |
| 46 | ugagguaguagξ Phvul.007G035900.2 | 5 | -1 | 1 | 22 |
| 47 | ugagguaguagξ Phvul.007G035900.2 | 5 | -1 | 1 | 22 |
| 48 | ugagguaguagξ Phvul.007G035900.2 | 5 | -1 | 1 | 22 |
| 49 | ugagguaguagξ Phvul.007G069900.3 | 5 | -1 | 1 | 22 |
| 50 | ugagguaguagξ Phvul.007G069900.5 | 5 | -1 | 1 | 22 |
| 51 | ugagguaguagξ Phvul.007G069900.1 | 5 | -1 | 1 | 22 |
| 52 | ugagguaguagξ Phvul.007G069900.4 | 5 | -1 | 1 | 22 |
| 53 | ugagguaguagξ Phvul.007G069900.3 | 5 | -1 | 1 | 22 |
| 54 | ugagguaguagξ Phvul.007G069900.5 | 5 | -1 | 1 | 22 |
| 55 | ugagguaguagξ Phvul.007G069900.1 | 5 | -1 | 1 | 22 |
| 56 | ugagguaguagξ Phvul.007G069900.4 | 5 | -1 | 1 | 22 |
| 57 | ugagguaguagξ Phvul.007G069900.3 | 5 | -1 | 1 | 22 |
| 58 | ugagguaguagξ Phvul.007G069900.5 | 5 | -1 | 1 | 22 |
| 59 | ugagguaguagξ Phvul.007G069900.1 | 5 | -1 | 1 | 22 |
| 60 | ugagguaguagξ Phvul.007G069900.4 | 5 | -1 | 1 | 22 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagξ Phvul.007G069900.3 | 5 | -1 | 1 | 22 |
| 4 | ugagguaguagξ Phvul.007G069900.5 | 5 | -1 | 1 | 22 |
| 5 | ugagguaguagξ Phvul.007G069900.5 | 5 | -1 | 1 | 22 |
| 6 | ugagguaguagξ Phvul.007G069900.1 | 5 | -1 | 1 | 22 |
| 7 | ugagguaguagξ Phvul.007G069900.4 | 5 | -1 | 1 | 22 |
| 8 | ugagguaguagξ Phvul.007G069900.3 | 5 | -1 | 1 | 22 |
| 9 | ugagguaguagξ Phvul.007G069900.3 | 5 | -1 | 1 | 22 |
| 10 | ugagguaguagξ Phvul.007G069900.5 | 5 | -1 | 1 | 22 |
| 11 | ugagguaguagξ Phvul.007G069900.1 | 5 | -1 | 1 | 22 |
| 12 | ugagguaguagξ Phvul.007G069900.1 | 5 | -1 | 1 | 22 |
| 13 | ugagguaguagξ Phvul.007G069900.4 | 5 | -1 | 1 | 22 |
| 14 | agagguaguagξ Phvul.007G099300.1 | 5 | -1 | 1 | 24 |
| 15 | ugagguaguagξ Phvul.007G114100.1 | 5 | -1 | 1 | 22 |
| 16 | ugagguaguagξ Phvul.007G114100.1 | 5 | -1 | 1 | 22 |
| 17 | ugagguaguagξ Phvul.007G114100.1 | 5 | -1 | 1 | 22 |
| 18 | ugagguaguagξ Phvul.007G114100.1 | 5 | -1 | 1 | 22 |
| 19 | ugagguaguagξ Phvul.007G114100.1 | 5 | -1 | 1 | 22 |
| 20 | ugagguaguagξ Phvul.007G114100.1 | 5 | -1 | 1 | 22 |
| 21 | ugagguaguagξ Phvul.007G184600.1 | 5 | -1 | 1 | 22 |
| 22 | ugagguaguagξ Phvul.007G184600.1 | 5 | -1 | 1 | 22 |
| 23 | agagguaguagξ Phvul.007G192300.1 | 5 | -1 | 1 | 24 |
| 24 | ugagguaguagξ Phvul.007G210400.1 | 5 | -1 | 1 | 22 |
| 25 | ugagguaguagξ Phvul.007G210400.1 | 5 | -1 | 1 | 22 |
| 26 | ugagguaguagξ Phvul.007G210400.1 | 5 | -1 | 1 | 22 |
| 27 | ugagguaguagξ Phvul.007G210400.1 | 5 | -1 | 1 | 22 |
| 28 | ugagguaguagξ Phvul.007G210400.1 | 5 | -1 | 1 | 22 |
| 29 | ugagguaguagξ Phvul.007G210400.1 | 5 | -1 | 1 | 22 |
| 30 | ugagguaguagξ Phvul.007G210400.1 | 5 | -1 | 1 | 22 |
| 31 | ugagguaguagξ Phvul.007G210400.1 | 5 | -1 | 1 | 22 |
| 32 | ugagguaguagξ Phvul.007G210400.1 | 5 | -1 | 1 | 22 |
| 33 | ugagguaguagξ Phvul.007G215300.1 | 5 | -1 | 1 | 22 |
| 34 | ugagguaguagξ Phvul.007G215300.1 | 5 | -1 | 1 | 22 |
| 35 | ugagguaguagξ Phvul.007G215300.1 | 5 | -1 | 1 | 22 |
| 36 | ugagguaguagξ Phvul.007G215300.1 | 5 | -1 | 1 | 22 |
| 37 | ugagguaguagξ Phvul.007G215300.1 | 5 | -1 | 1 | 22 |
| 38 | agagguaguagξ Phvul.007G251800.1 | 5 | -1 | 1 | 24 |
| 39 | agagguaguagξ Phvul.008G043400.1 | 5 | -1 | 1 | 24 |
| 40 | agagguaguagξ Phvul.008G043400.1 | 5 | -1 | 1 | 24 |
| 41 | agagguaguagξ Phvul.008G043400.1 | 5 | -1 | 1 | 24 |
| 42 | ugagguaguagξ Phvul.008G067300.1 | 5 | -1 | 1 | 22 |
| 43 | ugagguaguagξ Phvul.008G067300.1 | 5 | -1 | 1 | 22 |
| 44 | ugagguaguagξ Phvul.008G110100.1 | 5 | -1 | 1 | 22 |
| 45 | ugagguaguagξ Phvul.008G110100.1 | 5 | -1 | 1 | 22 |
| 46 | ugagguaguagξ Phvul.008G110100.1 | 5 | -1 | 1 | 22 |
| 47 | ugagguaguagξ Phvul.008G110100.1 | 5 | -1 | 1 | 22 |
| 48 | ugagguaguagξ Phvul.008G110100.1 | 5 | -1 | 1 | 22 |
| 49 | ugagguaguagξ Phvul.008G110100.1 | 5 | -1 | 1 | 22 |
| 50 | ugagguaguagξ Phvul.008G110200.1 | 5 | -1 | 1 | 22 |
| 51 | ugagguaguagξ Phvul.008G110200.1 | 5 | -1 | 1 | 22 |
| 52 | ugagguaguagξ Phvul.008G110200.1 | 5 | -1 | 1 | 22 |
| 53 | ugagguaguagξ Phvul.008G110200.1 | 5 | -1 | 1 | 22 |
| 54 | ugagguaguagξ Phvul.008G110200.1 | 5 | -1 | 1 | 22 |
| 55 | ugagguaguagξ Phvul.008G110500.1 | 5 | -1 | 1 | 22 |
| 56 | ugagguaguagξ Phvul.008G110500.1 | 5 | -1 | 1 | 22 |
| 57 | ugagguaguagξ Phvul.008G110500.1 | 5 | -1 | 1 | 22 |
| 58 | ugagguaguagξ Phvul.008G110500.1 | 5 | -1 | 1 | 22 |
| 59 | ugagguaguagξ Phvul.008G110500.1 | 5 | -1 | 1 | 22 |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagã Phvul.008G125400.2 | 5 | -1 | 1 | 22 |
| 4 | ugagguaguagã Phvul.008G125400.1 | 5 | -1 | 1 | 22 |
| 5 | ugagguaguagã Phvul.008G125400.2 | 5 | -1 | 1 | 22 |
| 6 | ugagguaguagã Phvul.008G125400.1 | 5 | -1 | 1 | 22 |
| 7 | agagguaguagę Phvul.008G229100.1 | 5 | -1 | 1 | 24 |
| 8 | ugagguaguagã Phvul.008G279750.1 | 5 | -1 | 1 | 22 |
| 9 | ugagguaguagã Phvul.008G279750.1 | 5 | -1 | 1 | 22 |
| 10 | ugagguaguagã Phvul.009G010800.1 | 5 | -1 | 1 | 22 |
| 11 | ugagguaguagã Phvul.009G010800.1 | 5 | -1 | 1 | 22 |
| 12 | agagguaguagę Phvul.009G034800.1 | 5 | -1 | 1 | 24 |
| 13 | ugagguaguagę Phvul.009G060200.1 | 5 | -1 | 1 | 22 |
| 14 | ugagguaguagę Phvul.009G060200.2 | 5 | -1 | 1 | 22 |
| 15 | ugagguaguagę Phvul.009G060200.1 | 5 | -1 | 1 | 22 |
| 16 | ugagguaguagę Phvul.009G060200.2 | 5 | -1 | 1 | 22 |
| 17 | ugagguaguagę Phvul.009G060200.1 | 5 | -1 | 1 | 22 |
| 18 | ugagguaguagę Phvul.009G060200.2 | 5 | -1 | 1 | 22 |
| 19 | ugagguaguagę Phvul.009G060200.1 | 5 | -1 | 1 | 22 |
| 20 | ugagguaguagę Phvul.009G060200.2 | 5 | -1 | 1 | 22 |
| 21 | ugagguaguagę Phvul.009G060200.1 | 5 | -1 | 1 | 22 |
| 22 | ugagguaguagę Phvul.009G060200.2 | 5 | -1 | 1 | 22 |
| 23 | ugagguaguagę Phvul.009G060200.1 | 5 | -1 | 1 | 22 |
| 24 | ugagguaguagę Phvul.009G060200.1 | 5 | -1 | 1 | 22 |
| 25 | ugagguaguagę Phvul.009G060200.2 | 5 | -1 | 1 | 22 |
| 26 | ugagguaguagã Phvul.009G115500.1 | 5 | -1 | 1 | 22 |
| 27 | ugagguaguagã Phvul.009G115500.1 | 5 | -1 | 1 | 22 |
| 28 | ugagguaguagę Phvul.009G158700.1 | 5 | -1 | 1 | 22 |
| 29 | ugagguaguagę Phvul.009G158700.1 | 5 | -1 | 1 | 22 |
| 30 | ugagguaguagę Phvul.009G158700.1 | 5 | -1 | 1 | 22 |
| 31 | ugagguaguagę Phvul.009G158700.1 | 5 | -1 | 1 | 22 |
| 32 | ugagguaguagę Phvul.009G158700.1 | 5 | -1 | 1 | 22 |
| 33 | ugagguaguagę Phvul.009G158700.1 | 5 | -1 | 1 | 22 |
| 34 | agagguaguagę Phvul.009G203100.1 | 5 | -1 | 1 | 24 |
| 35 | ugagguaguagę Phvul.009G232500.1 | 5 | -1 | 1 | 22 |
| 36 | ugagguaguagę Phvul.009G232500.1 | 5 | -1 | 1 | 22 |
| 37 | ugagguaguagę Phvul.009G232500.1 | 5 | -1 | 1 | 22 |
| 38 | ugagguaguagę Phvul.009G232500.1 | 5 | -1 | 1 | 22 |
| 39 | ugagguaguagã Phvul.009G255100.1 | 5 | -1 | 1 | 22 |
| 40 | ugagguaguagã Phvul.009G255100.2 | 5 | -1 | 1 | 22 |
| 41 | ugagguaguagã Phvul.009G255100.1 | 5 | -1 | 1 | 22 |
| 42 | ugagguaguagã Phvul.009G255100.2 | 5 | -1 | 1 | 22 |
| 43 | ugagguaguagę Phvul.010G026500.1 | 5 | -1 | 1 | 22 |
| 44 | ugagguaguagę Phvul.010G026500.1 | 5 | -1 | 1 | 22 |
| 45 | ugagguaguagę Phvul.010G026500.1 | 5 | -1 | 1 | 22 |
| 46 | ugagguaguagę Phvul.010G026500.1 | 5 | -1 | 1 | 22 |
| 47 | ugagguaguagã Phvul.010G028900.2 | 5 | -1 | 1 | 22 |
| 48 | ugagguaguagã Phvul.010G028900.1 | 5 | -1 | 1 | 22 |
| 49 | ugagguaguagã Phvul.010G028900.2 | 5 | -1 | 1 | 22 |
| 50 | ugagguaguagã Phvul.010G028900.1 | 5 | -1 | 1 | 22 |
| 51 | ugagguaguagę Phvul.010G067900.1 | 5 | -1 | 1 | 22 |
| 52 | ugagguaguagę Phvul.010G067900.1 | 5 | -1 | 1 | 22 |
| 53 | ugagguaguagę Phvul.010G067900.1 | 5 | -1 | 1 | 22 |
| 54 | ugagguaguagę Phvul.010G067900.1 | 5 | -1 | 1 | 22 |
| 55 | ugagguaguagę Phvul.010G067900.1 | 5 | -1 | 1 | 22 |
| 56 | ugagguaguagę Phvul.010G067900.1 | 5 | -1 | 1 | 22 |
| 57 | ugagguaguagę Phvul.010G067900.1 | 5 | -1 | 1 | 22 |
| 58 | ugagguaguagę Phvul.010G067900.1 | 5 | -1 | 1 | 22 |
| 59 | ugagguaguagę Phvul.010G067900.1 | 5 | -1 | 1 | 22 |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ugagguaguagξ Phvul.010G067900.1 | 5 | -1 | 1 | 22 |
| 4 | ugagguaguagξ Phvul.010G067900.1 | 5 | -1 | 1 | 22 |
| 5 | ugagguaguagξ Phvul.010G089200.1 | 5 | -1 | 1 | 22 |
| 6 | ugagguaguagξ Phvul.010G089200.1 | 5 | -1 | 1 | 22 |
| 7 | ugagguaguagξ Phvul.010G089200.2 | 5 | -1 | 1 | 22 |
| 8 | ugagguaguagξ Phvul.010G089200.1 | 5 | -1 | 1 | 22 |
| 9 | ugagguaguagξ Phvul.010G089200.1 | 5 | -1 | 1 | 22 |
| 10 | ugagguaguagξ Phvul.010G089200.2 | 5 | -1 | 1 | 22 |
| 11 | ugagguaguagξ Phvul.010G089200.1 | 5 | -1 | 1 | 22 |
| 12 | ugagguaguagξ Phvul.010G089200.2 | 5 | -1 | 1 | 22 |
| 13 | ugagguaguagξ Phvul.010G089200.2 | 5 | -1 | 1 | 22 |
| 14 | ugagguaguagξ Phvul.010G089200.1 | 5 | -1 | 1 | 22 |
| 15 | ugagguaguagξ Phvul.010G089200.2 | 5 | -1 | 1 | 22 |
| 16 | ugagguaguagξ Phvul.010G094450.1 | 5 | -1 | 1 | 22 |
| 17 | ugagguaguagξ Phvul.010G094450.1 | 5 | -1 | 1 | 22 |
| 18 | ugagguaguagξ Phvul.010G094450.1 | 5 | -1 | 1 | 22 |
| 19 | ugagguaguagξ Phvul.010G094450.1 | 5 | -1 | 1 | 22 |
| 20 | ugagguaguagξ Phvul.010G094450.1 | 5 | -1 | 1 | 22 |
| 21 | ugagguaguagξ Phvul.010G094450.1 | 5 | -1 | 1 | 22 |
| 22 | ugagguaguagξ Phvul.011G001200.2 | 5 | -1 | 1 | 22 |
| 23 | ugagguaguagξ Phvul.011G001200.1 | 5 | -1 | 1 | 22 |
| 24 | ugagguaguagξ Phvul.011G001200.2 | 5 | -1 | 1 | 22 |
| 25 | ugagguaguagξ Phvul.011G001200.1 | 5 | -1 | 1 | 22 |
| 26 | ugagguaguagξ Phvul.011G001200.1 | 5 | -1 | 1 | 22 |
| 27 | ugagguaguagξ Phvul.011G001200.2 | 5 | -1 | 1 | 22 |
| 28 | ugagguaguagξ Phvul.011G001200.1 | 5 | -1 | 1 | 22 |
| 29 | ugagguaguagξ Phvul.011G001200.2 | 5 | -1 | 1 | 22 |
| 30 | ugagguaguagξ Phvul.011G001200.2 | 5 | -1 | 1 | 22 |
| 31 | ugagguaguagξ Phvul.011G001200.1 | 5 | -1 | 1 | 22 |
| 32 | agagguaguagξ Phvul.011G004200.1 | 5 | -1 | 1 | 24 |
| 33 | ugagguaguagξ Phvul.011G203450.1 | 5 | -1 | 1 | 22 |
| 34 | ugagguaguagξ Phvul.011G203450.1 | 5 | -1 | 1 | 22 |
| 35 | ugagguaguagξ Phvul.011G203450.1 | 5 | -1 | 1 | 22 |
| 36 | ugagguaguagξ Phvul.011G203450.1 | 5 | -1 | 1 | 22 |
| 37 | ugagguaguagξ Phvul.011G203450.1 | 5 | -1 | 1 | 22 |
| 38 | ugagguaguagξ Phvul.011G203450.1 | 5 | -1 | 1 | 22 |
| 39 | ugagguaguagç Phvul.L001679.1 | 5 | -1 | 1 | 22 |
| 40 | ugagguaguagç Phvul.L001679.1 | 5 | -1 | 1 | 22 |
| 41 | ugagguaguagç Phvul.L002537.1 | 5 | -1 | 1 | 22 |
| 42 | ugagguaguagç Phvul.L002537.1 | 5 | -1 | 1 | 22 |
| 43 | ugagguaguagç Phvul.L002537.1 | 5 | -1 | 1 | 22 |
| 44 | ugagguaguagç Phvul.L009843.2 | 5 | -1 | 1 | 22 |
| 45 | ugagguaguagç Phvul.L009843.1 | 5 | -1 | 1 | 22 |
| 46 | ugagguaguagç Phvul.L009843.1 | 5 | -1 | 1 | 22 |
| 47 | ugagguaguagç Phvul.L009843.2 | 5 | -1 | 1 | 22 |
| 48 | ugagguaguagç Phvul.L009843.1 | 5 | -1 | 1 | 22 |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| Target_start | Target_end | miRNA_aligne | alignment | Target_aligne | Inhibition | Target_Desc. |
|--------------|------------|--------------|------------------|---------------|--------------|--------------|
| 1480 | 1501 | UGAGGUAGU |:UCUUAUACA | Cleavage | pacid=371762 | |
| 1480 | 1501 | UGAGGUAGU |:UCUUAUACA | Cleavage | pacid=371762 | |
| 1331 | 1352 | UGAGGUAGU |:GUCCAUACA | Cleavage | pacid=371768 | |
| 1331 | 1352 | UGAGGUAGU |:GUCCAUACA | Cleavage | pacid=371768 | |
| 1331 | 1352 | UGAGGUAGU |:GUCCAUACA | Cleavage | pacid=371768 | |
| 1331 | 1352 | UGAGGUAGU |:GUCCAUACA | Cleavage | pacid=371768 | |
| 697 | 720 | AGAGGUAGU | ...:AGUCCUAGG | Cleavage | pacid=371733 | |
| 878 | 899 | UGAGGUAGU |:GAAGGUUAU | Cleavage | pacid=371486 | |
| 878 | 899 | UGAGGUAGU |:GAAGGUUAU | Cleavage | pacid=371486 | |
| 2017 | 2040 | AGAGGUAGU |:UUCUUUAUG | Cleavage | pacid=371513 | |
| 1035 | 1056 | UGAGGUAGU |:AUGCAAACA | Cleavage | pacid=371429 | |
| 1035 | 1056 | UGAGGUAGU |:AUGCAAACA | Cleavage | pacid=371429 | |
| 1035 | 1056 | UGAGGUAGU |:AUGCAAACA | Cleavage | pacid=371429 | |
| 1035 | 1056 | UGAGGUAGU |:AUGCAAACA | Cleavage | pacid=371429 | |
| 3821 | 3842 | UGAGGUAGU |:GCGCAUGAA | Cleavage | pacid=371789 | |
| 3821 | 3842 | UGAGGUAGU |:GCGCAUGAA | Cleavage | pacid=371789 | |
| 3821 | 3842 | UGAGGUAGU |:GCGCAUGAA | Cleavage | pacid=371789 | |
| 3821 | 3842 | UGAGGUAGU |:GCGCAUGAA | Cleavage | pacid=371789 | |
| 348 | 369 | UGAGGUAGU |:UCCCAUCCAA | Cleavage | pacid=371701 | |
| 348 | 369 | UGAGGUAGU |:UCCCAUCCAA | Cleavage | pacid=371701 | |
| 348 | 369 | UGAGGUAGU |:UCCCAUCCAA | Cleavage | pacid=371701 | |
| 348 | 369 | UGAGGUAGU |:UCCCAUCCAA | Cleavage | pacid=371701 | |
| 99 | 120 | UGAGGUAGU | ...:CGUUGCAAA | Cleavage | pacid=371684 | |
| 99 | 120 | UGAGGUAGU | ...:CGUUGCAAA | Cleavage | pacid=371684 | |
| 99 | 120 | UGAGGUAGU | ...:CGUUGCAAA | Cleavage | pacid=371684 | |
| 99 | 120 | UGAGGUAGU | ...:CGUUGCAAA | Cleavage | pacid=371684 | |
| 1480 | 1501 | UGAGGUAGU |:UCUUAUACA | Cleavage | pacid=371762 | |
| 1480 | 1501 | UGAGGUAGU |:UCUUAUACA | Cleavage | pacid=371762 | |
| 1480 | 1501 | UGAGGUAGU |:UCUUAUACA | Cleavage | pacid=371762 | |
| 1480 | 1501 | UGAGGUAGU |:UCUUAUACA | Cleavage | pacid=371762 | |
| 806 | 827 | UGAGGUAGU |:UGCCAUACA | Cleavage | pacid=371750 | |
| 806 | 827 | UGAGGUAGU |:UGCCAUACA | Cleavage | pacid=371750 | |
| 806 | 827 | UGAGGUAGU |:UGCCAUACA | Cleavage | pacid=371750 | |
| 806 | 827 | UGAGGUAGU |:UGCCAUACA | Cleavage | pacid=371750 | |
| 1989 | 2012 | AGAGGUAGU | ...:AAGUCUAUG | Translation | pacid=371619 | |
| 442 | 465 | AGAGGUAGU | ...:UCAGAUCUG | Cleavage | pacid=371741 | |
| 3299 | 3320 | UGAGGUAGU |:UUCCAUUAU | Cleavage | pacid=371576 | |
| 3299 | 3320 | UGAGGUAGU |:UUCCAUUAU | Cleavage | pacid=371576 | |
| 3299 | 3320 | UGAGGUAGU |:UUCCAUUAU | Cleavage | pacid=371576 | |
| 3299 | 3320 | UGAGGUAGU |:UUCCAUUAU | Cleavage | pacid=371576 | |
| 1023 | 1046 | AGAGGUAGU |:CAAUUGUGI | Cleavage | pacid=371614 | |
| 927 | 950 | AGAGGUAGU |:CAAUUGUGI | Cleavage | pacid=371601 | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | | | |
|------|------|-----------|------------------|----------|--------------|
| 1298 | 1319 | UGAGGUAGU |UUUCAUCCA/ | Cleavage | pacid=371603 |
| 1298 | 1319 | UGAGGUAGU |UUUCAUCCA/ | Cleavage | pacid=371603 |
| 1298 | 1319 | UGAGGUAGU |UUUCAUCCA/ | Cleavage | pacid=371603 |
| 1298 | 1319 | UGAGGUAGU |UUUCAUCCA/ | Cleavage | pacid=371603 |
| 1298 | 1319 | UGAGGUAGU |UUUCAUCCA/ | Cleavage | pacid=371603 |
| 1298 | 1319 | UGAGGUAGU |UUUCAUCCA/ | Cleavage | pacid=371603 |
| 1298 | 1319 | UGAGGUAGU |UUUCAUCCA/ | Cleavage | pacid=371603 |
| 1298 | 1319 | UGAGGUAGU |UUUCAUCCA/ | Cleavage | pacid=371603 |
| 1298 | 1319 | UGAGGUAGU |UUUCAUCCA/ | Cleavage | pacid=371603 |
| 1298 | 1319 | UGAGGUAGU |UUUCAUCCA/ | Cleavage | pacid=371603 |
| 1298 | 1319 | UGAGGUAGU |UUUCAUCCA/ | Cleavage | pacid=371603 |
| 1298 | 1319 | UGAGGUAGU |UUUCAUCCA/ | Cleavage | pacid=371603 |
| 1298 | 1319 | UGAGGUAGU |UUUCAUCCA/ | Cleavage | pacid=371603 |
| 1298 | 1319 | UGAGGUAGU |UUUCAUCCA/ | Cleavage | pacid=371603 |
| 878 | 899 | UGAGGUAGU |GAAGGUUAU/ | Cleavage | pacid=371486 |
| 878 | 899 | UGAGGUAGU |GAAGGUUAU/ | Cleavage | pacid=371486 |
| 878 | 899 | UGAGGUAGU |GAAGGUUAU/ | Cleavage | pacid=371486 |
| 878 | 899 | UGAGGUAGU |GAAGGUUAU/ | Cleavage | pacid=371486 |
| 1826 | 1847 | UGAGGUAGU |UAAUAUGCU/ | Cleavage | pacid=371420 |
| 1826 | 1847 | UGAGGUAGU |UAAUAUGCU/ | Cleavage | pacid=371420 |
| 2732 | 2753 | UGAGGUAGU |GAGUUUGCA/ | Cleavage | pacid=371691 |
| 2732 | 2753 | UGAGGUAGU |GAGUUUGCA/ | Cleavage | pacid=371691 |
| 348 | 369 | UGAGGUAGU |UCCCAUCCAA | Cleavage | pacid=371701 |
| 348 | 369 | UGAGGUAGU |UCCCAUCCAA | Cleavage | pacid=371701 |
| 2435 | 2456 | UGAGGUAGU |ACUUAUGUA/ | Cleavage | pacid=371684 |
| 2435 | 2456 | UGAGGUAGU |ACUUAUGUA/ | Cleavage | pacid=371684 |
| 184 | 205 | UGAGGUAGU |CGACAUUAU/ | Cleavage | pacid=371689 |
| 184 | 205 | UGAGGUAGU |CGACAUUAU/ | Cleavage | pacid=371689 |
| 184 | 205 | UGAGGUAGU |CGACAUUAU/ | Cleavage | pacid=371689 |
| 184 | 205 | UGAGGUAGU |CGACAUUAU/ | Cleavage | pacid=371689 |
| 16 | 37 | UGAGGUAGU |CGACAUUAU/ | Cleavage | pacid=371701 |
| 16 | 37 | UGAGGUAGU |CGACAUUAU/ | Cleavage | pacid=371701 |
| 16 | 37 | UGAGGUAGU |CGACAUUAU/ | Cleavage | pacid=371701 |
| 16 | 37 | UGAGGUAGU |CGACAUUAU/ | Cleavage | pacid=371701 |
| 290 | 311 | UGAGGUAGU |AUUCUUGCA(| Cleavage | pacid=371710 |
| 290 | 311 | UGAGGUAGU |AUUCUUGCA(| Cleavage | pacid=371710 |
| 290 | 311 | UGAGGUAGU |AUUCUUGCA(| Cleavage | pacid=371710 |
| 290 | 311 | UGAGGUAGU |AUUCUUGCA(| Cleavage | pacid=371710 |
| 111 | 134 | AGAGGUAGU |CCUUCUCUG(| Cleavage | pacid=371699 |
| 111 | 134 | AGAGGUAGU |CCUUCUCUG(| Cleavage | pacid=371699 |
| 3957 | 3977 | UGAGGUAGU |CAUCAU-CAA/ | Cleavage | pacid=371677 |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | | |
|------|----------------|----------------------|----------|--------------|
| 3957 | 3977 UGAGGUAGU | ::: :::::CAUCAU-CAA | Cleavage | pacid=371677 |
| 3957 | 3977 UGAGGUAGU | ::: :::::CAUCAU-CAA | Cleavage | pacid=371677 |
| 3957 | 3977 UGAGGUAGU | ::: :::::CAUCAU-CAA | Cleavage | pacid=371677 |
| 3957 | 3977 UGAGGUAGU | ::: :::::CAUCAU-CAA | Cleavage | pacid=371677 |
| 3957 | 3977 UGAGGUAGU | ::: :::::CAUCAU-CAA | Cleavage | pacid=371677 |
| 3957 | 3977 UGAGGUAGU | ::: :::::CAUCAU-CAA | Cleavage | pacid=371677 |
| 3957 | 3977 UGAGGUAGU | ::: :::::CAUCAU-CAA | Cleavage | pacid=371677 |
| 956 | 977 UGAGGUAGU | ::: :::::CAUGACACAA | Cleavage | pacid=371706 |
| 956 | 977 UGAGGUAGU | ::: :::::CAUGACACAA | Cleavage | pacid=371706 |
| 956 | 977 UGAGGUAGU | ::: :::::CAUGACACAA | Cleavage | pacid=371706 |
| 956 | 977 UGAGGUAGU | ::: :::::CAUGACACAA | Cleavage | pacid=371706 |
| 143 | 166 AGAGGUAGU | ::: :::::CGGAUUGUG | Cleavage | pacid=371689 |
| 145 | 166 UGAGGUAGU | ::: :::::GAUUGUGCA | Cleavage | pacid=371689 |
| 145 | 166 UGAGGUAGU | ::: :::::GAUUGUGCA | Cleavage | pacid=371689 |
| 145 | 166 UGAGGUAGU | ::: :::::GAUUGUGCA | Cleavage | pacid=371689 |
| 145 | 166 UGAGGUAGU | ::: :::::GAUUGUGCA | Cleavage | pacid=371689 |
| 371 | 392 UGAGGUAGU | ::: :::::CAUUGGAUA | Cleavage | pacid=371781 |
| 371 | 392 UGAGGUAGU | ::: :::::CAUUGGAUA | Cleavage | pacid=371781 |
| 740 | 761 UGAGGUAGU | ::: :::::CAUUGGAUA | Cleavage | pacid=371781 |
| 813 | 834 UGAGGUAGU | ::: :::::CAUUGGAUA | Cleavage | pacid=371781 |
| 872 | 893 UGAGGUAGU | ::: :::::CAUUGGAUA | Cleavage | pacid=371781 |
| 903 | 924 UGAGGUAGU | ::: :::::CAUUGGAUA | Cleavage | pacid=371781 |
| 945 | 966 UGAGGUAGU | ::: :::::CAUUGGAUA | Cleavage | pacid=371781 |
| 1034 | 1055 UGAGGUAGU | ::: :::::CAUUGGAUA | Cleavage | pacid=371781 |
| 371 | 392 UGAGGUAGU | ::: :::::CAUUGGAUA | Cleavage | pacid=371781 |
| 371 | 392 UGAGGUAGU | ::: :::::CAUUGGAUA | Cleavage | pacid=371781 |
| 740 | 761 UGAGGUAGU | ::: :::::CAUUGGAUA | Cleavage | pacid=371781 |
| 813 | 834 UGAGGUAGU | ::: :::::CAUUGGAUA | Cleavage | pacid=371781 |
| 872 | 893 UGAGGUAGU | ::: :::::CAUUGGAUA | Cleavage | pacid=371781 |
| 903 | 924 UGAGGUAGU | ::: :::::CAUUGGAUA | Cleavage | pacid=371781 |
| 945 | 966 UGAGGUAGU | ::: :::::CAUUGGAUA | Cleavage | pacid=371781 |
| 1034 | 1055 UGAGGUAGU | ::: :::::CAUUGGAUA | Cleavage | pacid=371781 |
| 615 | 636 UGAGGUAGU | ::: :::::..AAGUGUACA | Cleavage | pacid=371771 |
| 615 | 636 UGAGGUAGU | ::: :::::..AAGUGUACA | Cleavage | pacid=371771 |
| 1331 | 1352 UGAGGUAGU | ::: :::::GUCCAUACA | Cleavage | pacid=371768 |
| 1331 | 1352 UGAGGUAGU | ::: :::::GUCCAUACA | Cleavage | pacid=371768 |
| 961 | 982 UGAGGUAGU | ::: :::::CAUCAUGUA | Cleavage | pacid=371787 |
| 961 | 982 UGAGGUAGU | ::: :::::CAUCAUGUA | Cleavage | pacid=371787 |
| 961 | 982 UGAGGUAGU | ::: :::::CAUCAUGUA | Cleavage | pacid=371787 |
| 961 | 982 UGAGGUAGU | ::: :::::CAUCAUGUA | Cleavage | pacid=371787 |
| 70 | 93 AGAGGUAGU | ::: :::::ACAAUAUG | Cleavage | pacid=371770 |
| 70 | 93 AGAGGUAGU | ::: :::::ACAAUAUG | Cleavage | pacid=371770 |
| 70 | 93 AGAGGUAGU | ::: :::::ACAAUAUG | Cleavage | pacid=371770 |

| | | | | |
|----|------|--|---|--------------|
| 1 | | | | |
| 2 | | | | |
| 3 | | | | |
| 4 | | 256 | 279 AGAGGUAGU, :: :::::UGAAGUGUG Cleavage | pacid=371749 |
| 5 | 3469 | 3490 UGAGGUAGU : : : :::::ACCAGUAGA/ Cleavage | | pacid=371472 |
| 6 | 3469 | 3490 UGAGGUAGU : : : :::::ACCAGUAGA/ Cleavage | | pacid=371472 |
| 7 | 2097 | 2120 AGAGGUAGU, : : ::::: CAGUCUAUG(Translation | | pacid=371618 |
| 8 | 891 | 914 AGAGGUAGU, : : ::::: CUUGCUAUG(Cleavage | | pacid=371618 |
| 9 | 2005 | 2026 UGAGGUAGU : : ::::: GUGUGUAUG Cleavage | | pacid=371626 |
| 10 | 2005 | 2026 UGAGGUAGU : : ::::: GUGUGUAUG Cleavage | | pacid=371626 |
| 11 | 972 | 993 UGAGGUAGU : : ::::: GCUCAUGUA/ Translation | | pacid=371622 |
| 12 | 972 | 993 UGAGGUAGU : : ::::: GCUCAUGUA/ Translation | | pacid=371622 |
| 13 | 972 | 993 UGAGGUAGU : : ::::: GCUCAUGUA/ Translation | | pacid=371622 |
| 14 | 972 | 993 UGAGGUAGU : : ::::: GCUCAUGUA/ Translation | | pacid=371622 |
| 15 | 417 | 440 AGAGGUAGU, : : ::::: CCCAUUAUG(Cleavage | | pacid=371542 |
| 16 | 735 | 756 UGAGGUAGU : : ::::: AGUUAGAUA/ Cleavage | | pacid=371529 |
| 17 | 825 | 846 UGAGGUAGU : : ::::: AGUUAGAUA/ Cleavage | | pacid=371529 |
| 18 | 735 | 756 UGAGGUAGU : : ::::: AGUUAGAUA/ Cleavage | | pacid=371529 |
| 19 | 825 | 846 UGAGGUAGU : : ::::: AGUUAGAUA/ Cleavage | | pacid=371529 |
| 20 | 2997 | 3018 UGAGGUAGU : : ::::: ACCUCUGCAA/ Cleavage | | pacid=371532 |
| 21 | 2997 | 3018 UGAGGUAGU : : ::::: ACCUCUGCAA/ Cleavage | | pacid=371532 |
| 22 | 126 | 147 UGAGGUAGU : : ::::: CAGCAUACAA/ Cleavage | | pacid=371723 |
| 23 | 126 | 147 UGAGGUAGU : : ::::: CAGCAUACAA/ Cleavage | | pacid=371723 |
| 24 | 126 | 147 UGAGGUAGU : : ::::: CAGCAUACAA/ Cleavage | | pacid=371723 |
| 25 | 126 | 147 UGAGGUAGU : : ::::: CAGCAUACAA/ Cleavage | | pacid=371723 |
| 26 | 3724 | 3745 UGAGGUAGU : : ::::: UUCUGUACA/ Cleavage | | pacid=371728 |
| 27 | 3724 | 3745 UGAGGUAGU : : ::::: UUCUGUACA/ Cleavage | | pacid=371728 |
| 28 | 3724 | 3745 UGAGGUAGU : : ::::: UUCUGUACA/ Cleavage | | pacid=371728 |
| 29 | 3724 | 3745 UGAGGUAGU : : ::::: UUCUGUACA/ Cleavage | | pacid=371728 |
| 30 | 1362 | 1385 AGAGGUAGU, : : ::::: UUCAUUACGI Cleavage | | pacid=371720 |
| 31 | 1380 | 1403 AGAGGUAGU, : : ::::: UUCAUUACGI Cleavage | | pacid=371720 |
| 32 | 7 | 30 AGAGGUAGU, : : ::::: CUAUCUAUG(Translation | | pacid=371716 |
| 33 | 7 | 30 AGAGGUAGU, : : ::::: CUAUCUAUG(Translation | | pacid=371716 |
| 34 | 459 | 480 UGAGGUAGU : : ::::: GAAUAUUCA/ Translation | | pacid=371672 |
| 35 | 459 | 480 UGAGGUAGU : : ::::: GAAUAUUCA/ Translation | | pacid=371672 |
| 36 | 588 | 609 UGAGGUAGU : : ::::: CAUUAUUCA/ Cleavage | | pacid=371667 |
| 37 | 588 | 609 UGAGGUAGU : : ::::: CAUUAUUCA/ Cleavage | | pacid=371667 |
| 38 | 495 | 516 UGAGGUAGU : : ::::: AUUUGUAGA/ Cleavage | | pacid=371662 |
| 39 | 495 | 516 UGAGGUAGU : : ::::: AUUUGUAGA/ Cleavage | | pacid=371662 |
| 40 | 3299 | 3320 UGAGGUAGU : : ::::: UUCAUAUA/ Cleavage | | pacid=371576 |
| 41 | 3299 | 3320 UGAGGUAGU : : ::::: UUCAUAUA/ Cleavage | | pacid=371576 |
| 42 | 44 | 65 UGAGGUAGU : : ::::: CAUAUAACA/ Cleavage | | pacid=371601 |
| 43 | 44 | 65 UGAGGUAGU : : ::::: CAUAUAACA/ Cleavage | | pacid=371601 |
| 44 | 270 | 291 UGAGGUAGU : : ::::: CGGUGUGCG/ Translation | | pacid=371580 |
| 45 | 270 | 291 UGAGGUAGU : : ::::: CGGUGUGCG/ Translation | | pacid=371580 |
| 46 | 1032 | 1053 UGAGGUAGU : : ::::: UUCUGCAUA/ Cleavage | | pacid=371582 |
| 47 | | | | |
| 48 | | | | |
| 49 | | | | |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

| | | | | |
|----|------|----------------|--|--------------|
| 1 | | | | |
| 2 | | | | |
| 3 | | | | |
| 4 | 1287 | 1308 UGAGGUAGU | ::: ::: : ::: ::: : CUCCAUGCAL Cleavage | pacid=371474 |
| 5 | 1360 | 1381 UGAGGUAGU | ::: ::: : ::: ::: : CUCCAUGCAL Cleavage | pacid=371474 |
| 6 | 1287 | 1308 UGAGGUAGU | ::: ::: : ::: ::: : CUCCAUGCAL Cleavage | pacid=371474 |
| 7 | 1360 | 1381 UGAGGUAGU | ::: ::: : ::: ::: : CUCCAUGCAL Cleavage | pacid=371474 |
| 8 | 1287 | 1308 UGAGGUAGU | ::: ::: : ::: ::: : CUCCAUGCAL Cleavage | pacid=371474 |
| 9 | 1360 | 1381 UGAGGUAGU | ::: ::: : ::: ::: : CUCCAUGCAL Cleavage | pacid=371474 |
| 10 | 1287 | 1308 UGAGGUAGU | ::: ::: : ::: ::: : CUCCAUGCAL Cleavage | pacid=371474 |
| 11 | 1360 | 1381 UGAGGUAGU | ::: ::: : ::: ::: : CUCCAUGCAL Cleavage | pacid=371474 |
| 12 | 575 | 596 UGAGGUAGU | ::: ::: : ::: ::: : : : : : AGCUAUACA/ Cleavage | pacid=371471 |
| 13 | 575 | 596 UGAGGUAGU | ::: ::: : ::: ::: : : : : : AGCUAUACA/ Cleavage | pacid=371471 |
| 14 | 1400 | 1421 UGAGGUAGU | ::: ::: : ::: ::: : : : : : CAUUGUAUC/ Cleavage | pacid=371474 |
| 15 | 1400 | 1421 UGAGGUAGU | ::: ::: : ::: ::: : : : : : CAUUGUAUC/ Cleavage | pacid=371474 |
| 16 | 1154 | 1175 UGAGGUAGU | ::: ::: : ::: ::: : : : : : AAAUAUAUG(Cleavage | pacid=371474 |
| 17 | 1154 | 1175 UGAGGUAGU | ::: ::: : ::: ::: : : : : : AAAUAUAUG(Cleavage | pacid=371474 |
| 18 | 1154 | 1175 UGAGGUAGU | ::: ::: : ::: ::: : : : : : AAAUAUAUG(Cleavage | pacid=371474 |
| 19 | 1154 | 1175 UGAGGUAGU | ::: ::: : ::: ::: : : : : : AAAUAUAUG(Cleavage | pacid=371474 |
| 20 | 389 | 412 AGAGGUAGU | ::: ::: : ::: ::: : : : : : CUAGCCAUGC Cleavage | pacid=371474 |
| 21 | 1354 | 1377 AGAGGUAGU | ::: ::: : ::: ::: : : : : : CUAGCCAUGC Cleavage | pacid=371451 |
| 22 | 1492 | 1515 AGAGGUAGU | ::: ::: : ::: ::: : : : : : CUAGCCAUGC Cleavage | pacid=371451 |
| 23 | 763 | 784 UGAGGUAGU | ::: ::: : ::: ::: : : : : : CACCUUAAAA Cleavage | pacid=371631 |
| 24 | 763 | 784 UGAGGUAGU | ::: ::: : ::: ::: : : : : : CACCUUAAAA Cleavage | pacid=371631 |
| 25 | 763 | 784 UGAGGUAGU | ::: ::: : ::: ::: : : : : : CACCUUAAAA Cleavage | pacid=371631 |
| 26 | 763 | 784 UGAGGUAGU | ::: ::: : ::: ::: : : : : : CACCUUAAAA Cleavage | pacid=371631 |
| 27 | 724 | 747 AGAGGUAGU | ::: ::: : ::: ::: : : : : : CAUACAAUGC Cleavage | pacid=371634 |
| 28 | 1991 | 2012 UGAGGUAGU | ::: ::: : ::: ::: : : : : : GUCUAUGCA/ Translation | pacid=371619 |
| 29 | 1991 | 2012 UGAGGUAGU | ::: ::: : ::: ::: : : : : : GUCUAUGCA/ Translation | pacid=371619 |
| 30 | 1035 | 1057 AGAGGUAGU | ::: ::: : ::: ::: : : : : : UAUACUAUG(Translation | pacid=371623 |
| 31 | 1488 | 1511 AGAGGUAGU | ::: ::: : ::: ::: : : : : : UCAACUAUG(Cleavage | pacid=371545 |
| 32 | 1497 | 1518 UGAGGUAGU | ::: ::: : ::: ::: : : : : : UAUCAUCCA/ Cleavage | pacid=371529 |
| 33 | 1539 | 1560 UGAGGUAGU | ::: ::: : ::: ::: : : : : : UAUCAUCCA/ Cleavage | pacid=371529 |
| 34 | 1497 | 1518 UGAGGUAGU | ::: ::: : ::: ::: : : : : : UAUCAUCCA/ Cleavage | pacid=371529 |
| 35 | 1539 | 1560 UGAGGUAGU | ::: ::: : ::: ::: : : : : : UAUCAUCCA/ Cleavage | pacid=371529 |
| 36 | 1497 | 1518 UGAGGUAGU | ::: ::: : ::: ::: : : : : : UAUCAUCCA/ Cleavage | pacid=371529 |
| 37 | 1539 | 1560 UGAGGUAGU | ::: ::: : ::: ::: : : : : : UAUCAUCCA/ Cleavage | pacid=371529 |
| 38 | 1497 | 1518 UGAGGUAGU | ::: ::: : ::: ::: : : : : : UAUCAUCCA/ Cleavage | pacid=371529 |
| 39 | 1539 | 1560 UGAGGUAGU | ::: ::: : ::: ::: : : : : : UAUCAUCCA/ Cleavage | pacid=371529 |
| 40 | 854 | 875 UGAGGUAGU | ::: ::: : ::: ::: : : : : : GAAUAUACA(Translation | pacid=371522 |
| 41 | 854 | 875 UGAGGUAGU | ::: ::: : ::: ::: : : : : : GAAUAUACA(Translation | pacid=371522 |
| 42 | 10 | 32 UGAGGUAGU | ::: ::: : ::: ::: : : : : : AACUACAACA Cleavage | pacid=371524 |
| 43 | 190 | 212 UGAGGUAGU | ::: ::: : ::: ::: : : : : : AACUACAACA Cleavage | pacid=371524 |
| 44 | 190 | 212 UGAGGUAGU | ::: ::: : ::: ::: : : : : : AACUACAACA Cleavage | pacid=371524 |
| 45 | 10 | 32 UGAGGUAGU | ::: ::: : ::: ::: : : : : : AACUACAACA Cleavage | pacid=371524 |
| 46 | 190 | 212 UGAGGUAGU | ::: ::: : ::: ::: : : : : : AACUACAACA Cleavage | pacid=371524 |
| 47 | | | | |
| 48 | | | | |
| 49 | | | | |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | |
|------|--|--------------|
| 190 | 212 UGAGGUAGU :::: : ::::: : AACUACAACA Cleavage | pacid=371524 |
| 500 | 521 UGAGGUAGU :: : :::: : ::::: : UAUUUUAUA Translation | pacid=371722 |
| 500 | 521 UGAGGUAGU :: : :::: : ::::: : UAUUUUAUA Translation | pacid=371722 |
| 1609 | 1630 UGAGGUAGU ::::: : : : : : : : : : : : : : UAUUGUACA/ Cleavage | pacid=371714 |
| 1609 | 1630 UGAGGUAGU ::::: : : : : : : : : : : : : : UAUUGUACA/ Cleavage | pacid=371714 |
| 716 | 739 AGAGGUAGU : AUAGUUAUG Cleavage | pacid=371719 |
| 716 | 739 AGAGGUAGU : AUAGUUAUG Cleavage | pacid=371719 |
| 824 | 847 AGAGGUAGU : AUAGUUAUG Cleavage | pacid=371719 |
| 824 | 847 AGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ AUAGUUAUG Cleavage | pacid=371719 |
| 379 | 402 AGAGGUAGU : CGAGUUAUA(Cleavage | pacid=371660 |
| 379 | 402 AGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ CGAGUUAUA(Cleavage | pacid=371660 |
| 609 | 630 UGAGGUAGU : GACUAUGCC/ Cleavage | pacid=371662 |
| 609 | 630 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ GACUAUGCC/ Cleavage | pacid=371662 |
| 557 | 580 AGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ AGAGUUUA Cleavage | pacid=371662 |
| 388 | 409 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ GGCUUGACA(Cleavage | pacid=371654 |
| 388 | 409 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ GGCUUGACA(Cleavage | pacid=371654 |
| 2987 | 3008 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ ACCUGUAUC/ Cleavage | pacid=371649 |
| 2987 | 3008 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ ACCUGUAUC/ Cleavage | pacid=371649 |
| 2987 | 3008 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ ACCUGUAUC/ Cleavage | pacid=371649 |
| 2987 | 3008 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ ACCUGUAUC/ Cleavage | pacid=371649 |
| 2341 | 2362 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ ACCUGUGCU/ Cleavage | pacid=371589 |
| 2361 | 2382 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ ACCUGUGCU/ Cleavage | pacid=371589 |
| 2341 | 2362 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ ACCUGUGCU/ Cleavage | pacid=371589 |
| 2361 | 2382 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ ACCUGUGCU/ Cleavage | pacid=371589 |
| 2361 | 2382 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ ACCUGUGCU/ Cleavage | pacid=371589 |
| 2341 | 2362 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ ACCUGUGCU/ Cleavage | pacid=371589 |
| 2361 | 2382 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ ACCUGUGCU/ Cleavage | pacid=371589 |
| 2341 | 2362 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ ACCUGUGCU/ Cleavage | pacid=371589 |
| 2361 | 2382 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ ACCUGUGCU/ Cleavage | pacid=371589 |
| 3008 | 3029 UGAGGUAGU :: AAGCAUAUA/ Translation | pacid=371595 |
| 3008 | 3029 UGAGGUAGU :: : : : : ~ : : : : ~ : : : : ~ : : : : ~ AAGCAUAUA/ Translation | pacid=371595 |
| 3008 | 3029 UGAGGUAGU :: : : : : ~ : : : : ~ : : : : ~ : : : : ~ AAGCAUAUA/ Translation | pacid=371595 |
| 3008 | 3029 UGAGGUAGU :: : : : : ~ : : : : ~ : : : : ~ : : : : ~ AAGCAUAUA/ Translation | pacid=371595 |
| 1469 | 1490 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ CGUUAUACA/ Translation | pacid=371599 |
| 1469 | 1490 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ CGUUAUACA/ Translation | pacid=371599 |
| 866 | 887 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ CCUUAUACA/ Cleavage | pacid=371576 |
| 883 | 904 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ CCUUAUACA/ Cleavage | pacid=371576 |
| 1146 | 1167 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ CCUUAUACA/ Cleavage | pacid=371576 |
| 866 | 887 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ CCUUAUACA/ Cleavage | pacid=371576 |
| 883 | 904 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ CCUUAUACA/ Cleavage | pacid=371576 |
| 1146 | 1167 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ CCUUAUACA/ Cleavage | pacid=371576 |
| 593 | 614 UGAGGUAGU : : : : ~ : : : : ~ : : : : ~ : : : : ~ AGUGAUUCA/ Translation | pacid=371587 |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | |
|------|----------------------|-----------------------|--------------|
| 886 | 907 UGAGGUAGU | ::GGCCAUGCA/ Cleavage | pacid=371426 |
| 892 | 913 UGAGGUAGU | ::GGCCAUGCA/ Cleavage | pacid=371425 |
| 886 | 907 UGAGGUAGU | ::GGCCAUGCA/ Cleavage | pacid=371425 |
| 892 | 913 UGAGGUAGU | ::GGCCAUGCA/ Cleavage | pacid=371425 |
| 886 | 907 UGAGGUAGU | ::GGCCAUGCA/ Cleavage | pacid=371426 |
| 892 | 913 UGAGGUAGU | ::GGCCAUGCA/ Cleavage | pacid=371425 |
| 886 | 907 UGAGGUAGU | ::GGCCAUGCA/ Cleavage | pacid=371425 |
| 892 | 913 UGAGGUAGU | ::GGCCAUGCA/ Cleavage | pacid=371425 |
| 2329 | 2350 UGAGGUAGU | ::AAUCGUGCA/ Cleavage | pacid=371429 |
| 2329 | 2350 UGAGGUAGU | ::AAUCGUGCA/ Cleavage | pacid=371429 |
| 2329 | 2350 UGAGGUAGU | ::AAUCGUGCA/ Cleavage | pacid=371429 |
| 2329 | 2350 UGAGGUAGU | ::AAUCGUGCA/ Cleavage | pacid=371429 |
| 3280 | 3301 UGAGGUAGU | ::UACUAUACU/ Cleavage | pacid=371551 |
| 3280 | 3301 UGAGGUAGU | ::UACUAUACU/ Cleavage | pacid=371551 |
| 3280 | 3301 UGAGGUAGU | ::UACUAUACU/ Cleavage | pacid=371551 |
| 3280 | 3301 UGAGGUAGU | ::UACUAUACU/ Cleavage | pacid=371551 |
| 278 | 299 UGAGGUAGU | ::AACCAAACAA Cleavage | pacid=371552 |
| 278 | 299 UGAGGUAGU | ::AACCAAACAA Cleavage | pacid=371552 |
| 278 | 299 UGAGGUAGU | ::AACCAAACAA Cleavage | pacid=371552 |
| 278 | 299 UGAGGUAGU | ::AACCAAACAA Cleavage | pacid=371552 |
| 405 | 426 UGAGGUAGU | ::UGCUAUACA/ Cleavage | pacid=371559 |
| 410 | 431 UGAGGUAGU | ::UGCUAUACA/ Cleavage | pacid=371559 |
| 405 | 426 UGAGGUAGU | ::UGCUAUACA/ Cleavage | pacid=371559 |
| 405 | 426 UGAGGUAGU | ::UGCUAUACA/ Cleavage | pacid=371559 |
| 410 | 431 UGAGGUAGU | ::UGCUAUACA/ Cleavage | pacid=371559 |
| 405 | 426 UGAGGUAGU | ::UGCUAUACA/ Cleavage | pacid=371559 |
| 25 | 46 UGAGGUAGU | ::CAUCAUUUA/ Cleavage | pacid=371573 |
| 25 | 46 UGAGGUAGU | ::CAUCAUUUA/ Cleavage | pacid=371573 |
| 25 | 46 UGAGGUAGU | ::CAUCAUUUA/ Cleavage | pacid=371573 |
| 25 | 46 UGAGGUAGU | ::CAUCAUUUA/ Cleavage | pacid=371573 |
| 317 | 340 AGAGGUAGU | ::AAAUCUCUU(Cleavage | pacid=371549 |
| 317 | 340 AGAGGUAGU | ::AAAUCUCUU(Cleavage | pacid=371549 |
| 28 | 48 UGAGGUAGU | ::CACUAUUA/ Cleavage | pacid=371700 |
| 28 | 48 UGAGGUAGU | ::CACUAUUA/ Cleavage | pacid=371700 |
| 1608 | 1629 UGAGGUAGU | ::GACCAAUAC Cleavage | pacid=371703 |
| 1614 | 1635 UGAGGUAGU | ::GACCAAUAC Cleavage | pacid=371703 |
| 1617 | 1638 UGAGGUAGU | ::GACCAAUAC Cleavage | pacid=371703 |
| 1670 | 1691 UGAGGUAGU | ::GACCAAUAC Cleavage | pacid=371703 |
| 1608 | 1629 UGAGGUAGU | ::GACCAAUAC Cleavage | pacid=371703 |
| 1614 | 1635 UGAGGUAGU | ::GACCAAUAC Cleavage | pacid=371703 |
| 1617 | 1638 UGAGGUAGU | ::GACCAAUAC Cleavage | pacid=371703 |
| 1670 | 1691 UGAGGUAGU | ::GACCAAUAC Cleavage | pacid=371703 |
| 1608 | 1629 UGAGGUAGU | ::GACCAAUAC Cleavage | pacid=371703 |

| | | | |
|----|------|----------------------|------------------------------------|
| 1 | | | |
| 2 | | | |
| 3 | | | |
| 4 | 1614 | 1635 UGAGGUAGU | GACCAAAUAC Cleavage pacid=371703 |
| 5 | 1617 | 1638 UGAGGUAGU | GACCAAAUAC Cleavage pacid=371703 |
| 6 | 1670 | 1691 UGAGGUAGU | GACCAAAUAC Cleavage pacid=371703 |
| 7 | 1608 | 1629 UGAGGUAGU | GACCAAAUAC Cleavage pacid=371703 |
| 8 | 1614 | 1635 UGAGGUAGU | GACCAAAUAC Cleavage pacid=371703 |
| 9 | 1617 | 1638 UGAGGUAGU | GACCAAAUAC Cleavage pacid=371703 |
| 10 | 1670 | 1691 UGAGGUAGU | GACCAAAUAC Cleavage pacid=371703 |
| 11 | 1670 | 1691 UGAGGUAGU | GACCAAAUAC Cleavage pacid=371703 |
| 12 | 1388 | 1412 AGAGGUAGU | UAGGCUAUG Translation pacid=371689 |
| 13 | 12 | 33 UGAGGUAGU | AGCCACAGAA Cleavage pacid=371689 |
| 14 | 12 | 33 UGAGGUAGU | AGCCACAGAA Cleavage pacid=371689 |
| 15 | 12 | 33 UGAGGUAGU | AGCCACAGAA Cleavage pacid=371689 |
| 16 | 12 | 33 UGAGGUAGU | AGCCACAGAA Cleavage pacid=371689 |
| 17 | 12 | 33 UGAGGUAGU | AGCCACAGAA Cleavage pacid=371689 |
| 18 | 145 | 166 UGAGGUAGU | GAUUGUGCA Cleavage pacid=371689 |
| 19 | 145 | 166 UGAGGUAGU | GAUUGUGCA Cleavage pacid=371689 |
| 20 | 1118 | 1139 UGAGGUAGU | UAUCAUACA Translation pacid=371696 |
| 21 | 1118 | 1139 UGAGGUAGU | UAUCAUACA Translation pacid=371696 |
| 22 | 1118 | 1139 UGAGGUAGU | UAUCAUACA Translation pacid=371696 |
| 23 | 1118 | 1139 UGAGGUAGU | UAUCAUACA Translation pacid=371696 |
| 24 | 1118 | 1139 UGAGGUAGU | UAUCAUACA Translation pacid=371696 |
| 25 | 1118 | 1139 UGAGGUAGU | UAUCAUACA Translation pacid=371696 |
| 26 | 1118 | 1139 UGAGGUAGU | UAUCAUACA Translation pacid=371696 |
| 27 | 1118 | 1139 UGAGGUAGU | UAUCAUACA Translation pacid=371696 |
| 28 | 1118 | 1139 UGAGGUAGU | UAUCAUACA Translation pacid=371696 |
| 29 | 1118 | 1139 UGAGGUAGU | UAUCAUACA Translation pacid=371696 |
| 30 | 1118 | 1139 UGAGGUAGU | UAUCAUACA Translation pacid=371696 |
| 31 | 1118 | 1139 UGAGGUAGU | UAUCAUACA Translation pacid=371696 |
| 32 | 40 | 63 AGAGGUAGU | GGAAAUGUG Cleavage pacid=371689 |
| 33 | 1077 | 1098 UGAGGUAGU | CGCUGUGCA Cleavage pacid=371690 |
| 34 | 1077 | 1098 UGAGGUAGU | CGCUGUGCA Cleavage pacid=371690 |
| 35 | 1175 | 1196 UGAGGUAGU | AGUGAUACA Cleavage pacid=371755 |
| 36 | 1175 | 1196 UGAGGUAGU | AGUGAUACA Cleavage pacid=371755 |
| 37 | 615 | 636 UGAGGUAGU | AAGUGUACA Cleavage pacid=371771 |
| 38 | 615 | 636 UGAGGUAGU | AAGUGUACA Cleavage pacid=371771 |
| 39 | 615 | 636 UGAGGUAGU | AAGUGUACA Cleavage pacid=371771 |
| 40 | 615 | 636 UGAGGUAGU | AAGUGUACA Cleavage pacid=371771 |
| 41 | 958 | 979 UGAGGUAGU | AAUUCUACA Cleavage pacid=371766 |
| 42 | 958 | 979 UGAGGUAGU | AAUUCUACA Cleavage pacid=371766 |
| 43 | 1506 | 1527 UGAGGUAGU | AACCAAAGAA Cleavage pacid=371744 |
| 44 | 1506 | 1527 UGAGGUAGU | AACCAAAGAA Cleavage pacid=371744 |
| 45 | 1506 | 1527 UGAGGUAGU | AACCAAAGAA Cleavage pacid=371744 |
| 46 | 1506 | 1527 UGAGGUAGU | AACCAAAGAA Cleavage pacid=371744 |
| 47 | 102 | 123 UGAGGUAGU | AAUUAUUA Cleavage pacid=371753 |
| 48 | 102 | 123 UGAGGUAGU | AAUUAUUA Cleavage pacid=371753 |
| 49 | 102 | 123 UGAGGUAGU | AAUUAUUA Cleavage pacid=371753 |
| 50 | 102 | 123 UGAGGUAGU | AAUUAUUA Cleavage pacid=371753 |
| 51 | 628 | 649 UGAGGUAGU | GAUUAUGUA Translation pacid=371766 |
| 52 | 628 | 649 UGAGGUAGU | GAUUAUGUA Translation pacid=371766 |
| 53 | | | |
| 54 | | | |
| 55 | | | |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | |
|------|--|--------------|
| 735 | 756 UGAGGUAGU :... :... :... :AGUUAGUA, Cleavage | pacid=371529 |
| 825 | 846 UGAGGUAGU :... :... :... :AGUUAGUA, Cleavage | pacid=371529 |
| 362 | 383 UGAGGUAGU :... :... :... :AGCUGAACAA, Cleavage | pacid=371534 |
| 362 | 383 UGAGGUAGU :... :... :... :AGCUGAACAA, Cleavage | pacid=371534 |
| 910 | 933 AGAGGUAGU :... :... :... :GGAAGUAUG, Cleavage | pacid=371741 |
| 160 | 181 UGAGGUAGU :... :... :... :CACCAUUCGA Translation | pacid=371736 |
| 160 | 181 UGAGGUAGU :... :... :... :CACCAUUCGA Translation | pacid=371736 |
| 160 | 181 UGAGGUAGU :... :... :... :CACCAUUCGA Translation | pacid=371736 |
| 160 | 181 UGAGGUAGU :... :... :... :CACCAUUCGA Translation | pacid=371736 |
| 160 | 181 UGAGGUAGU :... :... :... :CACCAUUCGA Translation | pacid=371736 |
| 160 | 181 UGAGGUAGU :... :... :... :CACCAUUCGA Translation | pacid=371736 |
| 160 | 181 UGAGGUAGU :... :... :... :CACCAUUCGA Translation | pacid=371736 |
| 160 | 181 UGAGGUAGU :... :... :... :CACCAUUCGA Translation | pacid=371736 |
| 160 | 181 UGAGGUAGU :... :... :... :CACCAUUCGA Translation | pacid=371736 |
| 451 | 472 UGAGGUAGU :... :... :... :AACUUUAGC, Cleavage | pacid=371712 |
| 451 | 472 UGAGGUAGU :... :... :... :AACUUUAGC, Cleavage | pacid=371712 |
| 451 | 472 UGAGGUAGU :... :... :... :AACUUUAGC, Cleavage | pacid=371712 |
| 451 | 472 UGAGGUAGU :... :... :... :AACUUUAGC, Cleavage | pacid=371712 |
| 2070 | 2092 UGAGGUAG-L :... :... :... :UACCAUUCA, Cleavage | pacid=371712 |
| 2070 | 2092 UGAGGUAG-L :... :... :... :UACCAUUCA, Cleavage | pacid=371712 |
| 2070 | 2092 UGAGGUAG-L :... :... :... :UACCAUUCA, Cleavage | pacid=371712 |
| 2070 | 2092 UGAGGUAG-L :... :... :... :UACCAUUCA, Cleavage | pacid=371712 |
| 1798 | 1821 AGAGGUAGU :... :... :... :CUUUUUGUG Cleavage | pacid=371741 |
| 267 | 288 UGAGGUAGU :... :... :... :GUGCAGGCAI Cleavage | pacid=371733 |
| 497 | 518 UGAGGUAGU :... :... :... :GUGCAGGCAI Cleavage | pacid=371733 |
| 267 | 288 UGAGGUAGU :... :... :... :GUGCAGGCAI Cleavage | pacid=371733 |
| 497 | 518 UGAGGUAGU :... :... :... :GUGCAGGCAI Cleavage | pacid=371733 |
| 1188 | 1209 UGAGGUAGU :... :... :... :AUCUAUAUG, Cleavage | pacid=371727 |
| 1188 | 1209 UGAGGUAGU :... :... :... :AUCUAUAUG, Cleavage | pacid=371727 |
| 2074 | 2095 UGAGGUAGU :... :... :... :AACCAUUCU Cleavage | pacid=371649 |
| 2074 | 2095 UGAGGUAGU :... :... :... :AACCAUUCU Cleavage | pacid=371649 |
| 2074 | 2095 UGAGGUAGU :... :... :... :AACCAUUCU Cleavage | pacid=371649 |
| 2074 | 2095 UGAGGUAGU :... :... :... :AACCAUUCU Cleavage | pacid=371649 |
| 2278 | 2299 UGAGGUAGU :... :... :... :AGUUUAUA, Translation | pacid=371664 |
| 2278 | 2299 UGAGGUAGU :... :... :... :AGUUUAUA, Translation | pacid=371664 |
| 737 | 764 AGAGGUAGU :... :... :... :UCGAUUGUG Cleavage | pacid=371676 |
| 86 | 108 UGAGGUAGU :... :... :... :AGCCACUGAA, Cleavage | pacid=371665 |
| 86 | 108 UGAGGUAGU :... :... :... :AGCCACUGAA, Cleavage | pacid=371665 |
| 86 | 108 UGAGGUAGU :... :... :... :AGCCACUGAA, Cleavage | pacid=371665 |
| 86 | 108 UGAGGUAGU :... :... :... :AGCCACUGAA, Cleavage | pacid=371665 |
| 1385 | 1406 UGAGGUAGU :... :... :... :CACCACUAA Cleavage | pacid=371664 |
| 1385 | 1406 UGAGGUAGU :... :... :... :CACCACUAA Cleavage | pacid=371664 |
| 1385 | 1406 UGAGGUAGU :... :... :... :CACCACUAA Cleavage | pacid=371664 |
| 1385 | 1406 UGAGGUAGU :... :... :... :CACCACUAA Cleavage | pacid=371664 |

| | | | |
|----|------|--|--------------|
| 1 | | | |
| 2 | | | |
| 3 | | | |
| 4 | 381 | 402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage | pacid=371660 |
| 5 | 381 | 402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage | pacid=371660 |
| 6 | 381 | 402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage | pacid=371660 |
| 7 | 381 | 402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage | pacid=371660 |
| 8 | 381 | 402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage | pacid=371660 |
| 9 | 381 | 402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage | pacid=371660 |
| 10 | 381 | 402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage | pacid=371660 |
| 11 | 381 | 402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage | pacid=371660 |
| 12 | 381 | 402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage | pacid=371660 |
| 13 | 381 | 402 UGAGGUAGU :..... :..... : AGUUAUACAI Cleavage | pacid=371660 |
| 14 | 607 | 630 AGAGGUAGU :..... :..... : CCGACUAUGC Cleavage | pacid=371662 |
| 15 | 609 | 630 UGAGGUAGU :..... :..... : GACUAUGCC/ Cleavage | pacid=371662 |
| 16 | 609 | 630 UGAGGUAGU :..... :..... : GACUAUGCC/ Cleavage | pacid=371662 |
| 17 | 609 | 630 UGAGGUAGU :..... :..... : GACUAUGCC/ Cleavage | pacid=371662 |
| 18 | 609 | 630 UGAGGUAGU :..... :..... : GACUAUGCC/ Cleavage | pacid=371662 |
| 19 | 609 | 630 UGAGGUAGU :..... :..... : GACUAUGCC/ Cleavage | pacid=371662 |
| 20 | 914 | 935 UGAGGUAGU :..... :..... : AAUCAUGUG(Cleavage | pacid=371654 |
| 21 | 914 | 935 UGAGGUAGU :..... :..... : AAUCAUGUG(Cleavage | pacid=371654 |
| 22 | 914 | 935 UGAGGUAGU :..... :..... : AAUCAUGUG(Cleavage | pacid=371654 |
| 23 | 914 | 935 UGAGGUAGU :..... :..... : AAUCAUGUG(Cleavage | pacid=371654 |
| 24 | 914 | 935 UGAGGUAGU :..... :..... : AAUCAUGUG(Cleavage | pacid=371654 |
| 25 | 48 | 69 UGAGGUAGU :..... :..... : AAUCAUGUC/ Cleavage | pacid=371676 |
| 26 | 48 | 69 UGAGGUAGU :..... :..... : AAUCAUGUC/ Cleavage | pacid=371676 |
| 27 | 48 | 69 UGAGGUAGU :..... :..... : AAUCAUGUC/ Cleavage | pacid=371676 |
| 28 | 48 | 69 UGAGGUAGU :..... :..... : AAUCAUGUC/ Cleavage | pacid=371676 |
| 29 | 48 | 69 UGAGGUAGU :..... :..... : AAUCAUGUC/ Cleavage | pacid=371676 |
| 30 | 48 | 69 UGAGGUAGU :..... :..... : AAUCAUGUC/ Cleavage | pacid=371676 |
| 31 | 42 | 63 UGAGGUAGU :..... :..... : CACCAUGCGA Cleavage | pacid=371666 |
| 32 | 42 | 63 UGAGGUAGU :..... :..... : CACCAUGCGA Cleavage | pacid=371666 |
| 33 | 42 | 63 UGAGGUAGU :..... :..... : CACCAUGCGA Cleavage | pacid=371666 |
| 34 | 42 | 63 UGAGGUAGU :..... :..... : CACCAUGCGA Cleavage | pacid=371666 |
| 35 | 42 | 63 UGAGGUAGU :..... :..... : CACCAUGCGA Cleavage | pacid=371666 |
| 36 | 559 | 580 UGAGGUAGU :..... :..... : AGUUUUACG, Cleavage | pacid=371662 |
| 37 | 559 | 580 UGAGGUAGU :..... :..... : AGUUUUACG, Cleavage | pacid=371662 |
| 38 | 559 | 580 UGAGGUAGU :..... :..... : AGUUUUACG, Cleavage | pacid=371662 |
| 39 | 559 | 580 UGAGGUAGU :..... :..... : AGUUUUACG, Cleavage | pacid=371662 |
| 40 | 559 | 580 UGAGGUAGU :..... :..... : AGUUUUACG, Cleavage | pacid=371662 |
| 41 | 559 | 580 UGAGGUAGU :..... :..... : AGUUUUACG, Cleavage | pacid=371662 |
| 42 | 337 | 358 UGAGGUAGU :..... :..... : UGCUAUUAUI Cleavage | pacid=371643 |
| 43 | 337 | 358 UGAGGUAGU :..... :..... : UGCUAUUAUI Cleavage | pacid=371643 |
| 44 | 496 | 516 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage | pacid=371669 |
| 45 | 833 | 853 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage | pacid=371669 |
| 46 | 496 | 516 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage | pacid=371669 |
| 47 | 833 | 853 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage | pacid=371669 |
| 48 | 496 | 516 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage | pacid=371669 |
| 49 | 833 | 853 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage | pacid=371669 |
| 50 | 496 | 516 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage | pacid=371669 |
| 51 | 833 | 853 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage | pacid=371669 |
| 52 | 496 | 516 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage | pacid=371669 |
| 53 | 833 | 853 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage | pacid=371669 |
| 54 | 833 | 853 UGAGGUAGU :..... :..... : AGUCAUAUA- Cleavage | pacid=371669 |
| 55 | 1110 | 1133 AGAGGUAGU :..... :..... : AAGACAAUG(Cleavage | pacid=371653 |
| 56 | 29 | 50 UGAGGUAGU :..... :..... : GACUAUGAA(Cleavage | pacid=371643 |
| 57 | 29 | 50 UGAGGUAGU :..... :..... : GACUAUGAA(Cleavage | pacid=371643 |
| 58 | 29 | 50 UGAGGUAGU :..... :..... : GACUAUGAA(Cleavage | pacid=371643 |
| 59 | 37 | 58 UGAGGUAGU :..... :..... : GACUAUGAA(Cleavage | pacid=371660 |
| 60 | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | | | |
|------|------|-----------|-------------------------------|-------------|--------------|
| 37 | 58 | UGAGGUAGU | :..... :.....GACUAUGAA | Cleavage | pacid=371660 |
| 37 | 58 | UGAGGUAGU | :..... :.....GAUUAUGAA | Cleavage | pacid=371647 |
| 37 | 58 | UGAGGUAGU | :..... :.....GAUUAUGAA | Cleavage | pacid=371647 |
| 816 | 837 | UGAGGUAGU | :: : : :.....:AACAAACGCCG | Cleavage | pacid=371581 |
| 816 | 837 | UGAGGUAGU | :: : : :.....:AACAAACGCCG | Cleavage | pacid=371581 |
| 816 | 837 | UGAGGUAGU | :: : : :.....:AACAAACGCCG | Cleavage | pacid=371581 |
| 816 | 837 | UGAGGUAGU | :: : : :.....:AACAAACGCCG | Cleavage | pacid=371581 |
| 2339 | 2362 | AGAGGUAGU | :: :..... :.....:CAACCUUGUG | Cleavage | pacid=371589 |
| 2359 | 2382 | AGAGGUAGU | :: :..... :.....:CAACCUUGUG | Cleavage | pacid=371589 |
| 2339 | 2362 | AGAGGUAGU | :: :..... :.....:CAACCUUGUG | Cleavage | pacid=371589 |
| 2359 | 2382 | AGAGGUAGU | :: :..... :.....:CAACCUUGUG | Cleavage | pacid=371589 |
| 2359 | 2382 | AGAGGUAGU | :: :..... :.....:CAACCUUGUG | Cleavage | pacid=371589 |
| 621 | 644 | AGAGGUAGU | :..... :.....GAAGGUGUG | Cleavage | pacid=371606 |
| 617 | 640 | AGAGGUAGU | :..... :.....GAAGGUGUG | Cleavage | pacid=371606 |
| 1243 | 1266 | AGAGGUAGU | :: :..... :.....:UAACCUAUG | Cleavage | pacid=371592 |
| 393 | 414 | UGAGGUAGU | :..... :.....GGUCAUAUG | Cleavage | pacid=371593 |
| 393 | 414 | UGAGGUAGU | :..... :.....GGUCAUAUG | Cleavage | pacid=371593 |
| 393 | 414 | UGAGGUAGU | :..... :.....GGUCAUAUG | Cleavage | pacid=371593 |
| 393 | 414 | UGAGGUAGU | :..... :.....GGUCAUAUG | Cleavage | pacid=371593 |
| 3769 | 3790 | UGAGGUAGU | :..... :.....UUACAUGUG | Cleavage | pacid=371576 |
| 3769 | 3790 | UGAGGUAGU | :..... :.....UUACAUGUG | Cleavage | pacid=371576 |
| 3769 | 3790 | UGAGGUAGU | :..... :.....UUACAUGUG | Cleavage | pacid=371576 |
| 3769 | 3790 | UGAGGUAGU | :..... :.....UUACAUGUG | Cleavage | pacid=371576 |
| 830 | 851 | UGAGGUAGU | :..... :.....UGUCAAAUA | Translation | pacid=371576 |
| 847 | 868 | UGAGGUAGU | :..... :.....UGUCAAAUA | Translation | pacid=371576 |
| 1110 | 1131 | UGAGGUAGU | :..... :.....UGUCAAAUA | Translation | pacid=371576 |
| 830 | 851 | UGAGGUAGU | :..... :.....UGUCAAAUA | Translation | pacid=371576 |
| 847 | 868 | UGAGGUAGU | :..... :.....UGUCAAAUA | Translation | pacid=371576 |
| 1110 | 1131 | UGAGGUAGU | :..... :.....UGUCAAAUA | Translation | pacid=371576 |
| 974 | 995 | UGAGGUAGU | :..... :.....AAUUGUCUA | Cleavage | pacid=371580 |
| 974 | 995 | UGAGGUAGU | :..... :.....AAUUGUCUA | Cleavage | pacid=371580 |
| 1023 | 1046 | AGAGGUAGU | :: :..... :.....:CAAUCCUGL | Cleavage | pacid=371596 |
| 842 | 863 | UGAGGUAGU | :..... :.....AAUUGUCUA | Cleavage | pacid=371613 |
| 842 | 863 | UGAGGUAGU | :..... :.....AAUUGUCUA | Cleavage | pacid=371613 |
| 1374 | 1395 | UGAGGUAGU | :: : :..... :.....:AAUGAUUCA | Cleavage | pacid=371588 |
| 1374 | 1395 | UGAGGUAGU | :: : :..... :.....:AAUGAUUCA | Cleavage | pacid=371588 |
| 79 | 100 | UGAGGUAGU | :: : :..... :.....:CACCAUUCAC | Cleavage | pacid=371604 |
| 79 | 100 | UGAGGUAGU | :: : :..... :.....:CACCAUUCAC | Cleavage | pacid=371604 |
| 79 | 100 | UGAGGUAGU | :: : :..... :.....:CACCAUUCAC | Cleavage | pacid=371604 |
| 79 | 100 | UGAGGUAGU | :: : :..... :.....:CACCAUUCAC | Cleavage | pacid=371604 |
| 60 | 81 | UGAGGUAGU | :: : :..... :.....:AACUCUAUCA | Cleavage | pacid=371615 |
| 61 | 82 | UGAGGUAGU | :: : :..... :.....:AACUCUAUCA | Cleavage | pacid=371615 |
| 60 | 81 | UGAGGUAGU | :: : :..... :.....:AACUCUAUCA | Cleavage | pacid=371615 |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | |
|------|------|--|--------------|
| 61 | 82 | UGAGGUAGU :::: :. ::::: :::: AACUCUAUCA Cleavage | pacid=371615 |
| 811 | 832 | UGAGGUAGU ::::: :. ::::: : AAUCAUACU Cleavage | pacid=371610 |
| 811 | 832 | UGAGGUAGU ::::: :. ::::: : AAUCAUACU Cleavage | pacid=371610 |
| 811 | 832 | UGAGGUAGU ::::: :. ::::: : AAUCAUACU Cleavage | pacid=371610 |
| 811 | 832 | UGAGGUAGU ::::: :. ::::: : AAUCAUACU Cleavage | pacid=371610 |
| 1742 | 1763 | UGAGGUAGU :::: :. ::::: : AGCCUGCG Cleavage | pacid=371608 |
| 1742 | 1763 | UGAGGUAGU :::: :. ::::: : AGCCUGCG Cleavage | pacid=371608 |
| 1742 | 1763 | UGAGGUAGU :::: :. ::::: : AGCCUGCG Cleavage | pacid=371608 |
| 1742 | 1763 | UGAGGUAGU :::: :. ::::: : AGCCUGCG Cleavage | pacid=371608 |
| 1434 | 1457 | AGAGGUAGU, :::: :. ::::: : UCAACUUGG Cleavage | pacid=371609 |
| 2135 | 2158 | AGAGGUAGU, :::: :. ::::: : UCAACUUGG Cleavage | pacid=371609 |
| 2140 | 2163 | AGAGGUAGU, :::: :. ::::: : UCAACUUGG Cleavage | pacid=371609 |
| 1671 | 1692 | UGAGGUAGU ::::: :. ::::: : AAUUAUGCU Cleavage | pacid=371575 |
| 1671 | 1692 | UGAGGUAGU ::::: :. ::::: : AAUUAUGCU Cleavage | pacid=371575 |
| 2511 | 2534 | AGAGGUAGU ::::: :. ::::: : AAAUUAAG Cleavage | pacid=371520 |
| 2873 | 2894 | UGAGGUAGU ::::: :. ::::: : AUUCAUACA Cleavage | pacid=371488 |
| 2905 | 2926 | UGAGGUAGU ::::: :. ::::: : AUUCAUACA Cleavage | pacid=371488 |
| 2873 | 2894 | UGAGGUAGU ::::: :. ::::: : AUUCAUACA Cleavage | pacid=371488 |
| 2905 | 2926 | UGAGGUAGU ::::: :. ::::: : AUUCAUACA Cleavage | pacid=371488 |
| 2496 | 2518 | UGAGGUAGU ::::: :. ::::: : GAUUAUAUC Cleavage | pacid=371517 |
| 2459 | 2481 | UGAGGUAGU ::::: :. ::::: : GAUUAUAUC Cleavage | pacid=371517 |
| 2496 | 2518 | UGAGGUAGU ::::: :. ::::: : GAUUAUAUC Cleavage | pacid=371517 |
| 2459 | 2481 | UGAGGUAGU ::::: :. ::::: : GAUUAUAUC Cleavage | pacid=371517 |
| 1402 | 1423 | UGAGGUAGU :::: :. ::::: : GACAAUAUG Cleavage | pacid=371510 |
| 1402 | 1423 | UGAGGUAGU :::: :. ::::: : GACAAUAUG Cleavage | pacid=371510 |
| 158 | 179 | UGAGGUAGU ::::: :. ::::: : UGCCAUACA Cleavage | pacid=371517 |
| 158 | 179 | UGAGGUAGU ::::: :. ::::: : UGCCAUACA Cleavage | pacid=371517 |
| 158 | 179 | UGAGGUAGU ::::: :. ::::: : UGCCAUACA Cleavage | pacid=371517 |
| 158 | 179 | UGAGGUAGU ::::: :. ::::: : UGCCAUACA Cleavage | pacid=371517 |
| 1956 | 1977 | UGAGGUAGU :::: :. ::::: : AGUCACACA Translation | pacid=371432 |
| 1956 | 1977 | UGAGGUAGU :::: :. ::::: : AGUCACACA Translation | pacid=371432 |
| 1956 | 1977 | UGAGGUAGU :::: :. ::::: : AGUCACACA Translation | pacid=371432 |
| 1956 | 1977 | UGAGGUAGU :::: :. ::::: : AGUCACACA Translation | pacid=371432 |
| 3980 | 4001 | UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage | pacid=371431 |
| 3970 | 3991 | UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage | pacid=371431 |
| 3992 | 4013 | UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage | pacid=371431 |
| 3993 | 4014 | UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage | pacid=371431 |
| 4085 | 4106 | UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage | pacid=371431 |
| 4062 | 4083 | UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage | pacid=371431 |
| 4669 | 4690 | UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage | pacid=371431 |
| 4681 | 4702 | UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage | pacid=371431 |
| 4774 | 4795 | UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage | pacid=371431 |
| 3980 | 4001 | UGAGGUAGU ::::: :. ::::: : GAUUAUGCG Cleavage | pacid=371431 |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | |
|------|----------------------|------------------------|--------------|
| 3970 | 3991 UGAGGUAGU | GAUUAUGCG(Cleavage | pacid=371431 |
| 3992 | 4013 UGAGGUAGU | GAUUAUGCG(Cleavage | pacid=371431 |
| 3993 | 4014 UGAGGUAGU | GAUUAUGCG(Cleavage | pacid=371431 |
| 4085 | 4106 UGAGGUAGU | GAUUAUGCG(Cleavage | pacid=371431 |
| 4062 | 4083 UGAGGUAGU | GAUUAUGCG(Cleavage | pacid=371431 |
| 4669 | 4690 UGAGGUAGU | GAUUAUGCG(Cleavage | pacid=371431 |
| 4681 | 4702 UGAGGUAGU | GAUUAUGCG(Cleavage | pacid=371431 |
| 4774 | 4795 UGAGGUAGU | GAUUAUGCG(Cleavage | pacid=371431 |
| 294 | 317 AGAGGUAGU..... | AAAACUAUG(Cleavage | pacid=371421 |
| 793 | 816 AGAGGUAGU..... | GAAACUAUG(Cleavage | pacid=371424 |
| 798 | 821 AGAGGUAGU..... | GAAACUAUG(Cleavage | pacid=371424 |
| 795 | 816 UGAGGUAGU | AACUAUGGA(Cleavage | pacid=371424 |
| 800 | 821 UGAGGUAGU | AACUAUGGA(Cleavage | pacid=371424 |
| 795 | 816 UGAGGUAGU | AACUAUGGA(Cleavage | pacid=371424 |
| 800 | 821 UGAGGUAGU | AACUAUGGA(Cleavage | pacid=371424 |
| 795 | 816 UGAGGUAGU | AACUAUGGA(Cleavage | pacid=371424 |
| 800 | 821 UGAGGUAGU | AACUAUGGA(Cleavage | pacid=371424 |
| 795 | 816 UGAGGUAGU | AACUAUGGA(Cleavage | pacid=371424 |
| 800 | 821 UGAGGUAGU | AACUAUGGA(Cleavage | pacid=371424 |
| 1427 | 1448 UGAGGUAGU | UGCCAUACAC Cleavage | pacid=371442 |
| 1427 | 1448 UGAGGUAGU | UGCCAUACAC Cleavage | pacid=371442 |
| 1427 | 1448 UGAGGUAGU | UGCCAUACAC Cleavage | pacid=371442 |
| 1427 | 1448 UGAGGUAGU | UGCCAUACAC Cleavage | pacid=371442 |
| 675 | 696 UGAGGUAGU | AAUCAUACU/ Cleavage | pacid=371556 |
| 675 | 696 UGAGGUAGU | AAUCAUACU/ Cleavage | pacid=371556 |
| 675 | 696 UGAGGUAGU | AAUCAUACU/ Cleavage | pacid=371556 |
| 675 | 696 UGAGGUAGU | AAUCAUACU/ Cleavage | pacid=371556 |
| 900 | 921 UGAGGUAGU | UAUUCUGCA(Translation | pacid=371548 |
| 900 | 921 UGAGGUAGU | UAUUCUGCA(Translation | pacid=371548 |
| 900 | 921 UGAGGUAGU | UAUUCUGCA(Translation | pacid=371548 |
| 900 | 921 UGAGGUAGU | UAUUCUGCA(Translation | pacid=371548 |
| 1830 | 1851 UGAGGUAGU | AUCUAUGUA(Cleavage | pacid=371559 |
| 1830 | 1851 UGAGGUAGU | AUCUAUGUA(Cleavage | pacid=371559 |
| 175 | 198 AGAGGUAGU..... | AAACUUAUU(Cleavage | pacid=371562 |
| 196 | 219 AGAGGUAGU..... | AAACUUAUU(Cleavage | pacid=371556 |
| 278 | 299 UGAGGUAGU | AACCAAACAA Cleavage | pacid=371552 |
| 278 | 299 UGAGGUAGU | AACCAAACAA Cleavage | pacid=371552 |
| 405 | 426 UGAGGUAGU | UGCUAUACA/ Cleavage | pacid=371559 |
| 410 | 431 UGAGGUAGU | UGCUAUACA/ Cleavage | pacid=371559 |
| 405 | 426 UGAGGUAGU | UGCUAUACA/ Cleavage | pacid=371559 |
| 405 | 426 UGAGGUAGU | UGCUAUACA/ Cleavage | pacid=371559 |
| 405 | 426 UGAGGUAGU | UGCUAUACA/ Cleavage | pacid=371559 |
| 410 | 431 UGAGGUAGU | UGCUAUACA/ Cleavage | pacid=371559 |
| 405 | 426 UGAGGUAGU | UGCUAUACA/ Cleavage | pacid=371559 |

| | | | |
|----|------|-----------------------|--------------------------------------|
| 1 | | | |
| 2 | | | |
| 3 | | | |
| 4 | 405 | 426 UGAGGUAGU | UGCUAUACA/ Cleavage pacid=371559 |
| 5 | 410 | 431 UGAGGUAGU | UGCUAUACA/ Cleavage pacid=371559 |
| 6 | 405 | 426 UGAGGUAGU | UGCUAUACA/ Cleavage pacid=371559 |
| 7 | 405 | 426 UGAGGUAGU | UGCUAUACA/ Cleavage pacid=371559 |
| 8 | 410 | 431 UGAGGUAGU | UGCUAUACA/ Cleavage pacid=371559 |
| 9 | 410 | 431 UGAGGUAGU | UGCUAUACA/ Cleavage pacid=371559 |
| 10 | 405 | 426 UGAGGUAGU | UGCUAUACA/ Cleavage pacid=371559 |
| 11 | 294 | 315 UGAGGUAGU | UACUGAACAC/ Cleavage pacid=371569 |
| 12 | 294 | 315 UGAGGUAGU | UACUGAACAC/ Cleavage pacid=371569 |
| 13 | 294 | 315 UGAGGUAGU | UACUGAACAC/ Cleavage pacid=371569 |
| 14 | 294 | 315 UGAGGUAGU | UACUGAACAC/ Cleavage pacid=371569 |
| 15 | 294 | 315 UGAGGUAGU | UACUGAACAC/ Cleavage pacid=371569 |
| 16 | 3916 | 3937 UGAGGUAGU | AGUCCUGCAC/ Cleavage pacid=371443 |
| 17 | 2706 | 2727 UGAGGUAGU | AGUCCUGCAC/ Cleavage pacid=371443 |
| 18 | 3916 | 3937 UGAGGUAGU | AGUCCUGCAC/ Cleavage pacid=371443 |
| 19 | 2706 | 2727 UGAGGUAGU | AGUCCUGCAC/ Cleavage pacid=371443 |
| 20 | 3916 | 3937 UGAGGUAGU | AGUCCUGCAC/ Cleavage pacid=371443 |
| 21 | 2706 | 2727 UGAGGUAGU | AGUCCUGCAC/ Cleavage pacid=371443 |
| 22 | 3916 | 3937 UGAGGUAGU | AGUCCUGCAC/ Cleavage pacid=371443 |
| 23 | 2706 | 2727 UGAGGUAGU | AGUCCUGCAC/ Cleavage pacid=371443 |
| 24 | 3916 | 3937 UGAGGUAGU | AGUCCUGCAC/ Cleavage pacid=371443 |
| 25 | 2706 | 2727 UGAGGUAGU | AGUCCUGCAC/ Cleavage pacid=371443 |
| 26 | 1727 | 1749 AGAGGUAGU | CAAGCUGU-C Cleavage pacid=371575 |
| 27 | 1223 | 1245 UGAGGUAGU | UACUAUAAC/ Translation pacid=371575 |
| 28 | 1223 | 1245 UGAGGUAGU | UACUAUAAC/ Translation pacid=371575 |
| 29 | 79 | 102 AGAGGUAGU | AAGUCUGUG/ Cleavage pacid=371789 |
| 30 | 986 | 1009 UGAGGU--AG .. | GAAUAUACA/ Cleavage pacid=371577 |
| 31 | 986 | 1009 UGAGGU--AG .. | GAAUAUACA/ Cleavage pacid=371577 |
| 32 | 753 | 776 AGAGGUAGU | AAGUCUAUG(Translation pacid=371678 |
| 33 | 695 | 718 AGAGGUAGU | AAGUCUAUG(Translation pacid=371680 |
| 34 | 2388 | 2409 UGAGGUAGU .. | AAAUCUGUA/ Cleavage pacid=371676 |
| 35 | 2388 | 2409 UGAGGUAGU .. | AAAUCUGUA/ Cleavage pacid=371676 |
| 36 | 2388 | 2409 UGAGGUAGU .. | AAAUCUGUA/ Cleavage pacid=371676 |
| 37 | 2388 | 2409 UGAGGUAGU .. | AAAUCUGUA/ Cleavage pacid=371676 |
| 38 | 1918 | 1941 AGAGGUAGU .. | AUAACUAUG(Cleavage pacid=371711 |
| 39 | 1601 | 1622 UGAGGUAGU | AAUUUUGCAC/ Cleavage pacid=371696 |
| 40 | 1601 | 1622 UGAGGUAGU | AAUUUUGCAC/ Cleavage pacid=371696 |
| 41 | 1983 | 2004 UGAGGUAGU .. | AGGUGUAUC, Cleavage pacid=371684 |
| 42 | 1983 | 2004 UGAGGUAGU .. | AGGUGUAUC, Cleavage pacid=371684 |
| 43 | 2640 | 2661 UGAGGUAGU | AAUUAUGUU Cleavage pacid=371712 |
| 44 | 2640 | 2661 UGAGGUAGU | AAUUAUGUU Cleavage pacid=371712 |
| 45 | 876 | 897 UGAGGUAGU | AACUGUACAC(Translation pacid=371709 |
| 46 | 876 | 897 UGAGGUAGU | AACUGUACAC(Translation pacid=371709 |
| 47 | 876 | 897 UGAGGUAGU | AACUGUACAC(Translation pacid=371709 |
| 48 | 876 | 897 UGAGGUAGU | AACUGUACAC(Translation pacid=371709 |
| 49 | 2372 | 2393 UGAGGUAGU | UACUGUGCAC(Cleavage pacid=371700 |
| 50 | 2372 | 2393 UGAGGUAGU | UACUGUGCAC(Cleavage pacid=371700 |
| 51 | | | |
| 52 | | | |
| 53 | | | |
| 54 | | | |
| 55 | | | |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | |
|------|----------------------|----------------------------------|--------------|
| 1237 | 1258 UGAGGUAGU | : : : : : GAUUAUACA(Cleavage | pacid=371711 |
| 1237 | 1258 UGAGGUAGU | : : : : : GAUUAUACA(Cleavage | pacid=371711 |
| 1650 | 1671 UGAGGUAGU | : : : : : AACCAUACUA Cleavage | pacid=371692 |
| 1650 | 1671 UGAGGUAGU | : : : : : AACCAUACUA Cleavage | pacid=371692 |
| 1650 | 1671 UGAGGUAGU | : : : : : AACCAUACUA Cleavage | pacid=371692 |
| 1650 | 1671 UGAGGUAGU | : : : : : AACCAUACUA Cleavage | pacid=371692 |
| 1650 | 1671 UGAGGUAGU | : : : : : AACCAUACUA Cleavage | pacid=371692 |
| 1650 | 1671 UGAGGUAGU | : : : : : AACCAUACUA Cleavage | pacid=371692 |
| 254 | 277 AGAGGUAGU | : : : : : GAAAGUGUG(Translation | pacid=371687 |
| 1804 | 1825 UGAGGUAGU | : : : : : AGCCAUUAUG(Cleavage | pacid=371711 |
| 1816 | 1837 UGAGGUAGU | : : : : : AGCCAUUAUG(Cleavage | pacid=371711 |
| 1804 | 1825 UGAGGUAGU | : : : : : AGCCAUUAUG(Cleavage | pacid=371711 |
| 1816 | 1837 UGAGGUAGU | : : : : : AGCCAUUAUG(Cleavage | pacid=371711 |
| 1804 | 1825 UGAGGUAGU | : : : : : AGCCAUUAUG(Cleavage | pacid=371711 |
| 1816 | 1837 UGAGGUAGU | : : : : : AGCCAUUAUG(Cleavage | pacid=371711 |
| 1804 | 1825 UGAGGUAGU | : : : : : AGCCAUUAUG(Cleavage | pacid=371711 |
| 1816 | 1837 UGAGGUAGU | : : : : : AGCCAUUAUG(Cleavage | pacid=371711 |
| 2325 | 2348 AGAGGUAGU | : : : : : UUAACUUAUU(Cleavage | pacid=371711 |
| 2445 | 2468 AGAGGUAGU | : : : : : UUAACUUAUU(Cleavage | pacid=371711 |
| 1874 | 1895 UGAGGUAGU | : : : : : CACCGUGUA(Cleavage | pacid=371687 |
| 1874 | 1895 UGAGGUAGU | : : : : : CACCGUGUA(Cleavage | pacid=371687 |
| 1874 | 1895 UGAGGUAGU | : : : : : CACCGUGUA(Cleavage | pacid=371687 |
| 1874 | 1895 UGAGGUAGU | : : : : : CACCGUGUA(Cleavage | pacid=371687 |
| 615 | 636 UGAGGUAGU | : : : : : GGCUAUACA(Cleavage | pacid=371766 |
| 615 | 636 UGAGGUAGU | : : : : : GGCUAUACA(Cleavage | pacid=371766 |
| 615 | 636 UGAGGUAGU | : : : : : GGCUAUACA(Cleavage | pacid=371766 |
| 615 | 636 UGAGGUAGU | : : : : : GGCUAUACA(Cleavage | pacid=371766 |
| 1026 | 1047 UGAGGUAGU | : : : : : AACCAUGUU(Cleavage | pacid=371749 |
| 1026 | 1047 UGAGGUAGU | : : : : : AACCAUGUU(Cleavage | pacid=371749 |
| 1026 | 1047 UGAGGUAGU | : : : : : AACCAUGUU(Cleavage | pacid=371749 |
| 1026 | 1047 UGAGGUAGU | : : : : : AACCAUGUU(Cleavage | pacid=371749 |
| 1126 | 1147 UGAGGUAGU | : : : : : GUUUUAUA. Cleavage | pacid=371755 |
| 1126 | 1147 UGAGGUAGU | : : : : : GUUUUAUA. Cleavage | pacid=371755 |
| 54 | 75 UGAGGUAGU | : : : : : AACUCUUCA(Cleavage | pacid=371767 |
| 54 | 75 UGAGGUAGU | : : : : : AACUCUUCA(Cleavage | pacid=371767 |
| 54 | 75 UGAGGUAGU | : : : : : AACUCUUCA(Cleavage | pacid=371767 |
| 54 | 75 UGAGGUAGU | : : : : : AACUCUUCA(Cleavage | pacid=371767 |
| 498 | 521 AGAGGUAGU | : : : : : UAAACUAUG(Translation | pacid=371764 |
| 628 | 649 UGAGGUAGU | : : : : : GAUUAUGUA. Translation | pacid=371766 |
| 628 | 649 UGAGGUAGU | : : : : : GAUUAUGUA. Translation | pacid=371766 |
| 628 | 649 UGAGGUAGU | : : : : : GAUUAUGUA. Translation | pacid=371766 |

| | | | |
|----|------|---|--------------|
| 1 | | | |
| 2 | | | |
| 3 | | | |
| 4 | 628 | 649 UGAGGUAGU ::GAUUAUGUA Translation | pacid=371766 |
| 5 | 868 | 889 UGAGGUAGU : :GAUUAUACA/ Cleavage | pacid=371774 |
| 6 | 868 | 889 UGAGGUAGU : :GAUUAUACA/ Cleavage | pacid=371774 |
| 7 | 169 | 192 AGAGGUAGU,:::: : :AAAAGGUG(Translation | pacid=371764 |
| 8 | 300 | 321 UGAGGUAGU ::CACUGUGUA/ Cleavage | pacid=371760 |
| 9 | 300 | 321 UGAGGUAGU ::CACUGUGUA/ Cleavage | pacid=371760 |
| 10 | 2595 | 2616 UGAGGUAGU : :CGUUGUAUA/ Cleavage | pacid=371445 |
| 11 | 2595 | 2616 UGAGGUAGU : :CGUUGUAUA/ Cleavage | pacid=371445 |
| 12 | 2031 | 2052 UGAGGUAGU : : GAUCAUGCA/ Cleavage | pacid=371470 |
| 13 | 2031 | 2052 UGAGGUAGU : : GAUCAUGCA/ Cleavage | pacid=371470 |
| 14 | 2031 | 2052 UGAGGUAGU : : GAUCAUGCA/ Cleavage | pacid=371470 |
| 15 | 2031 | 2052 UGAGGUAGU : : GAUCAUGCA/ Cleavage | pacid=371470 |
| 16 | 165 | 187 UGAGGUAGU ::GGCCAUGAA/ Cleavage | pacid=371454 |
| 17 | 165 | 187 UGAGGUAGU ::GGCCAUGAA/ Cleavage | pacid=371454 |
| 18 | 165 | 187 UGAGGUAGU ::GGCCAUGAA/ Cleavage | pacid=371454 |
| 19 | 165 | 187 UGAGGUAGU ::GGCCAUGAA/ Cleavage | pacid=371454 |
| 20 | 1526 | 1547 UGAGGUAGU ::GACUGUAAA/ Cleavage | pacid=371467 |
| 21 | 1526 | 1547 UGAGGUAGU ::GACUGUAAA/ Cleavage | pacid=371467 |
| 22 | 575 | 596 UGAGGUAGU ::AGCUAUACA/ Cleavage | pacid=371471 |
| 23 | 575 | 596 UGAGGUAGU ::AGCUAUACA/ Cleavage | pacid=371471 |
| 24 | 575 | 596 UGAGGUAGU ::AGCUAUACA/ Cleavage | pacid=371471 |
| 25 | 575 | 596 UGAGGUAGU ::AGCUAUACA/ Cleavage | pacid=371471 |
| 26 | 9208 | 9231 AGAGGUAGU,:: ::AGCACUGUG(Cleavage | pacid=371454 |
| 27 | 9208 | 9231 AGAGGUAGU,:: ::AGCACUGUG(Cleavage | pacid=371454 |
| 28 | 9208 | 9231 AGAGGUAGU,:: ::AGCACUGUG(Cleavage | pacid=371454 |
| 29 | 143 | 166 AGAGGUAGU,:::: : :AAAUAUGI Cleavage | pacid=371469 |
| 30 | 420 | 443 AGAGGUAGU,:::: : :GAAUUGGAG(Cleavage | pacid=371446 |
| 31 | 349 | 373 AGAGGUAGU, ::CUAGUUAUG(Translation | pacid=371637 |
| 32 | 4084 | 4104 UGAGGUAGU ::AAUCAUGCG- Cleavage | pacid=371622 |
| 33 | 4084 | 4104 UGAGGUAGU ::AAUCAUGCG- Cleavage | pacid=371622 |
| 34 | 4084 | 4104 UGAGGUAGU ::AAUCAUGCG- Cleavage | pacid=371622 |
| 35 | 4084 | 4104 UGAGGUAGU ::AAUCAUGCG- Cleavage | pacid=371622 |
| 36 | 2603 | 2624 UGAGGUAGU ::AACCAACCAA Cleavage | pacid=371635 |
| 37 | 2603 | 2624 UGAGGUAGU ::AACCAACCAA Cleavage | pacid=371635 |
| 38 | 2603 | 2624 UGAGGUAGU ::AACCAACCAA Cleavage | pacid=371635 |
| 39 | 2603 | 2624 UGAGGUAGU ::AACCAACCAA Cleavage | pacid=371635 |
| 40 | 971 | 993 UGAGGUAGU ::AGCUCAUGU/ Translation | pacid=371622 |
| 41 | 971 | 993 UGAGGUAGU ::AGCUCAUGU/ Translation | pacid=371622 |
| 42 | 2918 | 2939 UGAGGUAGU : :AGCUAUUUA/ Cleavage | pacid=371540 |
| 43 | 2918 | 2939 UGAGGUAGU : :AGCUAUUUA/ Cleavage | pacid=371540 |
| 44 | 297 | 320 AGAGGUAGU,:::: : :AAAGUUGUU Cleavage | pacid=371538 |
| 45 | 1539 | 1562 AGAGGUAGU,:::: : : AAAUUAUG(Cleavage | pacid=371546 |
| 46 | 10 | 32 UGAGGUAGU ::AACUACAACA Cleavage | pacid=371524 |
| 47 | | | |
| 48 | | | |
| 49 | | | |
| 50 | | | |
| 51 | | | |
| 52 | | | |
| 53 | | | |
| 54 | | | |
| 55 | | | |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | |
|------|--|--------------|
| 190 | 212 UGAGGUAGU ::::: : ::::: : AACUACAACA Cleavage | pacid=371524 |
| 190 | 212 UGAGGUAGU ::::: : ::::: : AACUACAACA Cleavage | pacid=371524 |
| 10 | 32 UGAGGUAGU ::::: : ::::: : AACUACAACA Cleavage | pacid=371524 |
| 190 | 212 UGAGGUAGU ::::: : ::::: : AACUACAACA Cleavage | pacid=371524 |
| 190 | 212 UGAGGUAGU ::::: : ::::: : AACUACAACA Cleavage | pacid=371524 |
| 10 | 32 UGAGGUAGU ::::: : ::::: : AACUACAACA Cleavage | pacid=371524 |
| 190 | 212 UGAGGUAGU ::::: : ::::: : AACUACAACA Cleavage | pacid=371524 |
| 190 | 212 UGAGGUAGU ::::: : ::::: : AACUACAACA Cleavage | pacid=371524 |
| 2173 | 2194 UGAGGUAGU ::::: : ::::: : AACUAUGCG(Translation | pacid=371530 |
| 2213 | 2234 UGAGGUAGU ::::: : ::::: : AACUAUGCG(Translation | pacid=371530 |
| 2421 | 2442 UGAGGUAGU ::::: : ::::: : AACUAUGCG(Translation | pacid=371530 |
| 2173 | 2194 UGAGGUAGU ::::: : ::::: : AACUAUGCG(Translation | pacid=371530 |
| 2213 | 2234 UGAGGUAGU ::::: : ::::: : AACUAUGCG(Translation | pacid=371530 |
| 2421 | 2442 UGAGGUAGU ::::: : ::::: : AACUAUGCG(Translation | pacid=371530 |
| 362 | 383 UGAGGUAGU ::::: : ::::: : AGCUGAACAA' Cleavage | pacid=371534 |
| 362 | 383 UGAGGUAGU ::::: : ::::: : AGCUGAACAA' Cleavage | pacid=371534 |
| 362 | 383 UGAGGUAGU ::::: : ::::: : AGCUGAACAA' Cleavage | pacid=371534 |
| 362 | 383 UGAGGUAGU ::::: : ::::: : AGCUGAACAA' Cleavage | pacid=371534 |
| 197 | 219 UGAGGUAGU ::::: : ::::: : AGCCAUGGC' Cleavage | pacid=371522 |
| 197 | 219 UGAGGUAGU ::::: : ::::: : AGCCAUGGC' Cleavage | pacid=371522 |
| 197 | 219 UGAGGUAGU ::::: : ::::: : AGCCAUGGC' Cleavage | pacid=371522 |
| 197 | 219 UGAGGUAGU ::::: : ::::: : AGCCAUGGC' Cleavage | pacid=371522 |
| 44 | 65 UGAGGUAGU ::::: : ::::: : AGCCAUGCAA' Cleavage | pacid=371713 |
| 44 | 65 UGAGGUAGU ::::: : ::::: : AGCCAUGCAA' Cleavage | pacid=371713 |
| 44 | 65 UGAGGUAGU ::::: : ::::: : AGCCAUGCAA' Cleavage | pacid=371713 |
| 44 | 65 UGAGGUAGU ::::: : ::::: : AGCCAUGCAA' Cleavage | pacid=371713 |
| 267 | 288 UGAGGUAGU ::::: : ::::: : GUGCAGGCAI Cleavage | pacid=371730 |
| 267 | 288 UGAGGUAGU ::::: : ::::: : GUGCAGGCAI Cleavage | pacid=371730 |
| 1870 | 1891 UGAGGUAGU ::::: : ::::: : CACUAUACAA' Cleavage | pacid=371645 |
| 1870 | 1891 UGAGGUAGU ::::: : ::::: : CACUAUACAA' Cleavage | pacid=371645 |
| 1870 | 1891 UGAGGUAGU ::::: : ::::: : CACUAUACAA' Cleavage | pacid=371645 |
| 1870 | 1891 UGAGGUAGU ::::: : ::::: : CACUAUACAA' Cleavage | pacid=371645 |
| 1971 | 1992 UGAGGUAGU ::::: : ::::: : AGCCAUUCA€ Cleavage | pacid=371648 |
| 1971 | 1992 UGAGGUAGU ::::: : ::::: : AGCCAUUCA€ Cleavage | pacid=371648 |
| 2125 | 2146 UGAGGUAGU ::::: : ::::: : AGCCAUUCA€ Cleavage | pacid=371648 |
| 2125 | 2146 UGAGGUAGU ::::: : ::::: : AGCCAUUCA€ Cleavage | pacid=371648 |
| 1971 | 1992 UGAGGUAGU ::::: : ::::: : AGCCAUUCA€ Cleavage | pacid=371648 |
| 1971 | 1992 UGAGGUAGU ::::: : ::::: : AGCCAUUCA€ Cleavage | pacid=371648 |
| 2125 | 2146 UGAGGUAGU ::::: : ::::: : AGCCAUUCA€ Cleavage | pacid=371648 |
| 2125 | 2146 UGAGGUAGU ::::: : ::::: : AGCCAUUCA€ Cleavage | pacid=371648 |

| | | | |
|----|------|--|--------------|
| 1 | | | |
| 2 | | | |
| 3 | | | |
| 4 | 1971 | 1992 UGAGGUAGU ::::: ::::: ::::: ::AGCCAUUCA€ Cleavage | pacid=371648 |
| 5 | 1971 | 1992 UGAGGUAGU ::::: ::::: ::::: ::AGCCAUUCA€ Cleavage | pacid=371648 |
| 6 | 2125 | 2146 UGAGGUAGU ::::: ::::: ::::: ::AGCCAUUCA€ Cleavage | pacid=371648 |
| 7 | 2125 | 2146 UGAGGUAGU ::::: ::::: ::::: ::AGCCAUUCA€ Cleavage | pacid=371648 |
| 8 | 1971 | 1992 UGAGGUAGU ::::: ::::: ::::: ::AGCCAUUCA€ Cleavage | pacid=371648 |
| 9 | 1971 | 1992 UGAGGUAGU ::::: ::::: ::::: ::AGCCAUUCA€ Cleavage | pacid=371648 |
| 10 | 1971 | 1992 UGAGGUAGU ::::: ::::: ::::: ::AGCCAUUCA€ Cleavage | pacid=371648 |
| 11 | 2125 | 2146 UGAGGUAGU ::::: ::::: ::::: ::AGCCAUUCA€ Cleavage | pacid=371648 |
| 12 | 2125 | 2146 UGAGGUAGU ::::: ::::: ::::: ::AGCCAUUCA€ Cleavage | pacid=371648 |
| 13 | 2125 | 2146 UGAGGUAGU ::::: ::::: ::::: ::AGCCAUUCA€ Cleavage | pacid=371648 |
| 14 | 46 | 69 AGAGGUAGU ::::: ::::: ::::: ::AAAUCAUGI Cleavage | pacid=371676 |
| 15 | 165 | 186 UGAGGUAGU ::::: ::::: ::::: ::AACCUUCCAG Cleavage | pacid=371643 |
| 16 | 165 | 186 UGAGGUAGU ::::: ::::: ::::: ::AACCUUCCAG Cleavage | pacid=371643 |
| 17 | 165 | 186 UGAGGUAGU ::::: ::::: ::::: ::AACCUUCCAG Cleavage | pacid=371643 |
| 18 | 165 | 186 UGAGGUAGU ::::: ::::: ::::: ::AACCUUCCAG Cleavage | pacid=371643 |
| 19 | 165 | 186 UGAGGUAGU ::::: ::::: ::::: ::AACCUUCCAG Cleavage | pacid=371643 |
| 20 | 833 | 854 UGAGGUAGU ::::: ::::: ::::: ::AAUUGCACA/ Translation | pacid=371669 |
| 21 | 833 | 854 UGAGGUAGU ::::: ::::: ::::: ::AAUUGCACA/ Translation | pacid=371669 |
| 22 | 833 | 854 UGAGGUAGU ::::: ::::: ::::: ::AAUUGCACA/ Translation | pacid=371669 |
| 23 | 365 | 388 AGAGGUAGU ::::: ::::: ::::: ::CAAACAAUGA/ Cleavage | pacid=371643 |
| 24 | 1112 | 1133 UGAGGUAGU ::::: ::::: ::::: ::GACAAUGCA/ Cleavage | pacid=371653 |
| 25 | 1112 | 1133 UGAGGUAGU ::::: ::::: ::::: ::GACAAUGCA/ Cleavage | pacid=371653 |
| 26 | 1112 | 1133 UGAGGUAGU ::::: ::::: ::::: ::GACAAUGCA/ Cleavage | pacid=371653 |
| 27 | 1112 | 1133 UGAGGUAGU ::::: ::::: ::::: ::GACAAUGCA/ Cleavage | pacid=371653 |
| 28 | 1112 | 1133 UGAGGUAGU ::::: ::::: ::::: ::GACAAUGCA/ Cleavage | pacid=371653 |
| 29 | 1112 | 1133 UGAGGUAGU ::::: ::::: ::::: ::GACAAUGCA/ Cleavage | pacid=371653 |
| 30 | 1112 | 1133 UGAGGUAGU ::::: ::::: ::::: ::GACAAUGCA/ Cleavage | pacid=371653 |
| 31 | 1112 | 1133 UGAGGUAGU ::::: ::::: ::::: ::GACAAUGCA/ Cleavage | pacid=371653 |
| 32 | 1919 | 1940 UGAGGUAGU ::::: ::::: ::::: ::AACCAAUUAC/ Cleavage | pacid=371670 |
| 33 | 1919 | 1940 UGAGGUAGU ::::: ::::: ::::: ::AACCAAUUAC/ Cleavage | pacid=371670 |
| 34 | 1919 | 1940 UGAGGUAGU ::::: ::::: ::::: ::AACCAAUUAC/ Cleavage | pacid=371670 |
| 35 | 1919 | 1940 UGAGGUAGU ::::: ::::: ::::: ::AACCAAUUAC/ Cleavage | pacid=371670 |
| 36 | 1919 | 1940 UGAGGUAGU ::::: ::::: ::::: ::AACCAAUUAC/ Cleavage | pacid=371670 |
| 37 | 1919 | 1940 UGAGGUAGU ::::: ::::: ::::: ::AACCAAUUAC/ Cleavage | pacid=371670 |
| 38 | 2013 | 2037 AGAGGUAGU ::::: ::::: ::::: ::GAAACUAAU(Cleavage | pacid=371654 |
| 39 | 2548 | 2571 AGAGGUAGU ::::: ::::: ::::: ::CAAAUAUUG(Cleavage | pacid=371606 |
| 40 | 1653 | 1676 AGAGGUAGU ::::: ::::: ::::: ::ACAAUAUUG(Cleavage | pacid=371606 |
| 41 | 1653 | 1676 AGAGGUAGU ::::: ::::: ::::: ::ACAAUAUUG(Cleavage | pacid=371606 |
| 42 | 1200 | 1221 UGAGGUAGU ::::: ::::: ::::: ::AAUUAUAGG(Cleavage | pacid=371586 |
| 43 | 1200 | 1221 UGAGGUAGU ::::: ::::: ::::: ::AAUUAUAGG(Cleavage | pacid=371586 |
| 44 | 1025 | 1046 UGAGGUAGU ::::: ::::: ::::: ::AAUCCUGUA/ Cleavage | pacid=371596 |
| 45 | 1025 | 1046 UGAGGUAGU ::::: ::::: ::::: ::AAUCCUGUA/ Cleavage | pacid=371596 |
| 46 | 1025 | 1046 UGAGGUAGU ::::: ::::: ::::: ::AAUCCUGUA/ Cleavage | pacid=371596 |
| 47 | 1025 | 1046 UGAGGUAGU ::::: ::::: ::::: ::AAUCCUGUA/ Cleavage | pacid=371596 |
| 48 | 1025 | 1046 UGAGGUAGU ::::: ::::: ::::: ::AAUCCUGUA/ Cleavage | pacid=371596 |
| 49 | 1025 | 1046 UGAGGUAGU ::::: ::::: ::::: ::AAUCCUGUA/ Cleavage | pacid=371596 |
| 50 | 1025 | 1046 UGAGGUAGU ::::: ::::: ::::: ::AAUUGUGUA. Cleavage | pacid=371614 |
| 51 | 1025 | 1046 UGAGGUAGU ::::: ::::: ::::: ::AAUUGUGUA. Cleavage | pacid=371614 |
| 52 | 1025 | 1046 UGAGGUAGU ::::: ::::: ::::: ::AAUUGUGUA. Cleavage | pacid=371614 |
| 53 | 1025 | 1046 UGAGGUAGU ::::: ::::: ::::: ::AAUUGUGUA. Cleavage | pacid=371614 |
| 54 | 1025 | 1046 UGAGGUAGU ::::: ::::: ::::: ::AAUUGUGUA. Cleavage | pacid=371614 |
| 55 | 929 | 950 UGAGGUAGU ::::: ::::: ::::: ::AAUUGUGUA. Cleavage | pacid=371601 |
| 56 | 929 | 950 UGAGGUAGU ::::: ::::: ::::: ::AAUUGUGUA. Cleavage | pacid=371601 |
| 57 | 929 | 950 UGAGGUAGU ::::: ::::: ::::: ::AAUUGUGUA. Cleavage | pacid=371601 |
| 58 | 929 | 950 UGAGGUAGU ::::: ::::: ::::: ::AAUUGUGUA. Cleavage | pacid=371601 |
| 59 | 929 | 950 UGAGGUAGU ::::: ::::: ::::: ::AAUUGUGUA. Cleavage | pacid=371601 |
| 60 | 929 | 950 UGAGGUAGU ::::: ::::: ::::: ::AAUUGUGUA. Cleavage | pacid=371601 |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | |
|------|------|--|--------------|
| 2973 | 2994 | UGAGGUAGU :GGCUGUGUA, Cleavage | pacid=371589 |
| 2979 | 3000 | UGAGGUAGU :GGCUGUGUA, Cleavage | pacid=371589 |
| 2973 | 2994 | UGAGGUAGU :GGCUGUGUA, Cleavage | pacid=371589 |
| 2979 | 3000 | UGAGGUAGU :GGCUGUGUA, Cleavage | pacid=371589 |
| 2270 | 2293 | AGAGGUAGU.....:GAGAUUGUG Cleavage | pacid=371586 |
| 2172 | 2193 | UGAGGUAGU ::: :..... :UUCUAUCAAC Cleavage | pacid=371611 |
| 2172 | 2193 | UGAGGUAGU ::: :..... :UUCUAUCAAC Cleavage | pacid=371611 |
| 1538 | 1559 | UGAGGUAGU :GGCUGUAUA, Cleavage | pacid=371502 |
| 1538 | 1559 | UGAGGUAGU :GGCUGUAUA, Cleavage | pacid=371502 |
| 612 | 635 | AGAGGUAGU.....:AAAGCUACGC Cleavage | pacid=371497 |
| 269 | 290 | UGAGGUAGU ::: :..... :AACCCCACAA Translation | pacid=371509 |
| 269 | 290 | UGAGGUAGU ::: :..... :AACCCCACAA Translation | pacid=371509 |
| 269 | 290 | UGAGGUAGU ::: :..... :AACCCCACAA Translation | pacid=371509 |
| 269 | 290 | UGAGGUAGU ::: :..... :AACCCCACAA Translation | pacid=371509 |
| 269 | 290 | UGAGGUAGU ::: :..... :AACCCCACAA Translation | pacid=371509 |
| 269 | 290 | UGAGGUAGU ::: :..... :AACCCCACAA Translation | pacid=371509 |
| 269 | 290 | UGAGGUAGU ::: :..... :AACCCCACAA Translation | pacid=371509 |
| 269 | 290 | UGAGGUAGU ::: :..... :AACCCCACAA Translation | pacid=371509 |
| 269 | 290 | UGAGGUAGU ::: :..... :AACCCCACAA Translation | pacid=371509 |
| 1680 | 1701 | UGAGGUAGU :GACUGUACAC Cleavage | pacid=371502 |
| 1680 | 1701 | UGAGGUAGU :GACUGUACAC Cleavage | pacid=371502 |
| 290 | 311 | UGAGGUAGU ::: :..... :AACGUUGUA, Cleavage | pacid=371491 |
| 290 | 311 | UGAGGUAGU ::: :..... :AACGUUGUA, Cleavage | pacid=371491 |
| 290 | 311 | UGAGGUAGU ::: :..... :AACGUUGUA, Cleavage | pacid=371491 |
| 290 | 311 | UGAGGUAGU ::: :..... :AACGUUGUA, Cleavage | pacid=371491 |
| 767 | 790 | AGAGGUAGU.....:AAGAUUGUG, Translation | pacid=371518 |
| 1402 | 1423 | UGAGGUAGU .. :..... :GACAAUAUG, Cleavage | pacid=371510 |
| 1402 | 1423 | UGAGGUAGU .. :..... :GACAAUAUG, Cleavage | pacid=371510 |
| 1402 | 1423 | UGAGGUAGU .. :..... :GACAAUAUG, Cleavage | pacid=371510 |
| 1402 | 1423 | UGAGGUAGU .. :..... :GACAAUAUG, Cleavage | pacid=371510 |
| 512 | 533 | UGAGGUAGU :GAUUGUGCA, Translation | pacid=371513 |
| 535 | 556 | UGAGGUAGU :GAUUGUGCA, Translation | pacid=371513 |
| 512 | 533 | UGAGGUAGU :GAUUGUGCA, Translation | pacid=371513 |
| 535 | 556 | UGAGGUAGU :GAUUGUGCA, Translation | pacid=371513 |
| 509 | 530 | UGAGGUAGU :AAUCAUACUL Cleavage | pacid=371431 |
| 509 | 530 | UGAGGUAGU :AAUCAUACUL Cleavage | pacid=371431 |
| 509 | 530 | UGAGGUAGU :AAUCAUACUL Cleavage | pacid=371431 |
| 509 | 530 | UGAGGUAGU :AAUCAUACUL Cleavage | pacid=371431 |
| 2465 | 2486 | UGAGGUAGU :AGUUAUACA, Cleavage | pacid=371430 |
| 2478 | 2499 | UGAGGUAGU :AGUUAUACA, Cleavage | pacid=371430 |
| 2465 | 2486 | UGAGGUAGU :AGUUAUACA, Cleavage | pacid=371430 |
| 2478 | 2499 | UGAGGUAGU :AGUUAUACA, Cleavage | pacid=371430 |
| 1001 | 1022 | UGAGGUAGU :AAUUAUAGA, Cleavage | pacid=371424 |
| 1001 | 1022 | UGAGGUAGU :AAUUAUAGA, Cleavage | pacid=371424 |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | |
|------|------|---|--------------|
| 1001 | 1022 | UGAGGUAGU ::::: : :::::AAUUAUAGA/ Cleavage | pacid=371424 |
| 1001 | 1022 | UGAGGUAGU ::::: : :::::AAUUAUAGA/ Cleavage | pacid=371424 |
| 1340 | 1361 | UGAGGUAGU ::::: : :::::UUCCAUGCCA/ Cleavage | pacid=371424 |
| 1345 | 1366 | UGAGGUAGU ::::: : :::::UUCCAUGCCA/ Cleavage | pacid=371424 |
| 1340 | 1361 | UGAGGUAGU ::::: : :::::UUCCAUGCCA/ Cleavage | pacid=371424 |
| 1345 | 1366 | UGAGGUAGU ::::: : :::::UUCCAUGCCA/ Cleavage | pacid=371424 |
| 1340 | 1361 | UGAGGUAGU ::::: : :::::UUCCAUGCCA/ Cleavage | pacid=371424 |
| 1345 | 1366 | UGAGGUAGU ::::: : :::::UUCCAUGCCA/ Cleavage | pacid=371424 |
| 1340 | 1361 | UGAGGUAGU ::::: : :::::UUCCAUGCCA/ Cleavage | pacid=371424 |
| 1345 | 1366 | UGAGGUAGU ::::: : :::::UUCCAUGCCA/ Cleavage | pacid=371424 |
| 1562 | 1583 | UGAGGUAGU ::::: : :::::AACCAUAUA/ Cleavage | pacid=371432 |
| 1562 | 1583 | UGAGGUAGU ::::: : :::::AACCAUAUA/ Cleavage | pacid=371432 |
| 1562 | 1583 | UGAGGUAGU ::::: : :::::AACCAUAUA/ Cleavage | pacid=371432 |
| 1562 | 1583 | UGAGGUAGU ::::: : :::::AACCAUAUA/ Cleavage | pacid=371432 |
| 534 | 555 | UGAGGUAGU ::::: : :::::GGCCAUGCA/ Cleavage | pacid=371560 |
| 534 | 555 | UGAGGUAGU ::::: : :::::GGCCAUGCA/ Cleavage | pacid=371560 |
| 534 | 555 | UGAGGUAGU ::::: : :::::GGCCAUGCA/ Cleavage | pacid=371560 |
| 534 | 555 | UGAGGUAGU ::::: : :::::GGCCAUGCA/ Cleavage | pacid=371560 |
| 534 | 555 | UGAGGUAGU ::::: : :::::GGCCAUGCA/ Cleavage | pacid=371560 |
| 534 | 555 | UGAGGUAGU ::::: : :::::GGCCAUGCA/ Cleavage | pacid=371560 |
| 534 | 555 | UGAGGUAGU ::::: : :::::GGCCAUGCA/ Cleavage | pacid=371560 |
| 534 | 555 | UGAGGUAGU ::::: : :::::GGCCAUGCA/ Cleavage | pacid=371560 |
| 534 | 555 | UGAGGUAGU ::::: : :::::GGCCAUGCA/ Cleavage | pacid=371560 |
| 589 | 611 | AGAGGUAGU::: : :::::AAUAUUAUG/ Cleavage | pacid=371566 |
| 299 | 320 | UGAGGUAGU ::::: : :::::AGCCAUUCA/ Translation | pacid=371558 |
| 299 | 320 | UGAGGUAGU ::::: : :::::AGCCAUUCA/ Translation | pacid=371558 |
| 299 | 320 | UGAGGUAGU ::::: : :::::AGCCAUUCA/ Translation | pacid=371558 |
| 299 | 320 | UGAGGUAGU ::::: : :::::AGCCAUUCA/ Translation | pacid=371558 |
| 1405 | 1426 | UGAGGUAGU ::::: : :::::GACUGUAAA/ Cleavage | pacid=371574 |
| 1405 | 1426 | UGAGGUAGU ::::: : :::::GACUGUAAA/ Cleavage | pacid=371574 |
| 1729 | 1749 | UGAGGUAGU ::::: : :::::AGCUGU-CAA Cleavage | pacid=371575 |
| 1729 | 1749 | UGAGGUAGU ::::: : :::::AGCUGU-CAA Cleavage | pacid=371575 |
| 121 | 142 | UGAGGUAGU ::::: : :::::AGCUGUAAA/ Cleavage | pacid=371790 |
| 121 | 142 | UGAGGUAGU ::::: : :::::AGCUGUAAA/ Cleavage | pacid=371790 |
| 121 | 142 | UGAGGUAGU ::::: : :::::AGCUGUAAA/ Cleavage | pacid=371790 |
| 121 | 142 | UGAGGUAGU ::::: : :::::AGCUGUAAA/ Cleavage | pacid=371790 |

| Multiplicity | Target_Acc. | ID | locusName | Pfam |
|--------------|--------------------|------------------|------------------|--------------|
| 1 | Phvul.002G267400.1 | Phvul.002G267400 | Phvul.002G267400 | PF02732 |
| 1 | Phvul.002G267400.1 | Phvul.002G267400 | Phvul.002G267400 | PF02732 |
| 1 | Phvul.002G071800.1 | Phvul.002G071800 | Phvul.002G071800 | PF06075 |
| 1 | Phvul.002G071800.1 | Phvul.002G071800 | Phvul.002G071800 | PF06075 |
| 1 | Phvul.002G071800.1 | Phvul.002G071800 | Phvul.002G071800 | PF06075 |
| 1 | Phvul.002G071800.1 | Phvul.002G071800 | Phvul.002G071800 | PF06075 |
| 1 | Phvul.002G071800.1 | Phvul.002G071800 | Phvul.002G071800 | PF06075 |
| 1 | Phvul.006G201700.1 | Phvul.006G201700 | Phvul.006G201700 | PF12014 |
| 1 | Phvul.009G057800.1 | Phvul.009G057800 | Phvul.009G057800 | PF04072 |
| 1 | Phvul.009G057800.1 | Phvul.009G057800 | Phvul.009G057800 | PF04072 |
| 1 | Phvul.009G086800.1 | Phvul.009G086800 | Phvul.009G086800 | PF02990 |
| 2 | Phvul.010G116400.1 | Phvul.010G116400 | Phvul.010G116400 | PF05659,PF04 |
| 2 | Phvul.010G116400.1 | Phvul.010G116400 | Phvul.010G116400 | PF05659,PF04 |
| 2 | Phvul.010G116400.1 | Phvul.010G116400 | Phvul.010G116400 | PF05659,PF04 |
| 2 | Phvul.010G116400.1 | Phvul.010G116400 | Phvul.010G116400 | PF05659,PF04 |
| 1 | Phvul.L009543.1 | Phvul.L009543 | Phvul.L009543 | PF00111,PF01 |
| 1 | Phvul.L009543.1 | Phvul.L009543 | Phvul.L009543 | PF00111,PF01 |
| 1 | Phvul.L009543.1 | Phvul.L009543 | Phvul.L009543 | PF00111,PF01 |
| 1 | Phvul.L009543.1 | Phvul.L009543 | Phvul.L009543 | PF00111,PF01 |
| 1 | Phvul.001G077200.2 | Phvul.001G077200 | Phvul.001G077200 | PF00170 |
| 1 | Phvul.001G077200.2 | Phvul.001G077200 | Phvul.001G077200 | PF00170 |
| 1 | Phvul.001G077200.2 | Phvul.001G077200 | Phvul.001G077200 | PF00170 |
| 1 | Phvul.001G077200.2 | Phvul.001G077200 | Phvul.001G077200 | PF00170 |
| 1 | Phvul.001G215300.1 | Phvul.001G215300 | Phvul.001G215300 | PF01501 |
| 1 | Phvul.001G215300.2 | Phvul.001G215300 | Phvul.001G215300 | PF01501 |
| 1 | Phvul.001G215300.1 | Phvul.001G215300 | Phvul.001G215300 | PF01501 |
| 1 | Phvul.001G215300.2 | Phvul.001G215300 | Phvul.001G215300 | PF01501 |
| 1 | Phvul.002G267400.1 | Phvul.002G267400 | Phvul.002G267400 | PF02732 |
| 1 | Phvul.002G267400.1 | Phvul.002G267400 | Phvul.002G267400 | PF02732 |
| 1 | Phvul.002G267400.1 | Phvul.002G267400 | Phvul.002G267400 | PF02732 |
| 1 | Phvul.002G267400.1 | Phvul.002G267400 | Phvul.002G267400 | PF02732 |
| 1 | Phvul.002G281100.1 | Phvul.002G281100 | Phvul.002G281100 | PF03016 |
| 1 | Phvul.002G281100.1 | Phvul.002G281100 | Phvul.002G281100 | PF03016 |
| 1 | Phvul.002G281100.1 | Phvul.002G281100 | Phvul.002G281100 | PF03016 |
| 1 | Phvul.002G281100.1 | Phvul.002G281100 | Phvul.002G281100 | PF03016 |
| 1 | Phvul.004G044900.1 | Phvul.004G044900 | Phvul.004G044900 | PF08263,PF00 |
| 2 | Phvul.006G158900.1 | Phvul.006G158900 | Phvul.006G158900 | PF15365 |
| 2 | Phvul.008G071966.1 | Phvul.008G071966 | Phvul.008G071966 | 0 |
| 2 | Phvul.008G071966.1 | Phvul.008G071966 | Phvul.008G071966 | 0 |
| 2 | Phvul.008G071966.1 | Phvul.008G071966 | Phvul.008G071966 | 0 |
| 2 | Phvul.008G071966.1 | Phvul.008G071966 | Phvul.008G071966 | 0 |
| 1 | Phvul.008G110200.1 | Phvul.008G110200 | Phvul.008G110200 | PF05056 |
| 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 | PF05056 |

| | | | | | |
|----|---|--------------------|------------------|------------------|--------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | 1 | Phvul.008G163350.4 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 4 | 1 | Phvul.008G163350.3 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 5 | 1 | Phvul.008G163350.2 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 6 | 1 | Phvul.008G163350.1 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 7 | 1 | Phvul.008G163350.4 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 8 | 1 | Phvul.008G163350.3 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 9 | 1 | Phvul.008G163350.2 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 10 | 1 | Phvul.008G163350.1 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 11 | 1 | Phvul.008G163350.4 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 12 | 1 | Phvul.008G163350.3 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 13 | 1 | Phvul.008G163350.2 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 14 | 1 | Phvul.008G163350.1 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 15 | 1 | Phvul.008G163350.4 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 16 | 1 | Phvul.008G163350.3 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 17 | 1 | Phvul.008G163350.2 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 18 | 1 | Phvul.008G163350.1 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 19 | 1 | Phvul.008G163350.4 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 20 | 1 | Phvul.008G163350.3 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 21 | 1 | Phvul.008G163350.2 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 22 | 1 | Phvul.008G163350.1 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 23 | 1 | Phvul.008G163350.4 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 24 | 1 | Phvul.008G163350.3 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 25 | 1 | Phvul.008G163350.2 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 26 | 1 | Phvul.008G163350.1 | Phvul.008G163350 | Phvul.008G163350 | 0 |
| 27 | 1 | Phvul.009G057800.1 | Phvul.009G057800 | Phvul.009G057800 | PF04072 |
| 28 | 1 | Phvul.009G057800.1 | Phvul.009G057800 | Phvul.009G057800 | PF04072 |
| 29 | 1 | Phvul.009G057800.1 | Phvul.009G057800 | Phvul.009G057800 | PF04072 |
| 30 | 1 | Phvul.009G057800.1 | Phvul.009G057800 | Phvul.009G057800 | PF04072 |
| 31 | 1 | Phvul.010G058700.1 | Phvul.010G058700 | Phvul.010G058700 | 0 |
| 32 | 1 | Phvul.010G058700.1 | Phvul.010G058700 | Phvul.010G058700 | 0 |
| 33 | 1 | Phvul.001G022400.1 | Phvul.001G022400 | Phvul.001G022400 | PF00497,PF00 |
| 34 | 1 | Phvul.001G022400.1 | Phvul.001G022400 | Phvul.001G022400 | PF00497,PF00 |
| 35 | 1 | Phvul.001G077200.2 | Phvul.001G077200 | Phvul.001G077200 | PF00170 |
| 36 | 1 | Phvul.001G077200.2 | Phvul.001G077200 | Phvul.001G077200 | PF00170 |
| 37 | 2 | Phvul.001G077700.1 | Phvul.001G077700 | Phvul.001G077700 | PF10509,PF00 |
| 38 | 2 | Phvul.001G077700.1 | Phvul.001G077700 | Phvul.001G077700 | PF10509,PF00 |
| 39 | 1 | Phvul.001G086466.1 | Phvul.001G086466 | Phvul.001G086466 | PF00022 |
| 40 | 1 | Phvul.001G086466.1 | Phvul.001G086466 | Phvul.001G086466 | PF00022 |
| 41 | 1 | Phvul.001G086466.1 | Phvul.001G086466 | Phvul.001G086466 | PF00022 |
| 42 | 1 | Phvul.001G086466.1 | Phvul.001G086466 | Phvul.001G086466 | PF00022 |
| 43 | 1 | Phvul.001G089600.1 | Phvul.001G089600 | Phvul.001G089600 | 0 |
| 44 | 1 | Phvul.001G089600.1 | Phvul.001G089600 | Phvul.001G089600 | 0 |
| 45 | 1 | Phvul.001G089600.1 | Phvul.001G089600 | Phvul.001G089600 | 0 |
| 46 | 1 | Phvul.001G089600.1 | Phvul.001G089600 | Phvul.001G089600 | 0 |
| 47 | 1 | Phvul.001G091100.1 | Phvul.001G091100 | Phvul.001G091100 | PF02365 |
| 48 | 1 | Phvul.001G091100.1 | Phvul.001G091100 | Phvul.001G091100 | PF02365 |
| 49 | 1 | Phvul.001G091100.1 | Phvul.001G091100 | Phvul.001G091100 | PF02365 |
| 50 | 1 | Phvul.001G091100.1 | Phvul.001G091100 | Phvul.001G091100 | PF02365 |
| 51 | 1 | Phvul.001G121000.1 | Phvul.001G121000 | Phvul.001G121000 | PF00682 |
| 52 | 1 | Phvul.001G121000.2 | Phvul.001G121000 | Phvul.001G121000 | PF00682 |
| 53 | 1 | Phvul.001G131150.1 | Phvul.001G131150 | Phvul.001G131150 | PF13304,PF00 |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | | |
|----|--------------------|------------------|------------------|--------------|
| 1 | Phvul.001G131150.2 | Phvul.001G131150 | Phvul.001G131150 | PF13304,PF00 |
| 2 | Phvul.001G131150.1 | Phvul.001G131150 | Phvul.001G131150 | PF13304,PF00 |
| 3 | Phvul.001G131150.2 | Phvul.001G131150 | Phvul.001G131150 | PF13304,PF00 |
| 4 | Phvul.001G131150.1 | Phvul.001G131150 | Phvul.001G131150 | PF13304,PF00 |
| 5 | Phvul.001G131150.2 | Phvul.001G131150 | Phvul.001G131150 | PF13304,PF00 |
| 6 | Phvul.001G131150.1 | Phvul.001G131150 | Phvul.001G131150 | PF13304,PF00 |
| 7 | Phvul.001G131150.2 | Phvul.001G131150 | Phvul.001G131150 | PF13304,PF00 |
| 8 | Phvul.001G131150.1 | Phvul.001G131150 | Phvul.001G131150 | PF13304,PF00 |
| 9 | Phvul.001G131150.2 | Phvul.001G131150 | Phvul.001G131150 | PF13304,PF00 |
| 10 | Phvul.001G131150.1 | Phvul.001G131150 | Phvul.001G131150 | PF13304,PF00 |
| 11 | Phvul.001G131150.2 | Phvul.001G131150 | Phvul.001G131150 | PF13304,PF00 |
| 12 | Phvul.001G141000.1 | Phvul.001G141000 | Phvul.001G141000 | PF03110 |
| 13 | Phvul.001G141000.1 | Phvul.001G141000 | Phvul.001G141000 | PF03110 |
| 14 | Phvul.001G141000.1 | Phvul.001G141000 | Phvul.001G141000 | PF03110 |
| 15 | Phvul.001G141000.1 | Phvul.001G141000 | Phvul.001G141000 | PF03110 |
| 16 | Phvul.001G179700.1 | Phvul.001G179700 | Phvul.001G179700 | PF00994,PF01 |
| 17 | Phvul.001G179700.1 | Phvul.001G179700 | Phvul.001G179700 | PF00994,PF01 |
| 18 | Phvul.001G179700.1 | Phvul.001G179700 | Phvul.001G179700 | PF00994,PF01 |
| 19 | Phvul.001G179700.1 | Phvul.001G179700 | Phvul.001G179700 | PF00994,PF01 |
| 20 | Phvul.001G179700.1 | Phvul.001G179700 | Phvul.001G179700 | PF00994,PF01 |
| 21 | Phvul.001G179700.1 | Phvul.001G179700 | Phvul.001G179700 | PF00994,PF01 |
| 22 | Phvul.001G179700.1 | Phvul.001G179700 | Phvul.001G179700 | PF00994,PF01 |
| 23 | Phvul.002G042000.2 | Phvul.002G042000 | Phvul.002G042000 | 0 |
| 24 | Phvul.002G042000.8 | Phvul.002G042000 | Phvul.002G042000 | 0 |
| 25 | Phvul.002G042000.7 | Phvul.002G042000 | Phvul.002G042000 | 0 |
| 26 | Phvul.002G042000.6 | Phvul.002G042000 | Phvul.002G042000 | 0 |
| 27 | Phvul.002G042000.5 | Phvul.002G042000 | Phvul.002G042000 | 0 |
| 28 | Phvul.002G042000.3 | Phvul.002G042000 | Phvul.002G042000 | 0 |
| 29 | Phvul.002G042000.4 | Phvul.002G042000 | Phvul.002G042000 | 0 |
| 30 | Phvul.002G042000.1 | Phvul.002G042000 | Phvul.002G042000 | 0 |
| 31 | Phvul.002G042000.2 | Phvul.002G042000 | Phvul.002G042000 | 0 |
| 32 | Phvul.002G042000.8 | Phvul.002G042000 | Phvul.002G042000 | 0 |
| 33 | Phvul.002G042000.7 | Phvul.002G042000 | Phvul.002G042000 | 0 |
| 34 | Phvul.002G042000.6 | Phvul.002G042000 | Phvul.002G042000 | 0 |
| 35 | Phvul.002G042000.5 | Phvul.002G042000 | Phvul.002G042000 | 0 |
| 36 | Phvul.002G042000.3 | Phvul.002G042000 | Phvul.002G042000 | 0 |
| 37 | Phvul.002G042000.4 | Phvul.002G042000 | Phvul.002G042000 | 0 |
| 38 | Phvul.002G042000.1 | Phvul.002G042000 | Phvul.002G042000 | 0 |
| 39 | Phvul.002G068200.1 | Phvul.002G068200 | Phvul.002G068200 | PF00085 |
| 40 | Phvul.002G068200.1 | Phvul.002G068200 | Phvul.002G068200 | PF00085 |
| 41 | Phvul.002G071800.1 | Phvul.002G071800 | Phvul.002G071800 | PF06075 |
| 42 | Phvul.002G071800.1 | Phvul.002G071800 | Phvul.002G071800 | PF06075 |
| 43 | Phvul.002G076600.1 | Phvul.002G076600 | Phvul.002G076600 | PF01471,PF00 |
| 44 | Phvul.002G076600.1 | Phvul.002G076600 | Phvul.002G076600 | PF01471,PF00 |
| 45 | Phvul.002G076600.1 | Phvul.002G076600 | Phvul.002G076600 | PF01471,PF00 |
| 46 | Phvul.002G076600.1 | Phvul.002G076600 | Phvul.002G076600 | PF01471,PF00 |
| 47 | Phvul.002G185150.2 | Phvul.002G185150 | Phvul.002G185150 | PF00999 |
| 48 | Phvul.002G185150.1 | Phvul.002G185150 | Phvul.002G185150 | PF00999 |
| 49 | Phvul.002G185150.3 | Phvul.002G185150 | Phvul.002G185150 | PF00999 |

| | | | | | |
|----|---|--------------------|------------------|------------------|--------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | | | | | |
| 4 | 1 | Phvul.002G304500.1 | Phvul.002G304500 | Phvul.002G304500 | PF07714 |
| 5 | 1 | Phvul.003G103100.2 | Phvul.003G103100 | Phvul.003G103100 | PF07496 |
| 6 | 1 | Phvul.003G103100.2 | Phvul.003G103100 | Phvul.003G103100 | PF07496 |
| 7 | 1 | Phvul.004G044800.1 | Phvul.004G044800 | Phvul.004G044800 | PF08263,PF00 |
| 8 | 1 | Phvul.004G106000.1 | Phvul.004G106000 | Phvul.004G106000 | PF01535 |
| 9 | 1 | Phvul.004G133400.1 | Phvul.004G133400 | Phvul.004G133400 | PF00571,PF00 |
| 10 | 1 | Phvul.004G133400.1 | Phvul.004G133400 | Phvul.004G133400 | PF00571,PF00 |
| 11 | 1 | Phvul.004G133400.1 | Phvul.004G133400 | Phvul.004G133400 | PF00571,PF00 |
| 12 | 1 | Phvul.004G176700.1 | Phvul.004G176700 | Phvul.004G176700 | PF00085 |
| 13 | 1 | Phvul.004G176700.1 | Phvul.004G176700 | Phvul.004G176700 | PF00085 |
| 14 | 1 | Phvul.004G176700.1 | Phvul.004G176700 | Phvul.004G176700 | PF00085 |
| 15 | 1 | Phvul.004G176700.1 | Phvul.004G176700 | Phvul.004G176700 | PF00085 |
| 16 | 1 | Phvul.004G176700.1 | Phvul.004G176700 | Phvul.004G176700 | PF00085 |
| 17 | 1 | Phvul.004G176700.1 | Phvul.004G176700 | Phvul.004G176700 | PF00085 |
| 18 | 1 | Phvul.005G087300.1 | Phvul.005G087300 | Phvul.005G087300 | PF12609 |
| 19 | 1 | Phvul.005G116100.2 | Phvul.005G116100 | Phvul.005G116100 | PF01738 |
| 20 | 1 | Phvul.005G116100.1 | Phvul.005G116100 | Phvul.005G116100 | PF01738 |
| 21 | 1 | Phvul.005G116100.2 | Phvul.005G116100 | Phvul.005G116100 | PF01738 |
| 22 | 1 | Phvul.005G116100.2 | Phvul.005G116100 | Phvul.005G116100 | PF01738 |
| 23 | 1 | Phvul.005G116100.1 | Phvul.005G116100 | Phvul.005G116100 | PF01738 |
| 24 | 1 | Phvul.005G180200.1 | Phvul.005G180200 | Phvul.005G180200 | PF16987 |
| 25 | 1 | Phvul.005G180200.1 | Phvul.005G180200 | Phvul.005G180200 | PF16987 |
| 26 | 1 | Phvul.005G180200.1 | Phvul.005G180200 | Phvul.005G180200 | PF16987 |
| 27 | 1 | Phvul.006G019800.1 | Phvul.006G019800 | Phvul.006G019800 | PF00736 |
| 28 | 1 | Phvul.006G019800.1 | Phvul.006G019800 | Phvul.006G019800 | PF00736 |
| 29 | 1 | Phvul.006G019800.1 | Phvul.006G019800 | Phvul.006G019800 | PF00736 |
| 30 | 1 | Phvul.006G019800.1 | Phvul.006G019800 | Phvul.006G019800 | PF00736 |
| 31 | 1 | Phvul.006G019800.1 | Phvul.006G019800 | Phvul.006G019800 | PF00736 |
| 32 | 1 | Phvul.006G067700.1 | Phvul.006G067700 | Phvul.006G067700 | PF14510,PF08 |
| 33 | 1 | Phvul.006G067700.1 | Phvul.006G067700 | Phvul.006G067700 | PF14510,PF08 |
| 34 | 1 | Phvul.006G067700.1 | Phvul.006G067700 | Phvul.006G067700 | PF14510,PF08 |
| 35 | 1 | Phvul.006G067700.1 | Phvul.006G067700 | Phvul.006G067700 | PF14510,PF08 |
| 36 | 1 | Phvul.006G067700.1 | Phvul.006G067700 | Phvul.006G067700 | PF14510,PF08 |
| 37 | 1 | Phvul.006G067700.1 | Phvul.006G067700 | Phvul.006G067700 | PF14510,PF08 |
| 38 | 1 | Phvul.006G106900.2 | Phvul.006G106900 | Phvul.006G106900 | PF14365,PF03 |
| 39 | 1 | Phvul.006G106900.1 | Phvul.006G106900 | Phvul.006G106900 | PF14365,PF03 |
| 40 | 1 | Phvul.006G137200.3 | Phvul.006G137200 | Phvul.006G137200 | PF03765 |
| 41 | 1 | Phvul.006G137200.2 | Phvul.006G137200 | Phvul.006G137200 | PF03765 |
| 42 | 1 | Phvul.006G137200.2 | Phvul.006G137200 | Phvul.006G137200 | PF03765 |
| 43 | 1 | Phvul.007G113800.1 | Phvul.007G113800 | Phvul.007G113800 | PF12697 |
| 44 | 1 | Phvul.007G113800.1 | Phvul.007G113800 | Phvul.007G113800 | PF12697 |
| 45 | 1 | Phvul.007G211400.1 | Phvul.007G211400 | Phvul.007G211400 | PF00295 |
| 46 | 1 | Phvul.007G211400.1 | Phvul.007G211400 | Phvul.007G211400 | PF00295 |
| 47 | 1 | Phvul.007G219400.1 | Phvul.007G219400 | Phvul.007G219400 | PF02519 |
| 48 | 1 | Phvul.007G219400.1 | Phvul.007G219400 | Phvul.007G219400 | PF02519 |
| 49 | 1 | Phvul.007G219400.1 | Phvul.007G219400 | Phvul.007G219400 | PF02519 |
| 50 | 1 | Phvul.007G219400.1 | Phvul.007G219400 | Phvul.007G219400 | PF02519 |
| 51 | 1 | Phvul.008G071966.1 | Phvul.008G071966 | Phvul.008G071966 | 0 |
| 52 | 1 | Phvul.008G071966.1 | Phvul.008G071966 | Phvul.008G071966 | 0 |
| 53 | 1 | Phvul.008G107300.1 | Phvul.008G107300 | Phvul.008G107300 | 0 |
| 54 | 1 | Phvul.008G107300.1 | Phvul.008G107300 | Phvul.008G107300 | 0 |
| 55 | 1 | Phvul.008G107300.1 | Phvul.008G107300 | Phvul.008G107300 | 0 |
| 56 | 1 | Phvul.008G115900.1 | Phvul.008G115900 | Phvul.008G115900 | PF08659 |
| 57 | 1 | Phvul.008G115900.1 | Phvul.008G115900 | Phvul.008G115900 | PF08659 |
| 58 | 1 | Phvul.008G115900.1 | Phvul.008G115900 | Phvul.008G115900 | PF08659 |
| 59 | 1 | Phvul.008G257700.2 | Phvul.008G257700 | Phvul.008G257700 | PF01370 |
| 60 | | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | | |
|----|--------------------|------------------|------------------|--------------|
| 1 | Phvul.008G257700.1 | Phvul.008G257700 | Phvul.008G257700 | PF01370 |
| 2 | Phvul.008G257700.2 | Phvul.008G257700 | Phvul.008G257700 | PF01370 |
| 3 | Phvul.008G257700.1 | Phvul.008G257700 | Phvul.008G257700 | PF01370 |
| 4 | Phvul.008G282700.1 | Phvul.008G282700 | Phvul.008G282700 | PF02628 |
| 5 | Phvul.008G289600.1 | Phvul.008G289600 | Phvul.008G289600 | PF02990 |
| 6 | Phvul.009G127300.1 | Phvul.009G127300 | Phvul.009G127300 | PF12937 |
| 7 | Phvul.009G127300.1 | Phvul.009G127300 | Phvul.009G127300 | PF12937 |
| 8 | Phvul.009G127300.1 | Phvul.009G127300 | Phvul.009G127300 | PF12937 |
| 9 | Phvul.009G127300.1 | Phvul.009G127300 | Phvul.009G127300 | PF12937 |
| 10 | Phvul.009G160700.1 | Phvul.009G160700 | Phvul.009G160700 | PF03016 |
| 11 | Phvul.009G160700.1 | Phvul.009G160700 | Phvul.009G160700 | PF03016 |
| 12 | Phvul.009G160700.1 | Phvul.009G160700 | Phvul.009G160700 | PF03016 |
| 13 | Phvul.009G160700.1 | Phvul.009G160700 | Phvul.009G160700 | PF03016 |
| 14 | Phvul.010G064700.1 | Phvul.010G064700 | Phvul.010G064700 | PF00931 |
| 15 | Phvul.010G064700.1 | Phvul.010G064700 | Phvul.010G064700 | PF00931 |
| 16 | Phvul.010G064700.1 | Phvul.010G064700 | Phvul.010G064700 | PF00931 |
| 17 | Phvul.010G064700.1 | Phvul.010G064700 | Phvul.010G064700 | PF00931 |
| 18 | Phvul.011G047100.1 | Phvul.011G047100 | Phvul.011G047100 | PF00170 |
| 19 | Phvul.011G047100.1 | Phvul.011G047100 | Phvul.011G047100 | PF00170 |
| 20 | Phvul.011G050300.1 | Phvul.011G050300 | Phvul.011G050300 | PF02260,PF15 |
| 21 | Phvul.011G050300.2 | Phvul.011G050300 | Phvul.011G050300 | PF02260,PF15 |
| 22 | Phvul.011G050300.1 | Phvul.011G050300 | Phvul.011G050300 | PF02260,PF15 |
| 23 | Phvul.011G050300.2 | Phvul.011G050300 | Phvul.011G050300 | PF02260,PF15 |
| 24 | Phvul.L007343.1 | Phvul.L007343 | Phvul.L007343 | PF07731,PF07 |
| 25 | Phvul.L007343.1 | Phvul.L007343 | Phvul.L007343 | PF07731,PF07 |
| 26 | Phvul.001G022700.1 | Phvul.001G022700 | Phvul.001G022700 | PF03763 |
| 27 | Phvul.001G022700.1 | Phvul.001G022700 | Phvul.001G022700 | PF03763 |
| 28 | Phvul.001G036800.1 | Phvul.001G036800 | Phvul.001G036800 | PF08244,PF00 |
| 29 | Phvul.001G100700.2 | Phvul.001G100700 | Phvul.001G100700 | PF00076 |
| 30 | Phvul.001G100700.2 | Phvul.001G100700 | Phvul.001G100700 | PF00076 |
| 31 | Phvul.001G153600.2 | Phvul.001G153600 | Phvul.001G153600 | PF14368 |
| 32 | Phvul.001G153600.2 | Phvul.001G153600 | Phvul.001G153600 | PF14368 |
| 33 | Phvul.001G153600.2 | Phvul.001G153600 | Phvul.001G153600 | PF14368 |
| 34 | Phvul.001G153600.2 | Phvul.001G153600 | Phvul.001G153600 | PF14368 |
| 35 | Phvul.001G247000.1 | Phvul.001G247000 | Phvul.001G247000 | PF00364 |
| 36 | Phvul.002G004100.1 | Phvul.002G004100 | Phvul.002G004100 | PF03330,PF01 |
| 37 | Phvul.002G013866.1 | Phvul.002G013866 | Phvul.002G013866 | PF13414 |
| 38 | Phvul.002G013866.1 | Phvul.002G013866 | Phvul.002G013866 | PF13414 |
| 39 | Phvul.002G212900.1 | Phvul.002G212900 | Phvul.002G212900 | PF12689 |
| 40 | Phvul.002G253200.1 | Phvul.002G253200 | Phvul.002G253200 | PF00415 |
| 41 | Phvul.002G253200.1 | Phvul.002G253200 | Phvul.002G253200 | PF00415 |
| 42 | Phvul.003G029000.2 | Phvul.003G029000 | Phvul.003G029000 | PF13646,PF02 |
| 43 | Phvul.003G029000.1 | Phvul.003G029000 | Phvul.003G029000 | PF13646,PF02 |

| | | | | |
|----|---|--------------------|------------------|-------------------------------|
| 1 | | | | |
| 2 | | | | |
| 3 | 1 | Phvul.003G087600.2 | Phvul.003G087600 | Phvul.003G087600 PF02803,PF00 |
| 4 | 1 | Phvul.003G087600.1 | Phvul.003G087600 | Phvul.003G087600 PF02803,PF00 |
| 5 | 1 | Phvul.003G087600.2 | Phvul.003G087600 | Phvul.003G087600 PF02803,PF00 |
| 6 | 1 | Phvul.003G087600.1 | Phvul.003G087600 | Phvul.003G087600 PF02803,PF00 |
| 7 | 1 | Phvul.003G087600.2 | Phvul.003G087600 | Phvul.003G087600 PF02803,PF00 |
| 8 | 1 | Phvul.003G087600.1 | Phvul.003G087600 | Phvul.003G087600 PF02803,PF00 |
| 9 | 1 | Phvul.003G087600.2 | Phvul.003G087600 | Phvul.003G087600 PF02803,PF00 |
| 10 | 1 | Phvul.003G087600.1 | Phvul.003G087600 | Phvul.003G087600 PF02803,PF00 |
| 11 | 1 | Phvul.003G087600.2 | Phvul.003G087600 | Phvul.003G087600 PF02803,PF00 |
| 12 | 1 | Phvul.003G087600.1 | Phvul.003G087600 | Phvul.003G087600 PF02803,PF00 |
| 13 | 1 | Phvul.003G104200.1 | Phvul.003G104200 | Phvul.003G104200 PF00153 |
| 14 | 1 | Phvul.003G104200.1 | Phvul.003G104200 | Phvul.003G104200 PF00153 |
| 15 | 1 | Phvul.003G141700.1 | Phvul.003G141700 | Phvul.003G141700 PF00566 |
| 16 | 1 | Phvul.003G141700.1 | Phvul.003G141700 | Phvul.003G141700 PF00566 |
| 17 | 1 | Phvul.003G231500.1 | Phvul.003G231500 | Phvul.003G231500 PF03953,PF00 |
| 18 | 1 | Phvul.003G231500.1 | Phvul.003G231500 | Phvul.003G231500 PF03953,PF00 |
| 19 | 1 | Phvul.003G231500.1 | Phvul.003G231500 | Phvul.003G231500 PF03953,PF00 |
| 20 | 1 | Phvul.003G231500.1 | Phvul.003G231500 | Phvul.003G231500 PF03953,PF00 |
| 21 | 1 | Phvul.003G294601.1 | Phvul.003G294601 | Phvul.003G294601 PF00076 |
| 22 | 1 | Phvul.003G294800.4 | Phvul.003G294800 | Phvul.003G294800 PF00076 |
| 23 | 1 | Phvul.003G294800.3 | Phvul.003G294800 | Phvul.003G294800 PF00076 |
| 24 | 1 | Phvul.004G015500.1 | Phvul.004G015500 | Phvul.004G015500 PF00646,PF08 |
| 25 | 1 | Phvul.004G015500.1 | Phvul.004G015500 | Phvul.004G015500 PF00646,PF08 |
| 26 | 1 | Phvul.004G015500.1 | Phvul.004G015500 | Phvul.004G015500 PF00646,PF08 |
| 27 | 1 | Phvul.004G015500.1 | Phvul.004G015500 | Phvul.004G015500 PF00646,PF08 |
| 28 | 1 | Phvul.004G032100.1 | Phvul.004G032100 | Phvul.004G032100 0 |
| 29 | 1 | Phvul.004G044900.1 | Phvul.004G044900 | Phvul.004G044900 PF08263,PF00 |
| 30 | 1 | Phvul.004G044900.1 | Phvul.004G044900 | Phvul.004G044900 PF08263,PF00 |
| 31 | 1 | Phvul.004G163200.1 | Phvul.004G163200 | Phvul.004G163200 PF00225 |
| 32 | 1 | Phvul.005G010700.2 | Phvul.005G010700 | Phvul.005G010700 PF11717,PF01 |
| 33 | 1 | Phvul.005G015800.2 | Phvul.005G015800 | Phvul.005G015800 PF00067 |
| 34 | 1 | Phvul.005G015800.1 | Phvul.005G015800 | Phvul.005G015800 PF00067 |
| 35 | 1 | Phvul.005G015800.2 | Phvul.005G015800 | Phvul.005G015800 PF00067 |
| 36 | 1 | Phvul.005G015800.1 | Phvul.005G015800 | Phvul.005G015800 PF00067 |
| 37 | 1 | Phvul.005G015800.2 | Phvul.005G015800 | Phvul.005G015800 PF00067 |
| 38 | 1 | Phvul.005G015800.1 | Phvul.005G015800 | Phvul.005G015800 PF00067 |
| 39 | 1 | Phvul.005G015800.2 | Phvul.005G015800 | Phvul.005G015800 PF00067 |
| 40 | 1 | Phvul.005G015800.1 | Phvul.005G015800 | Phvul.005G015800 PF00067 |
| 41 | 1 | Phvul.005G081600.1 | Phvul.005G081600 | Phvul.005G081600 PF13692,PF13 |
| 42 | 1 | Phvul.005G081600.1 | Phvul.005G081600 | Phvul.005G081600 PF13692,PF13 |
| 43 | 1 | Phvul.005G097200.3 | Phvul.005G097200 | Phvul.005G097200 PF03634 |
| 44 | 1 | Phvul.005G097200.6 | Phvul.005G097200 | Phvul.005G097200 PF03634 |
| 45 | 1 | Phvul.005G097200.5 | Phvul.005G097200 | Phvul.005G097200 PF03634 |
| 46 | 1 | Phvul.005G097200.3 | Phvul.005G097200 | Phvul.005G097200 PF03634 |
| 47 | 1 | Phvul.005G097200.6 | Phvul.005G097200 | Phvul.005G097200 PF03634 |
| 48 | | | | |
| 49 | | | | |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | | |
|----------------------|------------------|------------------|--------------|---|
| 1 Phvul.005G097200.5 | Phvul.005G097200 | Phvul.005G097200 | PF03634 | |
| 1 Phvul.006G062000.1 | Phvul.006G062000 | Phvul.006G062000 | | 0 |
| 1 Phvul.006G062000.1 | Phvul.006G062000 | Phvul.006G062000 | | 0 |
| 1 Phvul.006G130611.1 | Phvul.006G130611 | Phvul.006G130611 | PF00282 | |
| 1 Phvul.006G130611.1 | Phvul.006G130611 | Phvul.006G130611 | PF00282 | |
| 1 Phvul.006G192200.2 | Phvul.006G192200 | Phvul.006G192200 | PF00622,PF13 | |
| 1 Phvul.006G192200.1 | Phvul.006G192200 | Phvul.006G192200 | PF00622,PF13 | |
| 1 Phvul.006G192200.4 | Phvul.006G192200 | Phvul.006G192200 | PF00622,PF13 | |
| 1 Phvul.006G192200.3 | Phvul.006G192200 | Phvul.006G192200 | PF00622,PF13 | |
| 1 Phvul.007G058400.1 | Phvul.007G058400 | Phvul.007G058400 | PF04570 | |
| 1 Phvul.007G058400.2 | Phvul.007G058400 | Phvul.007G058400 | PF04570 | |
| 1 Phvul.007G064700.1 | Phvul.007G064700 | Phvul.007G064700 | PF12695 | |
| 1 Phvul.007G064700.1 | Phvul.007G064700 | Phvul.007G064700 | PF12695 | |
| 1 Phvul.007G182300.2 | Phvul.007G182300 | Phvul.007G182300 | | 0 |
| 1 Phvul.007G198500.1 | Phvul.007G198500 | Phvul.007G198500 | PF13414 | |
| 1 Phvul.007G198500.1 | Phvul.007G198500 | Phvul.007G198500 | PF13414 | |
| 1 Phvul.007G233800.1 | Phvul.007G233800 | Phvul.007G233800 | | 0 |
| 1 Phvul.007G233800.2 | Phvul.007G233800 | Phvul.007G233800 | | 0 |
| 1 Phvul.007G233800.1 | Phvul.007G233800 | Phvul.007G233800 | | 0 |
| 1 Phvul.007G233800.2 | Phvul.007G233800 | Phvul.007G233800 | | 0 |
| 1 Phvul.008G008300.6 | Phvul.008G008300 | Phvul.008G008300 | | 0 |
| 1 Phvul.008G008300.3 | Phvul.008G008300 | Phvul.008G008300 | | 0 |
| 1 Phvul.008G008300.5 | Phvul.008G008300 | Phvul.008G008300 | | 0 |
| 1 Phvul.008G008300.4 | Phvul.008G008300 | Phvul.008G008300 | | 0 |
| 1 Phvul.008G008300.2 | Phvul.008G008300 | Phvul.008G008300 | | 0 |
| 1 Phvul.008G008300.6 | Phvul.008G008300 | Phvul.008G008300 | | 0 |
| 1 Phvul.008G008300.3 | Phvul.008G008300 | Phvul.008G008300 | | 0 |
| 1 Phvul.008G008300.5 | Phvul.008G008300 | Phvul.008G008300 | | 0 |
| 1 Phvul.008G008300.4 | Phvul.008G008300 | Phvul.008G008300 | | 0 |
| 1 Phvul.008G008300.2 | Phvul.008G008300 | Phvul.008G008300 | | 0 |
| 1 Phvul.008G009200.2 | Phvul.008G009200 | Phvul.008G009200 | PF07522,PF04 | |
| 1 Phvul.008G009200.2 | Phvul.008G009200 | Phvul.008G009200 | PF07522,PF04 | |
| 1 Phvul.008G009200.2 | Phvul.008G009200 | Phvul.008G009200 | PF07522,PF04 | |
| 1 Phvul.008G009200.2 | Phvul.008G009200 | Phvul.008G009200 | PF07522,PF04 | |
| 1 Phvul.008G038300.1 | Phvul.008G038300 | Phvul.008G038300 | PF03105,PF03 | |
| 1 Phvul.008G038300.1 | Phvul.008G038300 | Phvul.008G038300 | PF03105,PF03 | |
| 2 Phvul.008G093200.3 | Phvul.008G093200 | Phvul.008G093200 | PF00560,PF08 | |
| 2 Phvul.008G093200.2 | Phvul.008G093200 | Phvul.008G093200 | PF00560,PF08 | |
| 2 Phvul.008G093200.1 | Phvul.008G093200 | Phvul.008G093200 | PF00560,PF08 | |
| 2 Phvul.008G093200.3 | Phvul.008G093200 | Phvul.008G093200 | PF00560,PF08 | |
| 2 Phvul.008G093200.2 | Phvul.008G093200 | Phvul.008G093200 | PF00560,PF08 | |
| 2 Phvul.008G093200.1 | Phvul.008G093200 | Phvul.008G093200 | PF00560,PF08 | |
| 2 Phvul.008G108800.2 | Phvul.008G108800 | Phvul.008G108800 | | 0 |

| | | | | | |
|----|---|--------------------|------------------|------------------|--------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | 2 | Phvul.008G108800.2 | Phvul.008G108800 | Phvul.008G108800 | 0 |
| 4 | 2 | Phvul.008G108800.2 | Phvul.008G108800 | Phvul.008G108800 | 0 |
| 5 | 2 | Phvul.008G108800.2 | Phvul.008G108800 | Phvul.008G108800 | 0 |
| 6 | 2 | Phvul.008G108800.2 | Phvul.008G108800 | Phvul.008G108800 | 0 |
| 7 | 1 | Phvul.008G110000.1 | Phvul.008G110000 | Phvul.008G110000 | PF05056 |
| 8 | 1 | Phvul.008G110200.1 | Phvul.008G110200 | Phvul.008G110200 | PF05056 |
| 9 | 1 | Phvul.008G110200.1 | Phvul.008G110200 | Phvul.008G110200 | PF05056 |
| 10 | 1 | Phvul.008G110200.1 | Phvul.008G110200 | Phvul.008G110200 | PF05056 |
| 11 | 1 | Phvul.008G110400.1 | Phvul.008G110400 | Phvul.008G110400 | PF05056 |
| 12 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 | PF05056 |
| 13 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 | PF05056 |
| 14 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 | PF05056 |
| 15 | 1 | Phvul.008G199500.1 | Phvul.008G199500 | Phvul.008G199500 | 0 |
| 16 | 1 | Phvul.008G290300.1 | Phvul.008G290300 | Phvul.008G290300 | PF00201 |
| 17 | 1 | Phvul.008G290300.1 | Phvul.008G290300 | Phvul.008G290300 | PF00201 |
| 18 | 1 | Phvul.008G290300.1 | Phvul.008G290300 | Phvul.008G290300 | PF00201 |
| 19 | 1 | Phvul.008G290300.1 | Phvul.008G290300 | Phvul.008G290300 | PF00201 |
| 20 | 1 | Phvul.008G290300.1 | Phvul.008G290300 | Phvul.008G290300 | PF00201 |
| 21 | 1 | Phvul.008G290300.1 | Phvul.008G290300 | Phvul.008G290300 | PF00201 |
| 22 | 1 | Phvul.009G026200.1 | Phvul.009G026200 | Phvul.009G026200 | PF02362,PF06 |
| 23 | 1 | Phvul.009G026200.1 | Phvul.009G026200 | Phvul.009G026200 | PF02362,PF06 |
| 24 | 1 | Phvul.009G040800.3 | Phvul.009G040800 | Phvul.009G040800 | 0 |
| 25 | 1 | Phvul.009G040800.1 | Phvul.009G040800 | Phvul.009G040800 | 0 |
| 26 | 1 | Phvul.009G040800.1 | Phvul.009G040800 | Phvul.009G040800 | 0 |
| 27 | 1 | Phvul.009G040800.2 | Phvul.009G040800 | Phvul.009G040800 | 0 |
| 28 | 1 | Phvul.009G121300.1 | Phvul.009G121300 | Phvul.009G121300 | PF15413,PF01 |
| 29 | 1 | Phvul.009G121300.2 | Phvul.009G121300 | Phvul.009G121300 | PF15413,PF01 |
| 30 | 1 | Phvul.009G121300.2 | Phvul.009G121300 | Phvul.009G121300 | PF15413,PF01 |
| 31 | 1 | Phvul.009G121300.1 | Phvul.009G121300 | Phvul.009G121300 | PF15413,PF01 |
| 32 | 1 | Phvul.009G121300.2 | Phvul.009G121300 | Phvul.009G121300 | PF15413,PF01 |
| 33 | 1 | Phvul.009G121300.2 | Phvul.009G121300 | Phvul.009G121300 | PF15413,PF01 |
| 34 | 1 | Phvul.009G121300.1 | Phvul.009G121300 | Phvul.009G121300 | PF15413,PF01 |
| 35 | 1 | Phvul.009G121300.2 | Phvul.009G121300 | Phvul.009G121300 | PF15413,PF01 |
| 36 | 1 | Phvul.009G121300.1 | Phvul.009G121300 | Phvul.009G121300 | PF15413,PF01 |
| 37 | 1 | Phvul.009G121300.2 | Phvul.009G121300 | Phvul.009G121300 | PF15413,PF01 |
| 38 | 1 | Phvul.009G121300.2 | Phvul.009G121300 | Phvul.009G121300 | PF15413,PF01 |
| 39 | 1 | Phvul.009G246900.4 | Phvul.009G246900 | Phvul.009G246900 | PF00153 |
| 40 | 1 | Phvul.009G246900.3 | Phvul.009G246900 | Phvul.009G246900 | PF00153 |
| 41 | 1 | Phvul.009G246900.1 | Phvul.009G246900 | Phvul.009G246900 | PF00153 |
| 42 | 1 | Phvul.009G246900.1 | Phvul.009G246900 | Phvul.009G246900 | PF00153 |
| 43 | 1 | Phvul.009G246900.2 | Phvul.009G246900 | Phvul.009G246900 | PF00153 |
| 44 | 1 | Phvul.009G246900.4 | Phvul.009G246900 | Phvul.009G246900 | PF00153 |
| 45 | 1 | Phvul.009G246900.3 | Phvul.009G246900 | Phvul.009G246900 | PF00153 |
| 46 | 1 | Phvul.009G246900.3 | Phvul.009G246900 | Phvul.009G246900 | PF00153 |
| 47 | 1 | Phvul.009G246900.1 | Phvul.009G246900 | Phvul.009G246900 | PF00153 |
| 48 | 1 | Phvul.009G246900.2 | Phvul.009G246900 | Phvul.009G246900 | PF00153 |
| 49 | 1 | Phvul.009G246900.2 | Phvul.009G246900 | Phvul.009G246900 | PF00153 |
| 50 | 1 | Phvul.010G048400.4 | Phvul.010G048400 | Phvul.010G048400 | PF08879 |
| 51 | 1 | Phvul.010G048400.3 | Phvul.010G048400 | Phvul.010G048400 | PF08879 |
| 52 | 1 | Phvul.010G048400.1 | Phvul.010G048400 | Phvul.010G048400 | PF08879 |
| 53 | 1 | Phvul.010G048400.2 | Phvul.010G048400 | Phvul.010G048400 | PF08879 |
| 54 | 1 | Phvul.010G048400.2 | Phvul.010G048400 | Phvul.010G048400 | PF08879 |
| 55 | 1 | Phvul.010G048400.4 | Phvul.010G048400 | Phvul.010G048400 | PF08879 |
| 56 | 1 | Phvul.010G048400.3 | Phvul.010G048400 | Phvul.010G048400 | PF08879 |
| 57 | 1 | Phvul.010G048400.3 | Phvul.010G048400 | Phvul.010G048400 | PF08879 |
| 58 | 1 | Phvul.010G048400.1 | Phvul.010G048400 | Phvul.010G048400 | PF08879 |
| 59 | 1 | Phvul.010G048400.2 | Phvul.010G048400 | Phvul.010G048400 | PF08879 |
| 60 | | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | | |
|----|--------------------|------------------|------------------|--------------|
| 1 | Phvul.010G048400.4 | Phvul.010G048400 | Phvul.010G048400 | PF08879 |
| 2 | Phvul.010G048400.3 | Phvul.010G048400 | Phvul.010G048400 | PF08879 |
| 3 | Phvul.010G048400.1 | Phvul.010G048400 | Phvul.010G048400 | PF08879 |
| 4 | Phvul.010G048400.2 | Phvul.010G048400 | Phvul.010G048400 | PF08879 |
| 5 | Phvul.010G048400.4 | Phvul.010G048400 | Phvul.010G048400 | PF08879 |
| 6 | Phvul.010G048400.3 | Phvul.010G048400 | Phvul.010G048400 | PF08879 |
| 7 | Phvul.010G048400.1 | Phvul.010G048400 | Phvul.010G048400 | PF08879 |
| 8 | Phvul.010G048400.2 | Phvul.010G048400 | Phvul.010G048400 | PF08879 |
| 9 | Phvul.010G116400.1 | Phvul.010G116400 | Phvul.010G116400 | PF05659,PF04 |
| 10 | Phvul.010G116400.1 | Phvul.010G116400 | Phvul.010G116400 | PF05659,PF04 |
| 11 | Phvul.010G116400.1 | Phvul.010G116400 | Phvul.010G116400 | PF05659,PF04 |
| 12 | Phvul.010G116400.1 | Phvul.010G116400 | Phvul.010G116400 | PF05659,PF04 |
| 13 | Phvul.011G013800.1 | Phvul.011G013800 | Phvul.011G013800 | PF00642,PF00 |
| 14 | Phvul.011G013800.1 | Phvul.011G013800 | Phvul.011G013800 | PF00642,PF00 |
| 15 | Phvul.011G013800.1 | Phvul.011G013800 | Phvul.011G013800 | PF00642,PF00 |
| 16 | Phvul.011G013800.1 | Phvul.011G013800 | Phvul.011G013800 | PF00642,PF00 |
| 17 | Phvul.011G123701.1 | Phvul.011G123701 | Phvul.011G123701 | 0 |
| 18 | Phvul.011G123701.1 | Phvul.011G123701 | Phvul.011G123701 | 0 |
| 19 | Phvul.011G123701.1 | Phvul.011G123701 | Phvul.011G123701 | 0 |
| 20 | Phvul.011G123701.1 | Phvul.011G123701 | Phvul.011G123701 | 0 |
| 21 | Phvul.011G160800.1 | Phvul.011G160800 | Phvul.011G160800 | PF01112 |
| 22 | Phvul.011G160800.3 | Phvul.011G160800 | Phvul.011G160800 | PF01112 |
| 23 | Phvul.011G160800.2 | Phvul.011G160800 | Phvul.011G160800 | PF01112 |
| 24 | Phvul.011G160800.1 | Phvul.011G160800 | Phvul.011G160800 | PF01112 |
| 25 | Phvul.011G160800.3 | Phvul.011G160800 | Phvul.011G160800 | PF01112 |
| 26 | Phvul.011G160800.2 | Phvul.011G160800 | Phvul.011G160800 | PF01112 |
| 27 | Phvul.011G173000.1 | Phvul.011G173000 | Phvul.011G173000 | PF01641 |
| 28 | Phvul.011G173000.1 | Phvul.011G173000 | Phvul.011G173000 | PF01641 |
| 29 | Phvul.011G173000.1 | Phvul.011G173000 | Phvul.011G173000 | PF01641 |
| 30 | Phvul.011G173000.1 | Phvul.011G173000 | Phvul.011G173000 | PF01641 |
| 31 | Phvul.011G190200.3 | Phvul.011G190200 | Phvul.011G190200 | PF05033,PF00 |
| 32 | Phvul.011G190200.2 | Phvul.011G190200 | Phvul.011G190200 | PF05033,PF00 |
| 33 | Phvul.001G098600.1 | Phvul.001G098600 | Phvul.001G098600 | PF05553 |
| 34 | Phvul.001G098600.1 | Phvul.001G098600 | Phvul.001G098600 | PF05553 |
| 35 | Phvul.001G102901.2 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |
| 36 | Phvul.001G102901.4 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |
| 37 | Phvul.001G102901.3 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |
| 38 | Phvul.001G102901.1 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |
| 39 | Phvul.001G102901.2 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |
| 40 | Phvul.001G102901.4 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |
| 41 | Phvul.001G102901.3 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |
| 42 | Phvul.001G102901.1 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |
| 43 | Phvul.001G102901.2 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |
| 44 | Phvul.001G102901.4 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |
| 45 | Phvul.001G102901.3 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |
| 46 | Phvul.001G102901.1 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |
| 47 | Phvul.001G102901.2 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |

| | | | | | |
|----|---|--------------------|------------------|------------------|--------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | | | | | |
| 4 | 1 | Phvul.001G102901.4 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |
| 5 | 1 | Phvul.001G102901.3 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |
| 6 | 1 | Phvul.001G102901.1 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |
| 7 | 1 | Phvul.001G102901.2 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |
| 8 | 1 | Phvul.001G102901.4 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |
| 9 | | | | | |
| 10 | 1 | Phvul.001G102901.3 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |
| 11 | 1 | Phvul.001G102901.1 | Phvul.001G102901 | Phvul.001G102901 | PF04818 |
| 12 | 1 | Phvul.001G147800.2 | Phvul.001G147800 | Phvul.001G147800 | 0 |
| 13 | | | | | |
| 14 | 1 | Phvul.001G173900.1 | Phvul.001G173900 | Phvul.001G173900 | PF13911 |
| 15 | 1 | Phvul.001G173900.1 | Phvul.001G173900 | Phvul.001G173900 | PF13911 |
| 16 | 1 | Phvul.001G173900.1 | Phvul.001G173900 | Phvul.001G173900 | PF13911 |
| 17 | 1 | Phvul.001G173900.1 | Phvul.001G173900 | Phvul.001G173900 | PF13911 |
| 18 | 1 | Phvul.001G173900.1 | Phvul.001G173900 | Phvul.001G173900 | PF13911 |
| 19 | 1 | Phvul.001G179700.1 | Phvul.001G179700 | Phvul.001G179700 | PF00994,PF01 |
| 20 | 1 | Phvul.001G179700.1 | Phvul.001G179700 | Phvul.001G179700 | PF00994,PF01 |
| 21 | | | | | |
| 22 | 1 | Phvul.001G200700.3 | Phvul.001G200700 | Phvul.001G200700 | PF15801,PF03 |
| 23 | 1 | Phvul.001G200700.1 | Phvul.001G200700 | Phvul.001G200700 | PF15801,PF03 |
| 24 | 1 | Phvul.001G200700.3 | Phvul.001G200700 | Phvul.001G200700 | PF15801,PF03 |
| 25 | 1 | Phvul.001G200700.1 | Phvul.001G200700 | Phvul.001G200700 | PF15801,PF03 |
| 26 | 1 | Phvul.001G200700.1 | Phvul.001G200700 | Phvul.001G200700 | PF15801,PF03 |
| 27 | 1 | Phvul.001G200700.3 | Phvul.001G200700 | Phvul.001G200700 | PF15801,PF03 |
| 28 | 1 | Phvul.001G200700.1 | Phvul.001G200700 | Phvul.001G200700 | PF15801,PF03 |
| 29 | 1 | Phvul.001G200700.3 | Phvul.001G200700 | Phvul.001G200700 | PF15801,PF03 |
| 30 | 1 | Phvul.001G200700.3 | Phvul.001G200700 | Phvul.001G200700 | PF15801,PF03 |
| 31 | 1 | Phvul.001G200700.1 | Phvul.001G200700 | Phvul.001G200700 | PF15801,PF03 |
| 32 | 1 | Phvul.001G260300.1 | Phvul.001G260300 | Phvul.001G260300 | PF04564 |
| 33 | | | | | |
| 34 | 1 | Phvul.001G268700.1 | Phvul.001G268700 | Phvul.001G268700 | PF08100,PF00 |
| 35 | 1 | Phvul.001G268700.1 | Phvul.001G268700 | Phvul.001G268700 | PF08100,PF00 |
| 36 | 2 | Phvul.002G058900.1 | Phvul.002G058900 | Phvul.002G058900 | PF13912 |
| 37 | 2 | Phvul.002G058900.1 | Phvul.002G058900 | Phvul.002G058900 | PF13912 |
| 38 | 1 | Phvul.002G068200.1 | Phvul.002G068200 | Phvul.002G068200 | PF00085 |
| 39 | 1 | Phvul.002G068200.1 | Phvul.002G068200 | Phvul.002G068200 | PF00085 |
| 40 | 1 | Phvul.002G068200.1 | Phvul.002G068200 | Phvul.002G068200 | PF00085 |
| 41 | 1 | Phvul.002G068200.1 | Phvul.002G068200 | Phvul.002G068200 | PF00085 |
| 42 | 1 | Phvul.002G068200.1 | Phvul.002G068200 | Phvul.002G068200 | PF00085 |
| 43 | 1 | Phvul.002G163400.1 | Phvul.002G163400 | Phvul.002G163400 | PF03106 |
| 44 | 1 | Phvul.002G163400.1 | Phvul.002G163400 | Phvul.002G163400 | PF03106 |
| 45 | 1 | Phvul.002G163400.1 | Phvul.002G163400 | Phvul.002G163400 | PF03106 |
| 46 | 1 | Phvul.002G165300.1 | Phvul.002G165300 | Phvul.002G165300 | PF07738 |
| 47 | 1 | Phvul.002G165300.1 | Phvul.002G165300 | Phvul.002G165300 | PF07738 |
| 48 | 1 | Phvul.002G165300.1 | Phvul.002G165300 | Phvul.002G165300 | PF07738 |
| 49 | 1 | Phvul.002G165300.1 | Phvul.002G165300 | Phvul.002G165300 | PF07738 |
| 50 | 1 | Phvul.002G165300.1 | Phvul.002G165300 | Phvul.002G165300 | PF07738 |
| 51 | 1 | Phvul.002G216700.3 | Phvul.002G216700 | Phvul.002G216700 | PF00010 |
| 52 | 1 | Phvul.002G216700.2 | Phvul.002G216700 | Phvul.002G216700 | PF00010 |
| 53 | 1 | Phvul.002G216700.3 | Phvul.002G216700 | Phvul.002G216700 | PF00010 |
| 54 | 1 | Phvul.002G216700.2 | Phvul.002G216700 | Phvul.002G216700 | PF00010 |
| 55 | 1 | Phvul.002G243300.1 | Phvul.002G243300 | Phvul.002G243300 | PF00657 |
| 56 | 1 | Phvul.002G243300.1 | Phvul.002G243300 | Phvul.002G243300 | PF00657 |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | | |
|----|--------------------|------------------|------------------|--------------|
| 1 | Phvul.002G253200.1 | Phvul.002G253200 | Phvul.002G253200 | PF00415 |
| 2 | Phvul.002G253200.1 | Phvul.002G253200 | Phvul.002G253200 | PF00415 |
| 3 | Phvul.002G253200.1 | Phvul.002G253200 | Phvul.002G253200 | PF00415 |
| 4 | Phvul.002G253200.1 | Phvul.002G253200 | Phvul.002G253200 | PF00415 |
| 5 | Phvul.002G253200.1 | Phvul.002G253200 | Phvul.002G253200 | PF00415 |
| 6 | Phvul.002G283800.1 | Phvul.002G283800 | Phvul.002G283800 | PF03083 |
| 7 | Phvul.002G283800.1 | Phvul.002G283800 | Phvul.002G283800 | PF03083 |
| 8 | Phvul.002G283800.1 | Phvul.002G283800 | Phvul.002G283800 | PF03083 |
| 9 | Phvul.002G283800.1 | Phvul.002G283800 | Phvul.002G283800 | PF03083 |
| 10 | Phvul.002G290904.1 | Phvul.002G290904 | Phvul.002G290904 | PF11940 |
| 11 | Phvul.002G290904.1 | Phvul.002G290904 | Phvul.002G290904 | PF11940 |
| 12 | Phvul.002G309100.1 | Phvul.002G309100 | Phvul.002G309100 | PF00481 |
| 13 | Phvul.002G309100.1 | Phvul.002G309100 | Phvul.002G309100 | PF00481 |
| 14 | Phvul.002G320900.1 | Phvul.002G320900 | Phvul.002G320900 | PF03152 |
| 15 | Phvul.002G320900.1 | Phvul.002G320900 | Phvul.002G320900 | PF03152 |
| 16 | Phvul.002G320900.1 | Phvul.002G320900 | Phvul.002G320900 | PF03152 |
| 17 | Phvul.002G320900.1 | Phvul.002G320900 | Phvul.002G320900 | PF03152 |
| 18 | Phvul.002G329900.2 | Phvul.002G329900 | Phvul.002G329900 | PF00153 |
| 19 | Phvul.002G329900.1 | Phvul.002G329900 | Phvul.002G329900 | PF00153 |
| 20 | Phvul.002G329900.2 | Phvul.002G329900 | Phvul.002G329900 | PF00153 |
| 21 | Phvul.002G329900.1 | Phvul.002G329900 | Phvul.002G329900 | PF00153 |
| 22 | Phvul.002G329900.2 | Phvul.002G329900 | Phvul.002G329900 | PF00153 |
| 23 | Phvul.002G329900.1 | Phvul.002G329900 | Phvul.002G329900 | PF00153 |
| 24 | Phvul.002G329900.1 | Phvul.002G329900 | Phvul.002G329900 | PF00153 |
| 25 | Phvul.002G329900.2 | Phvul.002G329900 | Phvul.002G329900 | PF00153 |
| 26 | Phvul.002G329900.1 | Phvul.002G329900 | Phvul.002G329900 | PF00153 |
| 27 | Phvul.002G329900.2 | Phvul.002G329900 | Phvul.002G329900 | PF00153 |
| 28 | Phvul.002G329900.1 | Phvul.002G329900 | Phvul.002G329900 | PF00153 |
| 29 | Phvul.002G329900.2 | Phvul.002G329900 | Phvul.002G329900 | PF00153 |
| 30 | Phvul.002G329900.1 | Phvul.002G329900 | Phvul.002G329900 | PF00153 |
| 31 | Phvul.002G329900.2 | Phvul.002G329900 | Phvul.002G329900 | PF00153 |
| 32 | Phvul.002G329900.1 | Phvul.002G329900 | Phvul.002G329900 | PF00153 |
| 33 | Phvul.002G329900.1 | Phvul.002G329900 | Phvul.002G329900 | PF00153 |
| 34 | Phvul.003G032300.1 | Phvul.003G032300 | Phvul.003G032300 | PF15628 |
| 35 | Phvul.003G032300.1 | Phvul.003G032300 | Phvul.003G032300 | PF15628 |
| 36 | Phvul.003G057700.1 | Phvul.003G057700 | Phvul.003G057700 | PF13641 |
| 37 | Phvul.003G057700.1 | Phvul.003G057700 | Phvul.003G057700 | PF13641 |
| 38 | Phvul.003G078900.1 | Phvul.003G078900 | Phvul.003G078900 | 0 |
| 39 | Phvul.003G078900.1 | Phvul.003G078900 | Phvul.003G078900 | 0 |
| 40 | Phvul.003G078900.1 | Phvul.003G078900 | Phvul.003G078900 | 0 |
| 41 | Phvul.003G078900.1 | Phvul.003G078900 | Phvul.003G078900 | 0 |
| 42 | Phvul.003G137000.1 | Phvul.003G137000 | Phvul.003G137000 | PF02140,PF01 |
| 43 | Phvul.003G137000.1 | Phvul.003G137000 | Phvul.003G137000 | PF02140,PF01 |
| 44 | Phvul.003G137000.1 | Phvul.003G137000 | Phvul.003G137000 | PF02140,PF01 |
| 45 | Phvul.003G137000.1 | Phvul.003G137000 | Phvul.003G137000 | PF02140,PF01 |
| 46 | Phvul.003G247200.2 | Phvul.003G247200 | Phvul.003G247200 | PF05659,PF00 |
| 47 | Phvul.003G247200.1 | Phvul.003G247200 | Phvul.003G247200 | PF05659,PF00 |
| 48 | Phvul.003G247200.2 | Phvul.003G247200 | Phvul.003G247200 | PF05659,PF00 |
| 49 | Phvul.003G247200.1 | Phvul.003G247200 | Phvul.003G247200 | PF05659,PF00 |
| 50 | Phvul.003G247200.2 | Phvul.003G247200 | Phvul.003G247200 | PF05659,PF00 |
| 51 | Phvul.003G247200.1 | Phvul.003G247200 | Phvul.003G247200 | PF05659,PF00 |
| 52 | Phvul.003G247200.2 | Phvul.003G247200 | Phvul.003G247200 | PF05659,PF00 |
| 53 | Phvul.003G247200.1 | Phvul.003G247200 | Phvul.003G247200 | PF05659,PF00 |
| 54 | Phvul.003G247200.2 | Phvul.003G247200 | Phvul.003G247200 | PF05659,PF00 |
| 55 | Phvul.003G247200.1 | Phvul.003G247200 | Phvul.003G247200 | PF05659,PF00 |
| 56 | Phvul.003G247200.2 | Phvul.003G247200 | Phvul.003G247200 | PF05659,PF00 |
| 57 | Phvul.003G247200.1 | Phvul.003G247200 | Phvul.003G247200 | PF05659,PF00 |
| 58 | Phvul.003G247200.2 | Phvul.003G247200 | Phvul.003G247200 | PF05659,PF00 |
| 59 | Phvul.003G247200.2 | Phvul.003G247200 | Phvul.003G247200 | PF05659,PF00 |
| 60 | | | | |

| | | | | | |
|----|---|--------------------|------------------|------------------|--------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | | | | | |
| 4 | 1 | Phvul.003G247200.1 | Phvul.003G247200 | Phvul.003G247200 | PF05659,PF00 |
| 5 | 1 | Phvul.003G280100.2 | Phvul.003G280100 | Phvul.003G280100 | PF03141 |
| 6 | 1 | Phvul.003G280100.2 | Phvul.003G280100 | Phvul.003G280100 | PF03141 |
| 7 | 1 | Phvul.003G294601.1 | Phvul.003G294601 | Phvul.003G294601 | PF00076 |
| 8 | 1 | Phvul.003G294601.1 | Phvul.003G294601 | Phvul.003G294601 | PF00076 |
| 9 | 1 | Phvul.003G294601.1 | Phvul.003G294601 | Phvul.003G294601 | PF00076 |
| 10 | 1 | Phvul.003G294601.1 | Phvul.003G294601 | Phvul.003G294601 | PF00076 |
| 11 | 1 | Phvul.003G294601.1 | Phvul.003G294601 | Phvul.003G294601 | PF00076 |
| 12 | 1 | Phvul.003G294800.4 | Phvul.003G294800 | Phvul.003G294800 | PF00076 |
| 13 | 1 | Phvul.003G294800.3 | Phvul.003G294800 | Phvul.003G294800 | PF00076 |
| 14 | 1 | Phvul.003G294800.4 | Phvul.003G294800 | Phvul.003G294800 | PF00076 |
| 15 | 1 | Phvul.003G294800.4 | Phvul.003G294800 | Phvul.003G294800 | PF00076 |
| 16 | 1 | Phvul.003G294800.3 | Phvul.003G294800 | Phvul.003G294800 | PF00076 |
| 17 | 1 | Phvul.003G294800.4 | Phvul.003G294800 | Phvul.003G294800 | PF00076 |
| 18 | 1 | Phvul.003G294800.3 | Phvul.003G294800 | Phvul.003G294800 | PF00076 |
| 19 | 1 | Phvul.003G294800.4 | Phvul.003G294800 | Phvul.003G294800 | PF00076 |
| 20 | 1 | Phvul.003G294800.4 | Phvul.003G294800 | Phvul.003G294800 | PF00076 |
| 21 | 1 | Phvul.003G294800.3 | Phvul.003G294800 | Phvul.003G294800 | PF00076 |
| 22 | 1 | Phvul.003G294800.3 | Phvul.003G294800 | Phvul.003G294800 | PF00076 |
| 23 | 1 | Phvul.004G032100.1 | Phvul.004G032100 | Phvul.004G032100 | 0 |
| 24 | 1 | Phvul.004G032100.1 | Phvul.004G032100 | Phvul.004G032100 | 0 |
| 25 | 1 | Phvul.004G032100.1 | Phvul.004G032100 | Phvul.004G032100 | 0 |
| 26 | 1 | Phvul.004G032100.1 | Phvul.004G032100 | Phvul.004G032100 | 0 |
| 27 | 1 | Phvul.004G032100.1 | Phvul.004G032100 | Phvul.004G032100 | 0 |
| 28 | 1 | Phvul.004G044800.1 | Phvul.004G044800 | Phvul.004G044800 | PF08263,PF00 |
| 29 | 1 | Phvul.004G044800.1 | Phvul.004G044800 | Phvul.004G044800 | PF08263,PF00 |
| 30 | 1 | Phvul.004G050550.1 | Phvul.004G050550 | Phvul.004G050550 | PF13650 |
| 31 | 1 | Phvul.004G050550.1 | Phvul.004G050550 | Phvul.004G050550 | PF13650 |
| 32 | 1 | Phvul.004G050550.1 | Phvul.004G050550 | Phvul.004G050550 | PF13650 |
| 33 | 1 | Phvul.004G050550.1 | Phvul.004G050550 | Phvul.004G050550 | PF13650 |
| 34 | 1 | Phvul.004G050550.1 | Phvul.004G050550 | Phvul.004G050550 | PF13650 |
| 35 | 1 | Phvul.004G173101.1 | Phvul.004G173101 | Phvul.004G173101 | PF06376 |
| 36 | 1 | Phvul.004G173101.1 | Phvul.004G173101 | Phvul.004G173101 | PF06376 |
| 37 | 1 | Phvul.004G173101.1 | Phvul.004G173101 | Phvul.004G173101 | PF06376 |
| 38 | 1 | Phvul.004G173101.1 | Phvul.004G173101 | Phvul.004G173101 | PF06376 |
| 39 | 1 | Phvul.004G173101.1 | Phvul.004G173101 | Phvul.004G173101 | PF06376 |
| 40 | 1 | Phvul.005G006400.1 | Phvul.005G006400 | Phvul.005G006400 | PF12796 |
| 41 | 1 | Phvul.005G006400.1 | Phvul.005G006400 | Phvul.005G006400 | PF12796 |
| 42 | 1 | Phvul.005G006400.1 | Phvul.005G006400 | Phvul.005G006400 | PF12796 |
| 43 | 1 | Phvul.005G006400.1 | Phvul.005G006400 | Phvul.005G006400 | PF12796 |
| 44 | 1 | Phvul.005G006400.1 | Phvul.005G006400 | Phvul.005G006400 | PF12796 |
| 45 | 1 | Phvul.005G014300.2 | Phvul.005G014300 | Phvul.005G014300 | PF00808 |
| 46 | 1 | Phvul.005G056400.1 | Phvul.005G056400 | Phvul.005G056400 | PF00651 |
| 47 | 1 | Phvul.005G095300.1 | Phvul.005G095300 | Phvul.005G095300 | PF00311 |
| 48 | 1 | Phvul.005G100300.1 | Phvul.005G100300 | Phvul.005G100300 | PF10551 |
| 49 | 1 | Phvul.005G116100.2 | Phvul.005G116100 | Phvul.005G116100 | PF01738 |
| 50 | 1 | Phvul.005G116100.1 | Phvul.005G116100 | Phvul.005G116100 | PF01738 |
| 51 | 1 | Phvul.005G116100.2 | Phvul.005G116100 | Phvul.005G116100 | PF01738 |
| 52 | 1 | Phvul.005G116100.1 | Phvul.005G116100 | Phvul.005G116100 | PF01738 |
| 53 | 1 | Phvul.005G116100.2 | Phvul.005G116100 | Phvul.005G116100 | PF01738 |
| 54 | 1 | Phvul.005G116100.1 | Phvul.005G116100 | Phvul.005G116100 | PF01738 |
| 55 | 1 | Phvul.005G116100.2 | Phvul.005G116100 | Phvul.005G116100 | PF01738 |
| 56 | 1 | Phvul.005G116100.1 | Phvul.005G116100 | Phvul.005G116100 | PF01738 |
| 57 | 1 | Phvul.005G116100.2 | Phvul.005G116100 | Phvul.005G116100 | PF01738 |
| 58 | 1 | Phvul.005G116100.1 | Phvul.005G116100 | Phvul.005G116100 | PF01738 |
| 59 | 1 | Phvul.005G116100.1 | Phvul.005G116100 | Phvul.005G116100 | PF01738 |
| 60 | | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | | |
|---|--------------------|------------------|------------------|--------------|
| 1 | Phvul.005G116100.2 | Phvul.005G116100 | Phvul.005G116100 | PF01738 |
| 1 | Phvul.005G116100.1 | Phvul.005G116100 | Phvul.005G116100 | PF01738 |
| 1 | Phvul.005G130100.1 | Phvul.005G130100 | Phvul.005G130100 | 0 |
| 1 | Phvul.005G130100.1 | Phvul.005G130100 | Phvul.005G130100 | 0 |
| 1 | Phvul.006G105800.1 | Phvul.006G105800 | Phvul.006G105800 | PF13499 |
| 1 | Phvul.006G113800.2 | Phvul.006G113800 | Phvul.006G113800 | PF14227,PF02 |
| 1 | Phvul.006G113800.1 | Phvul.006G113800 | Phvul.006G113800 | PF14227,PF02 |
| 1 | Phvul.006G113800.2 | Phvul.006G113800 | Phvul.006G113800 | PF14227,PF02 |
| 1 | Phvul.006G113800.1 | Phvul.006G113800 | Phvul.006G113800 | PF14227,PF02 |
| 1 | Phvul.006G113800.2 | Phvul.006G113800 | Phvul.006G113800 | PF14227,PF02 |
| 1 | Phvul.006G113800.1 | Phvul.006G113800 | Phvul.006G113800 | PF14227,PF02 |
| 1 | Phvul.006G113800.2 | Phvul.006G113800 | Phvul.006G113800 | PF14227,PF02 |
| 1 | Phvul.006G113800.1 | Phvul.006G113800 | Phvul.006G113800 | PF14227,PF02 |
| 1 | Phvul.006G121500.1 | Phvul.006G121500 | Phvul.006G121500 | PF00955 |
| 1 | Phvul.006G121500.2 | Phvul.006G121500 | Phvul.006G121500 | PF00955 |
| 1 | Phvul.006G121500.1 | Phvul.006G121500 | Phvul.006G121500 | PF00955 |
| 1 | Phvul.006G121500.2 | Phvul.006G121500 | Phvul.006G121500 | PF00955 |
| 1 | Phvul.006G121500.1 | Phvul.006G121500 | Phvul.006G121500 | PF00955 |
| 1 | Phvul.006G121500.1 | Phvul.006G121500 | Phvul.006G121500 | PF00955 |
| 1 | Phvul.006G121500.1 | Phvul.006G121500 | Phvul.006G121500 | PF00955 |
| 1 | Phvul.006G121500.1 | Phvul.006G121500 | Phvul.006G121500 | PF00955 |
| 2 | Phvul.006G158900.1 | Phvul.006G158900 | Phvul.006G158900 | PF15365 |
| 1 | Phvul.006G168154.1 | Phvul.006G168154 | Phvul.006G168154 | PF00450 |
| 1 | Phvul.006G168154.2 | Phvul.006G168154 | Phvul.006G168154 | PF00450 |
| 1 | Phvul.006G168154.1 | Phvul.006G168154 | Phvul.006G168154 | PF00450 |
| 1 | Phvul.006G168154.2 | Phvul.006G168154 | Phvul.006G168154 | PF00450 |
| 1 | Phvul.006G193700.1 | Phvul.006G193700 | Phvul.006G193700 | PF04641,PF15 |
| 1 | Phvul.006G193700.1 | Phvul.006G193700 | Phvul.006G193700 | PF04641,PF15 |
| 1 | Phvul.007G012500.1 | Phvul.007G012500 | Phvul.007G012500 | PF00326,PF02 |
| 1 | Phvul.007G012500.1 | Phvul.007G012500 | Phvul.007G012500 | PF00326,PF02 |
| 1 | Phvul.007G012500.1 | Phvul.007G012500 | Phvul.007G012500 | PF00326,PF02 |
| 1 | Phvul.007G012500.1 | Phvul.007G012500 | Phvul.007G012500 | PF00326,PF02 |
| 1 | Phvul.007G015000.1 | Phvul.007G015000 | Phvul.007G015000 | PF03634 |
| 1 | Phvul.007G015000.1 | Phvul.007G015000 | Phvul.007G015000 | PF03634 |
| 1 | Phvul.007G034000.1 | Phvul.007G034000 | Phvul.007G034000 | PF03034 |
| 1 | Phvul.007G051100.1 | Phvul.007G051100 | Phvul.007G051100 | PF01657,PF07 |
| 1 | Phvul.007G051100.1 | Phvul.007G051100 | Phvul.007G051100 | PF01657,PF07 |
| 1 | Phvul.007G051100.1 | Phvul.007G051100 | Phvul.007G051100 | PF01657,PF07 |
| 1 | Phvul.007G051100.1 | Phvul.007G051100 | Phvul.007G051100 | PF01657,PF07 |
| 1 | Phvul.007G056600.1 | Phvul.007G056600 | Phvul.007G056600 | PF02727,PF02 |
| 1 | Phvul.007G056600.1 | Phvul.007G056600 | Phvul.007G056600 | PF02727,PF02 |
| 1 | Phvul.007G056600.1 | Phvul.007G056600 | Phvul.007G056600 | PF02727,PF02 |
| 1 | Phvul.007G056600.1 | Phvul.007G056600 | Phvul.007G056600 | PF02727,PF02 |

| | | | | | |
|----|---|--------------------|------------------|------------------|--------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | | | | | |
| 4 | 1 | Phvul.007G058400.1 | Phvul.007G058400 | Phvul.007G058400 | PF04570 |
| 5 | 1 | Phvul.007G058400.2 | Phvul.007G058400 | Phvul.007G058400 | PF04570 |
| 6 | 1 | Phvul.007G058400.1 | Phvul.007G058400 | Phvul.007G058400 | PF04570 |
| 7 | 1 | Phvul.007G058400.2 | Phvul.007G058400 | Phvul.007G058400 | PF04570 |
| 8 | 1 | Phvul.007G058400.1 | Phvul.007G058400 | Phvul.007G058400 | PF04570 |
| 9 | 1 | Phvul.007G058400.2 | Phvul.007G058400 | Phvul.007G058400 | PF04570 |
| 10 | 1 | Phvul.007G058400.1 | Phvul.007G058400 | Phvul.007G058400 | PF04570 |
| 11 | 1 | Phvul.007G058400.2 | Phvul.007G058400 | Phvul.007G058400 | PF04570 |
| 12 | 1 | Phvul.007G058400.1 | Phvul.007G058400 | Phvul.007G058400 | PF04570 |
| 13 | 1 | Phvul.007G058400.2 | Phvul.007G058400 | Phvul.007G058400 | PF04570 |
| 14 | 1 | Phvul.007G064700.1 | Phvul.007G064700 | Phvul.007G064700 | PF12695 |
| 15 | 1 | Phvul.007G064700.1 | Phvul.007G064700 | Phvul.007G064700 | PF12695 |
| 16 | 1 | Phvul.007G064700.1 | Phvul.007G064700 | Phvul.007G064700 | PF12695 |
| 17 | 1 | Phvul.007G064700.1 | Phvul.007G064700 | Phvul.007G064700 | PF12695 |
| 18 | 1 | Phvul.007G064700.1 | Phvul.007G064700 | Phvul.007G064700 | PF12695 |
| 19 | 1 | Phvul.007G064700.1 | Phvul.007G064700 | Phvul.007G064700 | PF12695 |
| 20 | 1 | Phvul.007G073800.1 | Phvul.007G073800 | Phvul.007G073800 | PF01794,PF08 |
| 21 | 1 | Phvul.007G073800.1 | Phvul.007G073800 | Phvul.007G073800 | PF01794,PF08 |
| 22 | 1 | Phvul.007G073800.1 | Phvul.007G073800 | Phvul.007G073800 | PF01794,PF08 |
| 23 | 1 | Phvul.007G073800.1 | Phvul.007G073800 | Phvul.007G073800 | PF01794,PF08 |
| 24 | 1 | Phvul.007G073800.1 | Phvul.007G073800 | Phvul.007G073800 | PF01794,PF08 |
| 25 | 1 | Phvul.007G099300.1 | Phvul.007G099300 | Phvul.007G099300 | PF12646 |
| 26 | 1 | Phvul.007G099300.1 | Phvul.007G099300 | Phvul.007G099300 | PF12646 |
| 27 | 1 | Phvul.007G099300.1 | Phvul.007G099300 | Phvul.007G099300 | PF12646 |
| 28 | 1 | Phvul.007G099300.1 | Phvul.007G099300 | Phvul.007G099300 | PF12646 |
| 29 | 1 | Phvul.007G099300.1 | Phvul.007G099300 | Phvul.007G099300 | PF12646 |
| 30 | 1 | Phvul.007G107200.1 | Phvul.007G107200 | Phvul.007G107200 | PF00043,PF02 |
| 31 | 1 | Phvul.007G107200.1 | Phvul.007G107200 | Phvul.007G107200 | PF00043,PF02 |
| 32 | 1 | Phvul.007G107200.1 | Phvul.007G107200 | Phvul.007G107200 | PF00043,PF02 |
| 33 | 1 | Phvul.007G107200.1 | Phvul.007G107200 | Phvul.007G107200 | PF00043,PF02 |
| 34 | 1 | Phvul.007G107200.1 | Phvul.007G107200 | Phvul.007G107200 | PF00043,PF02 |
| 35 | 1 | Phvul.007G182300.2 | Phvul.007G182300 | Phvul.007G182300 | 0 |
| 36 | 1 | Phvul.007G182300.2 | Phvul.007G182300 | Phvul.007G182300 | 0 |
| 37 | 1 | Phvul.007G182300.2 | Phvul.007G182300 | Phvul.007G182300 | 0 |
| 38 | 1 | Phvul.007G182300.2 | Phvul.007G182300 | Phvul.007G182300 | 0 |
| 39 | 1 | Phvul.007G182300.2 | Phvul.007G182300 | Phvul.007G182300 | 0 |
| 40 | 1 | Phvul.007G189000.1 | Phvul.007G189000 | Phvul.007G189000 | 0 |
| 41 | 1 | Phvul.007G189000.1 | Phvul.007G189000 | Phvul.007G189000 | 0 |
| 42 | 1 | Phvul.007G189000.1 | Phvul.007G189000 | Phvul.007G189000 | 0 |
| 43 | 1 | Phvul.007G204300.2 | Phvul.007G204300 | Phvul.007G204300 | PF00069 |
| 44 | 1 | Phvul.007G204300.1 | Phvul.007G204300 | Phvul.007G204300 | PF00069 |
| 45 | 1 | Phvul.007G204300.2 | Phvul.007G204300 | Phvul.007G204300 | PF00069 |
| 46 | 1 | Phvul.007G204300.1 | Phvul.007G204300 | Phvul.007G204300 | PF00069 |
| 47 | 1 | Phvul.007G204300.2 | Phvul.007G204300 | Phvul.007G204300 | PF00069 |
| 48 | 1 | Phvul.007G204300.1 | Phvul.007G204300 | Phvul.007G204300 | PF00069 |
| 49 | 1 | Phvul.007G204300.2 | Phvul.007G204300 | Phvul.007G204300 | PF00069 |
| 50 | 1 | Phvul.007G204300.1 | Phvul.007G204300 | Phvul.007G204300 | PF00069 |
| 51 | 1 | Phvul.007G204300.2 | Phvul.007G204300 | Phvul.007G204300 | PF00069 |
| 52 | 1 | Phvul.007G204300.1 | Phvul.007G204300 | Phvul.007G204300 | PF00069 |
| 53 | 1 | Phvul.007G210400.1 | Phvul.007G210400 | Phvul.007G210400 | PF04043,PF01 |
| 54 | 1 | Phvul.007G275700.1 | Phvul.007G275700 | Phvul.007G275700 | PF00045 |
| 55 | 1 | Phvul.007G275700.1 | Phvul.007G275700 | Phvul.007G275700 | PF00045 |
| 56 | 1 | Phvul.007G276200.1 | Phvul.007G276200 | Phvul.007G276200 | PF00045 |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | |
|----------------------|------------------|------------------|--------------|
| 1 Phvul.007G276200.1 | Phvul.007G276200 | Phvul.007G276200 | PF00045 |
| 1 Phvul.007G276300.1 | Phvul.007G276300 | Phvul.007G276300 | PF00045 |
| 1 Phvul.007G276300.1 | Phvul.007G276300 | Phvul.007G276300 | PF00045 |
| 1 Phvul.008G003900.1 | Phvul.008G003900 | Phvul.008G003900 | 0 |
| 1 Phvul.008G003900.1 | Phvul.008G003900 | Phvul.008G003900 | 0 |
| 1 Phvul.008G003900.1 | Phvul.008G003900 | Phvul.008G003900 | 0 |
| 1 Phvul.008G003900.1 | Phvul.008G003900 | Phvul.008G003900 | 0 |
| 1 Phvul.008G008300.6 | Phvul.008G008300 | Phvul.008G008300 | 0 |
| 1 Phvul.008G008300.3 | Phvul.008G008300 | Phvul.008G008300 | 0 |
| 1 Phvul.008G008300.5 | Phvul.008G008300 | Phvul.008G008300 | 0 |
| 1 Phvul.008G008300.4 | Phvul.008G008300 | Phvul.008G008300 | 0 |
| 1 Phvul.008G008300.2 | Phvul.008G008300 | Phvul.008G008300 | 0 |
| 1 Phvul.008G012100.1 | Phvul.008G012100 | Phvul.008G012100 | PF02969,PF07 |
| 1 Phvul.008G012100.2 | Phvul.008G012100 | Phvul.008G012100 | PF02969,PF07 |
| 1 Phvul.008G048200.1 | Phvul.008G048200 | Phvul.008G048200 | PF02536 |
| 1 Phvul.008G069000.1 | Phvul.008G069000 | Phvul.008G069000 | 0 |
| 1 Phvul.008G069000.1 | Phvul.008G069000 | Phvul.008G069000 | 0 |
| 1 Phvul.008G069000.1 | Phvul.008G069000 | Phvul.008G069000 | 0 |
| 1 Phvul.008G069000.1 | Phvul.008G069000 | Phvul.008G069000 | 0 |
| 2 Phvul.008G071966.1 | Phvul.008G071966 | Phvul.008G071966 | 0 |
| 2 Phvul.008G071966.1 | Phvul.008G071966 | Phvul.008G071966 | 0 |
| 2 Phvul.008G071966.1 | Phvul.008G071966 | Phvul.008G071966 | 0 |
| 2 Phvul.008G071966.1 | Phvul.008G071966 | Phvul.008G071966 | 0 |
| 2 Phvul.008G093200.3 | Phvul.008G093200 | Phvul.008G093200 | PF00560,PF08 |
| 2 Phvul.008G093200.2 | Phvul.008G093200 | Phvul.008G093200 | PF00560,PF08 |
| 2 Phvul.008G093200.1 | Phvul.008G093200 | Phvul.008G093200 | PF00560,PF08 |
| 2 Phvul.008G093200.3 | Phvul.008G093200 | Phvul.008G093200 | PF00560,PF08 |
| 2 Phvul.008G093200.2 | Phvul.008G093200 | Phvul.008G093200 | PF00560,PF08 |
| 2 Phvul.008G093200.1 | Phvul.008G093200 | Phvul.008G093200 | PF00560,PF08 |
| 1 Phvul.008G110000.1 | Phvul.008G110000 | Phvul.008G110000 | PF05056 |
| 1 Phvul.008G110000.1 | Phvul.008G110000 | Phvul.008G110000 | PF05056 |
| 1 Phvul.008G110100.1 | Phvul.008G110100 | Phvul.008G110100 | PF05056 |
| 1 Phvul.008G110400.1 | Phvul.008G110400 | Phvul.008G110400 | PF05056 |
| 1 Phvul.008G110400.1 | Phvul.008G110400 | Phvul.008G110400 | PF05056 |
| 1 Phvul.008G118900.1 | Phvul.008G118900 | Phvul.008G118900 | PF00026 |
| 1 Phvul.008G118900.1 | Phvul.008G118900 | Phvul.008G118900 | PF00026 |
| 1 Phvul.008G157900.1 | Phvul.008G157900 | Phvul.008G157900 | 0 |
| 1 Phvul.008G157900.1 | Phvul.008G157900 | Phvul.008G157900 | 0 |
| 1 Phvul.008G157900.1 | Phvul.008G157900 | Phvul.008G157900 | 0 |
| 1 Phvul.008G157900.1 | Phvul.008G157900 | Phvul.008G157900 | 0 |
| 1 Phvul.008G206400.5 | Phvul.008G206400 | Phvul.008G206400 | PF01575 |
| 1 Phvul.008G206400.1 | Phvul.008G206400 | Phvul.008G206400 | PF01575 |
| 1 Phvul.008G206400.5 | Phvul.008G206400 | Phvul.008G206400 | PF01575 |

| | | | | | |
|----|---|--------------------|------------------|------------------|--------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | | | | | |
| 4 | 1 | Phvul.008G206400.1 | Phvul.008G206400 | Phvul.008G206400 | PF01575 |
| 5 | 1 | Phvul.008G225900.1 | Phvul.008G225900 | Phvul.008G225900 | 0 |
| 6 | 1 | Phvul.008G225900.1 | Phvul.008G225900 | Phvul.008G225900 | 0 |
| 7 | 1 | Phvul.008G225900.1 | Phvul.008G225900 | Phvul.008G225900 | 0 |
| 8 | | | | | |
| 9 | 1 | Phvul.008G225900.1 | Phvul.008G225900 | Phvul.008G225900 | 0 |
| 10 | 1 | Phvul.008G227600.1 | Phvul.008G227600 | Phvul.008G227600 | PF01490 |
| 11 | 1 | Phvul.008G227600.1 | Phvul.008G227600 | Phvul.008G227600 | PF01490 |
| 12 | | | | | |
| 13 | 1 | Phvul.008G227600.1 | Phvul.008G227600 | Phvul.008G227600 | PF01490 |
| 14 | 1 | Phvul.008G227600.1 | Phvul.008G227600 | Phvul.008G227600 | PF01490 |
| 15 | 1 | Phvul.008G274900.1 | Phvul.008G274900 | Phvul.008G274900 | PF00076 |
| 16 | 1 | Phvul.008G274900.2 | Phvul.008G274900 | Phvul.008G274900 | PF00076 |
| 17 | 1 | Phvul.008G274900.3 | Phvul.008G274900 | Phvul.008G274900 | PF00076 |
| 18 | | | | | |
| 19 | 1 | Phvul.008G282700.1 | Phvul.008G282700 | Phvul.008G282700 | PF02628 |
| 20 | 1 | Phvul.008G282700.1 | Phvul.008G282700 | Phvul.008G282700 | PF02628 |
| 21 | | | | | |
| 22 | 1 | Phvul.009G106700.1 | Phvul.009G106700 | Phvul.009G106700 | PF00249 |
| 23 | 1 | Phvul.009G121300.1 | Phvul.009G121300 | Phvul.009G121300 | PF15413,PF01 |
| 24 | 1 | Phvul.009G121300.2 | Phvul.009G121300 | Phvul.009G121300 | PF15413,PF01 |
| 25 | 1 | Phvul.009G121300.1 | Phvul.009G121300 | Phvul.009G121300 | PF15413,PF01 |
| 26 | 1 | Phvul.009G121300.2 | Phvul.009G121300 | Phvul.009G121300 | PF15413,PF01 |
| 27 | 1 | Phvul.009G173100.1 | Phvul.009G173100 | Phvul.009G173100 | PF00069 |
| 28 | 1 | Phvul.009G173100.3 | Phvul.009G173100 | Phvul.009G173100 | PF00069 |
| 29 | | | | | |
| 30 | 1 | Phvul.009G173100.1 | Phvul.009G173100 | Phvul.009G173100 | PF00069 |
| 31 | 1 | Phvul.009G173100.3 | Phvul.009G173100 | Phvul.009G173100 | PF00069 |
| 32 | | | | | |
| 33 | 1 | Phvul.009G232500.1 | Phvul.009G232500 | Phvul.009G232500 | PF01301 |
| 34 | 1 | Phvul.009G232500.1 | Phvul.009G232500 | Phvul.009G232500 | PF01301 |
| 35 | 1 | Phvul.009G259000.1 | Phvul.009G259000 | Phvul.009G259000 | PF08100,PF00 |
| 36 | 1 | Phvul.009G259000.1 | Phvul.009G259000 | Phvul.009G259000 | PF08100,PF00 |
| 37 | 1 | Phvul.009G259000.1 | Phvul.009G259000 | Phvul.009G259000 | PF08100,PF00 |
| 38 | 1 | Phvul.009G259000.1 | Phvul.009G259000 | Phvul.009G259000 | PF08100,PF00 |
| 39 | | | | | |
| 40 | 1 | Phvul.010G032400.1 | Phvul.010G032400 | Phvul.010G032400 | 0 |
| 41 | 1 | Phvul.010G032400.1 | Phvul.010G032400 | Phvul.010G032400 | 0 |
| 42 | 1 | Phvul.010G032400.1 | Phvul.010G032400 | Phvul.010G032400 | 0 |
| 43 | 1 | Phvul.010G032400.1 | Phvul.010G032400 | Phvul.010G032400 | 0 |
| 44 | 1 | Phvul.010G043700.5 | Phvul.010G043700 | Phvul.010G043700 | PF02847,PF02 |
| 45 | 1 | Phvul.010G043700.6 | Phvul.010G043700 | Phvul.010G043700 | PF02847,PF02 |
| 46 | 1 | Phvul.010G043700.4 | Phvul.010G043700 | Phvul.010G043700 | PF02847,PF02 |
| 47 | 1 | Phvul.010G043700.1 | Phvul.010G043700 | Phvul.010G043700 | PF02847,PF02 |
| 48 | 1 | Phvul.010G043700.3 | Phvul.010G043700 | Phvul.010G043700 | PF02847,PF02 |
| 49 | 1 | Phvul.010G043700.2 | Phvul.010G043700 | Phvul.010G043700 | PF02847,PF02 |
| 50 | 1 | Phvul.010G043700.9 | Phvul.010G043700 | Phvul.010G043700 | PF02847,PF02 |
| 51 | 1 | Phvul.010G043700.8 | Phvul.010G043700 | Phvul.010G043700 | PF02847,PF02 |
| 52 | 1 | Phvul.010G043700.7 | Phvul.010G043700 | Phvul.010G043700 | PF02847,PF02 |
| 53 | 1 | Phvul.010G043700.5 | Phvul.010G043700 | Phvul.010G043700 | PF02847,PF02 |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | | |
|----|----------------------|------------------|------------------|--------------|
| 1 | Phvul.010G043700.6 | Phvul.010G043700 | Phvul.010G043700 | PF02847,PF02 |
| 2 | 1 Phvul.010G043700.4 | Phvul.010G043700 | Phvul.010G043700 | PF02847,PF02 |
| 3 | 1 Phvul.010G043700.1 | Phvul.010G043700 | Phvul.010G043700 | PF02847,PF02 |
| 4 | 1 Phvul.010G043700.3 | Phvul.010G043700 | Phvul.010G043700 | PF02847,PF02 |
| 5 | 1 Phvul.010G043700.2 | Phvul.010G043700 | Phvul.010G043700 | PF02847,PF02 |
| 6 | 1 Phvul.010G043700.9 | Phvul.010G043700 | Phvul.010G043700 | PF02847,PF02 |
| 7 | 1 Phvul.010G043700.8 | Phvul.010G043700 | Phvul.010G043700 | PF02847,PF02 |
| 8 | 1 Phvul.010G043700.7 | Phvul.010G043700 | Phvul.010G043700 | PF02847,PF02 |
| 9 | 1 Phvul.010G070600.1 | Phvul.010G070600 | Phvul.010G070600 | PF00010 |
| 10 | 1 Phvul.010G089200.1 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 11 | 1 Phvul.010G089200.2 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 12 | 2 Phvul.010G089200.1 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 13 | 2 Phvul.010G089200.2 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 14 | 2 Phvul.010G089200.1 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 15 | 2 Phvul.010G089200.2 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 16 | 2 Phvul.010G089200.1 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 17 | 2 Phvul.010G089200.2 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 18 | 2 Phvul.010G089200.1 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 19 | 2 Phvul.010G089200.2 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 20 | 1 Phvul.010G135701.1 | Phvul.010G135701 | Phvul.010G135701 | PF00305 |
| 21 | 1 Phvul.010G135701.1 | Phvul.010G135701 | Phvul.010G135701 | PF00305 |
| 22 | 1 Phvul.010G135701.1 | Phvul.010G135701 | Phvul.010G135701 | PF00305 |
| 23 | 1 Phvul.010G135701.1 | Phvul.010G135701 | Phvul.010G135701 | PF00305 |
| 24 | 1 Phvul.011G013900.1 | Phvul.011G013900 | Phvul.011G013900 | PF00690,PF12 |
| 25 | 1 Phvul.011G013900.1 | Phvul.011G013900 | Phvul.011G013900 | PF00690,PF12 |
| 26 | 1 Phvul.011G013900.1 | Phvul.011G013900 | Phvul.011G013900 | PF00690,PF12 |
| 27 | 1 Phvul.011G013900.1 | Phvul.011G013900 | Phvul.011G013900 | PF00690,PF12 |
| 28 | 2 Phvul.011G050300.1 | Phvul.011G050300 | Phvul.011G050300 | PF02260,PF15 |
| 29 | 2 Phvul.011G050300.2 | Phvul.011G050300 | Phvul.011G050300 | PF02260,PF15 |
| 30 | 2 Phvul.011G050300.1 | Phvul.011G050300 | Phvul.011G050300 | PF02260,PF15 |
| 31 | 2 Phvul.011G050300.2 | Phvul.011G050300 | Phvul.011G050300 | PF02260,PF15 |
| 32 | 1 Phvul.011G061600.1 | Phvul.011G061600 | Phvul.011G061600 | PF05368 |
| 33 | 1 Phvul.011G061600.1 | Phvul.011G061600 | Phvul.011G061600 | PF05368 |
| 34 | 1 Phvul.011G114700.1 | Phvul.011G114700 | Phvul.011G114700 | PF05938 |
| 35 | 1 Phvul.011G123000.1 | Phvul.011G123000 | Phvul.011G123000 | PF05938 |
| 36 | 1 Phvul.011G123701.1 | Phvul.011G123701 | Phvul.011G123701 | 0 |
| 37 | 1 Phvul.011G123701.1 | Phvul.011G123701 | Phvul.011G123701 | 0 |
| 38 | 1 Phvul.011G160800.1 | Phvul.011G160800 | Phvul.011G160800 | PF01112 |
| 39 | 1 Phvul.011G160800.3 | Phvul.011G160800 | Phvul.011G160800 | PF01112 |
| 40 | 1 Phvul.011G160800.2 | Phvul.011G160800 | Phvul.011G160800 | PF01112 |
| 41 | 1 Phvul.011G160800.1 | Phvul.011G160800 | Phvul.011G160800 | PF01112 |
| 42 | 1 Phvul.011G160800.3 | Phvul.011G160800 | Phvul.011G160800 | PF01112 |
| 43 | 1 Phvul.011G160800.2 | Phvul.011G160800 | Phvul.011G160800 | PF01112 |

| | | | | | |
|----|---|--------------------|------------------|------------------|--------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | | | | | |
| 4 | 1 | Phvul.011G160800.1 | Phvul.011G160800 | Phvul.011G160800 | PF01112 |
| 5 | 1 | Phvul.011G160800.3 | Phvul.011G160800 | Phvul.011G160800 | PF01112 |
| 6 | 1 | Phvul.011G160800.2 | Phvul.011G160800 | Phvul.011G160800 | PF01112 |
| 7 | 1 | Phvul.011G160800.1 | Phvul.011G160800 | Phvul.011G160800 | PF01112 |
| 8 | 1 | Phvul.011G160800.3 | Phvul.011G160800 | Phvul.011G160800 | PF01112 |
| 9 | 1 | Phvul.011G160800.3 | Phvul.011G160800 | Phvul.011G160800 | PF01112 |
| 10 | 1 | Phvul.011G160800.2 | Phvul.011G160800 | Phvul.011G160800 | PF01112 |
| 11 | 1 | Phvul.011G202700.1 | Phvul.011G202700 | Phvul.011G202700 | 0 |
| 12 | 1 | Phvul.011G202700.1 | Phvul.011G202700 | Phvul.011G202700 | 0 |
| 13 | 1 | Phvul.011G202700.1 | Phvul.011G202700 | Phvul.011G202700 | 0 |
| 14 | 1 | Phvul.011G202700.1 | Phvul.011G202700 | Phvul.011G202700 | 0 |
| 15 | 1 | Phvul.011G202700.1 | Phvul.011G202700 | Phvul.011G202700 | 0 |
| 16 | 1 | Phvul.L002051.1 | Phvul.L002051 | Phvul.L002051 | PF01434,PF00 |
| 17 | 1 | Phvul.L002051.2 | Phvul.L002051 | Phvul.L002051 | PF01434,PF00 |
| 18 | 1 | Phvul.L002051.1 | Phvul.L002051 | Phvul.L002051 | PF01434,PF00 |
| 19 | 1 | Phvul.L002051.2 | Phvul.L002051 | Phvul.L002051 | PF01434,PF00 |
| 20 | 1 | Phvul.L002051.1 | Phvul.L002051 | Phvul.L002051 | PF01434,PF00 |
| 21 | 1 | Phvul.L002051.2 | Phvul.L002051 | Phvul.L002051 | PF01434,PF00 |
| 22 | 1 | Phvul.L002051.1 | Phvul.L002051 | Phvul.L002051 | PF01434,PF00 |
| 23 | 1 | Phvul.L002051.2 | Phvul.L002051 | Phvul.L002051 | PF01434,PF00 |
| 24 | 1 | Phvul.L002051.1 | Phvul.L002051 | Phvul.L002051 | PF01434,PF00 |
| 25 | 1 | Phvul.L002051.2 | Phvul.L002051 | Phvul.L002051 | PF01434,PF00 |
| 26 | 1 | Phvul.L002537.1 | Phvul.L002537 | Phvul.L002537 | PF16131,PF00 |
| 27 | 2 | Phvul.L002537.1 | Phvul.L002537 | Phvul.L002537 | PF16131,PF00 |
| 28 | 2 | Phvul.L002537.1 | Phvul.L002537 | Phvul.L002537 | PF16131,PF00 |
| 29 | 1 | Phvul.L007343.1 | Phvul.L007343 | Phvul.L007343 | PF07731,PF07 |
| 30 | 1 | Phvul.008G004400.1 | Phvul.008G004400 | Phvul.008G004400 | PF00107,PF16 |
| 31 | 1 | Phvul.008G004400.1 | Phvul.008G004400 | Phvul.008G004400 | PF00107,PF16 |
| 32 | 1 | Phvul.001G020300.1 | Phvul.001G020300 | Phvul.001G020300 | PF01734 |
| 33 | 1 | Phvul.001G020350.1 | Phvul.001G020350 | Phvul.001G020350 | PF01734 |
| 34 | 1 | Phvul.001G022700.1 | Phvul.001G022700 | Phvul.001G022700 | PF03763 |
| 35 | 1 | Phvul.001G022700.1 | Phvul.001G022700 | Phvul.001G022700 | PF03763 |
| 36 | 1 | Phvul.001G022700.1 | Phvul.001G022700 | Phvul.001G022700 | PF03763 |
| 37 | 1 | Phvul.001G022700.1 | Phvul.001G022700 | Phvul.001G022700 | PF03763 |
| 38 | 2 | Phvul.001G036800.1 | Phvul.001G036800 | Phvul.001G036800 | PF08244,PF00 |
| 39 | 1 | Phvul.001G057800.1 | Phvul.001G057800 | Phvul.001G057800 | PF10058 |
| 40 | 1 | Phvul.001G057800.1 | Phvul.001G057800 | Phvul.001G057800 | PF10058 |
| 41 | 2 | Phvul.001G077700.1 | Phvul.001G077700 | Phvul.001G077700 | PF10509,PF00 |
| 42 | 2 | Phvul.001G077700.1 | Phvul.001G077700 | Phvul.001G077700 | PF10509,PF00 |
| 43 | 1 | Phvul.001G097800.1 | Phvul.001G097800 | Phvul.001G097800 | PF16177,PF13 |
| 44 | 1 | Phvul.001G097800.1 | Phvul.001G097800 | Phvul.001G097800 | PF16177,PF13 |
| 45 | 1 | Phvul.001G109300.2 | Phvul.001G109300 | Phvul.001G109300 | PF04153,PF04 |
| 46 | 1 | Phvul.001G109300.1 | Phvul.001G109300 | Phvul.001G109300 | PF04153,PF04 |
| 47 | 1 | Phvul.001G109300.2 | Phvul.001G109300 | Phvul.001G109300 | PF04153,PF04 |
| 48 | 1 | Phvul.001G109300.1 | Phvul.001G109300 | Phvul.001G109300 | PF04153,PF04 |
| 49 | 1 | Phvul.001G114900.1 | Phvul.001G114900 | Phvul.001G114900 | PF01042,PF01 |
| 50 | 1 | Phvul.001G114900.1 | Phvul.001G114900 | Phvul.001G114900 | PF01042,PF01 |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | | |
|----|--------------------|------------------|------------------|--------------|
| 1 | Phvul.001G123000.2 | Phvul.001G123000 | Phvul.001G123000 | PF01055 |
| 2 | Phvul.001G123000.2 | Phvul.001G123000 | Phvul.001G123000 | PF01055 |
| 3 | Phvul.001G134100.2 | Phvul.001G134100 | Phvul.001G134100 | PF00931 |
| 4 | Phvul.001G134100.1 | Phvul.001G134100 | Phvul.001G134100 | PF00931 |
| 5 | Phvul.001G134100.2 | Phvul.001G134100 | Phvul.001G134100 | PF00931 |
| 6 | Phvul.001G134100.1 | Phvul.001G134100 | Phvul.001G134100 | PF00931 |
| 7 | Phvul.001G134100.2 | Phvul.001G134100 | Phvul.001G134100 | PF00931 |
| 8 | Phvul.001G134100.1 | Phvul.001G134100 | Phvul.001G134100 | PF00931 |
| 9 | Phvul.001G134100.2 | Phvul.001G134100 | Phvul.001G134100 | PF00931 |
| 10 | Phvul.001G134100.1 | Phvul.001G134100 | Phvul.001G134100 | PF00931 |
| 11 | Phvul.001G134100.2 | Phvul.001G134100 | Phvul.001G134100 | PF00931 |
| 12 | Phvul.001G134100.1 | Phvul.001G134100 | Phvul.001G134100 | PF00931 |
| 13 | Phvul.001G134100.2 | Phvul.001G134100 | Phvul.001G134100 | PF00931 |
| 14 | Phvul.001G134100.1 | Phvul.001G134100 | Phvul.001G134100 | PF00931 |
| 15 | Phvul.001G159300.1 | Phvul.001G159300 | Phvul.001G159300 | PF03195 |
| 16 | Phvul.001G163900.2 | Phvul.001G163900 | Phvul.001G163900 | PF00249,PF14 |
| 17 | Phvul.001G163900.1 | Phvul.001G163900 | Phvul.001G163900 | PF00249,PF14 |
| 18 | Phvul.001G163900.2 | Phvul.001G163900 | Phvul.001G163900 | PF00249,PF14 |
| 19 | Phvul.001G163900.1 | Phvul.001G163900 | Phvul.001G163900 | PF00249,PF14 |
| 20 | Phvul.001G163900.2 | Phvul.001G163900 | Phvul.001G163900 | PF00249,PF14 |
| 21 | Phvul.001G163900.1 | Phvul.001G163900 | Phvul.001G163900 | PF00249,PF14 |
| 22 | Phvul.001G163900.2 | Phvul.001G163900 | Phvul.001G163900 | PF00249,PF14 |
| 23 | Phvul.001G163900.1 | Phvul.001G163900 | Phvul.001G163900 | PF00249,PF14 |
| 24 | Phvul.001G163900.2 | Phvul.001G163900 | Phvul.001G163900 | PF00249,PF14 |
| 25 | Phvul.001G163900.1 | Phvul.001G163900 | Phvul.001G163900 | PF00249,PF14 |
| 26 | Phvul.001G163900.2 | Phvul.001G163900 | Phvul.001G163900 | PF00249,PF14 |
| 27 | Phvul.001G163900.1 | Phvul.001G163900 | Phvul.001G163900 | PF00249,PF14 |
| 28 | Phvul.001G214300.2 | Phvul.001G214300 | Phvul.001G214300 | PF05691 |
| 29 | Phvul.001G214300.1 | Phvul.001G214300 | Phvul.001G214300 | PF05691 |
| 30 | Phvul.001G220900.1 | Phvul.001G220900 | Phvul.001G220900 | PF01926,PF11 |
| 31 | Phvul.001G220900.1 | Phvul.001G220900 | Phvul.001G220900 | PF01926,PF11 |
| 32 | Phvul.001G220900.1 | Phvul.001G220900 | Phvul.001G220900 | PF01926,PF11 |
| 33 | Phvul.001G220900.1 | Phvul.001G220900 | Phvul.001G220900 | PF01926,PF11 |
| 34 | Phvul.002G013866.1 | Phvul.002G013866 | Phvul.002G013866 | PF13414 |
| 35 | Phvul.002G013866.1 | Phvul.002G013866 | Phvul.002G013866 | PF13414 |
| 36 | Phvul.002G013866.1 | Phvul.002G013866 | Phvul.002G013866 | PF13414 |
| 37 | Phvul.002G013866.1 | Phvul.002G013866 | Phvul.002G013866 | PF13414 |
| 38 | Phvul.002G043500.1 | Phvul.002G043500 | Phvul.002G043500 | PF14432,PF01 |
| 39 | Phvul.002G043500.1 | Phvul.002G043500 | Phvul.002G043500 | PF14432,PF01 |
| 40 | Phvul.002G043500.1 | Phvul.002G043500 | Phvul.002G043500 | PF14432,PF01 |
| 41 | Phvul.002G043500.1 | Phvul.002G043500 | Phvul.002G043500 | PF14432,PF01 |
| 42 | Phvul.002G058900.1 | Phvul.002G058900 | Phvul.002G058900 | PF13912 |
| 43 | Phvul.002G058900.1 | Phvul.002G058900 | Phvul.002G058900 | PF13912 |
| 44 | Phvul.002G152900.1 | Phvul.002G152900 | Phvul.002G152900 | PF03330,PF01 |
| 45 | Phvul.002G152900.1 | Phvul.002G152900 | Phvul.002G152900 | PF03330,PF01 |
| 46 | Phvul.002G152900.1 | Phvul.002G152900 | Phvul.002G152900 | PF03330,PF01 |
| 47 | Phvul.002G152900.1 | Phvul.002G152900 | Phvul.002G152900 | PF03330,PF01 |
| 48 | Phvul.002G153500.1 | Phvul.002G153500 | Phvul.002G153500 | PF04321 |
| 49 | Phvul.002G243300.1 | Phvul.002G243300 | Phvul.002G243300 | PF00657 |
| 50 | Phvul.002G243300.1 | Phvul.002G243300 | Phvul.002G243300 | PF00657 |
| 51 | Phvul.002G243300.1 | Phvul.002G243300 | Phvul.002G243300 | PF00657 |

| | | | | | |
|----|---|--------------------|------------------|------------------|--------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | | | | | |
| 4 | 1 | Phvul.002G243300.1 | Phvul.002G243300 | Phvul.002G243300 | PF00657 |
| 5 | 1 | Phvul.002G253100.1 | Phvul.002G253100 | Phvul.002G253100 | PF00415 |
| 6 | 1 | Phvul.002G253100.1 | Phvul.002G253100 | Phvul.002G253100 | PF00415 |
| 7 | 1 | Phvul.002G262600.1 | Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00 |
| 8 | 1 | Phvul.002G290000.3 | Phvul.002G290000 | Phvul.002G290000 | PF00010 |
| 9 | 1 | Phvul.002G290000.3 | Phvul.002G290000 | Phvul.002G290000 | PF00010 |
| 10 | 1 | Phvul.003G022200.1 | Phvul.003G022200 | Phvul.003G022200 | PF10508 |
| 11 | 1 | Phvul.003G022200.1 | Phvul.003G022200 | Phvul.003G022200 | PF10508 |
| 12 | 1 | Phvul.003G022200.1 | Phvul.003G022200 | Phvul.003G022200 | PF10508 |
| 13 | 1 | Phvul.003G022200.1 | Phvul.003G022200 | Phvul.003G022200 | PF10508 |
| 14 | 1 | Phvul.003G035400.1 | Phvul.003G035400 | Phvul.003G035400 | PF16863,PF01 |
| 15 | 1 | Phvul.003G035400.1 | Phvul.003G035400 | Phvul.003G035400 | PF16863,PF01 |
| 16 | 1 | Phvul.003G035400.1 | Phvul.003G035400 | Phvul.003G035400 | PF16863,PF01 |
| 17 | 1 | Phvul.003G035400.1 | Phvul.003G035400 | Phvul.003G035400 | PF16863,PF01 |
| 18 | 1 | Phvul.003G035400.1 | Phvul.003G035400 | Phvul.003G035400 | PF16863,PF01 |
| 19 | 1 | Phvul.003G050600.1 | Phvul.003G050600 | Phvul.003G050600 | PF02458 |
| 20 | 1 | Phvul.003G050600.1 | Phvul.003G050600 | Phvul.003G050600 | PF02458 |
| 21 | 1 | Phvul.003G050600.1 | Phvul.003G050600 | Phvul.003G050600 | PF02458 |
| 22 | 1 | Phvul.003G050600.1 | Phvul.003G050600 | Phvul.003G050600 | PF02458 |
| 23 | 1 | Phvul.003G050600.1 | Phvul.003G050600 | Phvul.003G050600 | PF02458 |
| 24 | 1 | Phvul.003G088200.1 | Phvul.003G088200 | Phvul.003G088200 | PF02893,PF00 |
| 25 | 1 | Phvul.003G088200.1 | Phvul.003G088200 | Phvul.003G088200 | PF02893,PF00 |
| 26 | 1 | Phvul.003G088200.1 | Phvul.003G088200 | Phvul.003G088200 | PF02893,PF00 |
| 27 | 1 | Phvul.003G104200.1 | Phvul.003G104200 | Phvul.003G104200 | PF00153 |
| 28 | 1 | Phvul.003G104200.1 | Phvul.003G104200 | Phvul.003G104200 | PF00153 |
| 29 | 1 | Phvul.003G104200.1 | Phvul.003G104200 | Phvul.003G104200 | PF00153 |
| 30 | 1 | Phvul.003G104200.1 | Phvul.003G104200 | Phvul.003G104200 | PF00153 |
| 31 | 1 | Phvul.003G104200.1 | Phvul.003G104200 | Phvul.003G104200 | PF00153 |
| 32 | 1 | Phvul.003G119100.3 | Phvul.003G119100 | Phvul.003G119100 | PF00169,PF06 |
| 33 | 1 | Phvul.003G119100.2 | Phvul.003G119100 | Phvul.003G119100 | PF00169,PF06 |
| 34 | 1 | Phvul.003G119100.1 | Phvul.003G119100 | Phvul.003G119100 | PF00169,PF06 |
| 35 | 1 | Phvul.003G119100.1 | Phvul.003G119100 | Phvul.003G119100 | PF00169,PF06 |
| 36 | 1 | Phvul.003G169700.1 | Phvul.003G169700 | Phvul.003G169700 | PF03016 |
| 37 | 1 | Phvul.003G292000.1 | Phvul.003G292000 | Phvul.003G292000 | PF00852 |
| 38 | 1 | Phvul.004G058600.1 | Phvul.004G058600 | Phvul.004G058600 | PF04193 |
| 39 | 1 | Phvul.004G058600.1 | Phvul.004G058600 | Phvul.004G058600 | PF04193 |
| 40 | 1 | Phvul.004G121666.1 | Phvul.004G121666 | Phvul.004G121666 | PF02874,PF00 |
| 41 | 1 | Phvul.004G121666.1 | Phvul.004G121666 | Phvul.004G121666 | PF02874,PF00 |
| 42 | 1 | Phvul.004G121666.1 | Phvul.004G121666 | Phvul.004G121666 | PF02874,PF00 |
| 43 | 1 | Phvul.004G121666.1 | Phvul.004G121666 | Phvul.004G121666 | PF02874,PF00 |
| 44 | 1 | Phvul.004G121666.1 | Phvul.004G121666 | Phvul.004G121666 | PF02874,PF00 |
| 45 | 1 | Phvul.004G133700.1 | Phvul.004G133700 | Phvul.004G133700 | PF02213,PF02 |
| 46 | 1 | Phvul.004G133700.1 | Phvul.004G133700 | Phvul.004G133700 | PF02213,PF02 |
| 47 | 1 | Phvul.004G133700.1 | Phvul.004G133700 | Phvul.004G133700 | PF02213,PF02 |
| 48 | 1 | Phvul.004G133700.1 | Phvul.004G133700 | Phvul.004G133700 | PF02213,PF02 |
| 49 | 1 | Phvul.004G133700.1 | Phvul.004G133700 | Phvul.004G133700 | PF02213,PF02 |
| 50 | 1 | Phvul.004G133700.1 | Phvul.004G133700 | Phvul.004G133700 | PF02213,PF02 |
| 51 | 1 | Phvul.004G176700.1 | Phvul.004G176700 | Phvul.004G176700 | PF00085 |
| 52 | 1 | Phvul.004G176700.1 | Phvul.004G176700 | Phvul.004G176700 | PF00085 |
| 53 | 1 | Phvul.005G056400.1 | Phvul.005G056400 | Phvul.005G056400 | PF00651 |
| 54 | 1 | Phvul.005G056400.1 | Phvul.005G056400 | Phvul.005G056400 | PF00651 |
| 55 | 1 | Phvul.005G056400.1 | Phvul.005G056400 | Phvul.005G056400 | PF00651 |
| 56 | 1 | Phvul.005G088800.1 | Phvul.005G088800 | Phvul.005G088800 | PF11883,PF08 |
| 57 | 1 | Phvul.005G088800.1 | Phvul.005G088800 | Phvul.005G088800 | PF11883,PF08 |
| 58 | 1 | Phvul.005G095600.1 | Phvul.005G095600 | Phvul.005G095600 | PF13419 |
| 59 | 1 | Phvul.005G097200.3 | Phvul.005G097200 | Phvul.005G097200 | PF03634 |
| 60 | | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | | |
|----|--------------------|------------------|------------------|--------------|
| 1 | Phvul.005G097200.6 | Phvul.005G097200 | Phvul.005G097200 | PF03634 |
| 2 | Phvul.005G097200.5 | Phvul.005G097200 | Phvul.005G097200 | PF03634 |
| 3 | Phvul.005G097200.3 | Phvul.005G097200 | Phvul.005G097200 | PF03634 |
| 4 | Phvul.005G097200.6 | Phvul.005G097200 | Phvul.005G097200 | PF03634 |
| 5 | Phvul.005G097200.5 | Phvul.005G097200 | Phvul.005G097200 | PF03634 |
| 6 | Phvul.005G097200.3 | Phvul.005G097200 | Phvul.005G097200 | PF03634 |
| 7 | Phvul.005G097200.6 | Phvul.005G097200 | Phvul.005G097200 | PF03634 |
| 8 | Phvul.005G097200.5 | Phvul.005G097200 | Phvul.005G097200 | PF03634 |
| 9 | Phvul.005G097200.3 | Phvul.005G097200 | Phvul.005G097200 | PF03634 |
| 10 | Phvul.005G097200.6 | Phvul.005G097200 | Phvul.005G097200 | PF03634 |
| 11 | Phvul.005G097200.5 | Phvul.005G097200 | Phvul.005G097200 | PF03634 |
| 12 | Phvul.005G097200.3 | Phvul.005G097200 | Phvul.005G097200 | PF03634 |
| 13 | Phvul.005G097200.6 | Phvul.005G097200 | Phvul.005G097200 | PF03634 |
| 14 | Phvul.005G097200.5 | Phvul.005G097200 | Phvul.005G097200 | PF03634 |
| 15 | Phvul.005G097200.3 | Phvul.005G097200 | Phvul.005G097200 | PF03634 |
| 16 | Phvul.005G097200.6 | Phvul.005G097200 | Phvul.005G097200 | PF03634 |
| 17 | Phvul.005G097200.5 | Phvul.005G097200 | Phvul.005G097200 | PF03634 |
| 18 | Phvul.005G101400.3 | Phvul.005G101400 | Phvul.005G101400 | PF00122,PF12 |
| 19 | Phvul.005G101400.2 | Phvul.005G101400 | Phvul.005G101400 | PF00122,PF12 |
| 20 | Phvul.005G101400.1 | Phvul.005G101400 | Phvul.005G101400 | PF00122,PF12 |
| 21 | Phvul.005G101400.3 | Phvul.005G101400 | Phvul.005G101400 | PF00122,PF12 |
| 22 | Phvul.005G101400.2 | Phvul.005G101400 | Phvul.005G101400 | PF00122,PF12 |
| 23 | Phvul.005G101400.1 | Phvul.005G101400 | Phvul.005G101400 | PF00122,PF12 |
| 24 | Phvul.005G130100.1 | Phvul.005G130100 | Phvul.005G130100 | 0 |
| 25 | Phvul.005G130100.1 | Phvul.005G130100 | Phvul.005G130100 | 0 |
| 26 | Phvul.005G130100.1 | Phvul.005G130100 | Phvul.005G130100 | 0 |
| 27 | Phvul.005G130100.1 | Phvul.005G130100 | Phvul.005G130100 | 0 |
| 28 | Phvul.005G173200.1 | Phvul.005G173200 | Phvul.005G173200 | 0 |
| 29 | Phvul.005G173200.1 | Phvul.005G173200 | Phvul.005G173200 | 0 |
| 30 | Phvul.005G173200.1 | Phvul.005G173200 | Phvul.005G173200 | 0 |
| 31 | Phvul.005G173200.1 | Phvul.005G173200 | Phvul.005G173200 | 0 |
| 32 | Phvul.006G143300.1 | Phvul.006G143300 | Phvul.006G143300 | 0 |
| 33 | Phvul.006G143300.1 | Phvul.006G143300 | Phvul.006G143300 | 0 |
| 34 | Phvul.006G143300.1 | Phvul.006G143300 | Phvul.006G143300 | 0 |
| 35 | Phvul.006G143300.1 | Phvul.006G143300 | Phvul.006G143300 | 0 |
| 36 | Phvul.006G168163.1 | Phvul.006G168163 | Phvul.006G168163 | PF00450 |
| 37 | Phvul.006G168163.1 | Phvul.006G168163 | Phvul.006G168163 | PF00450 |
| 38 | Phvul.007G035900.2 | Phvul.007G035900 | Phvul.007G035900 | PF00085,PF04 |
| 39 | Phvul.007G035900.2 | Phvul.007G035900 | Phvul.007G035900 | PF00085,PF04 |
| 40 | Phvul.007G035900.2 | Phvul.007G035900 | Phvul.007G035900 | PF00085,PF04 |
| 41 | Phvul.007G035900.2 | Phvul.007G035900 | Phvul.007G035900 | PF00085,PF04 |
| 42 | Phvul.007G069900.3 | Phvul.007G069900 | Phvul.007G069900 | PF13041 |
| 43 | Phvul.007G069900.5 | Phvul.007G069900 | Phvul.007G069900 | PF13041 |
| 44 | Phvul.007G069900.1 | Phvul.007G069900 | Phvul.007G069900 | PF13041 |
| 45 | Phvul.007G069900.4 | Phvul.007G069900 | Phvul.007G069900 | PF13041 |
| 46 | Phvul.007G069900.3 | Phvul.007G069900 | Phvul.007G069900 | PF13041 |
| 47 | Phvul.007G069900.5 | Phvul.007G069900 | Phvul.007G069900 | PF13041 |
| 48 | Phvul.007G069900.1 | Phvul.007G069900 | Phvul.007G069900 | PF13041 |
| 49 | Phvul.007G069900.4 | Phvul.007G069900 | Phvul.007G069900 | PF13041 |

| | | | | |
|----|---|--------------------|------------------|-------------------------------|
| 1 | | | | |
| 2 | | | | |
| 3 | 1 | Phvul.007G069900.3 | Phvul.007G069900 | Phvul.007G069900 PF13041 |
| 4 | 1 | Phvul.007G069900.5 | Phvul.007G069900 | Phvul.007G069900 PF13041 |
| 5 | 1 | Phvul.007G069900.1 | Phvul.007G069900 | Phvul.007G069900 PF13041 |
| 6 | 1 | Phvul.007G069900.4 | Phvul.007G069900 | Phvul.007G069900 PF13041 |
| 7 | 1 | Phvul.007G069900.3 | Phvul.007G069900 | Phvul.007G069900 PF13041 |
| 8 | 1 | Phvul.007G069900.5 | Phvul.007G069900 | Phvul.007G069900 PF13041 |
| 9 | 1 | Phvul.007G069900.1 | Phvul.007G069900 | Phvul.007G069900 PF13041 |
| 10 | 1 | Phvul.007G069900.4 | Phvul.007G069900 | Phvul.007G069900 PF13041 |
| 11 | 1 | Phvul.007G099300.1 | Phvul.007G099300 | Phvul.007G099300 PF12646 |
| 12 | 1 | Phvul.007G114100.1 | Phvul.007G114100 | Phvul.007G114100 PF00628 |
| 13 | 1 | Phvul.007G114100.1 | Phvul.007G114100 | Phvul.007G114100 PF00628 |
| 14 | 1 | Phvul.007G114100.1 | Phvul.007G114100 | Phvul.007G114100 PF00628 |
| 15 | 1 | Phvul.007G114100.1 | Phvul.007G114100 | Phvul.007G114100 PF00628 |
| 16 | 1 | Phvul.007G184600.1 | Phvul.007G184600 | Phvul.007G184600 PF07714,PF14 |
| 17 | 1 | Phvul.007G184600.1 | Phvul.007G184600 | Phvul.007G184600 PF07714,PF14 |
| 18 | 1 | Phvul.007G192300.1 | Phvul.007G192300 | Phvul.007G192300 PF04564,PF00 |
| 19 | 1 | Phvul.007G210400.1 | Phvul.007G210400 | Phvul.007G210400 PF04043,PF01 |
| 20 | 1 | Phvul.007G210400.1 | Phvul.007G210400 | Phvul.007G210400 PF04043,PF01 |
| 21 | 1 | Phvul.007G210400.1 | Phvul.007G210400 | Phvul.007G210400 PF04043,PF01 |
| 22 | 1 | Phvul.007G210400.1 | Phvul.007G210400 | Phvul.007G210400 PF04043,PF01 |
| 23 | 1 | Phvul.007G210400.1 | Phvul.007G210400 | Phvul.007G210400 PF04043,PF01 |
| 24 | 1 | Phvul.007G210400.1 | Phvul.007G210400 | Phvul.007G210400 PF04043,PF01 |
| 25 | 1 | Phvul.007G210400.1 | Phvul.007G210400 | Phvul.007G210400 PF04043,PF01 |
| 26 | 1 | Phvul.007G215300.1 | Phvul.007G215300 | Phvul.007G215300 PF00628,PF00 |
| 27 | 1 | Phvul.007G215300.1 | Phvul.007G215300 | Phvul.007G215300 PF00628,PF00 |
| 28 | 1 | Phvul.007G215300.1 | Phvul.007G215300 | Phvul.007G215300 PF00628,PF00 |
| 29 | 1 | Phvul.007G215300.1 | Phvul.007G215300 | Phvul.007G215300 PF00628,PF00 |
| 30 | 1 | Phvul.007G251800.1 | Phvul.007G251800 | Phvul.007G251800 PF00085,PF00 |
| 31 | 2 | Phvul.008G043400.1 | Phvul.008G043400 | Phvul.008G043400 PF08263,PF13 |
| 32 | 2 | Phvul.008G043400.1 | Phvul.008G043400 | Phvul.008G043400 PF08263,PF13 |
| 33 | 1 | Phvul.008G067300.1 | Phvul.008G067300 | Phvul.008G067300 PF00249 |
| 34 | 1 | Phvul.008G067300.1 | Phvul.008G067300 | Phvul.008G067300 PF00249 |
| 35 | 1 | Phvul.008G110100.1 | Phvul.008G110100 | Phvul.008G110100 PF05056 |
| 36 | 1 | Phvul.008G110100.1 | Phvul.008G110100 | Phvul.008G110100 PF05056 |
| 37 | 1 | Phvul.008G110100.1 | Phvul.008G110100 | Phvul.008G110100 PF05056 |
| 38 | 1 | Phvul.008G110100.1 | Phvul.008G110100 | Phvul.008G110100 PF05056 |
| 39 | 1 | Phvul.008G110200.1 | Phvul.008G110200 | Phvul.008G110200 PF05056 |
| 40 | 1 | Phvul.008G110200.1 | Phvul.008G110200 | Phvul.008G110200 PF05056 |
| 41 | 1 | Phvul.008G110200.1 | Phvul.008G110200 | Phvul.008G110200 PF05056 |
| 42 | 1 | Phvul.008G110200.1 | Phvul.008G110200 | Phvul.008G110200 PF05056 |
| 43 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 PF05056 |
| 44 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 PF05056 |
| 45 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 PF05056 |
| 46 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 PF05056 |
| 47 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 PF05056 |
| 48 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 PF05056 |
| 49 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 PF05056 |
| 50 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 PF05056 |
| 51 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 PF05056 |
| 52 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 PF05056 |
| 53 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 PF05056 |
| 54 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 PF05056 |
| 55 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 PF05056 |
| 56 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 PF05056 |
| 57 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 PF05056 |
| 58 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 PF05056 |
| 59 | 1 | Phvul.008G110500.1 | Phvul.008G110500 | Phvul.008G110500 PF05056 |
| 60 | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | |
|----------------------|------------------|------------------|--------------|
| 1 Phvul.008G125400.2 | Phvul.008G125400 | Phvul.008G125400 | PF08513,PF00 |
| 1 Phvul.008G125400.1 | Phvul.008G125400 | Phvul.008G125400 | PF08513,PF00 |
| 1 Phvul.008G125400.2 | Phvul.008G125400 | Phvul.008G125400 | PF08513,PF00 |
| 1 Phvul.008G125400.1 | Phvul.008G125400 | Phvul.008G125400 | PF08513,PF00 |
| 1 Phvul.008G229100.1 | Phvul.008G229100 | Phvul.008G229100 | PF02225,PF05 |
| 1 Phvul.008G279750.1 | Phvul.008G279750 | Phvul.008G279750 | PF03552 |
| 1 Phvul.008G279750.1 | Phvul.008G279750 | Phvul.008G279750 | PF03552 |
| 1 Phvul.009G010800.1 | Phvul.009G010800 | Phvul.009G010800 | PF00246 |
| 1 Phvul.009G010800.1 | Phvul.009G010800 | Phvul.009G010800 | PF00246 |
| 1 Phvul.009G034800.1 | Phvul.009G034800 | Phvul.009G034800 | 0 |
| 1 Phvul.009G060200.1 | Phvul.009G060200 | Phvul.009G060200 | PF01565,PF09 |
| 1 Phvul.009G060200.2 | Phvul.009G060200 | Phvul.009G060200 | PF01565,PF09 |
| 1 Phvul.009G060200.1 | Phvul.009G060200 | Phvul.009G060200 | PF01565,PF09 |
| 1 Phvul.009G060200.2 | Phvul.009G060200 | Phvul.009G060200 | PF01565,PF09 |
| 1 Phvul.009G060200.1 | Phvul.009G060200 | Phvul.009G060200 | PF01565,PF09 |
| 1 Phvul.009G060200.2 | Phvul.009G060200 | Phvul.009G060200 | PF01565,PF09 |
| 1 Phvul.009G060200.1 | Phvul.009G060200 | Phvul.009G060200 | PF01565,PF09 |
| 1 Phvul.009G060200.2 | Phvul.009G060200 | Phvul.009G060200 | PF01565,PF09 |
| 1 Phvul.009G115500.1 | Phvul.009G115500 | Phvul.009G115500 | PF07690 |
| 1 Phvul.009G115500.1 | Phvul.009G115500 | Phvul.009G115500 | PF07690 |
| 1 Phvul.009G158700.1 | Phvul.009G158700 | Phvul.009G158700 | 0 |
| 1 Phvul.009G158700.1 | Phvul.009G158700 | Phvul.009G158700 | 0 |
| 1 Phvul.009G158700.1 | Phvul.009G158700 | Phvul.009G158700 | 0 |
| 1 Phvul.009G158700.1 | Phvul.009G158700 | Phvul.009G158700 | 0 |
| 1 Phvul.009G203100.1 | Phvul.009G203100 | Phvul.009G203100 | PF04833 |
| 1 Phvul.009G232500.1 | Phvul.009G232500 | Phvul.009G232500 | PF01301 |
| 1 Phvul.009G232500.1 | Phvul.009G232500 | Phvul.009G232500 | PF01301 |
| 1 Phvul.009G232500.1 | Phvul.009G232500 | Phvul.009G232500 | PF01301 |
| 1 Phvul.009G232500.1 | Phvul.009G232500 | Phvul.009G232500 | PF01301 |
| 1 Phvul.009G255100.1 | Phvul.009G255100 | Phvul.009G255100 | PF02466 |
| 1 Phvul.009G255100.2 | Phvul.009G255100 | Phvul.009G255100 | PF02466 |
| 1 Phvul.009G255100.1 | Phvul.009G255100 | Phvul.009G255100 | PF02466 |
| 1 Phvul.009G255100.2 | Phvul.009G255100 | Phvul.009G255100 | PF02466 |
| 1 Phvul.010G026500.1 | Phvul.010G026500 | Phvul.010G026500 | 0 |
| 1 Phvul.010G026500.1 | Phvul.010G026500 | Phvul.010G026500 | 0 |
| 1 Phvul.010G026500.1 | Phvul.010G026500 | Phvul.010G026500 | 0 |
| 1 Phvul.010G026500.1 | Phvul.010G026500 | Phvul.010G026500 | 0 |
| 1 Phvul.010G028900.2 | Phvul.010G028900 | Phvul.010G028900 | PF01582,PF00 |
| 1 Phvul.010G028900.1 | Phvul.010G028900 | Phvul.010G028900 | PF01582,PF00 |
| 1 Phvul.010G028900.2 | Phvul.010G028900 | Phvul.010G028900 | PF01582,PF00 |
| 1 Phvul.010G028900.1 | Phvul.010G028900 | Phvul.010G028900 | PF01582,PF00 |
| 1 Phvul.010G067900.1 | Phvul.010G067900 | Phvul.010G067900 | PF00069 |
| 1 Phvul.010G067900.1 | Phvul.010G067900 | Phvul.010G067900 | PF00069 |

| | | | | | |
|----|---|--------------------|------------------|------------------|--------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | 1 | Phvul.010G067900.1 | Phvul.010G067900 | Phvul.010G067900 | PF00069 |
| 4 | 1 | Phvul.010G067900.1 | Phvul.010G067900 | Phvul.010G067900 | PF00069 |
| 5 | 2 | Phvul.010G089200.1 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 6 | 2 | Phvul.010G089200.2 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 7 | 2 | Phvul.010G089200.1 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 8 | 2 | Phvul.010G089200.2 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 9 | 2 | Phvul.010G089200.1 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 10 | 2 | Phvul.010G089200.2 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 11 | 2 | Phvul.010G089200.1 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 12 | 2 | Phvul.010G089200.2 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 13 | 2 | Phvul.010G089200.1 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 14 | 2 | Phvul.010G089200.2 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 15 | 2 | Phvul.010G089200.1 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 16 | 2 | Phvul.010G089200.2 | Phvul.010G089200 | Phvul.010G089200 | PF08610 |
| 17 | 1 | Phvul.010G094450.1 | Phvul.010G094450 | Phvul.010G094450 | 0 |
| 18 | 1 | Phvul.010G094450.1 | Phvul.010G094450 | Phvul.010G094450 | 0 |
| 19 | 1 | Phvul.010G094450.1 | Phvul.010G094450 | Phvul.010G094450 | 0 |
| 20 | 1 | Phvul.010G094450.1 | Phvul.010G094450 | Phvul.010G094450 | 0 |
| 21 | 1 | Phvul.010G094450.1 | Phvul.010G094450 | Phvul.010G094450 | 0 |
| 22 | 1 | Phvul.011G001200.2 | Phvul.011G001200 | Phvul.011G001200 | PF02383 |
| 23 | 1 | Phvul.011G001200.1 | Phvul.011G001200 | Phvul.011G001200 | PF02383 |
| 24 | 1 | Phvul.011G001200.2 | Phvul.011G001200 | Phvul.011G001200 | PF02383 |
| 25 | 1 | Phvul.011G001200.1 | Phvul.011G001200 | Phvul.011G001200 | PF02383 |
| 26 | 1 | Phvul.011G001200.2 | Phvul.011G001200 | Phvul.011G001200 | PF02383 |
| 27 | 1 | Phvul.011G001200.1 | Phvul.011G001200 | Phvul.011G001200 | PF02383 |
| 28 | 1 | Phvul.011G001200.2 | Phvul.011G001200 | Phvul.011G001200 | PF02383 |
| 29 | 1 | Phvul.011G001200.1 | Phvul.011G001200 | Phvul.011G001200 | PF02383 |
| 30 | 1 | Phvul.011G001200.2 | Phvul.011G001200 | Phvul.011G001200 | PF02383 |
| 31 | 1 | Phvul.011G001200.1 | Phvul.011G001200 | Phvul.011G001200 | PF02383 |
| 32 | 1 | Phvul.011G004200.1 | Phvul.011G004200 | Phvul.011G004200 | 0 |
| 33 | 1 | Phvul.011G203450.1 | Phvul.011G203450 | Phvul.011G203450 | PF05678 |
| 34 | 1 | Phvul.011G203450.1 | Phvul.011G203450 | Phvul.011G203450 | PF05678 |
| 35 | 1 | Phvul.011G203450.1 | Phvul.011G203450 | Phvul.011G203450 | PF05678 |
| 36 | 1 | Phvul.011G203450.1 | Phvul.011G203450 | Phvul.011G203450 | PF05678 |
| 37 | 1 | Phvul.011G203450.1 | Phvul.011G203450 | Phvul.011G203450 | PF05678 |
| 38 | 1 | Phvul.L001679.1 | Phvul.L001679 | Phvul.L001679 | PF00168 |
| 39 | 1 | Phvul.L001679.1 | Phvul.L001679 | Phvul.L001679 | PF00168 |
| 40 | 2 | Phvul.L002537.1 | Phvul.L002537 | Phvul.L002537 | PF16131,PF00 |
| 41 | 2 | Phvul.L002537.1 | Phvul.L002537 | Phvul.L002537 | PF16131,PF00 |
| 42 | 1 | Phvul.L009843.2 | Phvul.L009843 | Phvul.L009843 | PF00153 |
| 43 | 1 | Phvul.L009843.1 | Phvul.L009843 | Phvul.L009843 | PF00153 |
| 44 | 1 | Phvul.L009843.2 | Phvul.L009843 | Phvul.L009843 | PF00153 |
| 45 | 1 | Phvul.L009843.1 | Phvul.L009843 | Phvul.L009843 | PF00153 |
| 46 | 1 | Phvul.L009843.1 | Phvul.L009843 | Phvul.L009843 | PF00153 |
| 47 | 1 | Phvul.L009843.1 | Phvul.L009843 | Phvul.L009843 | PF00153 |
| 48 | 1 | Phvul.L009843.1 | Phvul.L009843 | Phvul.L009843 | PF00153 |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| Panther | KOG | KEGG | KOG | GO | Best-hit-arabi- |
|--------------------------|---------|------------|----------|----------------|-----------------|
| PTHR13451,P ⁻ | | 0 | 0 K10882 | GO:0004518,(| AT2G22140.1 |
| PTHR13451,P ⁻ | | 0 | 0 K10882 | GO:0004518,(| AT2G22140.1 |
| PTHR31928,P ⁻ | | 0 | 0 | 0 | 0 AT1G70340.1 |
| PTHR31928,P ⁻ | | 0 | 0 | 0 | 0 AT1G70340.1 |
| PTHR31928,P ⁻ | | 0 | 0 | 0 | 0 AT1G70340.1 |
| PTHR31928,P ⁻ | | 0 | 0 | 0 | 0 AT1G70340.1 |
| PTHR33917,P ⁻ | | 0 | 0 | 0 | 0 AT4G33630.1 |
| PTHR13600,P ⁻ | | 0 | 0 | 0 GO:0032259,(| AT5G42760.1 |
| PTHR13600,P ⁻ | | 0 | 0 | 0 GO:0032259,(| AT5G42760.1 |
| PTHR10766,P ⁻ | | 0 | 0 K17086 | GO:0016021 | AT5G10840.1 |
| PTHR22849,P ⁻ | | 0 6.3.2.19 | | 0 GO:0016567,(| AT1G76390.1 |
| PTHR22849,P ⁻ | | 0 6.3.2.19 | | 0 GO:0016567,(| AT1G76390.1 |
| PTHR22849,P ⁻ | | 0 6.3.2.19 | | 0 GO:0016567,(| AT1G76390.1 |
| PTHR22849,P ⁻ | | 0 6.3.2.19 | | 0 GO:0016567,(| AT1G76390.1 |
| PTHR11908,P ⁻ | | 0 1.17.1.4 | K00106 | GO:0051536,(| AT4G34890.1 |
| PTHR11908,P ⁻ | | 0 1.17.1.4 | K00106 | GO:0051536,(| AT4G34890.1 |
| PTHR11908,P ⁻ | | 0 1.17.1.4 | K00106 | GO:0051536,(| AT4G34890.1 |
| PTHR11908,P ⁻ | | 0 1.17.1.4 | K00106 | GO:0051536,(| AT4G34890.1 |
| PTHR22952,P ⁻ | | 0 | 0 | 0 GO:0043565,(| AT5G24800.1 |
| PTHR22952,P ⁻ | | 0 | 0 | 0 GO:0043565,(| AT5G24800.1 |
| PTHR22952,P ⁻ | | 0 | 0 | 0 GO:0043565,(| AT5G24800.1 |
| PTHR22952,P ⁻ | | 0 | 0 | 0 GO:0043565,(| AT5G24800.1 |
| PTHR11183,P ⁻ | KOG1950 | 2.4.1.123 | K18819 | GO:0016757 | AT2G47180.1 |
| PTHR11183,P ⁻ | KOG1950 | 2.4.1.123 | K18819 | GO:0016757 | AT2G47180.1 |
| PTHR11183,P ⁻ | KOG1950 | 2.4.1.123 | K18819 | GO:0016757 | AT2G47180.1 |
| PTHR11183,P ⁻ | KOG1950 | 2.4.1.123 | K18819 | GO:0016757 | AT2G47180.1 |
| PTHR13451,P ⁻ | | 0 | 0 K10882 | GO:0004518,(| AT2G22140.1 |
| PTHR13451,P ⁻ | | 0 | 0 K10882 | GO:0004518,(| AT2G22140.1 |
| PTHR13451,P ⁻ | | 0 | 0 K10882 | GO:0004518,(| AT2G22140.1 |
| PTHR13451,P ⁻ | | 0 | 0 K10882 | GO:0004518,(| AT2G22140.1 |
| PTHR11062,P ⁻ | KOG1021 | 2.4.2.41 | | 0 | 0 AT5G61840.1 |
| PTHR11062,P ⁻ | KOG1021 | 2.4.2.41 | | 0 | 0 AT5G61840.1 |
| PTHR11062,P ⁻ | KOG1021 | 2.4.2.41 | | 0 | 0 AT5G61840.1 |
| PTHR11062,P ⁻ | KOG1021 | 2.4.2.41 | | 0 | 0 AT5G61840.1 |
| PTHR27004,P ⁻ | KOG0472 | 2.7.11.1 | | 0 GO:0005515 | AT2G34930.1 |
| PTHR33670,P ⁻ | | 0 | 0 | 0 | 0 AT3G21570.1 |
| PTHR33463,P ⁻ | KOG1947 | | 0 | 0 | 0 AT1G61300.1 |
| PTHR33463,P ⁻ | KOG1947 | | 0 | 0 | 0 AT1G61300.1 |
| PTHR33463,P ⁻ | KOG1947 | | 0 | 0 | 0 AT1G61300.1 |
| PTHR33463,P ⁻ | KOG1947 | | 0 | 0 | 0 AT1G61300.1 |
| PTHR33103,P ⁻ | | 0 | 0 | 0 | 0 AT5G01150.1 |
| PTHR33103,P ⁻ | | 0 | 0 | 0 | 0 AT5G01120.1 |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | | |
|----|----------------------------------|-------------|--------|---------------------------|
| 1 | | | | |
| 2 | | | | |
| 3 | PTHR19229,P ⁻ KOG0059 | 3.6.3.25 | K05643 | GO:0005524,(AT2G41700.1 |
| 4 | PTHR19229,P ⁻ KOG0059 | 3.6.3.25 | K05643 | GO:0005524,(AT2G41700.1 |
| 5 | PTHR19229,P ⁻ KOG0059 | 3.6.3.25 | K05643 | GO:0005524,(AT2G41700.1 |
| 6 | PTHR19229,P ⁻ KOG0059 | 3.6.3.25 | K05643 | GO:0005524,(AT2G41700.1 |
| 7 | PTHR19229,P ⁻ KOG0059 | 3.6.3.25 | K05643 | GO:0005524,(AT2G41700.1 |
| 8 | PTHR19229,P ⁻ KOG0059 | 3.6.3.25 | K05643 | GO:0005524,(AT2G41700.1 |
| 9 | PTHR19229,P ⁻ KOG0059 | 3.6.3.25 | K05643 | GO:0005524,(AT2G41700.1 |
| 10 | PTHR19229,P ⁻ KOG0059 | 3.6.3.25 | K05643 | GO:0005524,(AT2G41700.1 |
| 11 | PTHR19229,P ⁻ KOG0059 | 3.6.3.25 | K05643 | GO:0005524,(AT2G41700.1 |
| 12 | PTHR31251,P ⁻ | 0 | 0 | 0 GO:0005634,(AT2G42200.1 |
| 13 | PTHR31251,P ⁻ | 0 | 0 | 0 GO:0005634,(AT2G42200.1 |
| 14 | PTHR31251,P ⁻ | 0 | 0 | 0 GO:0005634,(AT2G42200.1 |
| 15 | PTHR31251,P ⁻ | 0 | 0 | 0 GO:0005634,(AT2G42200.1 |
| 16 | PTHR31251,P ⁻ | 0 | 0 | 0 GO:0005634,(AT2G42200.1 |
| 17 | PTHR31251,P ⁻ | 0 | 0 | 0 GO:0005634,(AT2G42200.1 |
| 18 | PTHR23293,P ⁻ KOG2644 | 2.7.7.2 | | 0 GO:0008152,(AT5G03430.1 |
| 19 | PTHR23293,P ⁻ KOG2644 | 2.7.7.2 | | 0 GO:0008152,(AT5G03430.1 |
| 20 | PTHR23293,P ⁻ KOG2644 | 2.7.7.2 | | 0 GO:0008152,(AT5G03430.1 |
| 21 | PTHR23293,P ⁻ KOG2644 | 2.7.7.2 | | 0 GO:0008152,(AT5G03430.1 |
| 22 | PTHR23293,P ⁻ KOG2644 | 2.7.7.2 | | 0 GO:0008152,(AT5G03430.1 |
| 23 | PTHR23293,P ⁻ KOG2644 | 2.7.7.2 | | 0 GO:0008152,(AT5G03430.1 |
| 24 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 25 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 26 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 27 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 28 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 29 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 30 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 31 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 32 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 33 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 34 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 35 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 36 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 37 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 38 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 39 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 40 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 41 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 42 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 43 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 44 | PTHR13115,P ⁻ | 0 | 0 | 0 AT5G43630.1 |
| 45 | PTHR10438,P ⁻ KOG0907 | 1.6.5.4 | K03671 | GO:0045454,(AT5G39950.1 |
| 46 | PTHR10438,P ⁻ KOG0907 | 1.6.5.4 | K03671 | GO:0045454,(AT5G39950.1 |
| 47 | PTHR31928,P ⁻ | 0 | 0 | 0 AT1G70340.1 |
| 48 | PTHR31928,P ⁻ | 0 | 0 | 0 AT1G70340.1 |
| 49 | PTHR31928,P ⁻ | 0 | 0 | 0 AT1G70340.1 |
| 50 | PTHR10201,P ⁻ | 0 3.4.24.23 | | 0 GO:0031012,(AT1G70170.1 |
| 51 | PTHR10201,P ⁻ | 0 3.4.24.23 | | 0 GO:0031012,(AT1G70170.1 |
| 52 | PTHR10201,P ⁻ | 0 3.4.24.23 | | 0 GO:0031012,(AT1G70170.1 |
| 53 | PTHR10201,P ⁻ | 0 3.4.24.23 | | 0 GO:0031012,(AT1G70170.1 |
| 54 | PTHR10201,P ⁻ | 0 3.4.24.23 | | 0 GO:0031012,(AT1G70170.1 |
| 55 | PTHR10201,P ⁻ | 0 3.4.24.23 | | 0 GO:0031012,(AT1G70170.1 |
| 56 | PTHR10110,P ⁻ KOG1965 | | 0 | 0 GO:0055085,(AT2G01980.1 |
| 57 | PTHR10110,P ⁻ KOG1965 | | 0 | 0 GO:0055085,(AT2G01980.1 |
| 58 | PTHR10110,P ⁻ KOG1965 | | 0 | 0 GO:0055085,(AT2G01980.1 |
| 59 | PTHR10110,P ⁻ KOG1965 | | 0 | 0 GO:0055085,(AT2G01980.1 |
| 60 | | | | |

| | | | | |
|----|----------------------------------|------------|----------|---------------------------|
| 1 | | | | |
| 2 | | | | |
| 3 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G13690.1 |
| 4 | PTHR23336,P ⁻ | 0 | 0 | 0 GO:0008270 AT3G62900.1 |
| 5 | PTHR23336,P ⁻ | 0 | 0 | 0 GO:0008270 AT3G62900.1 |
| 6 | PTHR27004,P ⁻ KOG0472 | 2.7.11.1 | | 0 GO:0005515 AT2G34930.1 |
| 7 | PTHR24015,P ⁻ | 0 | 0 | 0 0 AT4G21190.1 |
| 8 | PTHR11689,P ⁻ | 0 | 0 K05016 | GO:0055085,(AT5G49890.1 |
| 9 | PTHR11689,P ⁻ | 0 | 0 K05016 | GO:0055085,(AT5G49890.1 |
| 10 | PTHR10438,P ⁻ KOG0907 | 3.5.1.52 | | 0 GO:0045454,(AT4G29670.1 |
| 11 | PTHR10438,P ⁻ KOG0907 | 3.5.1.52 | | 0 GO:0045454,(AT4G29670.1 |
| 12 | PTHR10438,P ⁻ KOG0907 | 3.5.1.52 | | 0 GO:0045454,(AT4G29670.1 |
| 13 | PTHR10438,P ⁻ KOG0907 | 3.5.1.52 | | 0 GO:0045454,(AT4G29670.1 |
| 14 | PTHR33090 | 0 | 0 | 0 0 AT4G10265.1 |
| 15 | PTHR17630 KOG3043 | 3.1.1.45 | | 0 GO:0016787 AT2G32520.1 |
| 16 | PTHR17630 KOG3043 | 3.1.1.45 | | 0 GO:0016787 AT2G32520.1 |
| 17 | PTHR17630 KOG3043 | 3.1.1.45 | | 0 GO:0016787 AT2G32520.1 |
| 18 | PTHR17630 KOG3043 | 3.1.1.45 | | 0 GO:0016787 AT2G32520.1 |
| 19 | PTHR33137,P ⁻ | 0 | 0 K14972 | 0 AT1G15780.1 |
| 20 | PTHR33137,P ⁻ | 0 | 0 K14972 | 0 AT1G15780.1 |
| 21 | PTHR11595,P ⁻ KOG1668 | | 0 K03232 | GO:0006414,(AT5G12110.1 |
| 22 | PTHR11595,P ⁻ KOG1668 | | 0 K03232 | GO:0006414,(AT5G12110.1 |
| 23 | PTHR11595,P ⁻ KOG1668 | | 0 K03232 | GO:0006414,(AT5G12110.1 |
| 24 | PTHR11595,P ⁻ KOG1668 | | 0 K03232 | GO:0006414,(AT5G12110.1 |
| 25 | PTHR19241,P ⁻ | 0 3.6.3.34 | | 0 GO:0016887,(AT2G29940.1 |
| 26 | PTHR19241,P ⁻ | 0 3.6.3.34 | | 0 GO:0016887,(AT2G29940.1 |
| 27 | PTHR19241,P ⁻ | 0 3.6.3.34 | | 0 GO:0016887,(AT2G29940.1 |
| 28 | PTHR19241,P ⁻ | 0 3.6.3.34 | | 0 GO:0016887,(AT2G29940.1 |
| 29 | PTHR31589,P ⁻ | 0 | 0 | 0 0 AT5G18460.1 |
| 30 | PTHR31589,P ⁻ | 0 | 0 | 0 0 AT5G18460.1 |
| 31 | PTHR23324,P ⁻ | 0 | 0 | 0 0 AT5G47730.1 |
| 32 | PTHR23324,P ⁻ | 0 | 0 | 0 0 AT5G47730.1 |
| 33 | PTHR10992,P ⁻ KOG1454 | | 0 | 0 0 AT5G38520.1 |
| 34 | PTHR10992,P ⁻ KOG1454 | | 0 | 0 0 AT5G38520.1 |
| 35 | PTHR31375,P ⁻ | 0 3.2.1.15 | | 0 GO:0005975,(AT1G02460.1 |
| 36 | PTHR31375,P ⁻ | 0 3.2.1.15 | | 0 GO:0005975,(AT1G02460.1 |
| 37 | PTHR31374,P ⁻ | 0 | 0 K14488 | GO:0009733 AT3G09870.1 |
| 38 | PTHR31374,P ⁻ | 0 | 0 K14488 | GO:0009733 AT3G09870.1 |
| 39 | PTHR33463,P ⁻ KOG1947 | | 0 | 0 0 AT1G61300.1 |
| 40 | PTHR33463,P ⁻ KOG1947 | | 0 | 0 0 AT1G61300.1 |
| 41 | PTHR35731,P ⁻ | 0 | 0 | 0 0 AT3G09050.1 |
| 42 | PTHR35731,P ⁻ | 0 | 0 | 0 0 AT3G09050.1 |
| 43 | PTHR24322,P ⁻ KOG0725 | 1.1.1.206 | K08081 | 0 AT5G06060.1 |
| 44 | PTHR24322,P ⁻ KOG0725 | 1.1.1.206 | K08081 | 0 AT5G06060.1 |
| 45 | PTHR10366,P ⁻ KOG1502 | 1.2.1.44 | | 0 GO:0050662,(AT5G58490.1 |
| 46 | | | | |
| 47 | | | | |
| 48 | | | | |
| 49 | | | | |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

| | | | | |
|----|----------------------------------|------------------|----------|---------------------------|
| 1 | | | | |
| 2 | | | | |
| 3 | PTHR10366,P ⁻ KOG1502 | 1.2.1.44 | | 0 GO:0050662,(AT5G58490.1 |
| 4 | PTHR10366,P ⁻ KOG1502 | 1.2.1.44 | | 0 GO:0050662,(AT5G58490.1 |
| 5 | PTHR10366,P ⁻ KOG1502 | 1.2.1.44 | | 0 GO:0050662,(AT5G58490.1 |
| 6 | PTHR23289,P ⁻ | 0 | 0 K02259 | GO:0055114,(AT5G56090.1 |
| 7 | PTHR10766,P ⁻ | 0 | 0 K17086 | GO:0016021 AT4G12650.1 |
| 8 | PTHR12874 KOG2997 | | 0 K10295 | GO:0005515 AT1G21760.1 |
| 9 | PTHR12874 KOG2997 | | 0 K10295 | GO:0005515 AT1G21760.1 |
| 10 | PTHR12874 KOG2997 | | 0 K10295 | GO:0005515 AT1G21760.1 |
| 11 | PTHR12874 KOG2997 | | 0 K10295 | GO:0005515 AT1G21760.1 |
| 12 | PTHR12874 KOG2997 | | 0 K10295 | GO:0005515 AT1G21760.1 |
| 13 | PTHR11062,P ⁻ KOG1021 | 2.4.2.41 | | 0 0 AT5G61840.1 |
| 14 | PTHR11062,P ⁻ KOG1021 | 2.4.2.41 | | 0 0 AT5G61840.1 |
| 15 | PTHR11062,P ⁻ KOG1021 | 2.4.2.41 | | 0 0 AT5G61840.1 |
| 16 | PTHR11062,P ⁻ KOG1021 | 2.4.2.41 | | 0 0 AT5G61840.1 |
| 17 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 |
| 18 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 |
| 19 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 |
| 20 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 |
| 21 | 0 | 0 | 0 | 0 GO:0043565,(AT4G36730.1 |
| 22 | 0 | 0 | 0 | 0 GO:0043565,(AT4G36730.1 |
| 23 | PTHR11139,P ⁻ | 0 2.7.11.1 | K08873 | GO:0005515,(AT1G50030.1 |
| 24 | PTHR11139,P ⁻ | 0 2.7.11.1 | K08873 | GO:0005515,(AT1G50030.1 |
| 25 | PTHR11139,P ⁻ | 0 2.7.11.1 | K08873 | GO:0005515,(AT1G50030.1 |
| 26 | PTHR11139,P ⁻ | 0 2.7.11.1 | K08873 | GO:0005515,(AT1G50030.1 |
| 27 | PTHR11709,P ⁻ | 0 1.10.3.2 | K05909 | GO:0055114,(AT2G29130.1 |
| 28 | PTHR11709,P ⁻ | 0 1.10.3.2 | K05909 | GO:0055114,(AT2G29130.1 |
| 29 | PTHR31471,P ⁻ | 0 | 0 | 0 0 AT1G45207.2 |
| 30 | PTHR31471,P ⁻ | 0 | 0 | 0 0 AT1G45207.2 |
| 31 | PTHR31953,P ⁻ | 0 3.2.1.153,3.2. | K01193 | 0 AT3G13790.1 |
| 32 | PTHR16105,P ⁻ | 0 | 0 K13157 | GO:0003676 AT1G09230.1 |
| 33 | PTHR16105,P ⁻ | 0 | 0 K13157 | GO:0003676 AT1G09230.1 |
| 34 | PTHR33044,P ⁻ | 0 | 0 | 0 0 AT2G48140.1 |
| 35 | PTHR33044,P ⁻ | 0 | 0 | 0 0 AT2G48140.1 |
| 36 | PTHR33044,P ⁻ | 0 | 0 | 0 0 AT2G48140.1 |
| 37 | PTHR33044,P ⁻ | 0 | 0 | 0 0 AT2G48140.1 |
| 38 | PTHR18866,P ⁻ | 0 | 0 | 0 0 AT3G56130.1 |
| 39 | PTHR31692,P ⁻ | 0 | 0 | 0 0 AT4G17030.1 |
| 40 | PTHR23083,P ⁻ | 0 | 0 | 0 0 AT4G37460.1 |
| 41 | PTHR23083,P ⁻ | 0 | 0 | 0 0 AT4G37460.1 |
| 42 | PTHR17901,P ⁻ KOG4549 | 3.1.3.48 | K17619 | GO:0016791 AT2G14110.1 |
| 43 | PTHR22870,P ⁻ | 0 | 0 | 0 0 AT3G26100.2 |
| 44 | PTHR22870,P ⁻ | 0 | 0 | 0 0 AT3G26100.2 |
| 45 | PTHR10648,P ⁻ | 0 | 0 K03456 | GO:0005515 AT3G25800.1 |
| 46 | PTHR10648,P ⁻ | 0 | 0 K03456 | GO:0005515 AT3G25800.1 |
| 47 | | | | |
| 48 | | | | |
| 49 | | | | |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

| | | | | |
|----|----------------------------------|----------------|----------|---------------------------|
| 1 | | | | |
| 2 | | | | |
| 3 | PTHR18919,P ⁻ | 0 2.3.1.9 | K00626 | GO:0016747,(AT5G47720.2 |
| 4 | PTHR18919,P ⁻ | 0 2.3.1.9 | K00626 | GO:0016747,(AT5G47720.2 |
| 5 | PTHR18919,P ⁻ | 0 2.3.1.9 | K00626 | GO:0016747,(AT5G47720.2 |
| 6 | PTHR18919,P ⁻ | 0 2.3.1.9 | K00626 | GO:0016747,(AT5G47720.2 |
| 7 | PTHR18919,P ⁻ | 0 2.3.1.9 | K00626 | GO:0016747,(AT5G47720.2 |
| 8 | PTHR18919,P ⁻ | 0 2.3.1.9 | K00626 | GO:0016747,(AT5G47720.2 |
| 9 | PTHR18919,P ⁻ | 0 2.3.1.9 | K00626 | GO:0016747,(AT5G47720.2 |
| 10 | PTHR18919,P ⁻ | 0 2.3.1.9 | K00626 | GO:0016747,(AT5G47720.2 |
| 11 | PTHR18919,P ⁻ | 0 2.3.1.9 | K00626 | GO:0016747,(AT5G47720.2 |
| 12 | PTHR18919,P ⁻ | 0 2.3.1.9 | K00626 | GO:0016747,(AT5G47720.2 |
| 13 | PTHR18919,P ⁻ | 0 2.3.1.9 | K00626 | GO:0016747,(AT5G47720.2 |
| 14 | PTHR24089,P ⁻ KOG0752 | | 0 K15108 | 0 AT5G48970.1 |
| 15 | PTHR24089,P ⁻ KOG0752 | | 0 K15108 | 0 AT5G48970.1 |
| 16 | PTHR22957,P ⁻ KOG1091 | | 0 K18469 | 0 AT4G29950.1 |
| 17 | PTHR22957,P ⁻ KOG1091 | | 0 K18469 | 0 AT4G29950.1 |
| 18 | PTHR22957,P ⁻ KOG1091 | | 0 K18469 | 0 AT4G29950.1 |
| 19 | PTHR11588,P ⁻ | 0 | 0 K07374 | GO:0003924,(AT1G04820.1 |
| 20 | PTHR11588,P ⁻ | 0 | 0 K07374 | GO:0003924,(AT1G04820.1 |
| 21 | PTHR11588,P ⁻ | 0 | 0 K07374 | GO:0003924,(AT1G04820.1 |
| 22 | PTHR11588,P ⁻ | 0 | 0 K07374 | GO:0003924,(AT1G04820.1 |
| 23 | PTHR11588,P ⁻ | 0 | 0 K07374 | GO:0003924,(AT1G04820.1 |
| 24 | PTHR24012,P ⁻ | 0 | 0 | 0 GO:0003676 AT1G49600.1 |
| 25 | PTHR24012,P ⁻ KOG0148 | | 0 | 0 GO:0003676 AT3G19130.1 |
| 26 | PTHR24012,P ⁻ KOG0148 | | 0 | 0 GO:0003676 AT3G19130.1 |
| 27 | PTHR24012,P ⁻ KOG0148 | | 0 | 0 GO:0003676 AT3G19130.1 |
| 28 | PTHR32212,P ⁻ | 0 | 0 | 0 GO:0005515 AT3G49030.1 |
| 29 | PTHR32212,P ⁻ | 0 | 0 | 0 GO:0005515 AT3G49030.1 |
| 30 | PTHR32212,P ⁻ | 0 | 0 | 0 GO:0005515 AT3G49030.1 |
| 31 | PTHR32212,P ⁻ | 0 | 0 | 0 GO:0005515 AT3G49030.1 |
| 32 | PTHR32212,P ⁻ | 0 | 0 | 0 GO:0005515 AT3G49030.1 |
| 33 | 0 | 0 | 0 | 0 0 0 |
| 34 | 0 | 0 | 0 | 0 0 0 |
| 35 | PTHR27004,P ⁻ KOG0472 | 2.7.11.1 | | 0 GO:0005515 AT2G34930.1 |
| 36 | PTHR27004,P ⁻ KOG0472 | 2.7.11.1 | | 0 GO:0005515 AT2G34930.1 |
| 37 | PTHR24115,P ⁻ | 0 3.6.4.4 | K10393 | GO:0008017,(AT3G16060.1 |
| 38 | PTHR10615,P ⁻ KOG2747 | 2.3.1.48 | K11308 | GO:0016747,(AT5G64610.1 |
| 39 | PTHR24286,P ⁻ KOG0157 | | 0 | 0 GO:0055114,(AT3G14620.1 |
| 40 | PTHR24286,P ⁻ KOG0157 | | 0 | 0 GO:0055114,(AT3G14620.1 |
| 41 | PTHR24286,P ⁻ KOG0157 | | 0 | 0 GO:0055114,(AT3G14620.1 |
| 42 | PTHR24286,P ⁻ KOG0157 | | 0 | 0 GO:0055114,(AT3G14620.1 |
| 43 | PTHR24286,P ⁻ KOG0157 | | 0 | 0 GO:0055114,(AT3G14620.1 |
| 44 | PTHR24286,P ⁻ KOG0157 | | 0 | 0 GO:0055114,(AT3G14620.1 |
| 45 | PTHR24286,P ⁻ KOG0157 | | 0 | 0 GO:0055114,(AT3G14620.1 |
| 46 | PTHR24286,P ⁻ KOG0157 | | 0 | 0 GO:0055114,(AT3G14620.1 |
| 47 | PTHR24286,P ⁻ KOG0157 | | 0 | 0 GO:0055114,(AT3G14620.1 |
| 48 | PTHR24286,P ⁻ KOG0157 | | 0 | 0 GO:0055114,(AT3G14620.1 |
| 49 | PTHR24286,P ⁻ KOG0157 | | 0 | 0 GO:0055114,(AT3G14620.1 |
| 50 | PTHR24286,P ⁻ KOG0157 | | 0 | 0 GO:0055114,(AT3G14620.1 |
| 51 | PTHR12526,P ⁻ KOG0853 | 2.4.1.132,2.4. | K03843 | 0 AT1G78800.1 |
| 52 | PTHR12526,P ⁻ KOG0853 | 2.4.1.132,2.4. | K03843 | 0 AT1G78800.1 |
| 53 | PTHR31072,P ⁻ | 0 | 0 | 0 0 AT3G15030.2 |
| 54 | PTHR31072,P ⁻ | 0 | 0 | 0 0 AT3G15030.2 |
| 55 | PTHR31072,P ⁻ | 0 | 0 | 0 0 AT3G15030.2 |
| 56 | PTHR31072,P ⁻ | 0 | 0 | 0 0 AT3G15030.2 |
| 57 | PTHR31072,P ⁻ | 0 | 0 | 0 0 AT3G15030.2 |
| 58 | PTHR31072,P ⁻ | 0 | 0 | 0 0 AT3G15030.2 |
| 59 | PTHR31072,P ⁻ | 0 | 0 | 0 0 AT3G15030.2 |
| 60 | | | | |

| | | | | | | |
|----|----------------------------------|----------|-----------------------|--------------|------------------------|-------------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G15030.2 | |
| 4 | PTHR37716,P ⁻ | 0 | 0 | 0 | 0 AT2G01870.1 | |
| 5 | PTHR37716,P ⁻ | 0 | 0 | 0 | 0 AT2G01870.1 | |
| 6 | PTHR11999,P ⁻ | 0 | 4.1.1.28,4.1.1 K01592 | GO:0030170,(| AT2G20340.1 | |
| 7 | PTHR11999,P ⁻ | 0 | 4.1.1.28,4.1.1 K01592 | GO:0030170,(| AT2G20340.1 | |
| 8 | PTHR12381,P ⁻ | 0 | 0 K15047 | GO:0005515 | 0 | |
| 9 | PTHR12381,P ⁻ | 0 | 0 K15047 | GO:0005515 | 0 | |
| 10 | PTHR12381,P ⁻ | 0 | 0 K15047 | GO:0005515 | 0 | |
| 11 | PTHR12381,P ⁻ | 0 | 0 K15047 | GO:0005515 | 0 | |
| 12 | PTHR33059,P ⁻ | 0 | 0 | 0 | 0 AT3G22550.1 | |
| 13 | PTHR33059,P ⁻ | 0 | 0 | 0 | 0 AT3G22550.1 | |
| 14 | PTHR23024,P ⁻ KOG1515 | 3.1.1.1 | | 0 | 0 AT5G62180.1 | |
| 15 | PTHR23024,P ⁻ KOG1515 | 3.1.1.1 | | 0 | 0 AT5G62180.1 | |
| 16 | PTHR37764,P ⁻ | 0 | 0 | 0 | 0 AT5G27390.1 | |
| 17 | 0 | 0 | 0 | 0 | 0 AT3G05625.1 | |
| 18 | 0 | 0 | 0 | 0 | 0 AT3G05625.1 | |
| 19 | PTHR33416,P ⁻ | 0 | 0 | 0 | 0 AT3G10650.1 | |
| 20 | PTHR33416,P ⁻ | 0 | 0 | 0 | 0 AT3G10650.1 | |
| 21 | PTHR33416,P ⁻ | 0 | 0 | 0 | 0 AT3G10650.1 | |
| 22 | PTHR33416,P ⁻ | 0 | 0 | 0 | 0 AT3G10650.1 | |
| 23 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 AT5G16210.1 | |
| 24 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 AT5G16210.1 | |
| 25 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 AT5G16210.1 | |
| 26 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 AT5G16210.1 | |
| 27 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 AT5G16210.1 | |
| 28 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 AT5G16210.1 | |
| 29 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 AT5G16210.1 | |
| 30 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 AT5G16210.1 | |
| 31 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 AT5G16210.1 | |
| 32 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 AT5G16210.1 | |
| 33 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 AT5G16210.1 | |
| 34 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 AT5G16210.1 | |
| 35 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 AT5G16210.1 | |
| 36 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 AT5G16210.1 | |
| 37 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 AT5G16210.1 | |
| 38 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 AT5G16210.1 | |
| 39 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 AT5G16210.1 | |
| 40 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 AT5G16210.1 | |
| 41 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 AT5G16210.1 | |
| 42 | PTHR23240,P ⁻ KOG1361 | 6.5.1.1 | K10747 | GO:0006310,(| AT1G66730.1 | |
| 43 | PTHR23240,P ⁻ KOG1361 | 6.5.1.1 | K10747 | GO:0006310,(| AT1G66730.1 | |
| 44 | PTHR23240,P ⁻ KOG1361 | 6.5.1.1 | K10747 | GO:0006310,(| AT1G66730.1 | |
| 45 | PTHR23240,P ⁻ KOG1361 | 6.5.1.1 | K10747 | GO:0006310,(| AT1G66730.1 | |
| 46 | PTHR10783,P ⁻ | 0 | 0 | 0 | GO:0016021 AT3G29060.1 | |
| 47 | PTHR10783,P ⁻ | 0 | 0 | 0 | GO:0016021 AT3G29060.1 | |
| 48 | PTHR27000,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0005515,(| AT3G47570.1 |
| 49 | PTHR27000,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0005515,(| AT3G47570.1 |
| 50 | PTHR27000,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0005515,(| AT3G47570.1 |
| 51 | PTHR27000,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0005515,(| AT3G47570.1 |
| 52 | PTHR27000,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0005515,(| AT3G47570.1 |
| 53 | PTHR27000,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0005515,(| AT3G47570.1 |
| 54 | PTHR13480 KOG2932 | | 0 K15685 | | 0 AT5G01160.1 | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | |
|----|--------------------------|---------|---|--------|-------------------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | PTHR13480 | KOG2932 | 0 | K15685 | 0 AT5G01160.1 |
| 4 | PTHR13480 | KOG2932 | 0 | K15685 | 0 AT5G01160.1 |
| 5 | PTHR13480 | KOG2932 | 0 | K15685 | 0 AT5G01160.1 |
| 6 | PTHR13480 | KOG2932 | 0 | K15685 | 0 AT5G01160.1 |
| 7 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01120.1 |
| 8 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01150.1 |
| 9 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01150.1 |
| 10 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01150.1 |
| 11 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01120.1 |
| 12 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01120.1 |
| 13 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01120.1 |
| 14 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01120.1 |
| 15 | PTHR13343,P ⁻ | 0 | 0 | 0 | 0 AT3G59300.1 |
| 16 | PTHR11926,P ⁻ | KOG1192 | 0 | 0 | GO:0016758,(AT3G21780.1 |
| 17 | PTHR11926,P ⁻ | KOG1192 | 0 | 0 | GO:0016758,(AT3G21780.1 |
| 18 | PTHR11926,P ⁻ | KOG1192 | 0 | 0 | GO:0016758,(AT3G21780.1 |
| 19 | PTHR11926,P ⁻ | KOG1192 | 0 | 0 | GO:0016758,(AT3G21780.1 |
| 20 | PTHR11926,P ⁻ | KOG1192 | 0 | 0 | GO:0016758,(AT3G21780.1 |
| 21 | PTHR11926,P ⁻ | KOG1192 | 0 | 0 | GO:0016758,(AT3G21780.1 |
| 22 | PTHR31384,P ⁻ | 0 | 0 | 0 | GO:0003677,(AT1G77850.1 |
| 23 | PTHR31384,P ⁻ | 0 | 0 | 0 | GO:0003677,(AT1G77850.1 |
| 24 | PTHR31851,P ⁻ | 0 | 0 | 0 | 0 AT4G27860.1 |
| 25 | PTHR31851,P ⁻ | 0 | 0 | 0 | 0 AT4G27860.1 |
| 26 | PTHR31851,P ⁻ | 0 | 0 | 0 | 0 AT4G27860.1 |
| 27 | PTHR31851,P ⁻ | 0 | 0 | 0 | 0 AT4G27860.1 |
| 28 | PTHR10972,P ⁻ | 0 | 0 | 0 | 0 AT4G08180.2 |
| 29 | PTHR10972,P ⁻ | 0 | 0 | 0 | 0 AT4G08180.2 |
| 30 | PTHR10972,P ⁻ | 0 | 0 | 0 | 0 AT4G08180.2 |
| 31 | PTHR10972,P ⁻ | 0 | 0 | 0 | 0 AT4G08180.2 |
| 32 | PTHR10972,P ⁻ | 0 | 0 | 0 | 0 AT4G08180.2 |
| 33 | PTHR10972,P ⁻ | 0 | 0 | 0 | 0 AT4G08180.2 |
| 34 | PTHR10972,P ⁻ | 0 | 0 | 0 | 0 AT4G08180.2 |
| 35 | PTHR10972,P ⁻ | 0 | 0 | 0 | 0 AT4G08180.2 |
| 36 | PTHR10972,P ⁻ | 0 | 0 | 0 | 0 AT4G08180.2 |
| 37 | PTHR10972,P ⁻ | 0 | 0 | 0 | 0 AT4G08180.2 |
| 38 | PTHR10972,P ⁻ | 0 | 0 | 0 | 0 AT4G08180.2 |
| 39 | PTHR24089,P ⁻ | 0 | 0 | 0 | 0 AT5G48970.1 |
| 40 | PTHR24089,P ⁻ | 0 | 0 | 0 | 0 AT5G48970.1 |
| 41 | PTHR24089,P ⁻ | 0 | 0 | 0 | 0 AT5G48970.1 |
| 42 | PTHR24089,P ⁻ | 0 | 0 | 0 | 0 AT5G48970.1 |
| 43 | PTHR24089,P ⁻ | 0 | 0 | 0 | 0 AT5G48970.1 |
| 44 | PTHR24089,P ⁻ | 0 | 0 | 0 | 0 AT5G48970.1 |
| 45 | PTHR24089,P ⁻ | 0 | 0 | 0 | 0 AT5G48970.1 |
| 46 | PTHR24089,P ⁻ | 0 | 0 | 0 | 0 AT5G48970.1 |
| 47 | PTHR24089,P ⁻ | 0 | 0 | 0 | 0 AT5G48970.1 |
| 48 | PTHR24089,P ⁻ | 0 | 0 | 0 | 0 AT5G48970.1 |
| 49 | PTHR24089,P ⁻ | 0 | 0 | 0 | 0 AT5G48970.1 |
| 50 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 51 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 52 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 53 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 54 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 55 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 56 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 57 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 58 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 59 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 60 | | | | | |

| | | | | | |
|----|----------------------------------|----------------|----------|--------|-------------------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 4 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 5 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 6 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 7 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 8 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 9 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 10 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 11 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 12 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 13 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0032502,(AT4G37740.1 |
| 14 | PTHR22849,P ⁻ | 0 | 6.3.2.19 | 0 | GO:0016567,(AT1G76390.1 |
| 15 | PTHR22849,P ⁻ | 0 | 6.3.2.19 | 0 | GO:0016567,(AT1G76390.1 |
| 16 | PTHR22849,P ⁻ | 0 | 6.3.2.19 | 0 | GO:0016567,(AT1G76390.1 |
| 17 | PTHR22849,P ⁻ | 0 | 6.3.2.19 | 0 | GO:0016567,(AT1G76390.1 |
| 18 | PTHR22849,P ⁻ | 0 | 6.3.2.19 | 0 | GO:0016567,(AT1G76390.1 |
| 19 | PTHR24009,P ⁻ | 0 | 0 | 0 | GO:0046872,(AT3G51950.2 |
| 20 | PTHR24009,P ⁻ | 0 | 0 | 0 | GO:0046872,(AT3G51950.2 |
| 21 | PTHR24009,P ⁻ | 0 | 0 | 0 | GO:0046872,(AT3G51950.2 |
| 22 | PTHR24009,P ⁻ | 0 | 0 | 0 | GO:0046872,(AT3G51950.2 |
| 23 | PTHR24009,P ⁻ | 0 | 0 | 0 | GO:0046872,(AT3G51950.2 |
| 24 | 0 | 0 | 0 | 0 | AT3G06985.1 |
| 25 | 0 | 0 | 0 | 0 | AT3G06985.1 |
| 26 | 0 | 0 | 0 | 0 | AT3G06985.1 |
| 27 | 0 | 0 | 0 | 0 | AT3G06985.1 |
| 28 | 0 | 0 | 0 | 0 | AT3G06985.1 |
| 29 | | | | | |
| 30 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 AT4G00590.1 |
| 31 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 AT4G00590.1 |
| 32 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 AT4G00590.1 |
| 33 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 AT4G00590.1 |
| 34 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 AT4G00590.1 |
| 35 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 AT4G00590.1 |
| 36 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 AT4G00590.1 |
| 37 | | | | | |
| 38 | PTHR10173,P ⁻ KOG0856 | 1.8.4.12 | K07305 | | GO:0055114,(AT1G53670.1 |
| 39 | PTHR10173,P ⁻ KOG0856 | 1.8.4.12 | K07305 | | GO:0055114,(AT1G53670.1 |
| 40 | PTHR10173,P ⁻ KOG0856 | 1.8.4.12 | K07305 | | GO:0055114,(AT1G53670.1 |
| 41 | PTHR10173,P ⁻ KOG0856 | 1.8.4.12 | K07305 | | GO:0055114,(AT1G53670.1 |
| 42 | PTHR10173,P ⁻ KOG0856 | 1.8.4.12 | K07305 | | GO:0055114,(AT1G53670.1 |
| 43 | PTHR22884,P ⁻ KOG1082 | 2.1.1.43 | K11420 | | GO:0034968,(AT5G04940.2 |
| 44 | PTHR22884,P ⁻ KOG1082 | 2.1.1.43 | K11420 | | GO:0034968,(AT5G04940.2 |
| 45 | | | | | |
| 46 | PTHR33265,P ⁻ | 0 | 0 | 0 | AT1G52140.1 |
| 47 | PTHR33265,P ⁻ | 0 | 0 | 0 | AT1G52140.1 |
| 48 | PTHR12460 KOG2669 | | 0 | K15559 | AT5G65180.1 |
| 49 | PTHR12460 KOG2669 | | 0 | K15559 | AT5G65180.1 |
| 50 | PTHR12460 KOG2669 | | 0 | K15559 | AT5G65180.1 |
| 51 | PTHR12460 KOG2669 | | 0 | K15559 | AT5G65180.1 |
| 52 | PTHR12460 KOG2669 | | 0 | K15559 | AT5G65180.1 |
| 53 | PTHR12460 KOG2669 | | 0 | K15559 | AT5G65180.1 |
| 54 | PTHR12460 KOG2669 | | 0 | K15559 | AT5G65180.1 |
| 55 | PTHR12460 KOG2669 | | 0 | K15559 | AT5G65180.1 |
| 56 | PTHR12460 KOG2669 | | 0 | K15559 | AT5G65180.1 |
| 57 | PTHR12460 KOG2669 | | 0 | K15559 | AT5G65180.1 |
| 58 | PTHR12460 KOG2669 | | 0 | K15559 | AT5G65180.1 |
| 59 | PTHR12460 KOG2669 | | 0 | K15559 | AT5G65180.1 |
| 60 | | | | | |

| | | | | | |
|----|-------------|---------|----------|--------|-------------------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | PTHR12460 | KOG2669 | 0 | K15559 | 0 AT5G65180.1 |
| 4 | PTHR12460 | KOG2669 | 0 | K15559 | 0 AT5G65180.1 |
| 5 | PTHR12460 | KOG2669 | 0 | K15559 | 0 AT5G65180.1 |
| 6 | PTHR12460 | KOG2669 | 0 | K15559 | 0 AT5G65180.1 |
| 7 | PTHR12460 | KOG2669 | 0 | K15559 | 0 AT5G65180.1 |
| 8 | PTHR12460 | KOG2669 | 0 | K15559 | 0 AT5G65180.1 |
| 9 | PTHR12460 | KOG2669 | 0 | K15559 | 0 AT5G65180.1 |
| 10 | PTHR12460 | KOG2669 | 0 | K15559 | 0 AT5G65180.1 |
| 11 | PTHR12460 | KOG2669 | 0 | K15559 | 0 AT5G65180.1 |
| 12 | PTHR31447,P | KOG4176 | 0 | 0 | 0 AT4G02940.1 |
| 13 | PTHR28630,P | KOG4498 | 0 | 0 | 0 AT2G37240.1 |
| 14 | PTHR28630,P | KOG4498 | 0 | 0 | 0 AT2G37240.1 |
| 15 | PTHR28630,P | KOG4498 | 0 | 0 | 0 AT2G37240.1 |
| 16 | PTHR28630,P | KOG4498 | 0 | 0 | 0 AT2G37240.1 |
| 17 | PTHR28630,P | KOG4498 | 0 | 0 | 0 AT2G37240.1 |
| 18 | PTHR23293,P | KOG2644 | 2.7.7.2 | 0 | GO:0008152,(AT5G03430.1 |
| 19 | PTHR23293,P | KOG2644 | 2.7.7.2 | 0 | GO:0008152,(AT5G03430.1 |
| 20 | PTHR12121,P | KOG0620 | 3.1.13.4 | K12603 | 0 AT3G58580.1 |
| 21 | PTHR12121,P | KOG0620 | 3.1.13.4 | K12603 | 0 AT3G58580.1 |
| 22 | PTHR12121,P | KOG0620 | 3.1.13.4 | K12603 | 0 AT3G58580.1 |
| 23 | PTHR12121,P | KOG0620 | 3.1.13.4 | K12603 | 0 AT3G58580.1 |
| 24 | PTHR12121,P | KOG0620 | 3.1.13.4 | K12603 | 0 AT3G58580.1 |
| 25 | PTHR12121,P | KOG0620 | 3.1.13.4 | K12603 | 0 AT3G58580.1 |
| 26 | PTHR12121,P | KOG0620 | 3.1.13.4 | K12603 | 0 AT3G58580.1 |
| 27 | PTHR12121,P | KOG0620 | 3.1.13.4 | K12603 | 0 AT3G58580.1 |
| 28 | PTHR12121,P | KOG0620 | 3.1.13.4 | K12603 | 0 AT3G58580.1 |
| 29 | PTHR12121,P | KOG0620 | 3.1.13.4 | K12603 | 0 AT3G58580.1 |
| 30 | PTHR12121,P | KOG0620 | 3.1.13.4 | K12603 | 0 AT3G58580.1 |
| 31 | PTHR12121,P | KOG0620 | 3.1.13.4 | K12603 | 0 AT3G58580.1 |
| 32 | PTHR22849,P | 0 | 6.3.2.19 | 0 | GO:0016567,(AT1G24330.1 |
| 33 | PTHR11746,P | KOG3178 | 0 | 0 | GO:0046983,(AT4G35160.1 |
| 34 | PTHR11746,P | KOG3178 | 0 | 0 | GO:0046983,(AT4G35160.1 |
| 35 | PTHR26374,P | 0 | 0 | 0 | 0 AT3G60580.1 |
| 36 | PTHR26374,P | 0 | 0 | 0 | 0 AT3G60580.1 |
| 37 | PTHR10438,P | KOG0907 | 1.6.5.4 | K03671 | GO:0045454,(AT5G39950.1 |
| 38 | PTHR10438,P | KOG0907 | 1.6.5.4 | K03671 | GO:0045454,(AT5G39950.1 |
| 39 | PTHR10438,P | KOG0907 | 1.6.5.4 | K03671 | GO:0045454,(AT5G39950.1 |
| 40 | PTHR10438,P | KOG0907 | 1.6.5.4 | K03671 | GO:0045454,(AT5G39950.1 |
| 41 | PTHR32096,P | 0 | 0 | 0 | GO:0043565,(AT4G11070.1 |
| 42 | PTHR32096,P | 0 | 0 | 0 | GO:0043565,(AT4G11070.1 |
| 43 | PTHR12953 | KOG1396 | 0 | 0 | 0 AT4G23950.1 |
| 44 | PTHR12953 | KOG1396 | 0 | 0 | 0 AT4G23950.1 |
| 45 | PTHR12953 | KOG1396 | 0 | 0 | 0 AT4G23950.1 |
| 46 | PTHR12953 | KOG1396 | 0 | 0 | 0 AT4G23950.1 |
| 47 | PTHR23042,P | 0 | 0 | 0 | GO:0046983 AT4G37850.1 |
| 48 | PTHR23042,P | 0 | 0 | 0 | GO:0046983 AT4G37850.1 |
| 49 | PTHR23042,P | 0 | 0 | 0 | GO:0046983 AT4G37850.1 |
| 50 | PTHR23042,P | 0 | 0 | 0 | GO:0046983 AT4G37850.1 |
| 51 | PTHR23042,P | 0 | 0 | 0 | GO:0046983 AT4G37850.1 |
| 52 | PTHR22835,P | 0 | 3.1.1.3 | 0 | GO:0016788 AT1G29670.1 |
| 53 | PTHR22835,P | 0 | 3.1.1.3 | 0 | GO:0016788 AT1G29670.1 |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|----------------------------------|-------------|----------|----------------|---------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | PTHR22870,P ⁻ | 0 | 0 | 0 | 0 AT3G26100.2 |
| 4 | PTHR22870,P ⁻ | 0 | 0 | 0 | 0 AT3G26100.2 |
| 5 | PTHR22870,P ⁻ | 0 | 0 | 0 | 0 AT3G26100.2 |
| 6 | PTHR22870,P ⁻ | 0 | 0 | 0 | 0 AT3G26100.2 |
| 7 | PTHR22870,P ⁻ | 0 | 0 | 0 | 0 AT3G26100.2 |
| 8 | PTHR10791,P ⁻ KOG1623 | | 0 K15382 | GO:0016021 | AT5G50800.1 |
| 9 | PTHR10791,P ⁻ KOG1623 | | 0 K15382 | GO:0016021 | AT5G50800.1 |
| 10 | PTHR10791,P ⁻ KOG1623 | | 0 K15382 | GO:0016021 | AT5G50800.1 |
| 11 | PTHR10791,P ⁻ KOG1623 | | 0 K15382 | GO:0016021 | AT5G50800.1 |
| 12 | PTHR10791,P ⁻ KOG1623 | | 0 K15382 | GO:0016021 | AT5G50800.1 |
| 13 | PTHR11533,P ⁻ | 0 3.4.11.14 | K01256 | GO:0006508 | AT1G63770.3 |
| 14 | PTHR11533,P ⁻ | 0 3.4.11.14 | K01256 | GO:0006508 | AT1G63770.3 |
| 15 | PTHR13832,P ⁻ KOG0698 | 3.1.3.16 | K14497 | GO:0003824,(| AT4G26080.1 |
| 16 | PTHR13832,P ⁻ KOG0698 | 3.1.3.16 | K14497 | GO:0003824,(| AT4G26080.1 |
| 17 | PTHR12555,P ⁻ KOG1816 | | 0 K14016 | GO:0006511 | AT2G21270.3 |
| 18 | PTHR12555,P ⁻ KOG1816 | | 0 K14016 | GO:0006511 | AT2G21270.3 |
| 19 | PTHR12555,P ⁻ KOG1816 | | 0 K14016 | GO:0006511 | AT2G21270.3 |
| 20 | PTHR12555,P ⁻ KOG1816 | | 0 K14016 | GO:0006511 | AT2G21270.3 |
| 21 | PTHR12555,P ⁻ KOG1816 | | 0 K14016 | GO:0006511 | AT2G21270.3 |
| 22 | PTHR12555,P ⁻ KOG1816 | | 0 K14016 | GO:0006511 | AT2G21270.3 |
| 23 | PTHR12555,P ⁻ KOG1816 | | 0 K14016 | GO:0006511 | AT2G21270.3 |
| 24 | PTHR24089,P ⁻ KOG0749 | | 0 K05863 | | 0 AT5G17400.1 |
| 25 | PTHR24089,P ⁻ KOG0749 | | 0 K05863 | | 0 AT5G17400.1 |
| 26 | PTHR24089,P ⁻ KOG0749 | | 0 K05863 | | 0 AT5G17400.1 |
| 27 | PTHR24089,P ⁻ KOG0749 | | 0 K05863 | | 0 AT5G17400.1 |
| 28 | PTHR24089,P ⁻ KOG0749 | | 0 K05863 | | 0 AT5G17400.1 |
| 29 | PTHR24089,P ⁻ KOG0749 | | 0 K05863 | | 0 AT5G17400.1 |
| 30 | PTHR24089,P ⁻ KOG0749 | | 0 K05863 | | 0 AT5G17400.1 |
| 31 | PTHR24089,P ⁻ KOG0749 | | 0 K05863 | | 0 AT5G17400.1 |
| 32 | PTHR24089,P ⁻ KOG0749 | | 0 K05863 | | 0 AT5G17400.1 |
| 33 | PTHR24089,P ⁻ KOG0749 | | 0 K05863 | | 0 AT5G17400.1 |
| 34 | PTHR24089,P ⁻ KOG0749 | | 0 K05863 | | 0 AT5G17400.1 |
| 35 | PTHR10359,P ⁻ | 0 4.2.99.18 | | 0 | 0 AT5G04560.2 |
| 36 | PTHR10359,P ⁻ | 0 4.2.99.18 | | 0 | 0 AT5G04560.2 |
| 37 | PTHR10859 KOG2978 | 2.4.1.83 | K00721 | | 0 AT1G20575.1 |
| 38 | PTHR10859 KOG2978 | 2.4.1.83 | K00721 | | 0 AT1G20575.1 |
| 39 | PTHR10859 KOG2978 | 2.4.1.83 | K00721 | | 0 AT1G20575.1 |
| 40 | PTHR34775,P ⁻ | 0 | 0 | 0 | 0 AT2G16270.1 |
| 41 | PTHR34775,P ⁻ | 0 | 0 | 0 | 0 AT2G16270.1 |
| 42 | PTHR34775,P ⁻ | 0 | 0 | 0 | 0 AT2G16270.1 |
| 43 | PTHR34775,P ⁻ | 0 | 0 | 0 | 0 AT2G16270.1 |
| 44 | PTHR34775,P ⁻ | 0 | 0 | 0 | 0 AT2G16270.1 |
| 45 | PTHR23421,P ⁻ | 0 3.2.1.23 | | 0 GO:0030246,(| AT3G13750.1 |
| 46 | PTHR23421,P ⁻ | 0 3.2.1.23 | | 0 GO:0030246,(| AT3G13750.1 |
| 47 | PTHR23421,P ⁻ | 0 3.2.1.23 | | 0 GO:0030246,(| AT3G13750.1 |
| 48 | PTHR23421,P ⁻ | 0 3.2.1.23 | | 0 GO:0030246,(| AT3G13750.1 |
| 49 | PTHR23421,P ⁻ | 0 3.2.1.23 | | 0 GO:0030246,(| AT3G13750.1 |
| 50 | PTHR23421,P ⁻ | 0 3.2.1.23 | | 0 GO:0030246,(| AT3G13750.1 |
| 51 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT5G66900.1 |
| 52 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT5G66900.1 |
| 53 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT5G66900.1 |
| 54 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT5G66900.1 |
| 55 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT5G66900.1 |
| 56 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT5G66900.1 |
| 57 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT5G66900.1 |
| 58 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT5G66900.1 |
| 59 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT5G66900.1 |
| 60 | | | | | |

| | | | | | | |
|----|--------------------------|------------|----------|--------------|-------------|-------------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | PTHR23155,P ⁻ | KOG4658 | 0 | 0 | GO:0043531 | AT5G66900.1 |
| 4 | PTHR10108,P ⁻ | 0 2.1.1.41 | | 0 | GO:0008168 | AT1G31850.2 |
| 5 | PTHR10108,P ⁻ | 0 2.1.1.41 | | 0 | GO:0008168 | AT1G31850.2 |
| 6 | PTHR24012,P ⁻ | 0 | 0 | 0 | GO:0003676 | AT1G49600.1 |
| 7 | PTHR24012,P ⁻ | 0 | 0 | 0 | GO:0003676 | AT1G49600.1 |
| 8 | PTHR24012,P ⁻ | 0 | 0 | 0 | GO:0003676 | AT1G49600.1 |
| 9 | PTHR24012,P ⁻ | 0 | 0 | 0 | GO:0003676 | AT1G49600.1 |
| 10 | PTHR24012,P ⁻ | 0 | 0 | 0 | GO:0003676 | AT1G49600.1 |
| 11 | PTHR24012,P ⁻ | 0 | 0 | 0 | GO:0003676 | AT1G49600.1 |
| 12 | PTHR24012,P ⁻ | KOG0148 | 0 | 0 | GO:0003676 | AT3G19130.1 |
| 13 | PTHR24012,P ⁻ | KOG0148 | 0 | 0 | GO:0003676 | AT3G19130.1 |
| 14 | PTHR24012,P ⁻ | KOG0148 | 0 | 0 | GO:0003676 | AT3G19130.1 |
| 15 | PTHR24012,P ⁻ | KOG0148 | 0 | 0 | GO:0003676 | AT3G19130.1 |
| 16 | PTHR24012,P ⁻ | KOG0148 | 0 | 0 | GO:0003676 | AT3G19130.1 |
| 17 | PTHR24012,P ⁻ | KOG0148 | 0 | 0 | GO:0003676 | AT3G19130.1 |
| 18 | PTHR24012,P ⁻ | KOG0148 | 0 | 0 | GO:0003676 | AT3G19130.1 |
| 19 | PTHR24012,P ⁻ | KOG0148 | 0 | 0 | GO:0003676 | AT3G19130.1 |
| 20 | PTHR24012,P ⁻ | KOG0148 | 0 | 0 | GO:0003676 | AT3G19130.1 |
| 21 | PTHR24012,P ⁻ | KOG0148 | 0 | 0 | GO:0003676 | AT3G19130.1 |
| 22 | PTHR24012,P ⁻ | KOG0148 | 0 | 0 | GO:0003676 | AT3G19130.1 |
| 23 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | 0 | 0 | 0 | 0 | 0 |
| 25 | 0 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | 0 | 0 | 0 | 0 | 0 |
| 27 | 0 | 0 | 0 | 0 | 0 | 0 |
| 28 | PTHR27004,P ⁻ | KOG0472 | 2.7.11.1 | 0 | GO:0005515 | AT2G34930.1 |
| 29 | PTHR27004,P ⁻ | KOG0472 | 2.7.11.1 | 0 | GO:0005515 | AT2G34930.1 |
| 30 | PTHR34482,P ⁻ | 0 | 0 | 0 | 0 | AT3G29750.1 |
| 31 | PTHR34482,P ⁻ | 0 | 0 | 0 | 0 | AT3G29750.1 |
| 32 | PTHR34482,P ⁻ | 0 | 0 | 0 | 0 | AT3G29750.1 |
| 33 | PTHR34482,P ⁻ | 0 | 0 | 0 | 0 | AT3G29750.1 |
| 34 | PTHR34482,P ⁻ | 0 | 0 | 0 | 0 | AT3G29750.1 |
| 35 | PTHR33374,P ⁻ | 0 | 0 | 0 | 0 | AT3G61640.1 |
| 36 | PTHR33374,P ⁻ | 0 | 0 | 0 | 0 | AT3G61640.1 |
| 37 | PTHR33374,P ⁻ | 0 | 0 | 0 | 0 | AT3G61640.1 |
| 38 | PTHR33374,P ⁻ | 0 | 0 | 0 | 0 | AT3G61640.1 |
| 39 | PTHR33374,P ⁻ | 0 | 0 | 0 | 0 | AT3G61640.1 |
| 40 | PTHR33374,P ⁻ | 0 | 0 | 0 | 0 | AT3G61640.1 |
| 41 | PTHR24193,P ⁻ | KOG4214 | 0 | 0 | 0 | AT2G17390.1 |
| 42 | PTHR24193,P ⁻ | KOG4214 | 0 | 0 | 0 | AT2G17390.1 |
| 43 | PTHR24193,P ⁻ | KOG4214 | 0 | 0 | 0 | AT2G17390.1 |
| 44 | PTHR24193,P ⁻ | KOG4214 | 0 | 0 | 0 | AT2G17390.1 |
| 45 | PTHR10252,P ⁻ | 0 | 0 | 0 | 0 | AT3G12480.1 |
| 46 | PTHR35918,P ⁻ | 0 | 0 | 0 | GO:0005515 | AT1G04390.1 |
| 47 | PTHR30523,P ⁻ | 0 4.1.1.31 | K01595 | GO:0015977,(| AT2G42600.2 | |
| 48 | PTHR31973,P ⁻ | 0 | 0 | 0 | 0 | AT1G64260.1 |
| 49 | PTHR17630 | KOG3043 | 3.1.1.45 | 0 | GO:0016787 | AT2G32520.1 |
| 50 | PTHR17630 | KOG3043 | 3.1.1.45 | 0 | GO:0016787 | AT2G32520.1 |
| 51 | PTHR17630 | KOG3043 | 3.1.1.45 | 0 | GO:0016787 | AT2G32520.1 |
| 52 | PTHR17630 | KOG3043 | 3.1.1.45 | 0 | GO:0016787 | AT2G32520.1 |
| 53 | PTHR17630 | KOG3043 | 3.1.1.45 | 0 | GO:0016787 | AT2G32520.1 |
| 54 | PTHR17630 | KOG3043 | 3.1.1.45 | 0 | GO:0016787 | AT2G32520.1 |
| 55 | PTHR17630 | KOG3043 | 3.1.1.45 | 0 | GO:0016787 | AT2G32520.1 |
| 56 | PTHR17630 | KOG3043 | 3.1.1.45 | 0 | GO:0016787 | AT2G32520.1 |
| 57 | PTHR17630 | KOG3043 | 3.1.1.45 | 0 | GO:0016787 | AT2G32520.1 |
| 58 | PTHR17630 | KOG3043 | 3.1.1.45 | 0 | GO:0016787 | AT2G32520.1 |
| 59 | PTHR17630 | KOG3043 | 3.1.1.45 | 0 | GO:0016787 | AT2G32520.1 |
| 60 | | | | | | |

| | | | | | |
|----|--------------------------|---------|-------------|--------|----------------------------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | PTHR17630 | KOG3043 | 3.1.1.45 | 0 | GO:0016787 AT2G32520.1 |
| 4 | PTHR17630 | KOG3043 | 3.1.1.45 | 0 | GO:0016787 AT2G32520.1 |
| 5 | PTHR10593,P ⁻ | | | 0 | 0 AT5G22890.1 |
| 6 | PTHR10593,P ⁻ | | | 0 | 0 AT5G22890.1 |
| 7 | PTHR14095,P ⁻ | | | 0 | 0 AT5G28850.2 |
| 8 | PTHR14095,P ⁻ | | | 0 | 0 AT5G28850.2 |
| 9 | PTHR13215,P ⁻ | | | 0 | GO:0006355,(AT4G00980.1 |
| 10 | PTHR13215,P ⁻ | | | 0 | GO:0006355,(AT4G00980.1 |
| 11 | PTHR13215,P ⁻ | | | 0 | GO:0006355,(AT4G00980.1 |
| 12 | PTHR13215,P ⁻ | | | 0 | GO:0006355,(AT4G00980.1 |
| 13 | PTHR13215,P ⁻ | | | 0 | GO:0006355,(AT4G00980.1 |
| 14 | PTHR13215,P ⁻ | | | 0 | GO:0006355,(AT4G00980.1 |
| 15 | PTHR13215,P ⁻ | | | 0 | GO:0006355,(AT4G00980.1 |
| 16 | PTHR13215,P ⁻ | | | 0 | GO:0006355,(AT4G00980.1 |
| 17 | PTHR13215,P ⁻ | | | 0 | GO:0006355,(AT4G00980.1 |
| 18 | PTHR13215,P ⁻ | | | 0 | GO:0006355,(AT4G00980.1 |
| 19 | PTHR13215,P ⁻ | | | 0 | GO:0006355,(AT4G00980.1 |
| 20 | PTHR11453,P ⁻ | | | 0 | GO:0016021,(AT3G62270.1 |
| 21 | PTHR11453,P ⁻ | | | 0 | GO:0016021,(AT3G62270.1 |
| 22 | PTHR11453,P ⁻ | | | 0 | GO:0016021,(AT3G62270.1 |
| 23 | PTHR11453,P ⁻ | | | 0 | GO:0016021,(AT3G62270.1 |
| 24 | PTHR11453,P ⁻ | | | 0 | GO:0016021,(AT3G62270.1 |
| 25 | PTHR11453,P ⁻ | | | 0 | GO:0016021,(AT3G62270.1 |
| 26 | PTHR11453,P ⁻ | | | 0 | GO:0016021,(AT3G62270.1 |
| 27 | PTHR11453,P ⁻ | | | 0 | GO:0016021,(AT3G62270.1 |
| 28 | PTHR11453,P ⁻ | | | 0 | GO:0016021,(AT3G62270.1 |
| 29 | PTHR11453,P ⁻ | | | 0 | GO:0016021,(AT3G62270.1 |
| 30 | PTHR11453,P ⁻ | | | 0 | GO:0016021,(AT3G62270.1 |
| 31 | PTHR33670,P ⁻ | | | 0 | 0 AT3G21570.1 |
| 32 | PTHR11802,P ⁻ | KOG1282 | | 0 | K16296 GO:0006508,(AT5G09640.1 |
| 33 | PTHR11802,P ⁻ | KOG1282 | | 0 | K16296 GO:0006508,(AT5G09640.1 |
| 34 | PTHR11802,P ⁻ | KOG1282 | | 0 | K16296 GO:0006508,(AT5G09640.1 |
| 35 | PTHR11802,P ⁻ | KOG1282 | | 0 | K16296 GO:0006508,(AT5G09640.1 |
| 36 | PTHR11802,P ⁻ | KOG1282 | | 0 | K16296 GO:0006508,(AT5G09640.1 |
| 37 | PTHR13063,P ⁻ | KOG3039 | | 0 | K13125 GO:0050999 AT1G61620.1 |
| 38 | PTHR13063,P ⁻ | KOG3039 | | 0 | K13125 GO:0050999 AT1G61620.1 |
| 39 | PTHR11757,P ⁻ | | 0 3.4.21.83 | K01354 | GO:0008236,(AT1G50380.1 |
| 40 | PTHR11757,P ⁻ | | 0 3.4.21.83 | K01354 | GO:0008236,(AT1G50380.1 |
| 41 | PTHR11757,P ⁻ | | 0 3.4.21.83 | K01354 | GO:0008236,(AT1G50380.1 |
| 42 | PTHR11757,P ⁻ | | 0 3.4.21.83 | K01354 | GO:0008236,(AT1G50380.1 |
| 43 | PTHR11757,P ⁻ | | 0 3.4.21.83 | K01354 | GO:0008236,(AT1G50380.1 |
| 44 | PTHR31072,P ⁻ | | | 0 | 0 AT5G23280.1 |
| 45 | PTHR31072,P ⁻ | | | 0 | 0 AT5G23280.1 |
| 46 | PTHR15362,P ⁻ | | 0 2.7.8.8 | K08730 | GO:0006659 AT1G15110.1 |
| 47 | PTHR27002 | KOG1187 | 2.7.10.2 | | 0 GO:0006468,(AT4G05200.1 |
| 48 | PTHR27002 | KOG1187 | 2.7.10.2 | | 0 GO:0006468,(AT4G05200.1 |
| 49 | PTHR27002 | KOG1187 | 2.7.10.2 | | 0 GO:0006468,(AT4G05200.1 |
| 50 | PTHR27002 | KOG1187 | 2.7.10.2 | | 0 GO:0006468,(AT4G05200.1 |
| 51 | PTHR10638,P ⁻ | | | 0 | 0 K00276 GO:0055114,(AT4G14940.1 |
| 52 | PTHR10638,P ⁻ | | | 0 | 0 K00276 GO:0055114,(AT4G14940.1 |
| 53 | PTHR10638,P ⁻ | | | 0 | 0 K00276 GO:0055114,(AT4G14940.1 |
| 54 | PTHR10638,P ⁻ | | | 0 | 0 K00276 GO:0055114,(AT4G14940.1 |
| 55 | PTHR10638,P ⁻ | | | 0 | 0 K00276 GO:0055114,(AT4G14940.1 |
| 56 | PTHR10638,P ⁻ | | | 0 | 0 K00276 GO:0055114,(AT4G14940.1 |
| 57 | PTHR10638,P ⁻ | | | 0 | 0 K00276 GO:0055114,(AT4G14940.1 |
| 58 | PTHR10638,P ⁻ | | | 0 | 0 K00276 GO:0055114,(AT4G14940.1 |
| 59 | PTHR10638,P ⁻ | | | 0 | 0 K00276 GO:0055114,(AT4G14940.1 |
| 60 | | | | | |

| | | | | | |
|----|----------------------------------|------------|--------|-------------------------|-------------------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | PTHR33059,P ⁻ | 0 | 0 | 0 | 0 AT3G22550.1 |
| 4 | PTHR33059,P ⁻ | 0 | 0 | 0 | 0 AT3G22550.1 |
| 5 | PTHR33059,P ⁻ | 0 | 0 | 0 | 0 AT3G22550.1 |
| 6 | PTHR33059,P ⁻ | 0 | 0 | 0 | 0 AT3G22550.1 |
| 7 | PTHR33059,P ⁻ | 0 | 0 | 0 | 0 AT3G22550.1 |
| 8 | PTHR33059,P ⁻ | 0 | 0 | 0 | 0 AT3G22550.1 |
| 9 | PTHR33059,P ⁻ | 0 | 0 | 0 | 0 AT3G22550.1 |
| 10 | PTHR33059,P ⁻ | 0 | 0 | 0 | 0 AT3G22550.1 |
| 11 | PTHR33059,P ⁻ | 0 | 0 | 0 | 0 AT3G22550.1 |
| 12 | PTHR33059,P ⁻ | 0 | 0 | 0 | 0 AT3G22550.1 |
| 13 | PTHR33059,P ⁻ | 0 | 0 | 0 | 0 AT3G22550.1 |
| 14 | PTHR23024,P ⁻ KOG1515 | 3.1.1.1 | | 0 | 0 AT5G62180.1 |
| 15 | PTHR23024,P ⁻ KOG1515 | 3.1.1.1 | | 0 | 0 AT5G62180.1 |
| 16 | PTHR23024,P ⁻ KOG1515 | 3.1.1.1 | | 0 | 0 AT5G62180.1 |
| 17 | PTHR23024,P ⁻ KOG1515 | 3.1.1.1 | | 0 | 0 AT5G62180.1 |
| 18 | PTHR23024,P ⁻ KOG1515 | 3.1.1.1 | | 0 | 0 AT5G62180.1 |
| 19 | PTHR23024,P ⁻ KOG1515 | 3.1.1.1 | | 0 | 0 AT5G62180.1 |
| 20 | PTHR11972,P ⁻ KOG0039 | 1.16.1.7 | | 0 | GO:0055114,(AT1G01580.1 |
| 21 | PTHR11972,P ⁻ KOG0039 | 1.16.1.7 | | 0 | GO:0055114,(AT1G01580.1 |
| 22 | PTHR11972,P ⁻ KOG0039 | 1.16.1.7 | | 0 | GO:0055114,(AT1G01580.1 |
| 23 | PTHR11972,P ⁻ KOG0039 | 1.16.1.7 | | 0 | GO:0055114,(AT1G01580.1 |
| 24 | PTHR11972,P ⁻ KOG0039 | 1.16.1.7 | | 0 | GO:0055114,(AT1G01580.1 |
| 25 | PTHR11972,P ⁻ KOG0039 | 1.16.1.7 | | 0 | GO:0055114,(AT1G01580.1 |
| 26 | PTHR35732,P ⁻ | 0 | 0 | 0 | 0 AT3G10405.1 |
| 27 | PTHR35732,P ⁻ | 0 | 0 | 0 | 0 AT3G10405.1 |
| 28 | PTHR35732,P ⁻ | 0 | 0 | 0 | 0 AT3G10405.1 |
| 29 | PTHR35732,P ⁻ | 0 | 0 | 0 | 0 AT3G10405.1 |
| 30 | PTHR35732,P ⁻ | 0 | 0 | 0 | 0 AT3G10405.1 |
| 31 | PTHR11260,P ⁻ KOG0867 | 2.5.1.18 | K00799 | GO:0005515 | AT1G02920.1 |
| 32 | PTHR11260,P ⁻ KOG0867 | 2.5.1.18 | K00799 | GO:0005515 | AT1G02920.1 |
| 33 | PTHR11260,P ⁻ KOG0867 | 2.5.1.18 | K00799 | GO:0005515 | AT1G02920.1 |
| 34 | PTHR11260,P ⁻ KOG0867 | 2.5.1.18 | K00799 | GO:0005515 | AT1G02920.1 |
| 35 | PTHR11260,P ⁻ KOG0867 | 2.5.1.18 | K00799 | GO:0005515 | AT1G02920.1 |
| 36 | PTHR37764,P ⁻ | 0 | 0 | 0 | 0 AT5G27390.1 |
| 37 | PTHR37764,P ⁻ | 0 | 0 | 0 | 0 AT5G27390.1 |
| 38 | PTHR37764,P ⁻ | 0 | 0 | 0 | 0 AT5G27390.1 |
| 39 | PTHR37764,P ⁻ | 0 | 0 | 0 | 0 AT5G27390.1 |
| 40 | PTHR37764,P ⁻ | 0 | 0 | 0 | 0 AT5G27390.1 |
| 41 | PTHR37764,P ⁻ | 0 | 0 | 0 | 0 AT5G27390.1 |
| 42 | PTHR33592 | 0 | 0 | 0 | 0 AT2G31345.1 |
| 43 | PTHR33592 | 0 | 0 | 0 | 0 AT2G31345.1 |
| 44 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G56720.1 |
| 45 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G56720.1 |
| 46 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G56720.1 |
| 47 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G56720.1 |
| 48 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G56720.1 |
| 49 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G56720.1 |
| 50 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G56720.1 |
| 51 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G56720.1 |
| 52 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G56720.1 |
| 53 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G56720.1 |
| 54 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G56720.1 |
| 55 | PTHR31707,P ⁻ | 0 3.1.1.11 | K01051 | GO:0004857,(AT3G05610.1 | |
| 56 | 0 | 0 | 0 | 0 | 0 |
| 57 | 0 | 0 | 0 | 0 | 0 |
| 58 | 0 | 0 | 0 | 0 | 0 |
| 59 | 0 | 0 | 0 | 0 | 0 |
| 60 | | | | | |

| | | | | | | |
|----|----------------------------------|-------------|----------|---|--------------|-------------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | 0 | 0 | 0 | 0 | 0 | 0 |
| 4 | 0 | 0 | 0 | 0 | 0 | 0 |
| 5 | 0 | 0 | 0 | 0 | 0 | 0 |
| 6 | 0 | 0 | 0 | 0 | 0 | 0 |
| 7 | PTHR35313,P ⁻ | 0 | 0 | 0 | 0 | AT5G13390.1 |
| 8 | PTHR35313,P ⁻ | 0 | 0 | 0 | 0 | AT5G13390.1 |
| 9 | PTHR35313,P ⁻ | 0 | 0 | 0 | 0 | AT5G13390.1 |
| 10 | PTHR35313,P ⁻ | 0 | 0 | 0 | 0 | AT5G13390.1 |
| 11 | PTHR35313,P ⁻ | 0 | 0 | 0 | 0 | AT5G13390.1 |
| 12 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 | AT5G16210.1 |
| 13 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 | AT5G16210.1 |
| 14 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 | AT5G16210.1 |
| 15 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 | AT5G16210.1 |
| 16 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 | AT5G16210.1 |
| 17 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 | AT5G16210.1 |
| 18 | PTHR32059,P ⁻ | 0 | 0 | 0 | 0 | AT5G16210.1 |
| 19 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | | GO:0006352,(| AT1G04950.1 |
| 20 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | | GO:0006352,(| AT1G04950.1 |
| 21 | PTHR13068,P ⁻ | 0 | 0 K15032 | | GO:0006355,(| AT3G18870.1 |
| 22 | PTHR13068,P ⁻ | 0 | 0 K15032 | | GO:0006355,(| AT3G18870.1 |
| 23 | PTHR35410,P ⁻ | 0 | 0 | 0 | 0 | 0 |
| 24 | PTHR35410,P ⁻ | 0 | 0 | 0 | 0 | 0 |
| 25 | PTHR35410,P ⁻ | 0 | 0 | 0 | 0 | 0 |
| 26 | PTHR35410,P ⁻ | 0 | 0 | 0 | 0 | 0 |
| 27 | PTHR35410,P ⁻ | 0 | 0 | 0 | 0 | 0 |
| 28 | PTHR33463,P ⁻ KOG1947 | | 0 | 0 | 0 | AT1G61300.1 |
| 29 | PTHR33463,P ⁻ KOG1947 | | 0 | 0 | 0 | AT1G61300.1 |
| 30 | PTHR33463,P ⁻ KOG1947 | | 0 | 0 | 0 | AT1G61300.1 |
| 31 | PTHR33463,P ⁻ KOG1947 | | 0 | 0 | 0 | AT1G61300.1 |
| 32 | PTHR33463,P ⁻ KOG1947 | | 0 | 0 | 0 | AT1G61300.1 |
| 33 | PTHR27000,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0005515,(| AT3G47570.1 |
| 34 | PTHR27000,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0005515,(| AT3G47570.1 |
| 35 | PTHR27000,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0005515,(| AT3G47570.1 |
| 36 | PTHR27000,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0005515,(| AT3G47570.1 |
| 37 | PTHR27000,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0005515,(| AT3G47570.1 |
| 38 | PTHR27000,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0005515,(| AT3G47570.1 |
| 39 | PTHR27000,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0005515,(| AT3G47570.1 |
| 40 | PTHR27000,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0005515,(| AT3G47570.1 |
| 41 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 | AT5G01120.1 |
| 42 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 | AT5G01120.1 |
| 43 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 | AT5G01120.1 |
| 44 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 | AT5G01120.1 |
| 45 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 | AT5G01120.1 |
| 46 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 | AT5G01120.1 |
| 47 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 | AT5G01120.1 |
| 48 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 | GO:0006508,(| AT5G02190.1 |
| 49 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 | GO:0006508,(| AT5G02190.1 |
| 50 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 | GO:0006508,(| AT5G02190.1 |
| 51 | 0 | 0 | 0 | 0 | 0 | 0 |
| 52 | 0 | 0 | 0 | 0 | 0 | 0 |
| 53 | 0 | 0 | 0 | 0 | 0 | 0 |
| 54 | 0 | 0 | 0 | 0 | 0 | 0 |
| 55 | 0 | 0 | 0 | 0 | 0 | 0 |
| 56 | PTHR13078 | 0 4.2.1.119 | | 0 | 0 | AT5G60335.1 |
| 57 | PTHR13078 | 0 4.2.1.119 | | 0 | 0 | AT5G60335.1 |
| 58 | PTHR13078 | 0 4.2.1.119 | | 0 | 0 | AT5G60335.1 |
| 59 | PTHR13078 | 0 4.2.1.119 | | 0 | 0 | AT5G60335.1 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------------------------|-------------|----------|--------------|--------------|---------------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | PTHR13078 | 0 4.2.1.119 | | 0 | | 0 AT5G60335.1 |
| 4 | | | | | | |
| 5 | 0 | 0 | 0 | 0 | 0 | 0 |
| 6 | 0 | 0 | 0 | 0 | 0 | 0 |
| 7 | 0 | 0 | 0 | 0 | 0 | 0 |
| 8 | 0 | 0 | 0 | 0 | 0 | 0 |
| 9 | | | | | | |
| 10 | PTHR22950,P ⁻ KOG1303 | | 0 | 0 | | 0 AT2G39890.1 |
| 11 | PTHR22950,P ⁻ KOG1303 | | 0 | 0 | | 0 AT2G39890.1 |
| 12 | PTHR22950,P ⁻ KOG1303 | | 0 | 0 | | 0 AT2G39890.1 |
| 13 | PTHR22950,P ⁻ KOG1303 | | 0 | 0 | | 0 AT2G39890.1 |
| 14 | PTHR24012,P ⁻ KOG4205 | | 0 K14411 | GO:0003676 | | AT3G07810.1 |
| 15 | PTHR24012,P ⁻ KOG4205 | | 0 K14411 | GO:0003676 | | AT3G07810.1 |
| 16 | PTHR24012,P ⁻ KOG4205 | | 0 K14411 | GO:0003676 | | AT3G07810.1 |
| 17 | PTHR23289,P ⁻ | 0 | 0 K02259 | GO:0055114,(| | AT5G56090.1 |
| 18 | PTHR23289,P ⁻ | 0 | 0 K02259 | GO:0055114,(| | AT5G56090.1 |
| 19 | PTHR10641,P ⁻ KOG0048 | | 0 | 0 | | 0 AT4G32730.2 |
| 20 | PTHR10972,P ⁻ | 0 | 0 | 0 | | 0 AT4G08180.2 |
| 21 | PTHR10972,P ⁻ | 0 | 0 | 0 | | 0 AT4G08180.2 |
| 22 | PTHR10972,P ⁻ | 0 | 0 | 0 | | 0 AT4G08180.2 |
| 23 | PTHR10972,P ⁻ | 0 | 0 | 0 | | 0 AT4G08180.2 |
| 24 | PTHR13902 KOG0198 | 2.7.11.1 | | 0 | GO:0006468,(| AT3G48260.1 |
| 25 | PTHR13902 KOG0198 | 2.7.11.1 | | 0 | GO:0006468,(| AT3G48260.1 |
| 26 | PTHR13902 KOG0198 | 2.7.11.1 | | 0 | GO:0006468,(| AT3G48260.1 |
| 27 | PTHR13902 KOG0198 | 2.7.11.1 | | 0 | GO:0006468,(| AT3G48260.1 |
| 28 | PTHR23421,P ⁻ | 0 3.2.1.23 | | 0 | GO:0005975,(| AT4G26140.1 |
| 29 | PTHR23421,P ⁻ | 0 3.2.1.23 | | 0 | GO:0005975,(| AT4G26140.1 |
| 30 | PTHR11746,P ⁻ KOG3178 | 2.1.1.68 | K13066 | GO:0046983,(| | AT5G54160.1 |
| 31 | PTHR11746,P ⁻ KOG3178 | 2.1.1.68 | K13066 | GO:0046983,(| | AT5G54160.1 |
| 32 | PTHR11746,P ⁻ KOG3178 | 2.1.1.68 | K13066 | GO:0046983,(| | AT5G54160.1 |
| 33 | PTHR11746,P ⁻ KOG3178 | 2.1.1.68 | K13066 | GO:0046983,(| | AT5G54160.1 |
| 34 | PTHR32387,P ⁻ | 0 | 0 K17592 | | | 0 AT3G48770.1 |
| 35 | PTHR32387,P ⁻ | 0 | 0 K17592 | | | 0 AT3G48770.1 |
| 36 | PTHR32387,P ⁻ | 0 | 0 K17592 | | | 0 AT3G48770.1 |
| 37 | PTHR32387,P ⁻ | 0 | 0 K17592 | | | 0 AT3G48770.1 |
| 38 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 39 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 40 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 41 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 42 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 43 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 44 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 45 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 46 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 47 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 48 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 49 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 50 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 51 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 52 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 53 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 54 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 55 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 56 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 57 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 58 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 59 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(| AT3G60240.4 |
| 60 | | | | | | |

| | | | | | |
|----|----------------------------------|----------------|--------|---|-------------------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(AT3G60240.4 |
| 4 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(AT3G60240.4 |
| 5 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(AT3G60240.4 |
| 6 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(AT3G60240.4 |
| 7 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(AT3G60240.4 |
| 8 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(AT3G60240.4 |
| 9 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(AT3G60240.4 |
| 10 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(AT3G60240.4 |
| 11 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(AT3G60240.4 |
| 12 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(AT3G60240.4 |
| 13 | PTHR23253,P ⁻ KOG0401 | | 0 | 0 | GO:0005515,(AT3G60240.4 |
| 14 | PTHR12565,P ⁻ | 0 | 0 | 0 | GO:0046983 AT4G00050.1 |
| 15 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | AT2G45690.1 |
| 16 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | AT2G45690.1 |
| 17 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | AT2G45690.1 |
| 18 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | AT2G45690.1 |
| 19 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | AT2G45690.1 |
| 20 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | AT2G45690.1 |
| 21 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | AT2G45690.1 |
| 22 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | AT2G45690.1 |
| 23 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | AT2G45690.1 |
| 24 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | AT2G45690.1 |
| 25 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | AT2G45690.1 |
| 26 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | AT2G45690.1 |
| 27 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | AT2G45690.1 |
| 28 | PTHR11771,P ⁻ | 0 1.13.11.58 | | 0 | GO:0055114,(AT1G55020.1 |
| 29 | PTHR11771,P ⁻ | 0 1.13.11.58 | | 0 | GO:0055114,(AT1G55020.1 |
| 30 | PTHR11771,P ⁻ | 0 1.13.11.58 | | 0 | GO:0055114,(AT1G55020.1 |
| 31 | PTHR11771,P ⁻ | 0 1.13.11.58 | | 0 | GO:0055114,(AT1G55020.1 |
| 32 | PTHR11771,P ⁻ | 0 1.13.11.58 | | 0 | GO:0055114,(AT1G55020.1 |
| 33 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT3G57330.1 |
| 34 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT3G57330.1 |
| 35 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT3G57330.1 |
| 36 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT3G57330.1 |
| 37 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT3G57330.1 |
| 38 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT3G57330.1 |
| 39 | PTHR11139,P ⁻ | 0 2.7.11.1 | K08873 | | GO:0005515,(AT1G50030.1 |
| 40 | PTHR11139,P ⁻ | 0 2.7.11.1 | K08873 | | GO:0005515,(AT1G50030.1 |
| 41 | PTHR11139,P ⁻ | 0 2.7.11.1 | K08873 | | GO:0005515,(AT1G50030.1 |
| 42 | PTHR11139,P ⁻ | 0 2.7.11.1 | K08873 | | GO:0005515,(AT1G50030.1 |
| 43 | PTHR11139,P ⁻ | 0 2.7.11.1 | K08873 | | GO:0005515,(AT1G50030.1 |
| 44 | PTHR14194,P ⁻ KOG1203 | | 0 | 0 | AT3G46780.1 |
| 45 | PTHR14194,P ⁻ KOG1203 | | 0 | 0 | AT3G46780.1 |
| 46 | PTHR31232 | 0 | 0 | 0 | AT1G04645.1 |
| 47 | PTHR31232 | 0 | 0 | 0 | AT4G16195.1 |
| 48 | PTHR31232 | 0 | 0 | 0 | AT4G16195.1 |
| 49 | 0 | 0 | 0 | 0 | AT3G06985.1 |
| 50 | 0 | 0 | 0 | 0 | AT3G06985.1 |
| 51 | 0 | 0 | 0 | 0 | AT3G06985.1 |
| 52 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 AT4G00590.1 |
| 53 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 AT4G00590.1 |
| 54 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 AT4G00590.1 |
| 55 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 AT4G00590.1 |
| 56 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 AT4G00590.1 |
| 57 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 AT4G00590.1 |
| 58 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 AT4G00590.1 |
| 59 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 AT4G00590.1 |
| 60 | | | | | |

| | | | | | | |
|----|----------------------------------|------------------|----------|---|--------------|-------------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 | AT4G00590.1 |
| 4 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 | AT4G00590.1 |
| 5 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 | AT4G00590.1 |
| 6 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 | AT4G00590.1 |
| 7 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 | AT4G00590.1 |
| 8 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 | AT4G00590.1 |
| 9 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 | AT4G00590.1 |
| 10 | PTHR10188,P ⁻ KOG1592 | 3.4.19.5,3.5.1 | | 0 | GO:0016787 | AT4G00590.1 |
| 11 | 0 | 0 | 0 | 0 | 0 | 0 |
| 12 | 0 | 0 | 0 | 0 | 0 | 0 |
| 13 | 0 | 0 | 0 | 0 | 0 | 0 |
| 14 | 0 | 0 | 0 | 0 | 0 | 0 |
| 15 | 0 | 0 | 0 | 0 | 0 | 0 |
| 16 | PTHR23076,P ⁻ KOG0737 | | 0 | 0 | GO:0006508,(| AT3G04340.1 |
| 17 | PTHR23076,P ⁻ KOG0737 | | 0 | 0 | GO:0006508,(| AT3G04340.1 |
| 18 | PTHR23076,P ⁻ KOG0737 | | 0 | 0 | GO:0006508,(| AT3G04340.1 |
| 19 | PTHR23076,P ⁻ KOG0737 | | 0 | 0 | GO:0006508,(| AT3G04340.1 |
| 20 | PTHR23076,P ⁻ KOG0737 | | 0 | 0 | GO:0006508,(| AT3G04340.1 |
| 21 | PTHR23076,P ⁻ KOG0737 | | 0 | 0 | GO:0006508,(| AT3G04340.1 |
| 22 | PTHR23076,P ⁻ KOG0737 | | 0 | 0 | GO:0006508,(| AT3G04340.1 |
| 23 | PTHR23076,P ⁻ KOG0737 | | 0 | 0 | GO:0006508,(| AT3G04340.1 |
| 24 | PTHR23076,P ⁻ KOG0737 | | 0 | 0 | GO:0006508,(| AT3G04340.1 |
| 25 | PTHR23076,P ⁻ KOG0737 | | 0 | 0 | GO:0006508,(| AT3G04340.1 |
| 26 | PTHR23076,P ⁻ KOG0737 | | 0 | 0 | GO:0006508,(| AT3G04340.1 |
| 27 | PTHR14089,P ⁻ | 0 | 0 K12872 | 0 | GO:0003676 | AT1G07360.1 |
| 28 | PTHR14089,P ⁻ | 0 | 0 K12872 | 0 | GO:0003676 | AT1G07360.1 |
| 29 | PTHR14089,P ⁻ | 0 | 0 K12872 | 0 | GO:0003676 | AT1G07360.1 |
| 30 | PTHR14089,P ⁻ | 0 | 0 K12872 | 0 | GO:0003676 | AT1G07360.1 |
| 31 | PTHR11709,P ⁻ | 0 1.10.3.2 | K05909 | 0 | GO:0055114,(| AT2G29130.1 |
| 32 | PTHR11695,P ⁻ | 0 1.1.1.54,1.3.1 | | 0 | GO:0055114,(| AT1G65560.1 |
| 33 | PTHR11695,P ⁻ | 0 1.1.1.54,1.3.1 | | 0 | GO:0055114,(| AT1G65560.1 |
| 34 | PTHR11695,P ⁻ | 0 1.1.1.54,1.3.1 | | 0 | GO:0055114,(| AT1G65560.1 |
| 35 | PTHR32176 KOG0513 | | 0 | 0 | GO:0006629 | AT2G26560.1 |
| 36 | PTHR32176 KOG0513 | | 0 | 0 | GO:0006629 | AT2G26560.1 |
| 37 | | | | | | |
| 38 | PTHR31471,P ⁻ | 0 | 0 | 0 | 0 | AT1G45207.2 |
| 39 | PTHR31471,P ⁻ | 0 | 0 | 0 | 0 | AT1G45207.2 |
| 40 | PTHR31471,P ⁻ | 0 | 0 | 0 | 0 | AT1G45207.2 |
| 41 | PTHR31471,P ⁻ | 0 | 0 | 0 | 0 | AT1G45207.2 |
| 42 | PTHR31471,P ⁻ | 0 | 0 | 0 | 0 | AT1G45207.2 |
| 43 | PTHR31953,P ⁻ | 0 3.2.1.153,3.2. | K01193 | 0 | | AT3G13790.1 |
| 44 | PTHR22166,P ⁻ KOG2846 | | 0 | 0 | 0 | AT4G31080.1 |
| 45 | PTHR22166,P ⁻ KOG2846 | | 0 | 0 | 0 | AT4G31080.1 |
| 46 | PTHR22166,P ⁻ KOG2846 | | 0 | 0 | 0 | AT4G31080.1 |
| 47 | PTHR10457,P ⁻ KOG0631 | 2.7.1.46 | K12446 | 0 | GO:0005524 | AT4G16130.1 |
| 48 | PTHR10457,P ⁻ KOG0631 | 2.7.1.46 | K12446 | 0 | GO:0005524 | AT4G16130.1 |
| 49 | PTHR24095,P ⁻ | 0 6.2.1.1 | K01895 | 0 | GO:0008152,(| AT5G36880.2 |
| 50 | PTHR24095,P ⁻ | 0 6.2.1.1 | K01895 | 0 | GO:0008152,(| AT5G36880.2 |
| 51 | PTHR24095,P ⁻ | 0 6.2.1.1 | K01895 | 0 | GO:0008152,(| AT5G36880.2 |
| 52 | PTHR23326,P ⁻ KOG2150 | | 0 K12580 | 0 | GO:0006355,(| AT5G18230.1 |
| 53 | PTHR23326,P ⁻ KOG2150 | | 0 K12580 | 0 | GO:0006355,(| AT5G18230.1 |
| 54 | PTHR23326,P ⁻ KOG2150 | | 0 K12580 | 0 | GO:0006355,(| AT5G18230.1 |
| 55 | PTHR23326,P ⁻ KOG2150 | | 0 K12580 | 0 | GO:0006355,(| AT5G18230.1 |
| 56 | PTHR23326,P ⁻ KOG2150 | | 0 K12580 | 0 | GO:0006355,(| AT5G18230.1 |
| 57 | PTHR12196 KOG2316 | 6.3.1.14 | K06927 | 0 | | AT3G04480.1 |
| 58 | PTHR12196 KOG2316 | 6.3.1.14 | K06927 | 0 | | AT3G04480.1 |
| 59 | PTHR12196 KOG2316 | 6.3.1.14 | K06927 | 0 | | AT3G04480.1 |
| 60 | | | | | | |

| | | | | | |
|----|----------------------------------|-------------|--------|----------------|---------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | PTHR22762,P ⁻ | 0 3.2.1.20 | | 0 GO:0005975,(| AT5G63840.1 |
| 4 | PTHR22762,P ⁻ | 0 3.2.1.20 | | 0 GO:0005975,(| AT5G63840.1 |
| 5 | | | | | |
| 6 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14470.1 |
| 7 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14470.1 |
| 8 | | | | | |
| 9 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14470.1 |
| 10 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14470.1 |
| 11 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14470.1 |
| 12 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14470.1 |
| 13 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14470.1 |
| 14 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14470.1 |
| 15 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14470.1 |
| 16 | | | | | |
| 17 | PTHR31529,P ⁻ | 0 | 0 | 0 | AT2G42430.1 |
| 18 | PTHR31314,P ⁻ | 0 | 0 | 0 | AT4G28610.1 |
| 19 | PTHR31314,P ⁻ | 0 | 0 | 0 | AT4G28610.1 |
| 20 | PTHR31314,P ⁻ | 0 | 0 | 0 | AT4G28610.1 |
| 21 | PTHR31314,P ⁻ | 0 | 0 | 0 | AT4G28610.1 |
| 22 | PTHR31314,P ⁻ | 0 | 0 | 0 | AT4G28610.1 |
| 23 | PTHR31314,P ⁻ | 0 | 0 | 0 | AT4G28610.1 |
| 24 | PTHR31314,P ⁻ | 0 | 0 | 0 | AT4G28610.1 |
| 25 | PTHR31314,P ⁻ | 0 | 0 | 0 | AT4G28610.1 |
| 26 | PTHR31314,P ⁻ | 0 | 0 | 0 | AT4G28610.1 |
| 27 | PTHR31314,P ⁻ | 0 | 0 | 0 | AT4G28610.1 |
| 28 | | | | | |
| 29 | PTHR31268,P ⁻ | 0 2.4.1.67 | K06611 | | 0 AT4G01970.1 |
| 30 | PTHR31268,P ⁻ | 0 2.4.1.67 | K06611 | | 0 AT4G01970.1 |
| 31 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02519 | GO:0005525 | AT4G11160.1 |
| 32 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02519 | GO:0005525 | AT4G11160.1 |
| 33 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02519 | GO:0005525 | AT4G11160.1 |
| 34 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02519 | GO:0005525 | AT4G11160.1 |
| 35 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02519 | GO:0005525 | AT4G11160.1 |
| 36 | PTHR23083,P ⁻ | 0 | 0 | 0 | AT4G37460.1 |
| 37 | PTHR23083,P ⁻ | 0 | 0 | 0 | AT4G37460.1 |
| 38 | PTHR23083,P ⁻ | 0 | 0 | 0 | AT4G37460.1 |
| 39 | PTHR23083,P ⁻ | 0 | 0 | 0 | AT4G37460.1 |
| 40 | PTHR23083,P ⁻ | 0 | 0 | 0 | AT4G37460.1 |
| 41 | | | | | |
| 42 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT3G22690.2 |
| 43 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT3G22690.2 |
| 44 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT3G22690.2 |
| 45 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT3G22690.2 |
| 46 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT3G22690.2 |
| 47 | PTHR26374,P ⁻ | 0 | 0 | 0 | AT3G60580.1 |
| 48 | PTHR26374,P ⁻ | 0 | 0 | 0 | AT3G60580.1 |
| 49 | | | | | |
| 50 | PTHR31867,P ⁻ | 0 | 0 | 0 | AT1G12560.1 |
| 51 | PTHR31867,P ⁻ | 0 | 0 | 0 | AT1G12560.1 |
| 52 | PTHR31867,P ⁻ | 0 | 0 | 0 | AT1G12560.1 |
| 53 | PTHR31867,P ⁻ | 0 | 0 | 0 | AT1G12560.1 |
| 54 | | | | | |
| 55 | PTHR10366,P ⁻ | 0 1.1.1.133 | K12451 | | 0 AT1G63000.1 |
| 56 | PTHR22835,P ⁻ | 0 3.1.1.3 | | 0 GO:0016788 | AT1G29670.1 |
| 57 | PTHR22835,P ⁻ | 0 3.1.1.3 | | 0 GO:0016788 | AT1G29670.1 |
| 58 | PTHR22835,P ⁻ | 0 3.1.1.3 | | 0 GO:0016788 | AT1G29670.1 |
| 59 | PTHR22835,P ⁻ | 0 3.1.1.3 | | 0 GO:0016788 | AT1G29670.1 |
| 60 | | | | | |

| | | | | | |
|----|----------------------------------|-------------------------|----------|---------------------------|---------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | PTHR22835,P ⁻ | 0 3.1.1.3 | | 0 GO:0016788 | AT1G29670.1 |
| 4 | PTHR22870,P ⁻ | 0 | 0 | 0 | 0 AT3G26100.2 |
| 5 | PTHR22870,P ⁻ | 0 | 0 | 0 | 0 AT3G26100.2 |
| 6 | PTHR23315,P ⁻ | 0 | 0 | 0 GO:0005515 | AT2G22125.1 |
| 7 | PTHR11514,P ⁻ | 0 | 0 | 0 GO:0046983 | AT5G41315.1 |
| 8 | PTHR11514,P ⁻ | 0 | 0 | 0 GO:0046983 | AT5G41315.1 |
| 9 | PTHR23315,P ⁻ | 0 | 0 | 0 GO:0043248 | AT1G23180.1 |
| 10 | PTHR23315,P ⁻ | 0 | 0 | 0 GO:0043248 | AT1G23180.1 |
| 11 | PTHR22762,P ⁻ | 0 3.2.1.177,3.2. K15925 | | GO:0005975,(AT1G68560.1 | |
| 12 | PTHR22762,P ⁻ | 0 3.2.1.177,3.2. K15925 | | GO:0005975,(AT1G68560.1 | |
| 13 | PTHR22762,P ⁻ | 0 3.2.1.177,3.2. K15925 | | GO:0005975,(AT1G68560.1 | |
| 14 | PTHR22762,P ⁻ | 0 3.2.1.177,3.2. K15925 | | GO:0005975,(AT1G68560.1 | |
| 15 | PTHR31642,P ⁻ | 0 2.3.1.99 | | 0 GO:0016747 | AT4G13840.1 |
| 16 | PTHR31642,P ⁻ | 0 2.3.1.99 | | 0 GO:0016747 | AT4G13840.1 |
| 17 | PTHR31642,P ⁻ | 0 2.3.1.99 | | 0 GO:0016747 | AT4G13840.1 |
| 18 | PTHR31642,P ⁻ | 0 2.3.1.99 | | 0 GO:0016747 | AT4G13840.1 |
| 19 | PTHR10774,P ⁻ KOG1032 | | 0 | 0 GO:0005515 | AT1G03370.1 |
| 20 | PTHR10774,P ⁻ KOG1032 | | 0 | 0 GO:0005515 | AT1G03370.1 |
| 21 | PTHR24089,P ⁻ KOG0752 | | 0 K15108 | | 0 AT5G48970.1 |
| 22 | PTHR24089,P ⁻ KOG0752 | | 0 K15108 | | 0 AT5G48970.1 |
| 23 | PTHR24089,P ⁻ KOG0752 | | 0 K15108 | | 0 AT5G48970.1 |
| 24 | PTHR24089,P ⁻ KOG0752 | | 0 K15108 | | 0 AT5G48970.1 |
| 25 | PTHR16166,P ⁻ KOG1809 | | 0 | 0 | 0 AT1G48090.1 |
| 26 | PTHR16166,P ⁻ KOG1809 | | 0 | 0 | 0 AT1G48090.1 |
| 27 | PTHR16166,P ⁻ KOG1809 | | 0 | 0 | 0 AT1G48090.1 |
| 28 | PTHR11062,P ⁻ KOG1021 | 2.4.2.41 | K18789 | | 0 AT5G33290.1 |
| 29 | PTHR11929,P ⁻ | 0 | 0 | 0 GO:0016020,(AT3G19280.1 | |
| 30 | PTHR13131,P ⁻ KOG2913 | | 0 K12386 | | 0 AT5G40670.1 |
| 31 | PTHR15184,P ⁻ | 0 3.6.3.14 | K02112 | GO:0046034,(ATCG00480.1 | |
| 32 | PTHR15184,P ⁻ | 0 3.6.3.14 | K02112 | GO:0046034,(ATCG00480.1 | |
| 33 | PTHR15184,P ⁻ | 0 3.6.3.14 | K02112 | GO:0046034,(ATCG00480.1 | |
| 34 | PTHR15184,P ⁻ | 0 3.6.3.14 | K02112 | GO:0046034,(ATCG00480.1 | |
| 35 | PTHR14445,P ⁻ | 0 | 0 | 0 GO:0005515,(AT5G08430.1 | |
| 36 | PTHR14445,P ⁻ | 0 | 0 | 0 GO:0005515,(AT5G08430.1 | |
| 37 | PTHR14445,P ⁻ | 0 | 0 | 0 GO:0005515,(AT5G08430.1 | |
| 38 | PTHR14445,P ⁻ | 0 | 0 | 0 GO:0005515,(AT5G08430.1 | |
| 39 | PTHR10438,P ⁻ KOG0907 | 3.5.1.52 | | 0 GO:0045454,(AT4G29670.1 | |
| 40 | PTHR10438,P ⁻ KOG0907 | 3.5.1.52 | | 0 GO:0045454,(AT4G29670.1 | |
| 41 | PTHR35918,P ⁻ | 0 | 0 | 0 GO:0005515 | AT1G04390.1 |
| 42 | PTHR35918,P ⁻ | 0 | 0 | 0 GO:0005515 | AT1G04390.1 |
| 43 | PTHR27002,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0004674,(AT4G21380.1 | |
| 44 | PTHR22749,P ⁻ KOG2914 | 2.7.1.26 | | 0 | 0 AT4G21470.1 |
| 45 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G15030.2 |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|----------------------------------|-----------|----------|--------------|---------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G15030.2 |
| 4 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G15030.2 |
| 5 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G15030.2 |
| 6 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G15030.2 |
| 7 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G15030.2 |
| 8 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G15030.2 |
| 9 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G15030.2 |
| 10 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G15030.2 |
| 11 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G15030.2 |
| 12 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G15030.2 |
| 13 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G15030.2 |
| 14 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G15030.2 |
| 15 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G15030.2 |
| 16 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G15030.2 |
| 17 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G15030.2 |
| 18 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(| AT5G44240.2 |
| 19 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(| AT5G44240.2 |
| 20 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(| AT5G44240.2 |
| 21 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(| AT5G44240.2 |
| 22 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(| AT5G44240.2 |
| 23 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(| AT5G44240.2 |
| 24 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(| AT5G44240.2 |
| 25 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(| AT5G44240.2 |
| 26 | PTHR10593,P ⁻ | 0 | 0 | 0 | 0 AT5G22890.1 |
| 27 | PTHR10593,P ⁻ | 0 | 0 | 0 | 0 AT5G22890.1 |
| 28 | PTHR10593,P ⁻ | 0 | 0 | 0 | 0 AT5G22890.1 |
| 29 | PTHR10593,P ⁻ | 0 | 0 | 0 | 0 AT5G22890.1 |
| 30 | PTHR10593,P ⁻ | 0 | 0 | 0 | 0 AT5G22890.1 |
| 31 | PTHR10285,P ⁻ KOG2878 | 2.7.1.31 | K15918 | 0 | AT1G80380.2 |
| 32 | PTHR10285,P ⁻ KOG2878 | 2.7.1.31 | K15918 | 0 | AT1G80380.2 |
| 33 | PTHR10285,P ⁻ KOG2878 | 2.7.1.31 | K15918 | 0 | AT1G80380.2 |
| 34 | PTHR10285,P ⁻ KOG2878 | 2.7.1.31 | K15918 | 0 | AT1G80380.2 |
| 35 | PTHR10285,P ⁻ KOG2878 | 2.7.1.31 | K15918 | 0 | AT1G80380.2 |
| 36 | 0 | 0 | 0 | 0 | 0 AT1G12064.1 |
| 37 | 0 | 0 | 0 | 0 | 0 AT1G12064.1 |
| 38 | 0 | 0 | 0 | 0 | 0 AT1G12064.1 |
| 39 | 0 | 0 | 0 | 0 | 0 AT1G12064.1 |
| 40 | 0 | 0 | 0 | 0 | 0 AT1G12064.1 |
| 41 | 0 | 0 | 0 | 0 | 0 AT1G12064.1 |
| 42 | PTHR11802,P ⁻ KOG1282 | | 0 K16296 | GO:0006508,(| AT1G73300.1 |
| 43 | PTHR11802,P ⁻ KOG1282 | | 0 K16296 | GO:0006508,(| AT1G73300.1 |
| 44 | PTHR22897 KOG1731 | 1.8.3.2 | K10758 | GO:0045454,(| AT1G15020.2 |
| 45 | PTHR22897 KOG1731 | 1.8.3.2 | K10758 | GO:0045454,(| AT1G15020.2 |
| 46 | PTHR22897 KOG1731 | 1.8.3.2 | K10758 | GO:0045454,(| AT1G15020.2 |
| 47 | PTHR22897 KOG1731 | 1.8.3.2 | K10758 | GO:0045454,(| AT1G15020.2 |
| 48 | PTHR22897 KOG1731 | 1.8.3.2 | K10758 | GO:0045454,(| AT1G15020.2 |
| 49 | PTHR22897 KOG1731 | 1.8.3.2 | K10758 | GO:0045454,(| AT1G15020.2 |
| 50 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 51 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 52 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 53 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 54 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 55 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 56 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 57 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 58 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 59 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 60 | | | | | |

| | | | | | |
|----|----------------------------------|------------|----------|---|-------------------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 4 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 5 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 6 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 7 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 8 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 9 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 10 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 11 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 12 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 13 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G55630.1 |
| 14 | PTHR35732,P ⁻ | 0 | 0 | 0 | 0 AT3G10405.1 |
| 15 | PTHR15856,P ⁻ KOG1844 | | 0 | 0 | GO:0005515 AT1G33420.1 |
| 16 | PTHR15856,P ⁻ KOG1844 | | 0 | 0 | GO:0005515 AT1G33420.1 |
| 17 | PTHR15856,P ⁻ KOG1844 | | 0 | 0 | GO:0005515 AT1G33420.1 |
| 18 | PTHR15856,P ⁻ KOG1844 | | 0 | 0 | GO:0005515 AT1G33420.1 |
| 19 | PTHR15856,P ⁻ KOG1844 | | 0 | 0 | GO:0005515 AT1G33420.1 |
| 20 | PTHR23257,P ⁻ KOG0192 | 2.7.11.1 | | 0 | GO:0006468,(AT1G08720.1 |
| 21 | PTHR23257,P ⁻ KOG0192 | 2.7.11.1 | | 0 | GO:0006468,(AT1G08720.1 |
| 22 | PTHR23315,P ⁻ | 0 6.3.2.19 | | 0 | GO:0016567,(AT3G54790.1 |
| 23 | PTHR31707,P ⁻ | 0 3.1.1.11 | K01051 | | GO:0004857,(AT3G05610.1 |
| 24 | PTHR31707,P ⁻ | 0 3.1.1.11 | K01051 | | GO:0004857,(AT3G05610.1 |
| 25 | PTHR31707,P ⁻ | 0 3.1.1.11 | K01051 | | GO:0004857,(AT3G05610.1 |
| 26 | PTHR31707,P ⁻ | 0 3.1.1.11 | K01051 | | GO:0004857,(AT3G05610.1 |
| 27 | PTHR31707,P ⁻ | 0 3.1.1.11 | K01051 | | GO:0004857,(AT3G05610.1 |
| 28 | PTHR31707,P ⁻ | 0 3.1.1.11 | K01051 | | GO:0004857,(AT3G05610.1 |
| 29 | PTHR31707,P ⁻ | 0 3.1.1.11 | K01051 | | GO:0004857,(AT3G05610.1 |
| 30 | PTHR31707,P ⁻ | 0 3.1.1.11 | K01051 | | GO:0004857,(AT3G05610.1 |
| 31 | PTHR31707,P ⁻ | 0 3.1.1.11 | K01051 | | GO:0004857,(AT3G05610.1 |
| 32 | PTHR13561,P ⁻ | 0 | 0 K10728 | | GO:0005515 AT4G02110.1 |
| 33 | PTHR13561,P ⁻ | 0 | 0 K10728 | | GO:0005515 AT4G02110.1 |
| 34 | PTHR13561,P ⁻ | 0 | 0 K10728 | | GO:0005515 AT4G02110.1 |
| 35 | PTHR13561,P ⁻ | 0 | 0 K10728 | | GO:0005515 AT4G02110.1 |
| 36 | PTHR13561,P ⁻ | 0 | 0 K10728 | | GO:0005515 AT4G02110.1 |
| 37 | PTHR22912,P ⁻ | 0 1.8.1.9 | K00384 | | GO:0045454,(AT2G41680.1 |
| 38 | PTHR27004,P ⁻ KOG0472 | | 0 | 0 | GO:0005515 AT1G47890.1 |
| 39 | PTHR27004,P ⁻ KOG0472 | | 0 | 0 | GO:0005515 AT1G47890.1 |
| 40 | PTHR10641,P ⁻ KOG0048 | | 0 K09422 | | 0 AT3G61250.1 |
| 41 | PTHR10641,P ⁻ KOG0048 | | 0 K09422 | | 0 AT3G61250.1 |
| 42 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01120.1 |
| 43 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01120.1 |
| 44 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01120.1 |
| 45 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01120.1 |
| 46 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01150.1 |
| 47 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01150.1 |
| 48 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01150.1 |
| 49 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01150.1 |
| 50 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01150.1 |
| 51 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01150.1 |
| 52 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01150.1 |
| 53 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01150.1 |
| 54 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01120.1 |
| 55 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01120.1 |
| 56 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01120.1 |
| 57 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01120.1 |
| 58 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01120.1 |
| 59 | PTHR33103,P ⁻ | 0 | 0 | 0 | 0 AT5G01120.1 |
| 60 | | | | | |

| | | | | | |
|----|----------------------------------|-------------|----------|----------------|-------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | PTHR22847,P ⁻ KOG0266 | | 0 | 0 GO:0005515 | AT2G32700.6 |
| 4 | PTHR22847,P ⁻ KOG0266 | | 0 | 0 GO:0005515 | AT2G32700.6 |
| 5 | PTHR22847,P ⁻ KOG0266 | | 0 | 0 GO:0005515 | AT2G32700.6 |
| 6 | PTHR22847,P ⁻ KOG0266 | | 0 | 0 GO:0005515 | AT2G32700.6 |
| 7 | PTHR22847,P ⁻ KOG0266 | | 0 | 0 GO:0005515 | AT2G32700.6 |
| 8 | PTHR10795,P ⁻ | 0 3.4.21.25 | | 0 GO:0006508,(| AT5G59100.1 |
| 9 | PTHR13301,P ⁻ | 0 2.4.1.12 | | 0 GO:0030244,(| AT1G55850.1 |
| 10 | PTHR13301,P ⁻ | 0 2.4.1.12 | | 0 GO:0030244,(| AT1G55850.1 |
| 11 | PTHR11705,P ⁻ KOG2650 | 3.4.17.1 | | 0 GO:0008270,(| AT5G42320.1 |
| 12 | PTHR11705,P ⁻ KOG2650 | 3.4.17.1 | | 0 GO:0008270,(| AT5G42320.1 |
| 13 | PTHR12791,P ⁻ | 0 | 0 K08505 | 0 AT4G14600.1 | |
| 14 | PTHR13878,P ⁻ KOG1231 | 1.5.99.12 | | 0 GO:0055114,(| AT1G75450.1 |
| 15 | PTHR13878,P ⁻ KOG1231 | 1.5.99.12 | | 0 GO:0055114,(| AT1G75450.1 |
| 16 | PTHR13878,P ⁻ KOG1231 | 1.5.99.12 | | 0 GO:0055114,(| AT1G75450.1 |
| 17 | PTHR13878,P ⁻ KOG1231 | 1.5.99.12 | | 0 GO:0055114,(| AT1G75450.1 |
| 18 | PTHR13878,P ⁻ KOG1231 | 1.5.99.12 | | 0 GO:0055114,(| AT1G75450.1 |
| 19 | PTHR13878,P ⁻ KOG1231 | 1.5.99.12 | | 0 GO:0055114,(| AT1G75450.1 |
| 20 | PTHR13878,P ⁻ KOG1231 | 1.5.99.12 | | 0 GO:0055114,(| AT1G75450.1 |
| 21 | PTHR13878,P ⁻ KOG1231 | 1.5.99.12 | | 0 GO:0055114,(| AT1G75450.1 |
| 22 | PTHR13878,P ⁻ KOG1231 | 1.5.99.12 | | 0 GO:0055114,(| AT1G75450.1 |
| 23 | PTHR13878,P ⁻ KOG1231 | 1.5.99.12 | | 0 GO:0055114,(| AT1G75450.1 |
| 24 | PTHR13878,P ⁻ KOG1231 | 1.5.99.12 | | 0 GO:0055114,(| AT1G75450.1 |
| 25 | PTHR13878,P ⁻ KOG1231 | 1.5.99.12 | | 0 GO:0055114,(| AT1G75450.1 |
| 26 | PTHR23500,P ⁻ KOG0254 | | 0 | 0 GO:0055085,(| AT4G35300.1 |
| 27 | PTHR23500,P ⁻ KOG0254 | | 0 | 0 GO:0055085,(| AT4G35300.1 |
| 28 | PTHR33880,P ⁻ | 0 | 0 | 0 AT4G14100.1 | |
| 29 | PTHR33880,P ⁻ | 0 | 0 | 0 AT4G14100.1 | |
| 30 | PTHR33880,P ⁻ | 0 | 0 | 0 AT4G14100.1 | |
| 31 | PTHR33880,P ⁻ | 0 | 0 | 0 AT4G14100.1 | |
| 32 | PTHR33880,P ⁻ | 0 | 0 | 0 AT4G14100.1 | |
| 33 | PTHR33880,P ⁻ | 0 | 0 | 0 AT4G14100.1 | |
| 34 | PTHR31673,P ⁻ | 0 | 0 | 0 GO:0031225,(| AT5G60920.1 |
| 35 | PTHR23421,P ⁻ | 0 3.2.1.23 | | 0 GO:0005975,(| AT4G26140.1 |
| 36 | PTHR23421,P ⁻ | 0 3.2.1.23 | | 0 GO:0005975,(| AT4G26140.1 |
| 37 | PTHR23421,P ⁻ | 0 3.2.1.23 | | 0 GO:0005975,(| AT4G26140.1 |
| 38 | PTHR23421,P ⁻ | 0 3.2.1.23 | | 0 GO:0005975,(| AT4G26140.1 |
| 39 | PTHR15371,P ⁻ | 0 | 0 | 0 AT4G16160.1 | |
| 40 | PTHR15371,P ⁻ | 0 | 0 | 0 AT4G16160.1 | |
| 41 | PTHR15371,P ⁻ | 0 | 0 | 0 AT4G16160.1 | |
| 42 | PTHR15371,P ⁻ | 0 | 0 | 0 AT4G16160.1 | |
| 43 | 0 | 0 | 0 | 0 | 0 |
| 44 | 0 | 0 | 0 | 0 | 0 |
| 45 | 0 | 0 | 0 | 0 | 0 |
| 46 | 0 | 0 | 0 | 0 | 0 |
| 47 | PTHR11017,P ⁻ | 0 | 0 | 0 GO:0007165,(| AT5G36930.2 |
| 48 | PTHR11017,P ⁻ | 0 | 0 | 0 GO:0007165,(| AT5G36930.2 |
| 49 | PTHR11017,P ⁻ | 0 | 0 | 0 GO:0007165,(| AT5G36930.2 |
| 50 | PTHR11017,P ⁻ | 0 | 0 | 0 GO:0007165,(| AT5G36930.2 |
| 51 | PTHR13902,P ⁻ | 0 2.7.11.1 | K08867 | GO:0006468,(| AT3G51630.1 |
| 52 | PTHR13902,P ⁻ | 0 2.7.11.1 | K08867 | GO:0006468,(| AT3G51630.1 |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|----------------------------------|------------|----------|--------------|---------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | PTHR13902,P ⁻ | 0 2.7.11.1 | K08867 | GO:0006468,(| AT3G51630.1 |
| 4 | PTHR13902,P ⁻ | 0 2.7.11.1 | K08867 | GO:0006468,(| AT3G51630.1 |
| 5 | | | | | |
| 6 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | 0 AT2G45690.1 |
| 7 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | 0 AT2G45690.1 |
| 8 | | | | | |
| 9 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | 0 AT2G45690.1 |
| 10 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | 0 AT2G45690.1 |
| 11 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | 0 AT2G45690.1 |
| 12 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | 0 AT2G45690.1 |
| 13 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | 0 AT2G45690.1 |
| 14 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | 0 AT2G45690.1 |
| 15 | PTHR13299,P ⁻ KOG4546 | | 0 | 0 | 0 AT2G45690.1 |
| 16 | | | | | |
| 17 | PTHR30573,P ⁻ | 0 2.5.1.72 | | 0 | 0 AT5G50210.1 |
| 18 | PTHR30573,P ⁻ | 0 2.5.1.72 | | 0 | 0 AT5G50210.1 |
| 19 | PTHR30573,P ⁻ | 0 2.5.1.72 | | 0 | 0 AT5G50210.1 |
| 20 | PTHR30573,P ⁻ | 0 2.5.1.72 | | 0 | 0 AT5G50210.1 |
| 21 | | | | | |
| 22 | PTHR11200,P ⁻ | 0 | 0 | 0 GO:0042578 | AT1G22620.1 |
| 23 | PTHR11200,P ⁻ | 0 | 0 | 0 GO:0042578 | AT1G22620.1 |
| 24 | PTHR11200,P ⁻ | 0 | 0 | 0 GO:0042578 | AT1G22620.1 |
| 25 | PTHR11200,P ⁻ | 0 | 0 | 0 GO:0042578 | AT1G22620.1 |
| 26 | PTHR11200,P ⁻ | 0 | 0 | 0 GO:0042578 | AT1G22620.1 |
| 27 | PTHR11200,P ⁻ | 0 | 0 | 0 GO:0042578 | AT1G22620.1 |
| 28 | PTHR11200,P ⁻ | 0 | 0 | 0 GO:0042578 | AT1G22620.1 |
| 29 | PTHR11200,P ⁻ | 0 | 0 | 0 GO:0042578 | AT1G22620.1 |
| 30 | PTHR11200,P ⁻ | 0 | 0 | 0 GO:0042578 | AT1G22620.1 |
| 31 | PTHR11200,P ⁻ | 0 | 0 | 0 GO:0042578 | AT1G22620.1 |
| 32 | | | | | |
| 33 | PTHR15852,P ⁻ | 0 5.3.4.1 | | 0 | 0 AT5G61670.1 |
| 34 | PTHR33624,P ⁻ | 0 | 0 | 0 | 0 AT3G56710.1 |
| 35 | PTHR33624,P ⁻ | 0 | 0 | 0 | 0 AT3G56710.1 |
| 36 | PTHR33624,P ⁻ | 0 | 0 | 0 | 0 AT3G56710.1 |
| 37 | PTHR33624,P ⁻ | 0 | 0 | 0 | 0 AT3G56710.1 |
| 38 | PTHR33624,P ⁻ | 0 | 0 | 0 | 0 AT3G56710.1 |
| 39 | PTHR10774,P ⁻ | 0 | 0 | 0 GO:0005515 | AT1G03370.1 |
| 40 | PTHR10774,P ⁻ | 0 | 0 | 0 GO:0005515 | AT1G03370.1 |
| 41 | | | | | |
| 42 | PTHR14089,P ⁻ | 0 | 0 K12872 | GO:0003676 | AT1G07360.1 |
| 43 | PTHR14089,P ⁻ | 0 | 0 K12872 | GO:0003676 | AT1G07360.1 |
| 44 | PTHR24089,P ⁻ KOG0749 | | 0 | 0 | 0 AT5G13490.1 |
| 45 | PTHR24089,P ⁻ KOG0749 | | 0 | 0 | 0 AT5G13490.1 |
| 46 | PTHR24089,P ⁻ KOG0749 | | 0 | 0 | 0 AT5G13490.1 |
| 47 | PTHR24089,P ⁻ KOG0749 | | 0 | 0 | 0 AT5G13490.1 |
| 48 | PTHR24089,P ⁻ KOG0749 | | 0 | 0 | 0 AT5G13490.1 |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| arabi-symbol | arabi-defline | ID |
|----------------------|--|----------------|
| ATEME1B,EME1B | essential meiotic endonuclease 1B | Phvul.002G26 |
| ATEME1B,EME1B | essential meiotic endonuclease 1B | Phvul.002G26 |
| | 0 Plant protein of unknown function (DUF936) | Phvul.002G07 |
| | 0 Plant protein of unknown function (DUF936) | Phvul.002G07 |
| | 0 Plant protein of unknown function (DUF936) | Phvul.002G07 |
| | 0 Plant protein of unknown function (DUF936) | Phvul.002G07 |
| EX1 | Protein of unknown function (DUF3506) | Phvul.006G20 |
| | 0 Leucine carboxyl methyltransferase | Phvul.009G05 |
| | 0 Leucine carboxyl methyltransferase | Phvul.009G05 |
| | 0 Endomembrane protein 70 protein family | Phvul.009G08 |
| | 0 ARM repeat superfamily protein | Phvul.010G11 |
| | 0 ARM repeat superfamily protein | Phvul.010G11 |
| | 0 ARM repeat superfamily protein | Phvul.010G11 |
| | 0 ARM repeat superfamily protein | Phvul.010G11 |
| ATXDH1,XDH1 | xanthine dehydrogenase 1 | Phvul.L009543 |
| ATXDH1,XDH1 | xanthine dehydrogenase 1 | Phvul.L009543 |
| ATXDH1,XDH1 | xanthine dehydrogenase 1 | Phvul.L009543 |
| ATXDH1,XDH1 | xanthine dehydrogenase 1 | Phvul.L009543 |
| ATBZIP9,BZIP9,BZO2H2 | basic leucine zipper 9 | Phvul.001G07 |
| ATBZIP9,BZIP9,BZO2H2 | basic leucine zipper 9 | Phvul.001G07 |
| ATBZIP9,BZIP9,BZO2H2 | basic leucine zipper 9 | Phvul.001G07 |
| ATBZIP9,BZIP9,BZO2H2 | basic leucine zipper 9 | Phvul.001G07 |
| AtGolS1,GolS1 | galactinol synthase 1 | Phvul.001G21 |
| AtGolS1,GolS1 | galactinol synthase 1 | Phvul.001G21 |
| AtGolS1,GolS1 | galactinol synthase 1 | Phvul.001G21 |
| AtGolS1,GolS1 | galactinol synthase 1 | Phvul.001G21 |
| ATEME1B,EME1B | essential meiotic endonuclease 1B | Phvul.002G26 |
| ATEME1B,EME1B | essential meiotic endonuclease 1B | Phvul.002G26 |
| ATEME1B,EME1B | essential meiotic endonuclease 1B | Phvul.002G26 |
| ATEME1B,EME1B | essential meiotic endonuclease 1B | Phvul.002G26 |
| GUT1 | Exostosin family protein | Phvul.002G28 |
| GUT1 | Exostosin family protein | Phvul.002G28 |
| GUT1 | Exostosin family protein | Phvul.002G28 |
| GUT1 | Exostosin family protein | Phvul.002G28 |
| | 0 disease resistance family protein / LRR family protein | Phvul.004G04 |
| | 0 | 0 Phvul.006G15 |
| | 0 LRR and NB-ARC domains-containing disease resistan | Phvul.008G07 |
| | 0 LRR and NB-ARC domains-containing disease resistan | Phvul.008G07 |
| | 0 LRR and NB-ARC domains-containing disease resistan | Phvul.008G07 |
| | 0 LRR and NB-ARC domains-containing disease resistan | Phvul.008G07 |
| | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| | 0 Protein of unknown function (DUF674) | Phvul.008G11 |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | |
|--|---|--------------|
| | 0 ARM repeat superfamily protein | Phvul.008G16 |
| | 0 ARM repeat superfamily protein | Phvul.008G16 |
| | 0 ARM repeat superfamily protein | Phvul.008G16 |
| | 0 ARM repeat superfamily protein | Phvul.008G16 |
| | 0 ARM repeat superfamily protein | Phvul.008G16 |
| | 0 ARM repeat superfamily protein | Phvul.008G16 |
| | 0 ARM repeat superfamily protein | Phvul.008G16 |
| | 0 ARM repeat superfamily protein | Phvul.008G16 |
| | 0 ARM repeat superfamily protein | Phvul.008G16 |
| | 0 ARM repeat superfamily protein | Phvul.008G16 |
| | 0 ARM repeat superfamily protein | Phvul.008G16 |
| | 0 ARM repeat superfamily protein | Phvul.008G16 |
| | 0 ARM repeat superfamily protein | Phvul.008G16 |
| | 0 ARM repeat superfamily protein | Phvul.008G16 |
| | 0 ARM repeat superfamily protein | Phvul.008G16 |
| | 0 ARM repeat superfamily protein | Phvul.008G16 |
| | 0 Leucine carboxyl methyltransferase | Phvul.009G05 |
| | 0 Leucine carboxyl methyltransferase | Phvul.009G05 |
| | 0 Leucine carboxyl methyltransferase | Phvul.009G05 |
| | 0 Leucine carboxyl methyltransferase | Phvul.009G05 |
| | 0 | 0 0 |
| | 0 | 0 0 |
| | ATGLR3.2,ATGLUR2,GLR3.2, glutamate receptor 2 | Phvul.001G02 |
| | ATGLR3.2,ATGLUR2,GLR3.2, glutamate receptor 2 | Phvul.001G02 |
| | ATBZIP9,BZIP9,BZO2H2 basic leucine zipper 9 | Phvul.001G07 |
| | ATBZIP9,BZIP9,BZO2H2 basic leucine zipper 9 | Phvul.001G07 |
| | ARA1,ATISA1,ISA1 arabinose kinase | Phvul.001G07 |
| | ARA1,ATISA1,ISA1 arabinose kinase | Phvul.001G07 |
| | ARP2,ATARP2,WRM actin related protein 2 | Phvul.001G08 |
| | ARP2,ATARP2,WRM actin related protein 2 | Phvul.001G08 |
| | ARP2,ATARP2,WRM actin related protein 2 | Phvul.001G08 |
| | ARP2,ATARP2,WRM actin related protein 2 | Phvul.001G08 |
| | ARP2,ATARP2,WRM actin related protein 2 | Phvul.001G08 |
| | ARP2,ATARP2,WRM actin related protein 2 | Phvul.001G08 |
| | ARP2,ATARP2,WRM actin related protein 2 | Phvul.001G08 |
| | ANAC041,NAC041 NAC domain containing protein 41 | Phvul.001G09 |
| | ANAC041,NAC041 NAC domain containing protein 41 | Phvul.001G09 |
| | ANAC041,NAC041 NAC domain containing protein 41 | Phvul.001G09 |
| | ANAC041,NAC041 NAC domain containing protein 41 | Phvul.001G09 |
| | 0 Aldolase superfamily protein | Phvul.001G12 |
| | 0 Aldolase superfamily protein | Phvul.001G12 |
| | ABCA1,AtABCA1 ATP-binding cassette A1 | Phvul.001G13 |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | |
|-------------------------|--|--------------|
| ABCA1,AtABCA1 | ATP-binding cassette A1 | Phvul.001G13 |
| ABCA1,AtABCA1 | ATP-binding cassette A1 | Phvul.001G13 |
| ABCA1,AtABCA1 | ATP-binding cassette A1 | Phvul.001G13 |
| ABCA1,AtABCA1 | ATP-binding cassette A1 | Phvul.001G13 |
| ABCA1,AtABCA1 | ATP-binding cassette A1 | Phvul.001G13 |
| ABCA1,AtABCA1 | ATP-binding cassette A1 | Phvul.001G13 |
| ABCA1,AtABCA1 | ATP-binding cassette A1 | Phvul.001G13 |
| SPL9 | squamosa promoter binding protein-like 9 | Phvul.001G14 |
| SPL9 | squamosa promoter binding protein-like 9 | Phvul.001G14 |
| SPL9 | squamosa promoter binding protein-like 9 | Phvul.001G14 |
| SPL9 | squamosa promoter binding protein-like 9 | Phvul.001G14 |
| | 0 phosphoadenosine phosphosulfate (PAPS) reductase | Phvul.001G17 |
| | 0 phosphoadenosine phosphosulfate (PAPS) reductase | Phvul.001G17 |
| | 0 phosphoadenosine phosphosulfate (PAPS) reductase | Phvul.001G17 |
| | 0 phosphoadenosine phosphosulfate (PAPS) reductase | Phvul.001G17 |
| | 0 phosphoadenosine phosphosulfate (PAPS) reductase | Phvul.001G17 |
| TZP | zinc knuckle (CCHC-type) family protein | Phvul.002G04 |
| TZP | zinc knuckle (CCHC-type) family protein | Phvul.002G04 |
| TZP | zinc knuckle (CCHC-type) family protein | Phvul.002G04 |
| TZP | zinc knuckle (CCHC-type) family protein | Phvul.002G04 |
| TZP | zinc knuckle (CCHC-type) family protein | Phvul.002G04 |
| TZP | zinc knuckle (CCHC-type) family protein | Phvul.002G04 |
| TZP | zinc knuckle (CCHC-type) family protein | Phvul.002G04 |
| TZP | zinc knuckle (CCHC-type) family protein | Phvul.002G04 |
| TZP | zinc knuckle (CCHC-type) family protein | Phvul.002G04 |
| TZP | zinc knuckle (CCHC-type) family protein | Phvul.002G04 |
| TZP | zinc knuckle (CCHC-type) family protein | Phvul.002G04 |
| TZP | zinc knuckle (CCHC-type) family protein | Phvul.002G04 |
| TZP | zinc knuckle (CCHC-type) family protein | Phvul.002G04 |
| TZP | zinc knuckle (CCHC-type) family protein | Phvul.002G04 |
| ATH2,ATTRX2,ATTRXH2,TRX | thioredoxin 2 | Phvul.002G06 |
| ATH2,ATTRX2,ATTRXH2,TRX | thioredoxin 2 | Phvul.002G06 |
| | 0 Plant protein of unknown function (DUF936) | Phvul.002G07 |
| | 0 Plant protein of unknown function (DUF936) | Phvul.002G07 |
| MMP | matrix metalloproteinase | Phvul.002G07 |
| MMP | matrix metalloproteinase | Phvul.002G07 |
| MMP | matrix metalloproteinase | Phvul.002G07 |
| MMP | matrix metalloproteinase | Phvul.002G07 |
| ATNHX7,ATSOS1,SOS1 | sodium proton exchanger, putative (NHX7) (SOS1) | Phvul.002G18 |
| ATNHX7,ATSOS1,SOS1 | sodium proton exchanger, putative (NHX7) (SOS1) | Phvul.002G18 |
| ATNHX7,ATSOS1,SOS1 | sodium proton exchanger, putative (NHX7) (SOS1) | Phvul.002G18 |

| | | | |
|----|---------------|--|----------------|
| 1 | | | |
| 2 | | | |
| 3 | | 0 Protein kinase protein with adenine nucleotide alpha | Phvul.002G30 |
| 4 | | 0 CW-type Zinc Finger | Phvul.003G10 |
| 5 | | 0 CW-type Zinc Finger | Phvul.003G10 |
| 6 | | 0 disease resistance family protein / LRR family protein | Phvul.004G04 |
| 7 | | | |
| 8 | emb1417 | Pentatricopeptide repeat (PPR) superfamily protein | Phvul.004G10 |
| 9 | | | |
| 10 | ATCLC-C,CLC-C | chloride channel C | Phvul.004G13 |
| 11 | ATCLC-C,CLC-C | chloride channel C | Phvul.004G13 |
| 12 | ACHT2 | atypical CYS HIS rich thioredoxin 2 | Phvul.004G17 |
| 13 | ACHT2 | atypical CYS HIS rich thioredoxin 2 | Phvul.004G17 |
| 14 | ACHT2 | atypical CYS HIS rich thioredoxin 2 | Phvul.004G17 |
| 15 | ACHT2 | atypical CYS HIS rich thioredoxin 2 | Phvul.004G17 |
| 16 | | | |
| 17 | | 0 Wound-responsive family protein | Phvul.005G08 |
| 18 | | | |
| 19 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.005G11 |
| 20 | | | |
| 21 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.005G11 |
| 22 | | | |
| 23 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.005G11 |
| 24 | | | |
| 25 | | 0 | 0 Phvul.005G18 |
| 26 | | 0 | 0 Phvul.005G18 |
| 27 | | 0 Glutathione S-transferase, C-terminal-like;Translation | Phvul.006G01 |
| 28 | | 0 Glutathione S-transferase, C-terminal-like;Translation | Phvul.006G01 |
| 29 | | 0 Glutathione S-transferase, C-terminal-like;Translation | Phvul.006G01 |
| 30 | | 0 Glutathione S-transferase, C-terminal-like;Translation | Phvul.006G01 |
| 31 | | | |
| 32 | ATPDR3,PDR3 | pleiotropic drug resistance 3 | Phvul.006G06 |
| 33 | ATPDR3,PDR3 | pleiotropic drug resistance 3 | Phvul.006G06 |
| 34 | ATPDR3,PDR3 | pleiotropic drug resistance 3 | Phvul.006G06 |
| 35 | ATPDR3,PDR3 | pleiotropic drug resistance 3 | Phvul.006G06 |
| 36 | | | |
| 37 | | 0 Protein of Unknown Function (DUF239) | Phvul.006G10 |
| 38 | | 0 Protein of Unknown Function (DUF239) | Phvul.006G10 |
| 39 | | | |
| 40 | | 0 Sec14p-like phosphatidylinositol transfer family prote | Phvul.006G13 |
| 41 | | 0 Sec14p-like phosphatidylinositol transfer family prote | Phvul.006G13 |
| 42 | | | |
| 43 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.007G11 |
| 44 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.007G11 |
| 45 | | | |
| 46 | | 0 Pectin lyase-like superfamily protein | Phvul.007G21 |
| 47 | | 0 Pectin lyase-like superfamily protein | Phvul.007G21 |
| 48 | | 0 SAUR-like auxin-responsive protein family | Phvul.007G21 |
| 49 | | 0 SAUR-like auxin-responsive protein family | Phvul.007G21 |
| 50 | | | |
| 51 | | 0 LRR and NB-ARC domains-containing disease resistan | Phvul.008G07 |
| 52 | | 0 LRR and NB-ARC domains-containing disease resistan | Phvul.008G07 |
| 53 | | | |
| 54 | | 0 | 0 0 |
| 55 | | 0 | 0 0 |
| 56 | | 0 NAD(P)-binding Rossmann-fold superfamily protein | Phvul.008G11 |
| 57 | | 0 NAD(P)-binding Rossmann-fold superfamily protein | Phvul.008G11 |
| 58 | | | |
| 59 | | 0 NAD(P)-binding Rossmann-fold superfamily protein | Phvul.008G25 |
| 60 | | | |

| | | | |
|----|--------------------------|---|---------------|
| 1 | | | |
| 2 | | | |
| 3 | | 0 NAD(P)-binding Rossmann-fold superfamily protein | Phvul.008G25 |
| 4 | | 0 NAD(P)-binding Rossmann-fold superfamily protein | Phvul.008G25 |
| 5 | | 0 NAD(P)-binding Rossmann-fold superfamily protein | Phvul.008G25 |
| 6 | | 0 NAD(P)-binding Rossmann-fold superfamily protein | Phvul.008G25 |
| 7 | COX15 | cytochrome c oxidase 15 | Phvul.008G28 |
| 8 | | 0 Endomembrane protein 70 protein family | Phvul.008G28 |
| 9 | | | |
| 10 | ATFBP7,FBP7 | F-box protein 7 | Phvul.009G12 |
| 11 | ATFBP7,FBP7 | F-box protein 7 | Phvul.009G12 |
| 12 | ATFBP7,FBP7 | F-box protein 7 | Phvul.009G12 |
| 13 | ATFBP7,FBP7 | F-box protein 7 | Phvul.009G12 |
| 14 | ATFBP7,FBP7 | F-box protein 7 | Phvul.009G12 |
| 15 | GUT1 | Exostosin family protein | Phvul.009G16 |
| 16 | GUT1 | Exostosin family protein | Phvul.009G16 |
| 17 | GUT1 | Exostosin family protein | Phvul.009G16 |
| 18 | GUT1 | Exostosin family protein | Phvul.009G16 |
| 19 | GUT1 | Exostosin family protein | Phvul.009G16 |
| 20 | | | |
| 21 | | 0 NB-ARC domain-containing disease resistance protei | Phvul.010G06 |
| 22 | | 0 NB-ARC domain-containing disease resistance protei | Phvul.010G06 |
| 23 | | 0 NB-ARC domain-containing disease resistance protei | Phvul.010G06 |
| 24 | | 0 NB-ARC domain-containing disease resistance protei | Phvul.010G06 |
| 25 | | | |
| 26 | GBF1 | G-box binding factor 1 | Phvul.011G04 |
| 27 | GBF1 | G-box binding factor 1 | Phvul.011G04 |
| 28 | TOR | target of rapamycin | Phvul.011G05 |
| 29 | TOR | target of rapamycin | Phvul.011G05 |
| 30 | TOR | target of rapamycin | Phvul.011G05 |
| 31 | TOR | target of rapamycin | Phvul.011G05 |
| 32 | TOR | target of rapamycin | Phvul.011G05 |
| 33 | | | |
| 34 | ATLAC2,LAC2 | laccase 2 | Phvul.L00734: |
| 35 | ATLAC2,LAC2 | laccase 2 | Phvul.L00734: |
| 36 | | 0 Remorin family protein | Phvul.001G02 |
| 37 | | 0 Remorin family protein | Phvul.001G02 |
| 38 | | | |
| 39 | ATBFRUCT1,ATCWINV1 | Glycosyl hydrolases family 32 protein | Phvul.001G03 |
| 40 | | 0 RNA-binding (RRM/RBD/RNP motifs) family protein | Phvul.001G10 |
| 41 | | 0 RNA-binding (RRM/RBD/RNP motifs) family protein | Phvul.001G10 |
| 42 | | | |
| 43 | EDA4 | Bifunctional inhibitor/lipid-transfer protein/seed stor | Phvul.001G15 |
| 44 | EDA4 | Bifunctional inhibitor/lipid-transfer protein/seed stor | Phvul.001G15 |
| 45 | EDA4 | Bifunctional inhibitor/lipid-transfer protein/seed stor | Phvul.001G15 |
| 46 | EDA4 | Bifunctional inhibitor/lipid-transfer protein/seed stor | Phvul.001G15 |
| 47 | EDA4 | Bifunctional inhibitor/lipid-transfer protein/seed stor | Phvul.001G15 |
| 48 | | 0 biotin/lipoyl attachment domain-containing protein | Phvul.001G24 |
| 49 | AT-EXPR,ATEXLB1,ATEXPR1, | expansin-like B1 | Phvul.002G00 |
| 50 | | | |
| 51 | SRFR1 | Tetratricopeptide repeat (TPR)-like superfamily prote | Phvul.002G01 |
| 52 | SRFR1 | Tetratricopeptide repeat (TPR)-like superfamily prote | Phvul.002G01 |
| 53 | | | |
| 54 | | 0 Haloacid dehalogenase-like hydrolase (HAD) superfan | Phvul.002G21 |
| 55 | | 0 Regulator of chromosome condensation (RCC1) famil | Phvul.002G25 |
| 56 | | 0 Regulator of chromosome condensation (RCC1) famil | Phvul.002G25 |
| 57 | PDF1,PP2AA2,PR 65 | protein phosphatase 2A subunit A2 | Phvul.003G02 |
| 58 | PDF1,PP2AA2,PR 65 | protein phosphatase 2A subunit A2 | Phvul.003G02 |
| 59 | | | |
| 60 | | | |

| | | | |
|----|-----------------|--|--------------|
| 1 | | | |
| 2 | | | |
| 3 | | 0 Thiolase family protein | Phvul.003G08 |
| 4 | | 0 Thiolase family protein | Phvul.003G08 |
| 5 | | 0 Thiolase family protein | Phvul.003G08 |
| 6 | | 0 Thiolase family protein | Phvul.003G08 |
| 7 | | 0 Thiolase family protein | Phvul.003G08 |
| 8 | | 0 Thiolase family protein | Phvul.003G08 |
| 9 | | 0 Thiolase family protein | Phvul.003G08 |
| 10 | | 0 Thiolase family protein | Phvul.003G08 |
| 11 | | 0 Thiolase family protein | Phvul.003G08 |
| 12 | | 0 Thiolase family protein | Phvul.003G08 |
| 13 | | 0 Thiolase family protein | Phvul.003G08 |
| 14 | | 0 Mitochondrial substrate carrier family protein | Phvul.003G10 |
| 15 | | 0 Mitochondrial substrate carrier family protein | Phvul.003G10 |
| 16 | | 0 Ypt/Rab-GAP domain of gyp1p superfamily protein | Phvul.003G14 |
| 17 | | 0 Ypt/Rab-GAP domain of gyp1p superfamily protein | Phvul.003G14 |
| 18 | | 0 Ypt/Rab-GAP domain of gyp1p superfamily protein | Phvul.003G14 |
| 19 | TOR2,TUA4 | tubulin alpha-4 chain | Phvul.003G23 |
| 20 | TOR2,TUA4 | tubulin alpha-4 chain | Phvul.003G23 |
| 21 | TOR2,TUA4 | tubulin alpha-4 chain | Phvul.003G23 |
| 22 | TOR2,TUA4 | tubulin alpha-4 chain | Phvul.003G23 |
| 23 | TOR2,TUA4 | tubulin alpha-4 chain | Phvul.003G23 |
| 24 | ATRBP47A,RBP47A | RNA-binding protein 47A | Phvul.003G29 |
| 25 | ATRBP47B,RBP47B | RNA-binding protein 47B | Phvul.003G29 |
| 26 | ATRBP47B,RBP47B | RNA-binding protein 47B | Phvul.003G29 |
| 27 | ATRBP47B,RBP47B | RNA-binding protein 47B | Phvul.003G29 |
| 28 | | 0 FBD, F-box and Leucine Rich Repeat domains containi | Phvul.004G01 |
| 29 | | 0 FBD, F-box and Leucine Rich Repeat domains containi | Phvul.004G01 |
| 30 | | 0 FBD, F-box and Leucine Rich Repeat domains containi | Phvul.004G01 |
| 31 | | 0 FBD, F-box and Leucine Rich Repeat domains containi | Phvul.004G01 |
| 32 | | 0 FBD, F-box and Leucine Rich Repeat domains containi | Phvul.004G01 |
| 33 | | 0 | 0 |
| 34 | | 0 | 0 |
| 35 | | 0 disease resistance family protein / LRR family protein | Phvul.004G04 |
| 36 | | 0 disease resistance family protein / LRR family protein | Phvul.004G04 |
| 37 | | 0 ATP binding microtubule motor family protein | Phvul.004G16 |
| 38 | | 0 ATP binding microtubule motor family protein | Phvul.004G16 |
| 39 | HAM1 | histone acetyltransferase of the MYST family 1 | Phvul.005G01 |
| 40 | CYP72A8 | cytochrome P450, family 72, subfamily A, polypeptide | Phvul.005G01 |
| 41 | CYP72A8 | cytochrome P450, family 72, subfamily A, polypeptide | Phvul.005G01 |
| 42 | CYP72A8 | cytochrome P450, family 72, subfamily A, polypeptide | Phvul.005G01 |
| 43 | CYP72A8 | cytochrome P450, family 72, subfamily A, polypeptide | Phvul.005G01 |
| 44 | CYP72A8 | cytochrome P450, family 72, subfamily A, polypeptide | Phvul.005G01 |
| 45 | CYP72A8 | cytochrome P450, family 72, subfamily A, polypeptide | Phvul.005G01 |
| 46 | CYP72A8 | cytochrome P450, family 72, subfamily A, polypeptide | Phvul.005G01 |
| 47 | CYP72A8 | cytochrome P450, family 72, subfamily A, polypeptide | Phvul.005G01 |
| 48 | CYP72A8 | cytochrome P450, family 72, subfamily A, polypeptide | Phvul.005G01 |
| 49 | CYP72A8 | cytochrome P450, family 72, subfamily A, polypeptide | Phvul.005G01 |
| 50 | CYP72A8 | cytochrome P450, family 72, subfamily A, polypeptide | Phvul.005G01 |
| 51 | | 0 UDP-Glycosyltransferase superfamily protein | Phvul.005G08 |
| 52 | | 0 UDP-Glycosyltransferase superfamily protein | Phvul.005G08 |
| 53 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 54 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 55 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 56 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 57 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 58 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 59 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 60 | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | |
|---------------|---|----------------|
| MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| | 0 | 0 0 |
| | 0 | 0 0 |
| | 0 Pyridoxal phosphate (PLP)-dependent transferases | suPhvul.006G13 |
| | 0 Pyridoxal phosphate (PLP)-dependent transferases | suPhvul.006G13 |
| | 0 | 0 Phvul.006G19 |
| | 0 | 0 Phvul.006G19 |
| | 0 | 0 Phvul.006G19 |
| | 0 | 0 Phvul.006G19 |
| | 0 Protein of unknown function (DUF581) | Phvul.007G05 |
| | 0 Protein of unknown function (DUF581) | Phvul.007G05 |
| AtCXE20,CXE20 | carboxyesterase 20 | Phvul.007G06 |
| AtCXE20,CXE20 | carboxyesterase 20 | Phvul.007G06 |
| | 0 Mog1/PsbP/DUF1795-like photosystem II reaction ce | Phvul.007G18 |
| | 0 Tetratricopeptide repeat (TPR)-like superfamily prote | Phvul.007G19 |
| | 0 Tetratricopeptide repeat (TPR)-like superfamily prote | Phvul.007G19 |
| | 0 | 0 0 |
| | 0 | 0 0 |
| | 0 | 0 0 |
| | 0 | 0 0 |
| | 0 HEAT repeat-containing protein | Phvul.008G00 |
| | 0 HEAT repeat-containing protein | Phvul.008G00 |
| | 0 HEAT repeat-containing protein | Phvul.008G00 |
| | 0 HEAT repeat-containing protein | Phvul.008G00 |
| | 0 HEAT repeat-containing protein | Phvul.008G00 |
| | 0 HEAT repeat-containing protein | Phvul.008G00 |
| | 0 HEAT repeat-containing protein | Phvul.008G00 |
| | 0 HEAT repeat-containing protein | Phvul.008G00 |
| | 0 HEAT repeat-containing protein | Phvul.008G00 |
| | 0 HEAT repeat-containing protein | Phvul.008G00 |
| AtLIG6,LIG6 | DNA LIGASE 6 | Phvul.008G00 |
| AtLIG6,LIG6 | DNA LIGASE 6 | Phvul.008G00 |
| AtLIG6,LIG6 | DNA LIGASE 6 | Phvul.008G00 |
| AtLIG6,LIG6 | DNA LIGASE 6 | Phvul.008G00 |
| | 0 EXS (ERD1/XPR1/SYG1) family protein | Phvul.008G03 |
| | 0 EXS (ERD1/XPR1/SYG1) family protein | Phvul.008G03 |
| | 0 Leucine-rich repeat protein kinase family protein | Phvul.008G09 |
| | 0 Leucine-rich repeat protein kinase family protein | Phvul.008G09 |
| | 0 Leucine-rich repeat protein kinase family protein | Phvul.008G09 |
| | 0 Leucine-rich repeat protein kinase family protein | Phvul.008G09 |
| | 0 Leucine-rich repeat protein kinase family protein | Phvul.008G09 |
| | 0 Leucine-rich repeat protein kinase family protein | Phvul.008G09 |
| | 0 RING/U-box superfamily protein | Phvul.008G10 |

| | | | |
|----|-------------|--|--------------|
| 1 | | | |
| 2 | | | |
| 3 | | 0 RING/U-box superfamily protein | Phvul.008G10 |
| 4 | | 0 RING/U-box superfamily protein | Phvul.008G10 |
| 5 | | 0 RING/U-box superfamily protein | Phvul.008G10 |
| 6 | | 0 RING/U-box superfamily protein | Phvul.008G10 |
| 7 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 8 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 9 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 10 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 11 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 12 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 13 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 14 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 15 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.008G19 |
| 16 | UGT71B6 | UDP-glucosyl transferase 71B6 | Phvul.008G29 |
| 17 | UGT71B6 | UDP-glucosyl transferase 71B6 | Phvul.008G29 |
| 18 | UGT71B6 | UDP-glucosyl transferase 71B6 | Phvul.008G29 |
| 19 | UGT71B6 | UDP-glucosyl transferase 71B6 | Phvul.008G29 |
| 20 | UGT71B6 | UDP-glucosyl transferase 71B6 | Phvul.008G29 |
| 21 | UGT71B6 | UDP-glucosyl transferase 71B6 | Phvul.008G29 |
| 22 | ARF17 | auxin response factor 17 | Phvul.009G02 |
| 23 | ARF17 | auxin response factor 17 | Phvul.009G02 |
| 24 | | | |
| 25 | | 0 vacuolar iron transporter (VIT) family protein | Phvul.009G04 |
| 26 | | 0 vacuolar iron transporter (VIT) family protein | Phvul.009G04 |
| 27 | | 0 vacuolar iron transporter (VIT) family protein | Phvul.009G04 |
| 28 | ORP1C | OSBP(oxysterol binding protein)-related protein 1C | Phvul.009G12 |
| 29 | ORP1C | OSBP(oxysterol binding protein)-related protein 1C | Phvul.009G12 |
| 30 | ORP1C | OSBP(oxysterol binding protein)-related protein 1C | Phvul.009G12 |
| 31 | ORP1C | OSBP(oxysterol binding protein)-related protein 1C | Phvul.009G12 |
| 32 | ORP1C | OSBP(oxysterol binding protein)-related protein 1C | Phvul.009G12 |
| 33 | ORP1C | OSBP(oxysterol binding protein)-related protein 1C | Phvul.009G12 |
| 34 | ORP1C | OSBP(oxysterol binding protein)-related protein 1C | Phvul.009G12 |
| 35 | ORP1C | OSBP(oxysterol binding protein)-related protein 1C | Phvul.009G12 |
| 36 | ORP1C | OSBP(oxysterol binding protein)-related protein 1C | Phvul.009G12 |
| 37 | ORP1C | OSBP(oxysterol binding protein)-related protein 1C | Phvul.009G12 |
| 38 | ORP1C | OSBP(oxysterol binding protein)-related protein 1C | Phvul.009G12 |
| 39 | | 0 Mitochondrial substrate carrier family protein | Phvul.009G24 |
| 40 | | 0 Mitochondrial substrate carrier family protein | Phvul.009G24 |
| 41 | | 0 Mitochondrial substrate carrier family protein | Phvul.009G24 |
| 42 | | 0 Mitochondrial substrate carrier family protein | Phvul.009G24 |
| 43 | | 0 Mitochondrial substrate carrier family protein | Phvul.009G24 |
| 44 | | 0 Mitochondrial substrate carrier family protein | Phvul.009G24 |
| 45 | | 0 Mitochondrial substrate carrier family protein | Phvul.009G24 |
| 46 | | 0 Mitochondrial substrate carrier family protein | Phvul.009G24 |
| 47 | | 0 Mitochondrial substrate carrier family protein | Phvul.009G24 |
| 48 | | 0 Mitochondrial substrate carrier family protein | Phvul.009G24 |
| 49 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 50 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 51 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 52 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 53 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 54 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 55 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 56 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 57 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 58 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 59 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 60 | | | |

| | | | |
|----|---------------|--|----------------|
| 1 | | | |
| 2 | | | |
| 3 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 4 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 5 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 6 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 7 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 8 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 9 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 10 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 11 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 12 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 13 | AtGRF2,GRF2 | growth-regulating factor 2 | Phvul.010G04 |
| 14 | | 0 ARM repeat superfamily protein | Phvul.010G11 |
| 15 | | 0 ARM repeat superfamily protein | Phvul.010G11 |
| 16 | | 0 ARM repeat superfamily protein | Phvul.010G11 |
| 17 | | 0 ARM repeat superfamily protein | Phvul.010G11 |
| 18 | | 0 ARM repeat superfamily protein | Phvul.010G11 |
| 19 | | 0 Zinc finger (CCCH-type) family protein / RNA recogniti | Phvul.011G01 |
| 20 | | 0 Zinc finger (CCCH-type) family protein / RNA recogniti | Phvul.011G01 |
| 21 | | 0 Zinc finger (CCCH-type) family protein / RNA recogniti | Phvul.011G01 |
| 22 | | 0 Zinc finger (CCCH-type) family protein / RNA recogniti | Phvul.011G01 |
| 23 | | 0 Zinc finger (CCCH-type) family protein / RNA recogniti | Phvul.011G01 |
| 24 | LCR44 | low-molecular-weight cysteine-rich 44 | 0 |
| 25 | LCR44 | low-molecular-weight cysteine-rich 44 | 0 |
| 26 | LCR44 | low-molecular-weight cysteine-rich 44 | 0 |
| 27 | LCR44 | low-molecular-weight cysteine-rich 44 | 0 |
| 28 | LCR44 | low-molecular-weight cysteine-rich 44 | 0 |
| 29 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolæ | Phvul.011G16 |
| 30 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolæ | Phvul.011G16 |
| 31 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolæ | Phvul.011G16 |
| 32 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolæ | Phvul.011G16 |
| 33 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolæ | Phvul.011G16 |
| 34 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolæ | Phvul.011G16 |
| 35 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolæ | Phvul.011G16 |
| 36 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolæ | Phvul.011G16 |
| 37 | ATMSRB1,MSRB1 | methionine sulfoxide reductase B 1 | Phvul.011G17 |
| 38 | ATMSRB1,MSRB1 | methionine sulfoxide reductase B 1 | Phvul.011G17 |
| 39 | ATMSRB1,MSRB1 | methionine sulfoxide reductase B 1 | Phvul.011G17 |
| 40 | ATMSRB1,MSRB1 | methionine sulfoxide reductase B 1 | Phvul.011G17 |
| 41 | ATMSRB1,MSRB1 | methionine sulfoxide reductase B 1 | Phvul.011G17 |
| 42 | ATMSRB1,MSRB1 | methionine sulfoxide reductase B 1 | Phvul.011G17 |
| 43 | SUVH1 | SU(VAR)3-9 homolog 1 | Phvul.011G19 |
| 44 | SUVH1 | SU(VAR)3-9 homolog 1 | Phvul.011G19 |
| 45 | | 0 | 0 Phvul.001G09 |
| 46 | | 0 | 0 Phvul.001G09 |
| 47 | | 0 ENTH/VHS family protein | Phvul.001G10 |
| 48 | | 0 ENTH/VHS family protein | Phvul.001G10 |
| 49 | | 0 ENTH/VHS family protein | Phvul.001G10 |
| 50 | | 0 ENTH/VHS family protein | Phvul.001G10 |
| 51 | | 0 ENTH/VHS family protein | Phvul.001G10 |
| 52 | | 0 ENTH/VHS family protein | Phvul.001G10 |
| 53 | | 0 ENTH/VHS family protein | Phvul.001G10 |
| 54 | | 0 ENTH/VHS family protein | Phvul.001G10 |
| 55 | | 0 ENTH/VHS family protein | Phvul.001G10 |
| 56 | | 0 ENTH/VHS family protein | Phvul.001G10 |
| 57 | | 0 ENTH/VHS family protein | Phvul.001G10 |
| 58 | | 0 ENTH/VHS family protein | Phvul.001G10 |
| 59 | | 0 ENTH/VHS family protein | Phvul.001G10 |
| 60 | | | |

| | | |
|----|---|--------------|
| 1 | | |
| 2 | | |
| 3 | 0 ENTH/VHS family protein | Phvul.001G10 |
| 4 | 0 ENTH/VHS family protein | Phvul.001G10 |
| 5 | 0 ENTH/VHS family protein | Phvul.001G10 |
| 6 | 0 ENTH/VHS family protein | Phvul.001G10 |
| 7 | 0 ENTH/VHS family protein | Phvul.001G10 |
| 8 | 0 ENTH/VHS family protein | Phvul.001G10 |
| 9 | 0 ENTH/VHS family protein | Phvul.001G10 |
| 10 | 0 ENTH/VHS family protein | Phvul.001G10 |
| 11 | 0 ENTH/VHS family protein | Phvul.001G10 |
| 12 | 0 ENTH/VHS family protein | Phvul.001G10 |
| 13 | 0 oxidoreductase, 2OG-Fe(II) oxygenase family protein | Phvul.001G14 |
| 14 | 0 Thioredoxin superfamily protein | Phvul.001G17 |
| 15 | 0 Thioredoxin superfamily protein | Phvul.001G17 |
| 16 | 0 Thioredoxin superfamily protein | Phvul.001G17 |
| 17 | 0 Thioredoxin superfamily protein | Phvul.001G17 |
| 18 | 0 Thioredoxin superfamily protein | Phvul.001G17 |
| 19 | 0 phosphoadenosine phosphosulfate (PAPS) reductase | Phvul.001G17 |
| 20 | 0 phosphoadenosine phosphosulfate (PAPS) reductase | Phvul.001G17 |
| 21 | 0 phosphoadenosine phosphosulfate (PAPS) reductase | Phvul.001G17 |
| 22 | 0 DNase I-like superfamily protein | Phvul.001G20 |
| 23 | 0 DNase I-like superfamily protein | Phvul.001G20 |
| 24 | 0 DNase I-like superfamily protein | Phvul.001G20 |
| 25 | 0 DNase I-like superfamily protein | Phvul.001G20 |
| 26 | 0 DNase I-like superfamily protein | Phvul.001G20 |
| 27 | 0 DNase I-like superfamily protein | Phvul.001G20 |
| 28 | 0 DNase I-like superfamily protein | Phvul.001G20 |
| 29 | 0 DNase I-like superfamily protein | Phvul.001G20 |
| 30 | 0 DNase I-like superfamily protein | Phvul.001G20 |
| 31 | 0 DNase I-like superfamily protein | Phvul.001G20 |
| 32 | 0 DNase I-like superfamily protein | Phvul.001G20 |
| 33 | 0 ARM repeat superfamily protein | Phvul.001G26 |
| 34 | 0 O-methyltransferase family protein | Phvul.001G26 |
| 35 | 0 O-methyltransferase family protein | Phvul.001G26 |
| 36 | 0 O-methyltransferase family protein | Phvul.001G26 |
| 37 | 0 C2H2-like zinc finger protein | Phvul.002G05 |
| 38 | 0 C2H2-like zinc finger protein | Phvul.002G05 |
| 39 | ATH2,ATTRX2,ATTRXH2,TRX thioredoxin 2 | Phvul.002G06 |
| 40 | ATH2,ATTRX2,ATTRXH2,TRX thioredoxin 2 | Phvul.002G06 |
| 41 | ATH2,ATTRX2,ATTRXH2,TRX thioredoxin 2 | Phvul.002G06 |
| 42 | ATH2,ATTRX2,ATTRXH2,TRX thioredoxin 2 | Phvul.002G06 |
| 43 | ATH2,ATTRX2,ATTRXH2,TRX thioredoxin 2 | Phvul.002G06 |
| 44 | AtWRKY41,WRKY41 WRKY family transcription factor | Phvul.002G16 |
| 45 | AtWRKY41,WRKY41 WRKY family transcription factor | Phvul.002G16 |
| 46 | AtWRKY41,WRKY41 WRKY family transcription factor | Phvul.002G16 |
| 47 | 0 Galactose-binding protein | Phvul.002G16 |
| 48 | 0 Galactose-binding protein | Phvul.002G16 |
| 49 | 0 Galactose-binding protein | Phvul.002G16 |
| 50 | 0 Galactose-binding protein | Phvul.002G16 |
| 51 | 0 Galactose-binding protein | Phvul.002G16 |
| 52 | 0 basic helix-loop-helix (bHLH) DNA-binding superfamily protein | Phvul.002G21 |
| 53 | 0 basic helix-loop-helix (bHLH) DNA-binding superfamily protein | Phvul.002G21 |
| 54 | 0 basic helix-loop-helix (bHLH) DNA-binding superfamily protein | Phvul.002G21 |
| 55 | 0 basic helix-loop-helix (bHLH) DNA-binding superfamily protein | Phvul.002G21 |
| 56 | 0 basic helix-loop-helix (bHLH) DNA-binding superfamily protein | Phvul.002G21 |
| 57 | 0 GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.002G24 |
| 58 | 0 GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.002G24 |
| 59 | 0 GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.002G24 |
| 60 | | |

| | | | |
|----|-------------|--|--------------|
| 1 | | | |
| 2 | | | |
| 3 | | 0 Regulator of chromosome condensation (RCC1) family | Phvul.002G25 |
| 4 | | 0 Regulator of chromosome condensation (RCC1) family | Phvul.002G25 |
| 5 | | 0 Regulator of chromosome condensation (RCC1) family | Phvul.002G25 |
| 6 | | 0 Regulator of chromosome condensation (RCC1) family | Phvul.002G25 |
| 7 | | 0 Regulator of chromosome condensation (RCC1) family | Phvul.002G25 |
| 8 | | 0 Nodulin MtN3 family protein | Phvul.002G28 |
| 9 | | 0 Nodulin MtN3 family protein | Phvul.002G28 |
| 10 | | 0 Nodulin MtN3 family protein | Phvul.002G28 |
| 11 | | 0 Nodulin MtN3 family protein | Phvul.002G28 |
| 12 | | 0 Nodulin MtN3 family protein | Phvul.002G28 |
| 13 | | 0 Peptidase M1 family protein | Phvul.002G29 |
| 14 | | 0 Peptidase M1 family protein | Phvul.002G29 |
| 15 | | 0 Peptidase M1 family protein | Phvul.002G29 |
| 16 | ABI1,AtABI1 | Protein phosphatase 2C family protein | Phvul.002G30 |
| 17 | ABI1,AtABI1 | Protein phosphatase 2C family protein | Phvul.002G30 |
| 18 | UFD1 | ubiquitin fusion degradation 1 | Phvul.002G32 |
| 19 | UFD1 | ubiquitin fusion degradation 1 | Phvul.002G32 |
| 20 | UFD1 | ubiquitin fusion degradation 1 | Phvul.002G32 |
| 21 | UFD1 | ubiquitin fusion degradation 1 | Phvul.002G32 |
| 22 | UFD1 | ubiquitin fusion degradation 1 | Phvul.002G32 |
| 23 | ER-ANT1 | endoplasmic reticulum-adenine nucleotide transport | Phvul.002G32 |
| 24 | ER-ANT1 | endoplasmic reticulum-adenine nucleotide transport | Phvul.002G32 |
| 25 | ER-ANT1 | endoplasmic reticulum-adenine nucleotide transport | Phvul.002G32 |
| 26 | ER-ANT1 | endoplasmic reticulum-adenine nucleotide transport | Phvul.002G32 |
| 27 | ER-ANT1 | endoplasmic reticulum-adenine nucleotide transport | Phvul.002G32 |
| 28 | ER-ANT1 | endoplasmic reticulum-adenine nucleotide transport | Phvul.002G32 |
| 29 | ER-ANT1 | endoplasmic reticulum-adenine nucleotide transport | Phvul.002G32 |
| 30 | ER-ANT1 | endoplasmic reticulum-adenine nucleotide transport | Phvul.002G32 |
| 31 | ER-ANT1 | endoplasmic reticulum-adenine nucleotide transport | Phvul.002G32 |
| 32 | ER-ANT1 | endoplasmic reticulum-adenine nucleotide transport | Phvul.002G32 |
| 33 | ER-ANT1 | endoplasmic reticulum-adenine nucleotide transport | Phvul.002G32 |
| 34 | DME | HhH-GPD base excision DNA repair family protein | Phvul.003G03 |
| 35 | DME | HhH-GPD base excision DNA repair family protein | Phvul.003G03 |
| 36 | | 0 Nucleotide-diphospho-sugar transferases superfamily | Phvul.003G05 |
| 37 | | 0 Nucleotide-diphospho-sugar transferases superfamily | Phvul.003G05 |
| 38 | | 0 | 0 |
| 39 | | 0 | 0 |
| 40 | | 0 | 0 |
| 41 | | 0 | 0 |
| 42 | | 0 | 0 |
| 43 | | 0 | 0 |
| 44 | | 0 | 0 |
| 45 | BGAL1 | beta galactosidase 1 | Phvul.003G13 |
| 46 | BGAL1 | beta galactosidase 1 | Phvul.003G13 |
| 47 | BGAL1 | beta galactosidase 1 | Phvul.003G13 |
| 48 | BGAL1 | beta galactosidase 1 | Phvul.003G13 |
| 49 | | 0 Disease resistance protein (CC-NBS-LRR class) family | Phvul.003G24 |
| 50 | | 0 Disease resistance protein (CC-NBS-LRR class) family | Phvul.003G24 |
| 51 | | 0 Disease resistance protein (CC-NBS-LRR class) family | Phvul.003G24 |
| 52 | | 0 Disease resistance protein (CC-NBS-LRR class) family | Phvul.003G24 |
| 53 | | 0 Disease resistance protein (CC-NBS-LRR class) family | Phvul.003G24 |
| 54 | | 0 Disease resistance protein (CC-NBS-LRR class) family | Phvul.003G24 |
| 55 | | 0 Disease resistance protein (CC-NBS-LRR class) family | Phvul.003G24 |
| 56 | | 0 Disease resistance protein (CC-NBS-LRR class) family | Phvul.003G24 |
| 57 | | 0 Disease resistance protein (CC-NBS-LRR class) family | Phvul.003G24 |
| 58 | | 0 Disease resistance protein (CC-NBS-LRR class) family | Phvul.003G24 |
| 59 | | 0 Disease resistance protein (CC-NBS-LRR class) family | Phvul.003G24 |
| 60 | | | |

| | | | |
|----|-----------------|--|--------------|
| 1 | | | |
| 2 | | | |
| 3 | | 0 Disease resistance protein (CC-NBS-LRR class) family | Phvul.003G24 |
| 4 | | 0 S-adenosyl-L-methionine-dependent methyltransferase | Phvul.003G28 |
| 5 | | 0 S-adenosyl-L-methionine-dependent methyltransferase | Phvul.003G28 |
| 6 | | | |
| 7 | ATRBP47A,RBP47A | RNA-binding protein 47A | Phvul.003G29 |
| 8 | ATRBP47A,RBP47A | RNA-binding protein 47A | Phvul.003G29 |
| 9 | ATRBP47A,RBP47A | RNA-binding protein 47A | Phvul.003G29 |
| 10 | ATRBP47A,RBP47A | RNA-binding protein 47A | Phvul.003G29 |
| 11 | ATRBP47A,RBP47A | RNA-binding protein 47A | Phvul.003G29 |
| 12 | ATRBP47B,RBP47B | RNA-binding protein 47B | Phvul.003G29 |
| 13 | ATRBP47B,RBP47B | RNA-binding protein 47B | Phvul.003G29 |
| 14 | ATRBP47B,RBP47B | RNA-binding protein 47B | Phvul.003G29 |
| 15 | ATRBP47B,RBP47B | RNA-binding protein 47B | Phvul.003G29 |
| 16 | ATRBP47B,RBP47B | RNA-binding protein 47B | Phvul.003G29 |
| 17 | ATRBP47B,RBP47B | RNA-binding protein 47B | Phvul.003G29 |
| 18 | ATRBP47B,RBP47B | RNA-binding protein 47B | Phvul.003G29 |
| 19 | ATRBP47B,RBP47B | RNA-binding protein 47B | Phvul.003G29 |
| 20 | ATRBP47B,RBP47B | RNA-binding protein 47B | Phvul.003G29 |
| 21 | ATRBP47B,RBP47B | RNA-binding protein 47B | Phvul.003G29 |
| 22 | ATRBP47B,RBP47B | RNA-binding protein 47B | Phvul.003G29 |
| 23 | | 0 | 0 0 |
| 24 | | 0 | 0 0 |
| 25 | | 0 | 0 0 |
| 26 | | 0 | 0 0 |
| 27 | | 0 | 0 0 |
| 28 | | 0 disease resistance family protein / LRR family protein | Phvul.004G04 |
| 29 | | 0 disease resistance family protein / LRR family protein | Phvul.004G04 |
| 30 | | | |
| 31 | | 0 Eukaryotic aspartyl protease family protein | Phvul.004G05 |
| 32 | | 0 Eukaryotic aspartyl protease family protein | Phvul.004G05 |
| 33 | | 0 Eukaryotic aspartyl protease family protein | Phvul.004G05 |
| 34 | | 0 Eukaryotic aspartyl protease family protein | Phvul.004G05 |
| 35 | | 0 Eukaryotic aspartyl protease family protein | Phvul.004G05 |
| 36 | AGP20,AtAGP20 | arabinogalactan protein 20 | Phvul.004G17 |
| 37 | AGP20,AtAGP20 | arabinogalactan protein 20 | Phvul.004G17 |
| 38 | AGP20,AtAGP20 | arabinogalactan protein 20 | Phvul.004G17 |
| 39 | AGP20,AtAGP20 | arabinogalactan protein 20 | Phvul.004G17 |
| 40 | AGP20,AtAGP20 | arabinogalactan protein 20 | Phvul.004G17 |
| 41 | AKR2B | ankyrin repeat-containing 2B | Phvul.005G00 |
| 42 | AKR2B | ankyrin repeat-containing 2B | Phvul.005G00 |
| 43 | AKR2B | ankyrin repeat-containing 2B | Phvul.005G00 |
| 44 | AKR2B | ankyrin repeat-containing 2B | Phvul.005G00 |
| 45 | AKR2B | ankyrin repeat-containing 2B | Phvul.005G00 |
| 46 | NF-YC11 | nuclear factor Y, subunit C11 | Phvul.005G01 |
| 47 | | 0 BTB/POZ domain-containing protein | Phvul.005G05 |
| 48 | | | |
| 49 | ATPPC2,PPC2 | phosphoenolpyruvate carboxylase 2 | Phvul.005G09 |
| 50 | | 0 MuDR family transposase | Phvul.005G10 |
| 51 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.005G11 |
| 52 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.005G11 |
| 53 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.005G11 |
| 54 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.005G11 |
| 55 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.005G11 |
| 56 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.005G11 |
| 57 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.005G11 |
| 58 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.005G11 |
| 59 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.005G11 |
| 60 | | | |

| | | | |
|----|-------------|---|----------------|
| 1 | | | |
| 2 | | | |
| 3 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.005G11 |
| 4 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.005G11 |
| 5 | | 0 C2H2 and C2HC zinc fingers superfamily protein | Phvul.005G13 |
| 6 | | 0 C2H2 and C2HC zinc fingers superfamily protein | Phvul.005G13 |
| 7 | | 0 Calcium-binding EF-hand family protein | Phvul.006G10 |
| 8 | | 0 zinc knuckle (CCHC-type) family protein | Phvul.006G11 |
| 9 | | 0 zinc knuckle (CCHC-type) family protein | Phvul.006G11 |
| 10 | | 0 zinc knuckle (CCHC-type) family protein | Phvul.006G11 |
| 11 | | 0 zinc knuckle (CCHC-type) family protein | Phvul.006G11 |
| 12 | | 0 zinc knuckle (CCHC-type) family protein | Phvul.006G11 |
| 13 | | 0 zinc knuckle (CCHC-type) family protein | Phvul.006G11 |
| 14 | | 0 zinc knuckle (CCHC-type) family protein | Phvul.006G11 |
| 15 | | 0 zinc knuckle (CCHC-type) family protein | Phvul.006G11 |
| 16 | | 0 zinc knuckle (CCHC-type) family protein | Phvul.006G11 |
| 17 | | 0 zinc knuckle (CCHC-type) family protein | Phvul.006G11 |
| 18 | | 0 zinc knuckle (CCHC-type) family protein | Phvul.006G11 |
| 19 | | 0 zinc knuckle (CCHC-type) family protein | Phvul.006G11 |
| 20 | | 0 HCO ₃ ⁻ transporter family | Phvul.006G12 |
| 21 | | 0 HCO ₃ ⁻ transporter family | Phvul.006G12 |
| 22 | | 0 HCO ₃ ⁻ transporter family | Phvul.006G12 |
| 23 | | 0 HCO ₃ ⁻ transporter family | Phvul.006G12 |
| 24 | | 0 HCO ₃ ⁻ transporter family | Phvul.006G12 |
| 25 | | 0 HCO ₃ ⁻ transporter family | Phvul.006G12 |
| 26 | | 0 HCO ₃ ⁻ transporter family | Phvul.006G12 |
| 27 | | 0 HCO ₃ ⁻ transporter family | Phvul.006G12 |
| 28 | | 0 HCO ₃ ⁻ transporter family | Phvul.006G12 |
| 29 | | 0 HCO ₃ ⁻ transporter family | Phvul.006G12 |
| 30 | | 0 | 0 Phvul.006G15 |
| 31 | | 0 | 0 Phvul.006G15 |
| 32 | SCPL19,SNG2 | serine carboxypeptidase-like 19 | Phvul.006G16 |
| 33 | SCPL19,SNG2 | serine carboxypeptidase-like 19 | Phvul.006G16 |
| 34 | SCPL19,SNG2 | serine carboxypeptidase-like 19 | Phvul.006G16 |
| 35 | SCPL19,SNG2 | serine carboxypeptidase-like 19 | Phvul.006G16 |
| 36 | SCPL19,SNG2 | serine carboxypeptidase-like 19 | Phvul.006G16 |
| 37 | | 0 phosphoinositide binding | Phvul.006G19 |
| 38 | | 0 phosphoinositide binding | Phvul.006G19 |
| 39 | | 0 Prolyl oligopeptidase family protein | Phvul.007G01 |
| 40 | | 0 Prolyl oligopeptidase family protein | Phvul.007G01 |
| 41 | | 0 Prolyl oligopeptidase family protein | Phvul.007G01 |
| 42 | | 0 Prolyl oligopeptidase family protein | Phvul.007G01 |
| 43 | | 0 TCP family transcription factor | Phvul.007G01 |
| 44 | | 0 TCP family transcription factor | Phvul.007G01 |
| 45 | | 0 phosphatidyl serine synthase family protein | Phvul.007G03 |
| 46 | | 0 phosphatidyl serine synthase family protein | Phvul.007G03 |
| 47 | | 0 phosphatidyl serine synthase family protein | Phvul.007G03 |
| 48 | | 0 phosphatidyl serine synthase family protein | Phvul.007G03 |
| 49 | CRK25 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.007G05 |
| 50 | CRK25 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.007G05 |
| 51 | CRK25 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.007G05 |
| 52 | CRK25 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.007G05 |
| 53 | CRK25 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.007G05 |
| 54 | CRK25 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.007G05 |
| 55 | AO1,ATAO1 | amine oxidase 1 | Phvul.007G05 |
| 56 | AO1,ATAO1 | amine oxidase 1 | Phvul.007G05 |
| 57 | AO1,ATAO1 | amine oxidase 1 | Phvul.007G05 |
| 58 | AO1,ATAO1 | amine oxidase 1 | Phvul.007G05 |
| 59 | AO1,ATAO1 | amine oxidase 1 | Phvul.007G05 |
| 60 | | | |

| | | | |
|----|-------------------------|---|----------------|
| 1 | | | |
| 2 | | | |
| 3 | | 0 Protein of unknown function (DUF581) | Phvul.007G05 |
| 4 | | 0 Protein of unknown function (DUF581) | Phvul.007G05 |
| 5 | | 0 Protein of unknown function (DUF581) | Phvul.007G05 |
| 6 | | 0 Protein of unknown function (DUF581) | Phvul.007G05 |
| 7 | | 0 Protein of unknown function (DUF581) | Phvul.007G05 |
| 8 | | 0 Protein of unknown function (DUF581) | Phvul.007G05 |
| 9 | | 0 Protein of unknown function (DUF581) | Phvul.007G05 |
| 10 | | 0 Protein of unknown function (DUF581) | Phvul.007G05 |
| 11 | | 0 Protein of unknown function (DUF581) | Phvul.007G05 |
| 12 | | 0 Protein of unknown function (DUF581) | Phvul.007G05 |
| 13 | | 0 Protein of unknown function (DUF581) | Phvul.007G05 |
| 14 | AtCXE20,CXE20 | carboxyesterase 20 | Phvul.007G06 |
| 15 | AtCXE20,CXE20 | carboxyesterase 20 | Phvul.007G06 |
| 16 | AtCXE20,CXE20 | carboxyesterase 20 | Phvul.007G06 |
| 17 | AtCXE20,CXE20 | carboxyesterase 20 | Phvul.007G06 |
| 18 | AtCXE20,CXE20 | carboxyesterase 20 | Phvul.007G06 |
| 19 | AtCXE20,CXE20 | carboxyesterase 20 | Phvul.007G06 |
| 20 | ATFRO2,FRD1,FRO2 | ferric reduction oxidase 2 | Phvul.007G07 |
| 21 | ATFRO2,FRD1,FRO2 | ferric reduction oxidase 2 | Phvul.007G07 |
| 22 | ATFRO2,FRD1,FRO2 | ferric reduction oxidase 2 | Phvul.007G07 |
| 23 | ATFRO2,FRD1,FRO2 | ferric reduction oxidase 2 | Phvul.007G07 |
| 24 | ATFRO2,FRD1,FRO2 | ferric reduction oxidase 2 | Phvul.007G07 |
| 25 | | | |
| 26 | | 0 | 0 Phvul.007G09 |
| 27 | | 0 | 0 Phvul.007G09 |
| 28 | | 0 | 0 Phvul.007G09 |
| 29 | | 0 | 0 Phvul.007G09 |
| 30 | | 0 | 0 Phvul.007G09 |
| 31 | ATGST11,ATGSTF7,ATGSTF8 | glutathione S-transferase 7 | Phvul.007G10 |
| 32 | ATGST11,ATGSTF7,ATGSTF8 | glutathione S-transferase 7 | Phvul.007G10 |
| 33 | ATGST11,ATGSTF7,ATGSTF8 | glutathione S-transferase 7 | Phvul.007G10 |
| 34 | ATGST11,ATGSTF7,ATGSTF8 | glutathione S-transferase 7 | Phvul.007G10 |
| 35 | ATGST11,ATGSTF7,ATGSTF8 | glutathione S-transferase 7 | Phvul.007G10 |
| 36 | | 0 Mog1/PsbP/DUF1795-like photosystem II reaction ce | Phvul.007G18 |
| 37 | | 0 Mog1/PsbP/DUF1795-like photosystem II reaction ce | Phvul.007G18 |
| 38 | | 0 Mog1/PsbP/DUF1795-like photosystem II reaction ce | Phvul.007G18 |
| 39 | | 0 Mog1/PsbP/DUF1795-like photosystem II reaction ce | Phvul.007G18 |
| 40 | | 0 Mog1/PsbP/DUF1795-like photosystem II reaction ce | Phvul.007G18 |
| 41 | | | |
| 42 | | 0 | 0 0 |
| 43 | | 0 | 0 0 |
| 44 | | 0 Protein kinase superfamily protein | Phvul.007G20 |
| 45 | | 0 Protein kinase superfamily protein | Phvul.007G20 |
| 46 | | 0 Protein kinase superfamily protein | Phvul.007G20 |
| 47 | | 0 Protein kinase superfamily protein | Phvul.007G20 |
| 48 | | 0 Protein kinase superfamily protein | Phvul.007G20 |
| 49 | | 0 Protein kinase superfamily protein | Phvul.007G20 |
| 50 | | 0 Protein kinase superfamily protein | Phvul.007G20 |
| 51 | | 0 Protein kinase superfamily protein | Phvul.007G20 |
| 52 | | 0 Protein kinase superfamily protein | Phvul.007G20 |
| 53 | | 0 Protein kinase superfamily protein | Phvul.007G20 |
| 54 | | 0 Protein kinase superfamily protein | Phvul.007G20 |
| 55 | | 0 Plant invertase/pectin methylesterase inhibitor super | Phvul.007G21 |
| 56 | | 0 | 0 Phvul.007G27 |
| 57 | | 0 | 0 Phvul.007G27 |
| 58 | | 0 | 0 Phvul.007G27 |
| 59 | | 0 | 0 Phvul.007G27 |
| 60 | | | |

| | | | | |
|----|--------------------|---|---|--------------|
| 1 | | | | |
| 2 | | | | |
| 3 | | 0 | 0 | Phvul.007G27 |
| 4 | | 0 | 0 | Phvul.007G27 |
| 5 | | 0 | 0 | Phvul.007G27 |
| 6 | | 0 | 0 | Phvul.007G27 |
| 7 | NEF1 | no exine formation 1 | | Phvul.008G00 |
| 8 | NEF1 | no exine formation 1 | | Phvul.008G00 |
| 9 | NEF1 | no exine formation 1 | | Phvul.008G00 |
| 10 | NEF1 | no exine formation 1 | | Phvul.008G00 |
| 11 | NEF1 | no exine formation 1 | | Phvul.008G00 |
| 12 | | 0 HEAT repeat-containing protein | | Phvul.008G00 |
| 13 | | 0 HEAT repeat-containing protein | | Phvul.008G00 |
| 14 | | 0 HEAT repeat-containing protein | | Phvul.008G00 |
| 15 | | 0 HEAT repeat-containing protein | | Phvul.008G00 |
| 16 | | 0 HEAT repeat-containing protein | | Phvul.008G00 |
| 17 | | 0 HEAT repeat-containing protein | | Phvul.008G00 |
| 18 | | 0 HEAT repeat-containing protein | | Phvul.008G00 |
| 19 | ATTA6,TAF6,TAFII59 | TATA BOX ASSOCIATED FACTOR II 59 | | Phvul.008G01 |
| 20 | ATTA6,TAF6,TAFII59 | TATA BOX ASSOCIATED FACTOR II 59 | | Phvul.008G01 |
| 21 | | 0 Mitochondrial transcription termination factor family | | Phvul.008G04 |
| 22 | | 0 | 0 | 0 |
| 23 | | 0 | 0 | 0 |
| 24 | | 0 | 0 | 0 |
| 25 | | 0 | 0 | 0 |
| 26 | | 0 | 0 | 0 |
| 27 | | 0 | 0 | 0 |
| 28 | | 0 LRR and NB-ARC domains-containing disease resistan | | Phvul.008G07 |
| 29 | | 0 LRR and NB-ARC domains-containing disease resistan | | Phvul.008G07 |
| 30 | | 0 LRR and NB-ARC domains-containing disease resistan | | Phvul.008G07 |
| 31 | | 0 LRR and NB-ARC domains-containing disease resistan | | Phvul.008G07 |
| 32 | | 0 LRR and NB-ARC domains-containing disease resistan | | Phvul.008G07 |
| 33 | | 0 Leucine-rich repeat protein kinase family protein | | Phvul.008G09 |
| 34 | | 0 Leucine-rich repeat protein kinase family protein | | Phvul.008G09 |
| 35 | | 0 Leucine-rich repeat protein kinase family protein | | Phvul.008G09 |
| 36 | | 0 Leucine-rich repeat protein kinase family protein | | Phvul.008G09 |
| 37 | | 0 Leucine-rich repeat protein kinase family protein | | Phvul.008G09 |
| 38 | | 0 Leucine-rich repeat protein kinase family protein | | Phvul.008G09 |
| 39 | | 0 Leucine-rich repeat protein kinase family protein | | Phvul.008G09 |
| 40 | | 0 Leucine-rich repeat protein kinase family protein | | Phvul.008G09 |
| 41 | | 0 Protein of unknown function (DUF674) | | Phvul.008G11 |
| 42 | | 0 Protein of unknown function (DUF674) | | Phvul.008G11 |
| 43 | | 0 Protein of unknown function (DUF674) | | Phvul.008G11 |
| 44 | | 0 Protein of unknown function (DUF674) | | Phvul.008G11 |
| 45 | | 0 Protein of unknown function (DUF674) | | Phvul.008G11 |
| 46 | | 0 Protein of unknown function (DUF674) | | Phvul.008G11 |
| 47 | | 0 Protein of unknown function (DUF674) | | Phvul.008G11 |
| 48 | ATASP38,EMB24,PCS1 | Eukaryotic aspartyl protease family protein | | Phvul.008G11 |
| 49 | ATASP38,EMB24,PCS1 | Eukaryotic aspartyl protease family protein | | Phvul.008G11 |
| 50 | | 0 | 0 | 0 |
| 51 | | 0 | 0 | 0 |
| 52 | | 0 | 0 | 0 |
| 53 | | 0 | 0 | 0 |
| 54 | | 0 | 0 | 0 |
| 55 | | 0 Thioesterase superfamily protein | | Phvul.008G20 |
| 56 | | 0 Thioesterase superfamily protein | | Phvul.008G20 |
| 57 | | 0 Thioesterase superfamily protein | | Phvul.008G20 |
| 58 | | 0 Thioesterase superfamily protein | | Phvul.008G20 |
| 59 | | 0 Thioesterase superfamily protein | | Phvul.008G20 |
| 60 | | | | |

| | | | |
|----|------------------------|--|--------------|
| 1 | | | |
| 2 | | | |
| 3 | | 0 Thioesterase superfamily protein | Phvul.008G20 |
| 4 | | 0 | 0 |
| 5 | | 0 | 0 |
| 6 | | 0 | 0 |
| 7 | | 0 | 0 |
| 8 | | 0 | 0 |
| 9 | | 0 | 0 |
| 10 | ATPROT1,PROT1 | proline transporter 1 | Phvul.008G22 |
| 11 | ATPROT1,PROT1 | proline transporter 1 | Phvul.008G22 |
| 12 | ATPROT1,PROT1 | proline transporter 1 | Phvul.008G22 |
| 13 | ATPROT1,PROT1 | proline transporter 1 | Phvul.008G22 |
| 14 | ATPROT1,PROT1 | proline transporter 1 | Phvul.008G22 |
| 15 | | 0 RNA-binding (RRM/RBD/RNP motifs) family protein | Phvul.008G27 |
| 16 | | 0 RNA-binding (RRM/RBD/RNP motifs) family protein | Phvul.008G27 |
| 17 | | 0 RNA-binding (RRM/RBD/RNP motifs) family protein | Phvul.008G27 |
| 18 | | 0 RNA-binding (RRM/RBD/RNP motifs) family protein | Phvul.008G27 |
| 19 | COX15 | cytochrome c oxidase 15 | Phvul.008G28 |
| 20 | COX15 | cytochrome c oxidase 15 | Phvul.008G28 |
| 21 | | | |
| 22 | ATMYB3R-1,ATMYB3R1,MYI | Homeodomain-like protein | Phvul.009G10 |
| 23 | ORP1C | OSBP(oxysterol binding protein)-related protein 1C | Phvul.009G12 |
| 24 | ORP1C | OSBP(oxysterol binding protein)-related protein 1C | Phvul.009G12 |
| 25 | ORP1C | OSBP(oxysterol binding protein)-related protein 1C | Phvul.009G12 |
| 26 | ORP1C | OSBP(oxysterol binding protein)-related protein 1C | Phvul.009G12 |
| 27 | ORP1C | OSBP(oxysterol binding protein)-related protein 1C | Phvul.009G12 |
| 28 | WNK3 | with no lysine (K) kinase 3 | Phvul.009G17 |
| 29 | WNK3 | with no lysine (K) kinase 3 | Phvul.009G17 |
| 30 | WNK3 | with no lysine (K) kinase 3 | Phvul.009G17 |
| 31 | WNK3 | with no lysine (K) kinase 3 | Phvul.009G17 |
| 32 | WNK3 | with no lysine (K) kinase 3 | Phvul.009G17 |
| 33 | BGAL12 | beta-galactosidase 12 | Phvul.009G23 |
| 34 | BGAL12 | beta-galactosidase 12 | Phvul.009G23 |
| 35 | ATOMT1,OMT1 | O-methyltransferase 1 | Phvul.009G25 |
| 36 | ATOMT1,OMT1 | O-methyltransferase 1 | Phvul.009G25 |
| 37 | ATOMT1,OMT1 | O-methyltransferase 1 | Phvul.009G25 |
| 38 | ATOMT1,OMT1 | O-methyltransferase 1 | Phvul.009G25 |
| 39 | ATOMT1,OMT1 | O-methyltransferase 1 | Phvul.009G25 |
| 40 | ATOMT1,OMT1 | O-methyltransferase 1 | Phvul.009G25 |
| 41 | | 0 DNA binding;ATP binding | Phvul.010G03 |
| 42 | | 0 DNA binding;ATP binding | Phvul.010G03 |
| 43 | | 0 DNA binding;ATP binding | Phvul.010G03 |
| 44 | | 0 DNA binding;ATP binding | Phvul.010G03 |
| 45 | | 0 DNA binding;ATP binding | Phvul.010G03 |
| 46 | | 0 DNA binding;ATP binding | Phvul.010G03 |
| 47 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 48 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 49 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 50 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 51 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 52 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 53 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 54 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 55 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 56 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 57 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 58 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 59 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 60 | | | |

| | | | |
|----|------------------------|--|--------------|
| 1 | | | |
| 2 | | | |
| 3 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 4 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 5 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 6 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 7 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 8 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 9 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 10 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 11 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 12 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 13 | CUM2,EIF4G | eukaryotic translation initiation factor 4G | Phvul.010G04 |
| 14 | UNE10 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.010G07 |
| 15 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 16 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 17 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 18 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 19 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 20 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 21 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 22 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 23 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 24 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 25 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 26 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 27 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 28 | ATLOX1,LOX1 | lipoxygenase 1 | Phvul.010G13 |
| 29 | ATLOX1,LOX1 | lipoxygenase 1 | Phvul.010G13 |
| 30 | ATLOX1,LOX1 | lipoxygenase 1 | Phvul.010G13 |
| 31 | ATLOX1,LOX1 | lipoxygenase 1 | Phvul.010G13 |
| 32 | ATLOX1,LOX1 | lipoxygenase 1 | Phvul.010G13 |
| 33 | ATLOX1,LOX1 | lipoxygenase 1 | Phvul.010G13 |
| 34 | ACA11 | autoinhibited Ca ²⁺ -ATPase 11 | Phvul.011G01 |
| 35 | ACA11 | autoinhibited Ca ²⁺ -ATPase 11 | Phvul.011G01 |
| 36 | ACA11 | autoinhibited Ca ²⁺ -ATPase 11 | Phvul.011G01 |
| 37 | ACA11 | autoinhibited Ca ²⁺ -ATPase 11 | Phvul.011G01 |
| 38 | ACA11 | autoinhibited Ca ²⁺ -ATPase 11 | Phvul.011G01 |
| 39 | TOR | target of rapamycin | Phvul.011G05 |
| 40 | TOR | target of rapamycin | Phvul.011G05 |
| 41 | TOR | target of rapamycin | Phvul.011G05 |
| 42 | TOR | target of rapamycin | Phvul.011G05 |
| 43 | TOR | target of rapamycin | Phvul.011G05 |
| 44 | PTAC16 | plastid transcriptionally active 16 | Phvul.011G06 |
| 45 | PTAC16 | plastid transcriptionally active 16 | Phvul.011G06 |
| 46 | | 0 Plant self-incompatibility protein S1 family | Phvul.011G11 |
| 47 | | 0 Plant self-incompatibility protein S1 family | Phvul.011G11 |
| 48 | | 0 Plant self-incompatibility protein S1 family | Phvul.011G12 |
| 49 | | 0 Plant self-incompatibility protein S1 family | Phvul.011G12 |
| 50 | LCR44 | low-molecular-weight cysteine-rich 44 | 0 |
| 51 | LCR44 | low-molecular-weight cysteine-rich 44 | 0 |
| 52 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolase) | Phvul.011G16 |
| 53 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolase) | Phvul.011G16 |
| 54 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolase) | Phvul.011G16 |
| 55 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolase) | Phvul.011G16 |
| 56 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolase) | Phvul.011G16 |
| 57 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolase) | Phvul.011G16 |
| 58 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolase) | Phvul.011G16 |
| 59 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolase) | Phvul.011G16 |
| 60 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolase) | Phvul.011G16 |

| | | | |
|----|--------------------|--|---------------|
| 1 | | | |
| 2 | | | |
| 3 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolase) | Phvul.011G16 |
| 4 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolase) | Phvul.011G16 |
| 5 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolase) | Phvul.011G16 |
| 6 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolase) | Phvul.011G16 |
| 7 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolase) | Phvul.011G16 |
| 8 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolase) | Phvul.011G16 |
| 9 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolase) | Phvul.011G16 |
| 10 | | 0 N-terminal nucleophile aminohydrolases (Ntn hydrolase) | Phvul.011G16 |
| 11 | | 0 | 0 0 |
| 12 | | 0 | 0 0 |
| 13 | | 0 | 0 0 |
| 14 | | 0 | 0 0 |
| 15 | | 0 | 0 0 |
| 16 | emb2458 | FtsH extracellular protease family | Phvul.L00205: |
| 17 | emb2458 | FtsH extracellular protease family | Phvul.L00205: |
| 18 | emb2458 | FtsH extracellular protease family | Phvul.L00205: |
| 19 | emb2458 | FtsH extracellular protease family | Phvul.L00205: |
| 20 | emb2458 | FtsH extracellular protease family | Phvul.L00205: |
| 21 | emb2458 | FtsH extracellular protease family | Phvul.L00205: |
| 22 | emb2458 | FtsH extracellular protease family | Phvul.L00205: |
| 23 | emb2458 | FtsH extracellular protease family | Phvul.L00205: |
| 24 | emb2458 | FtsH extracellular protease family | Phvul.L00205: |
| 25 | emb2458 | FtsH extracellular protease family | Phvul.L00205: |
| 26 | emb2458 | FtsH extracellular protease family | Phvul.L00205: |
| 27 | | 0 CCCH-type zinc fingerfamily protein with RNA-binding | Phvul.L00253: |
| 28 | | 0 CCCH-type zinc fingerfamily protein with RNA-binding | Phvul.L00253: |
| 29 | | 0 CCCH-type zinc fingerfamily protein with RNA-binding | Phvul.L00253: |
| 30 | | 0 CCCH-type zinc fingerfamily protein with RNA-binding | Phvul.L00253: |
| 31 | ATLAC2,LAC2 | laccase 2 | Phvul.L00734: |
| 32 | | 0 Zinc-binding dehydrogenase family protein | Phvul.008G00 |
| 33 | | 0 Zinc-binding dehydrogenase family protein | Phvul.008G00 |
| 34 | | 0 Zinc-binding dehydrogenase family protein | Phvul.008G00 |
| 35 | PLA IIA,PLA2A,PLP2 | phospholipase A 2A | Phvul.001G02 |
| 36 | PLA IIA,PLA2A,PLP2 | phospholipase A 2A | Phvul.001G02 |
| 37 | | 0 Remorin family protein | Phvul.001G02 |
| 38 | | 0 Remorin family protein | Phvul.001G02 |
| 39 | | 0 Remorin family protein | Phvul.001G02 |
| 40 | | 0 Remorin family protein | Phvul.001G02 |
| 41 | | 0 Remorin family protein | Phvul.001G02 |
| 42 | | 0 Remorin family protein | Phvul.001G02 |
| 43 | ATBFRUCT1,ATCWINV1 | Glycosyl hydrolases family 32 protein | Phvul.001G03 |
| 44 | | 0 Protein of unknown function (DUF2296) | Phvul.001G05 |
| 45 | | 0 Protein of unknown function (DUF2296) | Phvul.001G05 |
| 46 | | 0 Protein of unknown function (DUF2296) | Phvul.001G05 |
| 47 | ARA1,ATISA1,ISA1 | arabinose kinase | Phvul.001G07 |
| 48 | ARA1,ATISA1,ISA1 | arabinose kinase | Phvul.001G07 |
| 49 | ACS | acetyl-CoA synthetase | Phvul.001G09 |
| 50 | ACS | acetyl-CoA synthetase | Phvul.001G09 |
| 51 | ACS | acetyl-CoA synthetase | Phvul.001G09 |
| 52 | | 0 transcription regulator NOT2/NOT3/NOT5 family prot | Phvul.001G10 |
| 53 | | 0 transcription regulator NOT2/NOT3/NOT5 family prot | Phvul.001G10 |
| 54 | | 0 transcription regulator NOT2/NOT3/NOT5 family prot | Phvul.001G10 |
| 55 | | 0 transcription regulator NOT2/NOT3/NOT5 family prot | Phvul.001G10 |
| 56 | | 0 transcription regulator NOT2/NOT3/NOT5 family prot | Phvul.001G10 |
| 57 | | 0 endoribonucleases | Phvul.001G11 |
| 58 | | 0 endoribonucleases | Phvul.001G11 |
| 59 | | 0 endoribonucleases | Phvul.001G11 |
| 60 | | | |

| | | | |
|----|----------------------|---|----------------|
| 1 | | | |
| 2 | | | |
| 3 | PSL5,RSW3 | Glycosyl hydrolases family 31 protein | Phvul.001G12 |
| 4 | PSL5,RSW3 | Glycosyl hydrolases family 31 protein | Phvul.001G12 |
| 5 | | | |
| 6 | | 0 NB-ARC domain-containing disease resistance protei | Phvul.001G13 |
| 7 | | 0 NB-ARC domain-containing disease resistance protei | Phvul.001G13 |
| 8 | | 0 NB-ARC domain-containing disease resistance protei | Phvul.001G13 |
| 9 | | 0 NB-ARC domain-containing disease resistance protei | Phvul.001G13 |
| 10 | | 0 NB-ARC domain-containing disease resistance protei | Phvul.001G13 |
| 11 | | 0 NB-ARC domain-containing disease resistance protei | Phvul.001G13 |
| 12 | | 0 NB-ARC domain-containing disease resistance protei | Phvul.001G13 |
| 13 | | 0 NB-ARC domain-containing disease resistance protei | Phvul.001G13 |
| 14 | | 0 NB-ARC domain-containing disease resistance protei | Phvul.001G13 |
| 15 | | 0 NB-ARC domain-containing disease resistance protei | Phvul.001G13 |
| 16 | ASL18,LBD16 | lateral organ boundaries-domain 16 | Phvul.001G15 |
| 17 | AtPHR1,PHR1 | phosphate starvation response 1 | Phvul.001G16 |
| 18 | AtPHR1,PHR1 | phosphate starvation response 1 | Phvul.001G16 |
| 19 | AtPHR1,PHR1 | phosphate starvation response 1 | Phvul.001G16 |
| 20 | AtPHR1,PHR1 | phosphate starvation response 1 | Phvul.001G16 |
| 21 | AtPHR1,PHR1 | phosphate starvation response 1 | Phvul.001G16 |
| 22 | AtPHR1,PHR1 | phosphate starvation response 1 | Phvul.001G16 |
| 23 | AtPHR1,PHR1 | phosphate starvation response 1 | Phvul.001G16 |
| 24 | AtPHR1,PHR1 | phosphate starvation response 1 | Phvul.001G16 |
| 25 | AtPHR1,PHR1 | phosphate starvation response 1 | Phvul.001G16 |
| 26 | AtPHR1,PHR1 | phosphate starvation response 1 | Phvul.001G16 |
| 27 | AtPHR1,PHR1 | phosphate starvation response 1 | Phvul.001G16 |
| 28 | AtSTS,STS | stachyose synthase | Phvul.001G21 |
| 29 | AtSTS,STS | stachyose synthase | Phvul.001G21 |
| 30 | | | |
| 31 | | 0 Translation initiation factor 2, small GTP-binding prot | Phvul.001G22 |
| 32 | | 0 Translation initiation factor 2, small GTP-binding prot | Phvul.001G22 |
| 33 | | 0 Translation initiation factor 2, small GTP-binding prot | Phvul.001G22 |
| 34 | | 0 Translation initiation factor 2, small GTP-binding prot | Phvul.001G22 |
| 35 | | 0 Translation initiation factor 2, small GTP-binding prot | Phvul.001G22 |
| 36 | SRFR1 | Tetratricopeptide repeat (TPR)-like superfamily prote | Phvul.002G01 |
| 37 | SRFR1 | Tetratricopeptide repeat (TPR)-like superfamily prote | Phvul.002G01 |
| 38 | SRFR1 | Tetratricopeptide repeat (TPR)-like superfamily prote | Phvul.002G01 |
| 39 | SRFR1 | Tetratricopeptide repeat (TPR)-like superfamily prote | Phvul.002G01 |
| 40 | | | |
| 41 | | | |
| 42 | | 0 | 0 Phvul.002G04 |
| 43 | | 0 | 0 Phvul.002G04 |
| 44 | | 0 | 0 Phvul.002G04 |
| 45 | | 0 | 0 Phvul.002G04 |
| 46 | | | |
| 47 | | 0 C2H2-like zinc finger protein | Phvul.002G05 |
| 48 | | 0 C2H2-like zinc finger protein | Phvul.002G05 |
| 49 | | | |
| 50 | AEXP7,ATEXPA7,ATHEXP | Al expansin A7 | Phvul.002G15 |
| 51 | AEXP7,ATEXPA7,ATHEXP | Al expansin A7 | Phvul.002G15 |
| 52 | AEXP7,ATEXPA7,ATHEXP | Al expansin A7 | Phvul.002G15 |
| 53 | AEXP7,ATEXPA7,ATHEXP | Al expansin A7 | Phvul.002G15 |
| 54 | | | |
| 55 | NRS/ER,UER1 | nucleotide-rhamnose synthase/epimerase-reductase | Phvul.002G15 |
| 56 | | 0 GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.002G24 |
| 57 | | 0 GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.002G24 |
| 58 | | 0 GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.002G24 |
| 59 | | 0 GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.002G24 |
| 60 | | | |

| | | | |
|----|-------------------------|--|--------------|
| 1 | | | |
| 2 | | | |
| 3 | | 0 GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.002G24 |
| 4 | | 0 Regulator of chromosome condensation (RCC1) famil | Phvul.002G25 |
| 5 | | 0 Regulator of chromosome condensation (RCC1) famil | Phvul.002G25 |
| 6 | | 0 Regulator of chromosome condensation (RCC1) famil | Phvul.002G25 |
| 7 | CSI1 | binding | Phvul.002G26 |
| 8 | GL3,MYC6.2 | basic helix-loop-helix (bHLH) DNA-binding superfamil | Phvul.002G29 |
| 9 | GL3,MYC6.2 | basic helix-loop-helix (bHLH) DNA-binding superfamil | Phvul.002G29 |
| 10 | | 0 ARM repeat superfamily protein | Phvul.003G02 |
| 11 | | 0 ARM repeat superfamily protein | Phvul.003G02 |
| 12 | | 0 ARM repeat superfamily protein | Phvul.003G02 |
| 13 | | 0 ARM repeat superfamily protein | Phvul.003G02 |
| 14 | ATXYL1,TRG1,XYL1 | alpha-xylosidase 1 | Phvul.003G03 |
| 15 | ATXYL1,TRG1,XYL1 | alpha-xylosidase 1 | Phvul.003G03 |
| 16 | ATXYL1,TRG1,XYL1 | alpha-xylosidase 1 | Phvul.003G03 |
| 17 | ATXYL1,TRG1,XYL1 | alpha-xylosidase 1 | Phvul.003G03 |
| 18 | ATXYL1,TRG1,XYL1 | alpha-xylosidase 1 | Phvul.003G03 |
| 19 | | 0 HXXXD-type acyl-transferase family protein | Phvul.003G05 |
| 20 | | 0 HXXXD-type acyl-transferase family protein | Phvul.003G05 |
| 21 | | 0 HXXXD-type acyl-transferase family protein | Phvul.003G05 |
| 22 | | 0 HXXXD-type acyl-transferase family protein | Phvul.003G05 |
| 23 | | 0 HXXXD-type acyl-transferase family protein | Phvul.003G05 |
| 24 | | 0 C2 calcium/lipid-binding and GRAM domain containin | Phvul.003G08 |
| 25 | | 0 C2 calcium/lipid-binding and GRAM domain containin | Phvul.003G08 |
| 26 | | 0 Mitochondrial substrate carrier family protein | Phvul.003G10 |
| 27 | | 0 Mitochondrial substrate carrier family protein | Phvul.003G10 |
| 28 | | 0 Mitochondrial substrate carrier family protein | Phvul.003G10 |
| 29 | | 0 Mitochondrial substrate carrier family protein | Phvul.003G10 |
| 30 | | 0 Mitochondrial substrate carrier family protein | Phvul.003G10 |
| 31 | | 0 Mitochondrial substrate carrier family protein | Phvul.003G10 |
| 32 | | 0 calcium-dependent lipid-binding family protein | Phvul.003G11 |
| 33 | | 0 calcium-dependent lipid-binding family protein | Phvul.003G11 |
| 34 | | 0 calcium-dependent lipid-binding family protein | Phvul.003G11 |
| 35 | | 0 calcium-dependent lipid-binding family protein | Phvul.003G11 |
| 36 | XGD1 | xylogalacturonan deficient 1 | Phvul.003G16 |
| 37 | ATFUT11,FUCT1,FUCTA,FUT | fucosyltransferase 11 | Phvul.003G29 |
| 38 | | 0 PQ-loop repeat family protein / transmembrane fami | Phvul.004G05 |
| 39 | | 0 ATP synthase subunit beta | Phvul.004G12 |
| 40 | | 0 ATP synthase subunit beta | Phvul.004G12 |
| 41 | | 0 ATP synthase subunit beta | Phvul.004G12 |
| 42 | | 0 ATP synthase subunit beta | Phvul.004G12 |
| 43 | | 0 ATP synthase subunit beta | Phvul.004G12 |
| 44 | | 0 ATP synthase subunit beta | Phvul.004G12 |
| 45 | | 0 SWIB/MDM2 domain;Plus-3;GYF | Phvul.004G13 |
| 46 | | 0 SWIB/MDM2 domain;Plus-3;GYF | Phvul.004G13 |
| 47 | | 0 SWIB/MDM2 domain;Plus-3;GYF | Phvul.004G13 |
| 48 | | 0 SWIB/MDM2 domain;Plus-3;GYF | Phvul.004G13 |
| 49 | | 0 SWIB/MDM2 domain;Plus-3;GYF | Phvul.004G13 |
| 50 | | 0 SWIB/MDM2 domain;Plus-3;GYF | Phvul.004G13 |
| 51 | ACHT2 | atypical CYS HIS rich thioredoxin 2 | Phvul.004G17 |
| 52 | ACHT2 | atypical CYS HIS rich thioredoxin 2 | Phvul.004G17 |
| 53 | | 0 BTB/POZ domain-containing protein | Phvul.005G05 |
| 54 | | 0 BTB/POZ domain-containing protein | Phvul.005G05 |
| 55 | | 0 BTB/POZ domain-containing protein | Phvul.005G05 |
| 56 | ARK3,RK3 | receptor kinase 3 | Phvul.005G08 |
| 57 | ATFMN/FHY,FMN/FHY | riboflavin kinase/FMN hydrolase | Phvul.005G09 |
| 58 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 59 | | | |
| 60 | | | |

| | | | |
|----|--------------------|--|--------------|
| 1 | | | |
| 2 | | | |
| 3 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 4 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 5 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 6 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 7 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 8 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 9 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 10 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 11 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 12 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 13 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 14 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 15 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 16 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 17 | MEE35,TCP4 | TCP family transcription factor 4 | Phvul.005G09 |
| 18 | ALA2 | aminophospholipid ATPase 2 | Phvul.005G10 |
| 19 | ALA2 | aminophospholipid ATPase 2 | Phvul.005G10 |
| 20 | ALA2 | aminophospholipid ATPase 2 | Phvul.005G10 |
| 21 | ALA2 | aminophospholipid ATPase 2 | Phvul.005G10 |
| 22 | ALA2 | aminophospholipid ATPase 2 | Phvul.005G10 |
| 23 | ALA2 | aminophospholipid ATPase 2 | Phvul.005G10 |
| 24 | ALA2 | aminophospholipid ATPase 2 | Phvul.005G10 |
| 25 | ALA2 | aminophospholipid ATPase 2 | Phvul.005G10 |
| 26 | | 0 C2H2 and C2HC zinc fingers superfamily protein | Phvul.005G13 |
| 27 | | 0 C2H2 and C2HC zinc fingers superfamily protein | Phvul.005G13 |
| 28 | | 0 C2H2 and C2HC zinc fingers superfamily protein | Phvul.005G13 |
| 29 | | 0 C2H2 and C2HC zinc fingers superfamily protein | Phvul.005G13 |
| 30 | | 0 C2H2 and C2HC zinc fingers superfamily protein | Phvul.005G13 |
| 31 | | 0 P-loop containing nucleoside triphosphate hydrolases | Phvul.005G17 |
| 32 | | 0 P-loop containing nucleoside triphosphate hydrolases | Phvul.005G17 |
| 33 | | 0 P-loop containing nucleoside triphosphate hydrolases | Phvul.005G17 |
| 34 | | 0 P-loop containing nucleoside triphosphate hydrolases | Phvul.005G17 |
| 35 | | 0 P-loop containing nucleoside triphosphate hydrolases | Phvul.005G17 |
| 36 | | 0 | 0 |
| 37 | | 0 | 0 |
| 38 | | 0 | 0 |
| 39 | | 0 | 0 |
| 40 | | 0 | 0 |
| 41 | scpl2 | serine carboxypeptidase-like 2 | Phvul.006G16 |
| 42 | scpl2 | serine carboxypeptidase-like 2 | Phvul.006G16 |
| 43 | ATQSOX1,QSO2,QSOX1 | quiescin-sulfhydryl oxidase 1 | Phvul.007G03 |
| 44 | ATQSOX1,QSO2,QSOX1 | quiescin-sulfhydryl oxidase 1 | Phvul.007G03 |
| 45 | ATQSOX1,QSO2,QSOX1 | quiescin-sulfhydryl oxidase 1 | Phvul.007G03 |
| 46 | ATQSOX1,QSO2,QSOX1 | quiescin-sulfhydryl oxidase 1 | Phvul.007G03 |
| 47 | ATQSOX1,QSO2,QSOX1 | quiescin-sulfhydryl oxidase 1 | Phvul.007G03 |
| 48 | ATQSOX1,QSO2,QSOX1 | quiescin-sulfhydryl oxidase 1 | Phvul.007G03 |
| 49 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 50 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 51 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 52 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 53 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 54 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 55 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 56 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 57 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 58 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 59 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 60 | | | |

| | | | |
|----|---------------|---|----------------|
| 1 | | | |
| 2 | | | |
| 3 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 4 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 5 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 6 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 7 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 8 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 9 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 10 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 11 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 12 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 13 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G06 |
| 14 | | 0 | 0 Phvul.007G09 |
| 15 | | 0 RING/FYVE/PHD zinc finger superfamily protein | Phvul.007G11 |
| 16 | | 0 RING/FYVE/PHD zinc finger superfamily protein | Phvul.007G11 |
| 17 | | 0 RING/FYVE/PHD zinc finger superfamily protein | Phvul.007G11 |
| 18 | | 0 RING/FYVE/PHD zinc finger superfamily protein | Phvul.007G11 |
| 19 | | 0 RING/FYVE/PHD zinc finger superfamily protein | Phvul.007G11 |
| 20 | ATEDR1,EDR1 | Protein kinase superfamily protein | Phvul.007G18 |
| 21 | ATEDR1,EDR1 | Protein kinase superfamily protein | Phvul.007G18 |
| 22 | | 0 ARM repeat superfamily protein | Phvul.007G19 |
| 23 | | 0 Plant invertase/pectin methylesterase inhibitor super | Phvul.007G21 |
| 24 | | 0 Plant invertase/pectin methylesterase inhibitor super | Phvul.007G21 |
| 25 | | 0 Plant invertase/pectin methylesterase inhibitor super | Phvul.007G21 |
| 26 | | 0 Plant invertase/pectin methylesterase inhibitor super | Phvul.007G21 |
| 27 | | 0 Plant invertase/pectin methylesterase inhibitor super | Phvul.007G21 |
| 28 | | 0 Plant invertase/pectin methylesterase inhibitor super | Phvul.007G21 |
| 29 | | 0 Plant invertase/pectin methylesterase inhibitor super | Phvul.007G21 |
| 30 | | 0 Plant invertase/pectin methylesterase inhibitor super | Phvul.007G21 |
| 31 | | 0 Plant invertase/pectin methylesterase inhibitor super | Phvul.007G21 |
| 32 | | 0 transcription coactivators | Phvul.007G21 |
| 33 | | 0 transcription coactivators | Phvul.007G21 |
| 34 | | 0 transcription coactivators | Phvul.007G21 |
| 35 | | 0 transcription coactivators | Phvul.007G21 |
| 36 | | 0 transcription coactivators | Phvul.007G21 |
| 37 | NTRC | NADPH-dependent thioredoxin reductase C | Phvul.007G25 |
| 38 | AtRLP7,RLP7 | receptor like protein 7 | Phvul.008G04 |
| 39 | AtRLP7,RLP7 | receptor like protein 7 | Phvul.008G04 |
| 40 | AtMYB17,MYB17 | myb domain protein 17 | Phvul.008G06 |
| 41 | AtMYB17,MYB17 | myb domain protein 17 | Phvul.008G06 |
| 42 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 43 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 44 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 45 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 46 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 47 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 48 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 49 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 50 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 51 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 52 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 53 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 54 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 55 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 56 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 57 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 58 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 59 | | 0 Protein of unknown function (DUF674) | Phvul.008G11 |
| 60 | | | |

| | | | |
|----|---------------------|---|--------------|
| 1 | | | |
| 2 | | | |
| 3 | LUH | LEUNIG_homolog | Phvul.008G12 |
| 4 | LUH | LEUNIG_homolog | Phvul.008G12 |
| 5 | LUH | LEUNIG_homolog | Phvul.008G12 |
| 6 | LUH | LEUNIG_homolog | Phvul.008G12 |
| 7 | LUH | LEUNIG_homolog | Phvul.008G12 |
| 8 | | | |
| 9 | | 0 Subtilisin-like serine endopeptidase family protein | Phvul.008G22 |
| 10 | ATCSLE1,CSLE1 | cellulose synthase like E1 | Phvul.008G27 |
| 11 | ATCSLE1,CSLE1 | cellulose synthase like E1 | Phvul.008G27 |
| 12 | | | |
| 13 | | 0 Zn-dependent exopeptidases superfamily protein | Phvul.009G01 |
| 14 | | 0 Zn-dependent exopeptidases superfamily protein | Phvul.009G01 |
| 15 | | 0 Target SNARE coiled-coil domain protein | Phvul.009G03 |
| 16 | ATCKX5,ATCKX6,CKX5 | cytokinin oxidase 5 | Phvul.009G06 |
| 17 | ATCKX5,ATCKX6,CKX5 | cytokinin oxidase 5 | Phvul.009G06 |
| 18 | ATCKX5,ATCKX6,CKX5 | cytokinin oxidase 5 | Phvul.009G06 |
| 19 | ATCKX5,ATCKX6,CKX5 | cytokinin oxidase 5 | Phvul.009G06 |
| 20 | ATCKX5,ATCKX6,CKX5 | cytokinin oxidase 5 | Phvul.009G06 |
| 21 | ATCKX5,ATCKX6,CKX5 | cytokinin oxidase 5 | Phvul.009G06 |
| 22 | ATCKX5,ATCKX6,CKX5 | cytokinin oxidase 5 | Phvul.009G06 |
| 23 | ATCKX5,ATCKX6,CKX5 | cytokinin oxidase 5 | Phvul.009G06 |
| 24 | ATCKX5,ATCKX6,CKX5 | cytokinin oxidase 5 | Phvul.009G06 |
| 25 | ATCKX5,ATCKX6,CKX5 | cytokinin oxidase 5 | Phvul.009G06 |
| 26 | ATCKX5,ATCKX6,CKX5 | cytokinin oxidase 5 | Phvul.009G06 |
| 27 | TMT2 | tonoplast monosaccharide transporter2 | Phvul.009G11 |
| 28 | TMT2 | tonoplast monosaccharide transporter2 | Phvul.009G11 |
| 29 | | | |
| 30 | | 0 transferases, transferring glycosyl groups | 0 |
| 31 | | 0 transferases, transferring glycosyl groups | 0 |
| 32 | | 0 transferases, transferring glycosyl groups | 0 |
| 33 | | 0 transferases, transferring glycosyl groups | 0 |
| 34 | | 0 transferases, transferring glycosyl groups | 0 |
| 35 | COB | COBRA-like extracellular glycosyl-phosphatidyl inositol | Phvul.009G20 |
| 36 | BGAL12 | beta-galactosidase 12 | Phvul.009G23 |
| 37 | BGAL12 | beta-galactosidase 12 | Phvul.009G23 |
| 38 | BGAL12 | beta-galactosidase 12 | Phvul.009G23 |
| 39 | BGAL12 | beta-galactosidase 12 | Phvul.009G23 |
| 40 | BGAL12 | beta-galactosidase 12 | Phvul.009G23 |
| 41 | ATOEP16-2,ATOEP16-S | Mitochondrial import inner membrane translocase subunit | Phvul.009G25 |
| 42 | ATOEP16-2,ATOEP16-S | Mitochondrial import inner membrane translocase subunit | Phvul.009G25 |
| 43 | ATOEP16-2,ATOEP16-S | Mitochondrial import inner membrane translocase subunit | Phvul.009G25 |
| 44 | ATOEP16-2,ATOEP16-S | Mitochondrial import inner membrane translocase subunit | Phvul.009G25 |
| 45 | ATOEP16-2,ATOEP16-S | Mitochondrial import inner membrane translocase subunit | Phvul.009G25 |
| 46 | | | |
| 47 | | 0 | 0 0 |
| 48 | | 0 | 0 0 |
| 49 | | 0 | 0 0 |
| 50 | | 0 | 0 0 |
| 51 | | 0 | 0 0 |
| 52 | | 0 Disease resistance protein (TIR-NBS-LRR class) family | Phvul.010G02 |
| 53 | | 0 Disease resistance protein (TIR-NBS-LRR class) family | Phvul.010G02 |
| 54 | | 0 Disease resistance protein (TIR-NBS-LRR class) family | Phvul.010G02 |
| 55 | | 0 Disease resistance protein (TIR-NBS-LRR class) family | Phvul.010G02 |
| 56 | | 0 Disease resistance protein (TIR-NBS-LRR class) family | Phvul.010G02 |
| 57 | ATWNK5,WNK5,ZIK1 | with no lysine (K) kinase 5 | Phvul.010G06 |
| 58 | ATWNK5,WNK5,ZIK1 | with no lysine (K) kinase 5 | Phvul.010G06 |
| 59 | | | |
| 60 | | | |

| | | | |
|----|------------------------|--|----------------|
| 1 | | | |
| 2 | | | |
| 3 | ATWNK5,WNK5,ZIK1 | with no lysine (K) kinase 5 | Phvul.010G06 |
| 4 | ATWNK5,WNK5,ZIK1 | with no lysine (K) kinase 5 | Phvul.010G06 |
| 5 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 6 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 7 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 8 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 9 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 10 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 11 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 12 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 13 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 14 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 15 | ATPEX16,PEX16,SSE,SSE1 | shrunk seed protein (SSE1) | Phvul.010G08 |
| 16 | OLD5,QS,SUFE3 | quinolinate synthase | Phvul.010G09 |
| 17 | OLD5,QS,SUFE3 | quinolinate synthase | Phvul.010G09 |
| 18 | OLD5,QS,SUFE3 | quinolinate synthase | Phvul.010G09 |
| 19 | OLD5,QS,SUFE3 | quinolinate synthase | Phvul.010G09 |
| 20 | OLD5,QS,SUFE3 | quinolinate synthase | Phvul.010G09 |
| 21 | OLD5,QS,SUFE3 | quinolinate synthase | Phvul.010G09 |
| 22 | ATSAC1 | Phosphoinositide phosphatase family protein | Phvul.011G00 |
| 23 | ATSAC1 | Phosphoinositide phosphatase family protein | Phvul.011G00 |
| 24 | ATSAC1 | Phosphoinositide phosphatase family protein | Phvul.011G00 |
| 25 | ATSAC1 | Phosphoinositide phosphatase family protein | Phvul.011G00 |
| 26 | ATSAC1 | Phosphoinositide phosphatase family protein | Phvul.011G00 |
| 27 | ATSAC1 | Phosphoinositide phosphatase family protein | Phvul.011G00 |
| 28 | ATSAC1 | Phosphoinositide phosphatase family protein | Phvul.011G00 |
| 29 | ATSAC1 | Phosphoinositide phosphatase family protein | Phvul.011G00 |
| 30 | ATSAC1 | Phosphoinositide phosphatase family protein | Phvul.011G00 |
| 31 | ATSAC1 | Phosphoinositide phosphatase family protein | Phvul.011G00 |
| 32 | | 0 | 0 Phvul.011G00 |
| 33 | | | |
| 34 | SIB1 | sigma factor binding protein 1 | Phvul.011G20 |
| 35 | SIB1 | sigma factor binding protein 1 | Phvul.011G20 |
| 36 | SIB1 | sigma factor binding protein 1 | Phvul.011G20 |
| 37 | SIB1 | sigma factor binding protein 1 | Phvul.011G20 |
| 38 | SIB1 | sigma factor binding protein 1 | Phvul.011G20 |
| 39 | | 0 C2 calcium/lipid-binding and GRAM domain containin | Phvul.L001679 |
| 40 | | 0 C2 calcium/lipid-binding and GRAM domain containin | Phvul.L001679 |
| 41 | | | |
| 42 | | 0 CCCH-type zinc fingerfamily protein with RNA-binding | Phvul.L002537 |
| 43 | | 0 CCCH-type zinc fingerfamily protein with RNA-binding | Phvul.L002537 |
| 44 | AAC2 | ADP/ATP carrier 2 | Phvul.L009843 |
| 45 | AAC2 | ADP/ATP carrier 2 | Phvul.L009843 |
| 46 | AAC2 | ADP/ATP carrier 2 | Phvul.L009843 |
| 47 | AAC2 | ADP/ATP carrier 2 | Phvul.L009843 |
| 48 | AAC2 | ADP/ATP carrier 2 | Phvul.L009843 |
| 49 | | | |
| 50 | | | |
| 51 | | | |
| 52 | | | |
| 53 | | | |
| 54 | | | |
| 55 | | | |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

| Annot_defline | IDENTIFIER | NAME | DESCRIPTION |
|----------------|---------------|--|---|
| K10882 - cros: | Phvul.002G26 | Cell cycle orga | component EME1 of MUS81-EME1 Holliday junction clea |
| K10882 - cros: | Phvul.002G26 | Cell cycle orga | component EME1 of MUS81-EME1 Holliday junction clea |
| PF06075 - Plai | Phvul.002G07 | Cytoskeleton (regulatory protein (CORD) of cortical microtubule organi | |
| PF06075 - Plai | Phvul.002G07 | Cytoskeleton (regulatory protein (CORD) of cortical microtubule organi | |
| PF06075 - Plai | Phvul.002G07 | Cytoskeleton (regulatory protein (CORD) of cortical microtubule organi | |
| PF06075 - Plai | Phvul.002G07 | Cytoskeleton (regulatory protein (CORD) of cortical microtubule organi | |
| PTHR33917:Sf | Phvul.006G20 | not assigned. | ã (original description: pacid=37173374 transcript=Phvul.) |
| PTHR13600:Sf | Phvul.009G05 | not assigned. | r no hits & (original description: pacid=37148617 transcri |
| PTHR13600:Sf | Phvul.009G05 | not assigned. | r no hits & (original description: pacid=37148617 transcri |
| PTHR10766:Sf | Phvul.009G08 | not assigned. | ã (original description: pacid=37151360 transcript=Phvul.) |
| PTHR22849//I | Phvul.010G11 | Protein home | E3 ubiquitin ligase (PUB) (original description: pacid=371 |
| PTHR22849//I | Phvul.010G11 | Protein home | E3 ubiquitin ligase (PUB) (original description: pacid=371 |
| PTHR22849//I | Phvul.010G11 | Protein home | E3 ubiquitin ligase (PUB) (original description: pacid=371 |
| PTHR22849//I | Phvul.010G11 | Protein home | E3 ubiquitin ligase (PUB) (original description: pacid=371 |
| 1.17.1.4 - Xan | Phvul.L00954: | Redox homeo | xanthine dehydrogenase (original description: pacid=371 |
| 1.17.1.4 - Xan | Phvul.L00954: | Redox homeo | xanthine dehydrogenase (original description: pacid=371 |
| 1.17.1.4 - Xan | Phvul.L00954: | Redox homeo | xanthine dehydrogenase (original description: pacid=371 |
| 1.17.1.4 - Xan | Phvul.L00954: | Redox homeo | xanthine dehydrogenase (original description: pacid=371 |
| PTHR22952//I | Phvul.001G07 | RNA biosynth | transcription factor (bZIP9/10/25) (original description: p |
| PTHR22952//I | Phvul.001G07 | RNA biosynth | transcription factor (bZIP9/10/25) (original description: p |
| PTHR22952//I | Phvul.001G07 | RNA biosynth | transcription factor (bZIP9/10/25) (original description: p |
| PTHR22952//I | Phvul.001G07 | RNA biosynth | transcription factor (bZIP9/10/25) (original description: p |
| PTHR11183//I | Phvul.001G21 | Carbohydrate | galactinol synthase (original description: pacid=3716845 |
| PTHR11183//I | Phvul.001G21 | Carbohydrate | galactinol synthase (original description: pacid=3716845 |
| PTHR11183//I | Phvul.001G21 | Carbohydrate | galactinol synthase (original description: pacid=3716845 |
| PTHR11183//I | Phvul.001G21 | Carbohydrate | galactinol synthase (original description: pacid=3716845 |
| K10882 - cros: | Phvul.002G26 | Cell cycle orga | component EME1 of MUS81-EME1 Holliday junction clea |
| K10882 - cros: | Phvul.002G26 | Cell cycle orga | component EME1 of MUS81-EME1 Holliday junction clea |
| K10882 - cros: | Phvul.002G26 | Cell cycle orga | component EME1 of MUS81-EME1 Holliday junction clea |
| K10882 - cros: | Phvul.002G26 | Cell cycle orga | component EME1 of MUS81-EME1 Holliday junction clea |
| PTHR11062:Sf | Phvul.002G28 | Cell wall orga | xylosyltransferase (IRX10) (original description: pacid=37 |
| PTHR11062:Sf | Phvul.002G28 | Cell wall orga | xylosyltransferase (IRX10) (original description: pacid=37 |
| PTHR11062:Sf | Phvul.002G28 | Cell wall orga | xylosyltransferase (IRX10) (original description: pacid=37 |
| PTHR11062:Sf | Phvul.002G28 | Cell wall orga | xylosyltransferase (IRX10) (original description: pacid=37 |
| PF00560//PFC | Phvul.004G04 | not assigned. | ã (original description: pacid=37161946 transcript=Phvul.) |
| PF15365 - Pro | Phvul.006G15 | not assigned. | r no hits & (original description: pacid=37174157 transcri |
| KOG1947 - Lei | Phvul.008G07 | not assigned. | r no hits & (original description: pacid=37157631 transcri |
| KOG1947 - Lei | Phvul.008G07 | not assigned. | r no hits & (original description: pacid=37157631 transcri |
| KOG1947 - Lei | Phvul.008G07 | not assigned. | r no hits & (original description: pacid=37157631 transcri |
| KOG1947 - Lei | Phvul.008G07 | not assigned. | r no hits & (original description: pacid=37157631 transcri |
| PTHR33103:Sf | Phvul.008G11 | not assigned. | r no hits & (original description: pacid=37161406 transcri |
| PTHR33103:Sf | Phvul.008G11 | not assigned. | r no hits & (original description: pacid=37160139 transcri |

1
2
3 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
4 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
5 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
6 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
7 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
8 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
9 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
10 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
11 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
12 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
13 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
14 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
15 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
16 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
17 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
18 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
19 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
20 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
21 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
22 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
23 PTHR12663:SlPhvul.008G16Cell cycle orga cohesin cofactor (PDS5) (original description: pacid=371
24 PTHR13600:SlPhvul.009G05not assigned.r no hits & (original description: pacid=37148617 transcri
25 PTHR13600:SlPhvul.009G05not assigned.r no hits & (original description: pacid=37148617 transcri
26 PTHR13600:SlPhvul.009G05not assigned.r no hits & (original description: pacid=37148617 transcri
27 PTHR13600:SlPhvul.009G05not assigned.r no hits & (original description: pacid=37148617 transcri
28 PTHR13600:SlPhvul.009G05not assigned.r no hits & (original description: pacid=37148617 transcri
29 0 Phvul.010G05not assigned.r no hits & (original description: pacid=37142098 transcri
30 0 Phvul.010G05not assigned.r no hits & (original description: pacid=37142098 transcri
31 PF01094 - RecPhvul.001G02Solute transpcligand-gated cation channel (GLR) (original description: p
32 PF01094 - RecPhvul.001G02Solute transpcligand-gated cation channel (GLR) (original description: p
33 PTHR22952//IPhvul.001G07RNA biosynthtranscription factor (bZIP9/10/25) (original description: p
34 PTHR22952//IPhvul.001G07RNA biosynthtranscription factor (bZIP9/10/25) (original description: p
35 K12446 - L-arçPhvul.001G07Carbohydrate L-arabinose kinase (original description: pacid=3716845z
36 K12446 - L-arçPhvul.001G07Carbohydrate L-arabinose kinase (original description: pacid=3716845z
37 PTHR11937:SlPhvul.001G08not assigned.ç (original description: pacid=37168999 transcript=Phvul.
38 PTHR11937:SlPhvul.001G08not assigned.ç (original description: pacid=37168999 transcript=Phvul.
39 PTHR11937:SlPhvul.001G08not assigned.ç (original description: pacid=37168999 transcript=Phvul.
40 K17260 - actirPhvul.001G08not assigned.ç (original description: pacid=37170199 transcript=Phvul.
41 K17260 - actirPhvul.001G08not assigned.ç (original description: pacid=37170199 transcript=Phvul.
42 K17260 - actirPhvul.001G08not assigned.ç (original description: pacid=37170199 transcript=Phvul.
43 K17260 - actirPhvul.001G08not assigned.ç (original description: pacid=37170199 transcript=Phvul.
44 PTHR31719:SlPhvul.001G09RNA biosynthtranscription factor (NAC) (original description: pacid=37
45 PTHR31719:SlPhvul.001G09RNA biosynthtranscription factor (NAC) (original description: pacid=37
46 PTHR31719:SlPhvul.001G09RNA biosynthtranscription factor (NAC) (original description: pacid=37
47 PTHR31719:SlPhvul.001G09RNA biosynthtranscription factor (NAC) (original description: pacid=37
48 PTHR10277//IPhvul.001G12Amino acid m-hydroxymethylglutaryl-CoA lyase (original description: p
49 PTHR10277//IPhvul.001G12Amino acid m-hydroxymethylglutaryl-CoA lyase (original description: p
50 K05643 - ATP-Phvul.001G13Solute transpcsubfamily ABCA transporter (original description: pacid=

1
2
3 K05643 - ATP-Phvul.001G13 Solute transp_c subfamily ABCA transporter (original description: pacid=
4 K05643 - ATP-Phvul.001G13 Solute transp_c subfamily ABCA transporter (original description: pacid=
5 K05643 - ATP-Phvul.001G13 Solute transp_c subfamily ABCA transporter (original description: pacid=
6 K05643 - ATP-Phvul.001G13 Solute transp_c subfamily ABCA transporter (original description: pacid=
7 K05643 - ATP-Phvul.001G13 Solute transp_c subfamily ABCA transporter (original description: pacid=
8 K05643 - ATP-Phvul.001G13 Solute transp_c subfamily ABCA transporter (original description: pacid=
9 K05643 - ATP-Phvul.001G13 Solute transp_c subfamily ABCA transporter (original description: pacid=
10 K05643 - ATP-Phvul.001G13 Solute transp_c subfamily ABCA transporter (original description: pacid=
11 K05643 - ATP-Phvul.001G13 Solute transp_c subfamily ABCA transporter (original description: pacid=
12 PF03110 - SBFP_h vul.001G14 RNA biosynth_e transcription factor (SBP) (original description: pacid=37
13 PF03110 - SBFP_h vul.001G14 RNA biosynth_e transcription factor (SBP) (original description: pacid=37
14 PF03110 - SBFP_h vul.001G14 RNA biosynth_e transcription factor (SBP) (original description: pacid=37
15 PF03110 - SBFP_h vul.001G14 RNA biosynth_e transcription factor (SBP) (original description: pacid=37
16 2.7.7.2 - FAD_s Phvul.001G17 not assigned.r no hits & (original description: pacid=37168919 transcri
17 2.7.7.2 - FAD_s Phvul.001G17 not assigned.r no hits & (original description: pacid=37168919 transcri
18 2.7.7.2 - FAD_s Phvul.001G17 not assigned.r no hits & (original description: pacid=37168919 transcri
19 2.7.7.2 - FAD_s Phvul.001G17 not assigned.r no hits & (original description: pacid=37168919 transcri
20 2.7.7.2 - FAD_s Phvul.001G17 not assigned.r no hits & (original description: pacid=37168919 transcri
21 2.7.7.2 - FAD_s Phvul.001G17 not assigned.r no hits & (original description: pacid=37168919 transcri
22 2.7.7.2 - FAD_s Phvul.001G17 not assigned.r no hits & (original description: pacid=37168919 transcri
23 2.7.7.2 - FAD_s Phvul.001G17 not assigned.r no hits & (original description: pacid=37168919 transcri
24 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
25 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
26 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
27 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
28 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
29 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
30 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
31 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
32 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
33 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
34 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
35 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
36 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
37 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
38 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
39 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
40 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
41 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
42 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
43 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
44 PF03126 - Plu:Phvul.002G04 Multi-process TZP circadian clock repression factor (original descriptio
45 PTHR10438:SI_f Phvul.002G06 Redox homeo H-type thioredoxin (original description: pacid=3717719!
46 PTHR10438:SI_f Phvul.002G06 Redox homeo H-type thioredoxin (original description: pacid=3717719!
47 PTHR10438:SI_f Phvul.002G06 Redox homeo H-type thioredoxin (original description: pacid=3717719!
48 PF06075 - Plai_f Phvul.002G07 Cytoskeleton (regulatory protein (CORD) of cortical microtubule organi
49 PF06075 - Plai_f Phvul.002G07 Cytoskeleton (regulatory protein (CORD) of cortical microtubule organi
50 3.4.24.23 - M_z Phvul.002G07 Protein home_e Matrixin-type metalloprotease (original description: paci
51 3.4.24.23 - M_z Phvul.002G07 Protein home_e Matrixin-type metalloprotease (original description: paci
52 3.4.24.23 - M_z Phvul.002G07 Protein home_e Matrixin-type metalloprotease (original description: paci
53 3.4.24.23 - M_z Phvul.002G07 Protein home_e Matrixin-type metalloprotease (original description: paci
54 3.4.24.23 - M_z Phvul.002G07 Protein home_e Matrixin-type metalloprotease (original description: paci
55 PTHR10110:SI_f Phvul.002G18 External stim_e sodium:proton antiporter (SOS1) (original description: p
56 PTHR10110:SI_f Phvul.002G18 External stim_e sodium:proton antiporter (SOS1) (original description: p
57 PTHR10110:SI_f Phvul.002G18 External stim_e sodium:proton antiporter (SOS1) (original description: p
58 PTHR10110:SI_f Phvul.002G18 External stim_e sodium:proton antiporter (SOS1) (original description: p
59 PTHR10110:SI_f Phvul.002G18 External stim_e sodium:proton antiporter (SOS1) (original description: p
60

2.7.11.1 - NonPhvul.002G30Protein modif protein kinase (PERK-related) (original description: pacid
 PTHR23336:SIPhvul.003G10not assigned.r no hits & (original description: pacid=37147291 transcri
 PTHR23336:SIPhvul.003G10not assigned.r no hits & (original description: pacid=37147291 transcri
 PF00560//PFPhvul.004G04not assigned.ã (original description: pacid=37161823 transcript=Phvul.
 PF01535 - PPPhvul.004G10not assigned.ã (original description: pacid=37161859 transcript=Phvul.
 PTHR11689:SIPhvul.004G13Solute transpñanion channel / anion:proton antiporter (CLC) (original d
 PTHR11689:SIPhvul.004G13Solute transpñanion channel / anion:proton antiporter (CLC) (original d
 PTHR10438:SIPhvul.004G17Redox homeo atypical thioredoxin (ACHT) (original description: pacid=:
 PTHR10438:SIPhvul.004G17Redox homeo atypical thioredoxin (ACHT) (original description: pacid=:
 PTHR10438:SIPhvul.004G17Redox homeo atypical thioredoxin (ACHT) (original description: pacid=:
 PTHR10438:SIPhvul.004G17Redox homeo atypical thioredoxin (ACHT) (original description: pacid=:
 PF12609 - WoPhvul.005G08not assigned.r no hits & (original description: pacid=37154279 transcri
 K01061 - carb Phvul.005G11not assigned.r no hits & (original description: pacid=37152909 transcri
 K01061 - carb Phvul.005G11not assigned.r no hits & (original description: pacid=37152909 transcri
 K01061 - carb Phvul.005G11not assigned.r no hits & (original description: pacid=37152909 transcri
 K01061 - carb Phvul.005G11not assigned.r no hits & (original description: pacid=37152909 transcri
 K14972 - PAX-Phvul.005G18RNA biosynthcomponent MED15 of tail module of MEDIATOR transcri
 K14972 - PAX-Phvul.005G18RNA biosynthcomponent MED15 of tail module of MEDIATOR transcri
 PTHR11595:SIPhvul.006G01Protein biosyr component eEF1B-beta/-delta of eEF1B eEF1A-GDP-recy
 PTHR11595:SIPhvul.006G01Protein biosyr component eEF1B-beta/-delta of eEF1B eEF1A-GDP-recy
 PTHR11595:SIPhvul.006G01Protein biosyr component eEF1B-beta/-delta of eEF1B eEF1A-GDP-recy
 PTHR11595:SIPhvul.006G01Protein biosyr component eEF1B-beta/-delta of eEF1B eEF1A-GDP-recy
 PTHR19241:SIPhvul.006G06Solute transpñsubfamily ABCG transporter (original description: pacid=
 PTHR19241:SIPhvul.006G06Solute transpñsubfamily ABCG transporter (original description: pacid=
 PTHR19241:SIPhvul.006G06Solute transpñsubfamily ABCG transporter (original description: pacid=
 PTHR19241:SIPhvul.006G06Solute transpñsubfamily ABCG transporter (original description: pacid=
 PF14365 - DorPhvul.006G10not assigned.r no hits & (original description: pacid=37172094 transcri
 PF14365 - DorPhvul.006G10not assigned.r no hits & (original description: pacid=37172094 transcri
 PTHR23324//IPhvul.006G13not assigned.r no hits & (original description: pacid=37171658 transcri
 PTHR23324//IPhvul.006G13not assigned.r no hits & (original description: pacid=37171658 transcri
 PTHR10992:SIPhvul.007G11Coenzyme mechlorophyll dephytylase (CLD) (original description: pacid
 PTHR10992:SIPhvul.007G11Coenzyme mechlorophyll dephytylase (CLD) (original description: pacid
 PTHR31375:SIPhvul.007G21Enzyme classii Polygalacturonase At1g48100 OS=Arabidopsis thaliana (:
 PTHR31375:SIPhvul.007G21Enzyme classii Polygalacturonase At1g48100 OS=Arabidopsis thaliana (:
 K14488 - SAUIPhvul.007G21not assigned.r no hits & (original description: pacid=37166206 transcri
 K14488 - SAUIPhvul.007G21not assigned.r no hits & (original description: pacid=37166206 transcri
 KOG1947 - LeiPhvul.008G07not assigned.r no hits & (original description: pacid=37157631 transcri
 KOG1947 - LeiPhvul.008G07not assigned.r no hits & (original description: pacid=37157631 transcri
 O Phvul.008G10not assigned.r no hits & (original description: pacid=37160112 transcri
 O Phvul.008G10not assigned.r no hits & (original description: pacid=37160112 transcri
 K08081 - TropPhvul.008G11Enzyme classii Enzyme classification.EC_1 oxidoreductases.EC_1.1 oxid
 K08081 - TropPhvul.008G11Enzyme classii Enzyme classification.EC_1 oxidoreductases.EC_1.1 oxid
 PTHR10366:SIPhvul.008G25not assigned.ã (original description: pacid=37158298 transcript=Phvul.

1
2
3 PTHR10366:SlPhvul.008G25 not assigned.ã (original description: pacid=37158298 transcript=Phvul.
4 PTHR10366:SlPhvul.008G25 not assigned.ã (original description: pacid=37158298 transcript=Phvul.
5 PTHR10366:SlPhvul.008G25 not assigned.ã (original description: pacid=37158298 transcript=Phvul.
6 K02259 - cytoPhvul.008G28 Cellular respir component COX15 of cytochrome c oxidase assembly (o
7 PTHR10766:SlPhvul.008G28 not assigned.ã (original description: pacid=37158021 transcript=Phvul.
8 K10295 - F-bo Phvul.009G12 Protein home component FBX of SCF E3 ubiquitin ligase complex (origi
9 K10295 - F-bo Phvul.009G12 Protein home component FBX of SCF E3 ubiquitin ligase complex (origi
10 K10295 - F-bo Phvul.009G12 Protein home component FBX of SCF E3 ubiquitin ligase complex (origi
11 K10295 - F-bo Phvul.009G12 Protein home component FBX of SCF E3 ubiquitin ligase complex (origi
12 PTHR11062:SlPhvul.009G16 Cell wall orgar xylosyltransferase (IRX10) (original description: pacid=37
13 PTHR11062:SlPhvul.009G16 Cell wall orgar xylosyltransferase (IRX10) (original description: pacid=37
14 PTHR11062:SlPhvul.009G16 Cell wall orgar xylosyltransferase (IRX10) (original description: pacid=37
15 PTHR11062:SlPhvul.009G16 Cell wall orgar xylosyltransferase (IRX10) (original description: pacid=37
16 PTHR23155//IPhvul.010G06 not assigned.ã (original description: pacid=37142899 transcript=Phvul.
17 PTHR23155//IPhvul.010G06 not assigned.ã (original description: pacid=37142899 transcript=Phvul.
18 PTHR23155//IPhvul.010G06 not assigned.ã (original description: pacid=37142899 transcript=Phvul.
19 PTHR23155//IPhvul.010G06 not assigned.ã (original description: pacid=37142899 transcript=Phvul.
20 PF00170 - bZlIPhvul.011G04 not assigned.r no hits & (original description: pacid=37157418 transcri
21 PF00170 - bZlIPhvul.011G04 not assigned.r no hits & (original description: pacid=37157418 transcri
22 **K08873 - PI-3-Phvul.011G05 Protein modif protein kinase (PIKK) (original description: pacid=371548**
23 **K08873 - PI-3-Phvul.011G05 Protein modif protein kinase (PIKK) (original description: pacid=371548**
24 **K08873 - PI-3-Phvul.011G05 Protein modif protein kinase (PIKK) (original description: pacid=371548**
25 **K08873 - PI-3-Phvul.011G05 Protein modif protein kinase (PIKK) (original description: pacid=371548**
26 PTHR11709//IPhvul.L00734:Cell wall orgar lignin laccase (original description: pacid=37178902 tran
27 PTHR11709//IPhvul.L00734:Cell wall orgar lignin laccase (original description: pacid=37178902 tran
28 **PTHR31471:SlPhvul.001G02 not assigned.r no hits & (original description: pacid=37167696 transcri**
29 **PTHR31471:SlPhvul.001G02 not assigned.r no hits & (original description: pacid=37167696 transcri**
30 3.2.1.153 - FrPhvul.001G03 Carbohydrate acid beta-fructofuranosidase (CWIN) (original descriptio
31 K13157 - U11,Phvul.001G10 RNA processir protein factor U11/U12-65K of U11/U12 small nuclear ri
32 K13157 - U11,Phvul.001G10 RNA processir protein factor U11/U12-65K of U11/U12 small nuclear ri
33 PF14368 - ProPhvul.001G15 not assigned.r no hits & (original description: pacid=37169901 transcri
34 PF14368 - ProPhvul.001G15 not assigned.r no hits & (original description: pacid=37169901 transcri
35 PF14368 - ProPhvul.001G15 not assigned.r no hits & (original description: pacid=37169901 transcri
36 PF14368 - ProPhvul.001G15 not assigned.r no hits & (original description: pacid=37169901 transcri
37 PTHR18866//IPhvul.001G24 Lipid metaboli acetyl-CoA carboxylase regulator (BADDC) (original descriq
38 PF01357//PFCPhvul.002G00 Cell wall orgar beta-like-class expansin (original description: pacid=371
39 PTHR23083//IPhvul.002G01 not assigned.ã (original description: pacid=37176692 transcript=Phvul.
40 PTHR23083//IPhvul.002G01 not assigned.ã (original description: pacid=37176692 transcript=Phvul.
41 K17619 - magPhvul.002G21 not assigned.r no hits & (original description: pacid=37177891 transcri
42 PTHR22870:SlPhvul.002G25 not assigned.ã (original description: pacid=37175448 transcript=Phvul.
43 PTHR22870:SlPhvul.002G25 not assigned.ã (original description: pacid=37175448 transcript=Phvul.
44 K03456 - serirPhvul.003G02 Protein modif scaffold component A of PP2A phosphatase complexes (
45 K03456 - serirPhvul.003G02 Protein modif scaffold component A of PP2A phosphatase complexes (
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

K00626 - acet:Phvul.003G08Secondary me acetyl-CoA C-acyltransferase (original description: pacid:
K00626 - acet:Phvul.003G08Secondary me acetyl-CoA C-acyltransferase (original description: pacid:
K00626 - acet:Phvul.003G08Secondary me acetyl-CoA C-acyltransferase (original description: pacid:
K00626 - acet:Phvul.003G08Secondary me acetyl-CoA C-acyltransferase (original description: pacid:
K00626 - acet:Phvul.003G08Secondary me acetyl-CoA C-acyltransferase (original description: pacid:
K00626 - acet:Phvul.003G08Secondary me acetyl-CoA C-acyltransferase (original description: pacid:
K00626 - acet:Phvul.003G08Secondary me acetyl-CoA C-acyltransferase (original description: pacid:
K00626 - acet:Phvul.003G08Secondary me acetyl-CoA C-acyltransferase (original description: pacid:
K15108 - solu:Phvul.003G10Solute transp:solute transporter (MTCC) (original description: pacid=3:
K15108 - solu:Phvul.003G10Solute transp:solute transporter (MTCC) (original description: pacid=3:
PTHR22957:SI:Phvul.003G14Vesicle traffi:RAB-GTPase-activating protein (RAB-GAP) (original descr
PTHR22957:SI:Phvul.003G14Vesicle traffi:RAB-GTPase-activating protein (RAB-GAP) (original descr
K07374 - tubu:Phvul.003G23Cytoskeleton :component alpha-Tubulin of alpha-beta-Tubulin heteroc
K07374 - tubu:Phvul.003G23Cytoskeleton :component alpha-Tubulin of alpha-beta-Tubulin heteroc
K07374 - tubu:Phvul.003G23Cytoskeleton :component alpha-Tubulin of alpha-beta-Tubulin heteroc
K07374 - tubu:Phvul.003G23Cytoskeleton :component alpha-Tubulin of alpha-beta-Tubulin heteroc
PTHR24012:SI:Phvul.003G29not assigned.ã (original description: pacid=37147487 transcript=Phvul.
PTHR24012:SI:Phvul.003G29RNA processir:mRNA-binding regulatory factor (RBP45/47) (original des
PTHR24012:SI:Phvul.003G29RNA processir:mRNA-binding regulatory factor (RBP45/47) (original des
PTHR32212:SI:Phvul.004G01not assigned.r no hits & (original description: pacid=37163167 transcri
PTHR32212:SI:Phvul.004G01not assigned.r no hits & (original description: pacid=37163167 transcri
PTHR32212:SI:Phvul.004G01not assigned.r no hits & (original description: pacid=37163167 transcri
PTHR32212:SI:Phvul.004G01not assigned.r no hits & (original description: pacid=37163167 transcri
0 Phvul.004G03not assigned.r no hits & (original description: pacid=37163425 transcri
PF00560//PFC:Phvul.004G04not assigned.ã (original description: pacid=37161946 transcript=Phvul.
PF00560//PFC:Phvul.004G04not assigned.ã (original description: pacid=37161946 transcript=Phvul.
K10393 - kine:Phvul.004G16Cytoskeleton :motor protein (Kinesin-13) (original description: pacid=3
K11308 - histc:Phvul.005G01Chromatin orç:acetyltransferase component HAM of NuA4 histone acet
1.14.13.37 - N:Phvul.005G01Enzyme classii: Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic
1.14.13.37 - N:Phvul.005G01Enzyme classii: Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic
1.14.13.37 - N:Phvul.005G01Enzyme classii: Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic
1.14.13.37 - N:Phvul.005G01Enzyme classii: Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic
1.14.13.37 - N:Phvul.005G01Enzyme classii: Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic
1.14.13.37 - N:Phvul.005G01Enzyme classii: Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic
1.14.13.37 - N:Phvul.005G01Enzyme classii: Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic
1.14.13.37 - N:Phvul.005G01Enzyme classii: Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic
2.4.1.132 - GC:Phvul.005G08Protein modif:alpha-1,3/1,6-mannosyltransferase (ALG2) (original desc
2.4.1.132 - GC:Phvul.005G08Protein modif:alpha-1,3/1,6-mannosyltransferase (ALG2) (original desc
PTHR31072:SI:Phvul.005G09RNA biosynth:transcription factor (TCP) (original description: pacid=37
PTHR31072:SI:Phvul.005G09RNA biosynth:transcription factor (TCP) (original description: pacid=37
PTHR31072:SI:Phvul.005G09RNA biosynth:transcription factor (TCP) (original description: pacid=37
PTHR31072:SI:Phvul.005G09RNA biosynth:transcription factor (TCP) (original description: pacid=37
PTHR31072:SI:Phvul.005G09RNA biosynth:transcription factor (TCP) (original description: pacid=37

1
2
3 PTHR31072:SI Phvul.005G09 RNA biosynthesis transcription factor (TCP) (original description: pacid=37
4 0 Phvul.006G06 not assigned.r no hits & (original description: pacid=37172254 transcri
5 0 Phvul.006G06 not assigned.r no hits & (original description: pacid=37172254 transcri
6 4.1.1.28 - AroI Phvul.006G13 Secondary aromatic L-amino acid decarboxylase (original descriptio
7 4.1.1.28 - AroI Phvul.006G13 Secondary aromatic L-amino acid decarboxylase (original descriptio
8 K15047 - hete Phvul.006G19 not assigned.r no hits & (original description: pacid=37171957 transcri
9 K15047 - hete Phvul.006G19 not assigned.r no hits & (original description: pacid=37171957 transcri
10 K15047 - hete Phvul.006G19 not assigned.r no hits & (original description: pacid=37171957 transcri
11 K15047 - hete Phvul.006G19 not assigned.r no hits & (original description: pacid=37171957 transcri
12 PF04570 - zinc Phvul.007G05 Multi-process SnRK1-interacting factor (FLZ) (original description: pacid
13 PF04570 - zinc Phvul.007G05 Multi-process SnRK1-interacting factor (FLZ) (original description: pacid
14 PTHR23024:SI Phvul.007G06 not assigned.a (original description: pacid=37166219 transcript=Phvul.
15 PTHR23024:SI Phvul.007G06 not assigned.a (original description: pacid=37166219 transcript=Phvul.
16 PTHR37764:SI Phvul.007G18 not assigned.r no hits & (original description: pacid=37166249 transcri
17 PF13414 - TPF Phvul.007G19 not assigned.r no hits & (original description: pacid=37165459 transcri
18 PF13414 - TPF Phvul.007G19 not assigned.r no hits & (original description: pacid=37165459 transcri
19 0 Phvul.007G23 Protein translocator NUP1/NUP136 nucleoporin of nuclear pore complex (ori
20 0 Phvul.007G23 Protein translocator NUP1/NUP136 nucleoporin of nuclear pore complex (ori
21 0 Phvul.007G23 Protein translocator NUP1/NUP136 nucleoporin of nuclear pore complex (ori
22 0 Phvul.007G23 Protein translocator NUP1/NUP136 nucleoporin of nuclear pore complex (ori
23 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
24 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
25 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
26 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
27 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
28 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
29 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
30 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
31 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
32 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
33 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
34 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
35 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
36 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
37 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
38 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
39 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
40 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
41 KOG0211 - PrC Phvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
42 PTHR23240//I Phvul.008G00 DNA damage DNA ligase (LIG6) (original description: pacid=37159578
43 PTHR23240//I Phvul.008G00 DNA damage DNA ligase (LIG6) (original description: pacid=37159578
44 PTHR23240//I Phvul.008G00 DNA damage DNA ligase (LIG6) (original description: pacid=37159578
45 PTHR23240//I Phvul.008G00 DNA damage DNA ligase (LIG6) (original description: pacid=37159578
46 PTHR23240//I Phvul.008G00 DNA damage DNA ligase (LIG6) (original description: pacid=37159578
47 PTHR10783:SI Phvul.008G03 Nutrient uptake phosphate transporter (PHO1) (original description: paci
48 PTHR10783:SI Phvul.008G03 Nutrient uptake phosphate transporter (PHO1) (original description: paci
49 PF00069//PFC Phvul.008G09 Protein modification protein kinase (LRR-XII) (original description: pacid=3715
50 PF00069//PFC Phvul.008G09 Protein modification protein kinase (LRR-XII) (original description: pacid=3715
51 PF00069//PFC Phvul.008G09 Protein modification protein kinase (LRR-XII) (original description: pacid=3715
52 PF00069//PFC Phvul.008G09 Protein modification protein kinase (LRR-XII) (original description: pacid=3715
53 PF00069//PFC Phvul.008G09 Protein modification protein kinase (LRR-XII) (original description: pacid=3715
54 PF00069//PFC Phvul.008G09 Protein modification protein kinase (LRR-XII) (original description: pacid=3715
55 PF00069//PFC Phvul.008G09 Protein modification protein kinase (LRR-XII) (original description: pacid=3715
56 PF00069//PFC Phvul.008G09 Protein modification protein kinase (LRR-XII) (original description: pacid=3715
57 PF00069//PFC Phvul.008G09 Protein modification protein kinase (LRR-XII) (original description: pacid=3715
58 K15685 - E3 ubiquitin ligase (HAKAI) (original description: pacid=3
59
60

1
2
3 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig
4 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig
5 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig
6 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig
7 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig
8 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig
9 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig
10 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig
11 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig
12 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig
13 PTHR31602:SlPhvul.010G04RNA biosynthesis component GRF of GRF-GIF transcriptional complex (orig
14 PTHR22849//lPhvul.010G11Protein home E3 ubiquitin ligase (PUB) (original description: pacid=371
15 PTHR22849//lPhvul.010G11Protein home E3 ubiquitin ligase (PUB) (original description: pacid=371
16 PTHR22849//lPhvul.010G11Protein home E3 ubiquitin ligase (PUB) (original description: pacid=371
17 PTHR22849//lPhvul.010G11Protein home E3 ubiquitin ligase (PUB) (original description: pacid=371
18 PTHR22849//lPhvul.010G11Protein home E3 ubiquitin ligase (PUB) (original description: pacid=371
19 PTHR24009:SlPhvul.011G01RNA biosynthesis C3H zinc finger transcription factor (original description:
20 PTHR24009:SlPhvul.011G01RNA biosynthesis C3H zinc finger transcription factor (original description:
21 PTHR24009:SlPhvul.011G01RNA biosynthesis C3H zinc finger transcription factor (original description:
22 PTHR24009:SlPhvul.011G01RNA biosynthesis C3H zinc finger transcription factor (original description:
23 PTHR24009:SlPhvul.011G01RNA biosynthesis C3H zinc finger transcription factor (original description:
24 0 Phvul.011G12not assigned.r no hits & (original description: pacid=37155251 transcri
25 0 Phvul.011G12not assigned.r no hits & (original description: pacid=37155251 transcri
26 0 Phvul.011G12not assigned.r no hits & (original description: pacid=37155251 transcri
27 0 Phvul.011G12not assigned.r no hits & (original description: pacid=37155251 transcri
28 0 Phvul.011G12not assigned.r no hits & (original description: pacid=37155251 transcri
29
30 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
31 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
32 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
33 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
34 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
35 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
36 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
37
38 PTHR10173:SlPhvul.011G17not assigned.a (original description: pacid=37157390 transcript=Phvul.
39 PTHR10173:SlPhvul.011G17not assigned.a (original description: pacid=37157390 transcript=Phvul.
40 PTHR10173:SlPhvul.011G17not assigned.a (original description: pacid=37157390 transcript=Phvul.
41 PTHR10173:SlPhvul.011G17not assigned.a (original description: pacid=37157390 transcript=Phvul.
42 PTHR10173:SlPhvul.011G17not assigned.a (original description: pacid=37157390 transcript=Phvul.
43 PTHR22884:SlPhvul.011G19Chromatin org methylated DNA binding component SUVH1/3 of SUVH-I
44 PTHR22884:SlPhvul.011G19Chromatin org methylated DNA binding component SUVH1/3 of SUVH-I
45 PF05553 - CotPhvul.001G09not assigned.r no hits & (original description: pacid=37170071 transcri
46 PF05553 - CotPhvul.001G09not assigned.r no hits & (original description: pacid=37170071 transcri
47 K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri
48 K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri
49 K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri
50 K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri
51 K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri
52 K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri
53 K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri
54 K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri
55 K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri
56 K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri
57 K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri
58 K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri
59 K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri
K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri
K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri
K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri
K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri
K15559 - reguPhvul.001G10not assigned.r no hits & (original description: pacid=37170360 transcri
PTHR31447:SIPhvul.001G14RNA processir N6-methyladenosine demethylase (ALKBH10) (original d
PTHR28630:SIPhvul.001G17not assigned.ã (original description: pacid=37168987 transcript=Phvul.
PTHR28630:SIPhvul.001G17not assigned.ã (original description: pacid=37168987 transcript=Phvul.
PTHR28630:SIPhvul.001G17not assigned.ã (original description: pacid=37168987 transcript=Phvul.
PTHR28630:SIPhvul.001G17not assigned.ã (original description: pacid=37168987 transcript=Phvul.
2.7.7.2 - FAD ðPhvul.001G17not assigned.r no hits & (original description: pacid=37168919 transcri
2.7.7.2 - FAD ðPhvul.001G17not assigned.r no hits & (original description: pacid=37168919 transcri
K12603 - CCR4Phvul.001G20RNA processir deadenylase component CCR4 of CCR4-NOT complex (or
K12603 - CCR4Phvul.001G20RNA processir deadenylase component CCR4 of CCR4-NOT complex (or
K12603 - CCR4Phvul.001G20RNA processir deadenylase component CCR4 of CCR4-NOT complex (or
K12603 - CCR4Phvul.001G20RNA processir deadenylase component CCR4 of CCR4-NOT complex (or
K12603 - CCR4Phvul.001G20RNA processir deadenylase component CCR4 of CCR4-NOT complex (or
K12603 - CCR4Phvul.001G20RNA processir deadenylase component CCR4 of CCR4-NOT complex (or
K12603 - CCR4Phvul.001G20RNA processir deadenylase component CCR4 of CCR4-NOT complex (or
K12603 - CCR4Phvul.001G20RNA processir deadenylase component CCR4 of CCR4-NOT complex (or
PTHR22849:SIPhvul.001G26not assigned.ã (original description: pacid=37168993 transcript=Phvul.
PTHR11746:SIPhvul.001G26Enzyme classii Acetylserotonin O-methyltransferase OS=Arabidopsis th
PTHR11746:SIPhvul.001G26Enzyme classii Acetylserotonin O-methyltransferase OS=Arabidopsis th
PF13912 - C2FPhvul.002G05RNA biosynthC2H2 zinc finger transcription factor (original descriptio
PF13912 - C2FPhvul.002G05RNA biosynthC2H2 zinc finger transcription factor (original descriptio
PTHR10438:SIPhvul.002G06Redox homeo H-type thioredoxin (original description: pacid=3717719!
PTHR10438:SIPhvul.002G06Redox homeo H-type thioredoxin (original description: pacid=3717719!
PTHR10438:SIPhvul.002G06Redox homeo H-type thioredoxin (original description: pacid=3717719!
PTHR10438:SIPhvul.002G06Redox homeo H-type thioredoxin (original description: pacid=3717719!
PF03106 - WRPhvul.002G16RNA biosynthtranscription factor (WRKY) (original description: pacid=:
PF03106 - WRPhvul.002G16RNA biosynthtranscription factor (WRKY) (original description: pacid=:
PTHR12953 - IPhvul.002G16Cytoskeleton ðregulatory factor (SUN3/4/5) nuclear shape determinati
PTHR12953 - IPhvul.002G16Cytoskeleton ðregulatory factor (SUN3/4/5) nuclear shape determinati
PTHR12953 - IPhvul.002G16Cytoskeleton ðregulatory factor (SUN3/4/5) nuclear shape determinati
PTHR12953 - IPhvul.002G16Cytoskeleton ðregulatory factor (SUN3/4/5) nuclear shape determinati
PTHR23042:SIPhvul.002G21Nutrient uptalbHLH-IVa-class iron homeostasis regulator (original desc
PTHR23042:SIPhvul.002G21Nutrient uptalbHLH-IVa-class iron homeostasis regulator (original desc
PTHR23042:SIPhvul.002G21Nutrient uptalbHLH-IVa-class iron homeostasis regulator (original desc
PTHR23042:SIPhvul.002G21Nutrient uptalbHLH-IVa-class iron homeostasis regulator (original desc
PTHR22835//IPhvul.002G24not assigned.ã (original description: pacid=37176697 transcript=Phvul.
PTHR22835//IPhvul.002G24not assigned.ã (original description: pacid=37176697 transcript=Phvul.

1
2
3 PTHR22870:SlPhvul.002G25 not assigned.ã (original description: pacid=37175448 transcript=Phvul.
4 PTHR22870:SlPhvul.002G25 not assigned.ã (original description: pacid=37175448 transcript=Phvul.
5 PTHR22870:SlPhvul.002G25 not assigned.ã (original description: pacid=37175448 transcript=Phvul.
6 PTHR22870:SlPhvul.002G25 not assigned.ã (original description: pacid=37175448 transcript=Phvul.
7 PTHR10791:SlPhvul.002G28 Solute transpç sugar efflux transporter (SWEET) (original description: pã
8 PTHR10791:SlPhvul.002G28 Solute transpç sugar efflux transporter (SWEET) (original description: pã
9 PTHR10791:SlPhvul.002G28 Solute transpç sugar efflux transporter (SWEET) (original description: pã
10 PTHR10791:SlPhvul.002G28 Solute transpç sugar efflux transporter (SWEET) (original description: pã
11 PTHR10791:SlPhvul.002G28 Solute transpç sugar efflux transporter (SWEET) (original description: pã
12 PTHR10791:SlPhvul.002G28 Solute transpç sugar efflux transporter (SWEET) (original description: pã
13 PTHR10791:SlPhvul.002G28 Solute transpç sugar efflux transporter (SWEET) (original description: pã
14 3.4.11.14 - CyPhvul.002G29 not assigned.ã (original description: pacid=37176433 transcript=Phvul.
15 3.4.11.14 - CyPhvul.002G29 not assigned.ã (original description: pacid=37176433 transcript=Phvul.
16 PTHR13832//lPhvul.002G30 Protein modif clade A phosphatase (original description: pacid=371752
17 PTHR13832//lPhvul.002G30 Protein modif clade A phosphatase (original description: pacid=371752
18 K14016 - ubiq Phvul.002G32 Protein home component UFD1 of ER-associated protein degradation (
19 K14016 - ubiq Phvul.002G32 Protein home component UFD1 of ER-associated protein degradation (
20 K14016 - ubiq Phvul.002G32 Protein home component UFD1 of ER-associated protein degradation (
21 K14016 - ubiq Phvul.002G32 Protein home component UFD1 of ER-associated protein degradation (
22 K14016 - ubiq Phvul.002G32 Protein home component UFD1 of ER-associated protein degradation (
23 K05863 - soluPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3
24 K05863 - soluPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3
25 K05863 - soluPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3
26 K05863 - soluPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3
27 K05863 - soluPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3
28 K05863 - soluPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3
29 K05863 - soluPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3
30 K05863 - soluPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3
31 K05863 - soluPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3
32 K05863 - soluPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3
33 K05863 - soluPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3
34 K05863 - soluPhvul.002G32 Solute transpç solute transporter (MTCC) (original description: pacid=3
35 PTHR10359:SlPhvul.003G03 Chromatin orç methylcytosine-specific DNA glycosylase (ROS1) (original
36 PTHR10359:SlPhvul.003G03 Chromatin orç methylcytosine-specific DNA glycosylase (ROS1) (original
37 K00721 - dolichPhvul.003G05 Protein modif catalytic component DPMS1 of DPMS dolichol-phosphat
38 K00721 - dolichPhvul.003G05 Protein modif catalytic component DPMS1 of DPMS dolichol-phosphat
39 0 Phvul.003G07 not assigned.r no hits & (original description: pacid=37147041 transcri
40 0 Phvul.003G07 not assigned.r no hits & (original description: pacid=37147041 transcri
41 0 Phvul.003G07 not assigned.r no hits & (original description: pacid=37147041 transcri
42 0 Phvul.003G07 not assigned.r no hits & (original description: pacid=37147041 transcri
43 PTHR23421:SlPhvul.003G13 Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=3
44 PTHR23421:SlPhvul.003G13 Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=3
45 PTHR23421:SlPhvul.003G13 Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=3
46 PTHR23421:SlPhvul.003G13 Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=3
47 PTHR23155//lPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.
48 PTHR23155//lPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.
49 PTHR23155//lPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.
50 PTHR23155//lPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.
51 PTHR23155//lPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.
52 PTHR23155//lPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.
53 PTHR23155//lPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.
54 PTHR23155//lPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.
55 PTHR23155//lPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.
56 PTHR23155//lPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.
57 PTHR23155//lPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.
58 PTHR23155//lPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.
59 PTHR23155//lPhvul.003G24 not assigned.ã (original description: pacid=37146857 transcript=Phvul.
60

1
2
3 K01061 - carb Phvul.005G11 not assigned.r no hits & (original description: pacid=37152909 transcri
4 K01061 - carb Phvul.005G11 not assigned.r no hits & (original description: pacid=37152909 transcri
5 PTHR10593//IPhvu.005G13RNA biosynth C2H2 zinc finger transcription factor (original descriptio
6 PTHR10593//IPhvu.005G13RNA biosynth C2H2 zinc finger transcription factor (original descriptio
7 K11583 - serir Phvul.006G10 Protein modif regulatory component B2 of PP2A phosphatase complex
8 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.
9 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.
10 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.
11 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.
12 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.
13 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.
14 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.
15 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.
16 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.
17 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.
18 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.
19 PTHR13215:SI Phvul.006G11 not assigned.a (original description: pacid=37173654 transcript=Phvu.
20 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:
21 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:
22 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:
23 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:
24 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:
25 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:
26 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:
27 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:
28 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:
29 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:
30 PTHR11453:SI Phvul.006G12 Solute transp borate transporter (BOR) (original description: pacid=37:
31 PF15365 - Pro Phvul.006G15 not assigned.r no hits & (original description: pacid=37174157 transcri
32 PTHR11802:SI Phvul.006G16 Protein home serine carboxypeptidase (original description: pacid=371
33 PTHR11802:SI Phvul.006G16 Protein home serine carboxypeptidase (original description: pacid=371
34 PTHR11802:SI Phvul.006G16 Protein home serine carboxypeptidase (original description: pacid=371
35 PTHR11802:SI Phvul.006G16 Protein home serine carboxypeptidase (original description: pacid=371
36 K13125 - nitri Phvul.006G19 not assigned.a (original description: pacid=37172724 transcript=Phvu.
37 K13125 - nitri Phvul.006G19 not assigned.a (original description: pacid=37172724 transcript=Phvu.
38 K01354 - oligc Phvul.007G01 not assigned.r no hits & (original description: pacid=37164997 transcri
39 K01354 - oligc Phvul.007G01 not assigned.r no hits & (original description: pacid=37164997 transcri
40 K01354 - oligc Phvul.007G01 not assigned.r no hits & (original description: pacid=37164997 transcri
41 K01354 - oligc Phvul.007G01 not assigned.r no hits & (original description: pacid=37164997 transcri
42 PTHR31072:SI Phvul.007G01 Multi-process CHE circadian clock repression factor (original descriptio
43 PTHR31072:SI Phvul.007G01 Multi-process CHE circadian clock repression factor (original descriptio
44 2.7.8.8 - CDP- Phvul.007G03 Lipid metaboli base-exchange-type phosphatidylserine synthase (origin
45 2.7.10.2 - NonPhvul.007G05 Protein modif protein kinase (SD-1) (original description: pacid=371665
46 2.7.10.2 - NonPhvul.007G05 Protein modif protein kinase (SD-1) (original description: pacid=371665
47 2.7.10.2 - NonPhvul.007G05 Protein modif protein kinase (SD-1) (original description: pacid=371665
48 2.7.10.2 - NonPhvul.007G05 Protein modif protein kinase (SD-1) (original description: pacid=371665
49 PTHR10638:SI Phvul.007G05 Polyamine me copper-containing amine oxidase (CuAO) (original descri
50 PTHR10638:SI Phvul.007G05 Polyamine me copper-containing amine oxidase (CuAO) (original descri
51 PTHR10638:SI Phvul.007G05 Polyamine me copper-containing amine oxidase (CuAO) (original descri
52 PTHR10638:SI Phvul.007G05 Polyamine me copper-containing amine oxidase (CuAO) (original descri
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

PF04570 - zincPhvul.007G05Multi-process SnRK1-interacting factor (FLZ) (original description: pacic
PF04570 - zincPhvul.007G05Multi-process SnRK1-interacting factor (FLZ) (original description: pacic
PF04570 - zincPhvul.007G05Multi-process SnRK1-interacting factor (FLZ) (original description: pacic
PF04570 - zincPhvul.007G05Multi-process SnRK1-interacting factor (FLZ) (original description: pacic
PF04570 - zincPhvul.007G05Multi-process SnRK1-interacting factor (FLZ) (original description: pacic
PF04570 - zincPhvul.007G05Multi-process SnRK1-interacting factor (FLZ) (original description: pacic
PTHR23024:SIPhvul.007G06not assigned.ã (original description: pacid=37166219 transcript=Phvul.
PTHR23024:SIPhvul.007G06not assigned.ã (original description: pacid=37166219 transcript=Phvul.
PTHR23024:SIPhvul.007G06not assigned.ã (original description: pacid=37166219 transcript=Phvul.
PTHR23024:SIPhvul.007G06not assigned.ã (original description: pacid=37166219 transcript=Phvul.
PTHR23024:SIPhvul.007G06not assigned.ã (original description: pacid=37166219 transcript=Phvul.
PTHR11972//IPhvul.007G07Nutrient uptalmetal ion-chelate reductase (FRO) (original description: |
PTHR11972//IPhvul.007G07Nutrient uptalmetal ion-chelate reductase (FRO) (original description: |
PTHR11972//IPhvul.007G07Nutrient uptalmetal ion-chelate reductase (FRO) (original description: |
PTHR11972//IPhvul.007G07Nutrient uptalmetal ion-chelate reductase (FRO) (original description: |
PF12646 - DorPhvul.007G09not assigned.r no hits & (original description: pacid=37167603 transcri
PF12646 - DorPhvul.007G09not assigned.r no hits & (original description: pacid=37167603 transcri
PF12646 - DorPhvul.007G09not assigned.r no hits & (original description: pacid=37167603 transcri
PF12646 - DorPhvul.007G09not assigned.r no hits & (original description: pacid=37167603 transcri
PTHR11260:SIPhvul.007G10Protein modif class phi glutathione S-transferase (original description: |
PTHR11260:SIPhvul.007G10Protein modif class phi glutathione S-transferase (original description: |
PTHR11260:SIPhvul.007G10Protein modif class phi glutathione S-transferase (original description: |
PTHR11260:SIPhvul.007G10Protein modif class phi glutathione S-transferase (original description: |
PTHR37764:SIPhvul.007G18not assigned.r no hits & (original description: pacid=37166249 transcri
PTHR37764:SIPhvul.007G18not assigned.r no hits & (original description: pacid=37166249 transcri
PTHR37764:SIPhvul.007G18not assigned.r no hits & (original description: pacid=37166249 transcri
PTHR37764:SIPhvul.007G18not assigned.r no hits & (original description: pacid=37166249 transcri
0 Phvul.007G18not assigned.r no hits & (original description: pacid=37164309 transcri
0 Phvul.007G18not assigned.r no hits & (original description: pacid=37164309 transcri
2.7.11.1 - NonPhvul.007G20Protein modif receptor-like protein kinase (RLCK-V) (original descriptio
2.7.11.1 - NonPhvul.007G20Protein modif receptor-like protein kinase (RLCK-V) (original descriptio
2.7.11.1 - NonPhvul.007G20Protein modif receptor-like protein kinase (RLCK-V) (original descriptio
2.7.11.1 - NonPhvul.007G20Protein modif receptor-like protein kinase (RLCK-V) (original descriptio
2.7.11.1 - NonPhvul.007G20Protein modif receptor-like protein kinase (RLCK-V) (original descriptio
2.7.11.1 - NonPhvul.007G20Protein modif receptor-like protein kinase (RLCK-V) (original descriptio
2.7.11.1 - NonPhvul.007G20Protein modif receptor-like protein kinase (RLCK-V) (original descriptio
PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165
PF00045 - HerPhvul.007G27not assigned.ã (original description: pacid=37164350 transcript=Phvul.
PF00045 - HerPhvul.007G27not assigned.ã (original description: pacid=37164350 transcript=Phvul.
PF00045 - HerPhvul.007G27not assigned.ã (original description: pacid=37166099 transcript=Phvul.

1
2
3 PF00045 - HerPhvul.007G27 not assigned.a (original description: pacid=37166099 transcript=Phvul.
4 PF00045 - HerPhvul.007G27 not assigned.a (original description: pacid=37164734 transcript=Phvul.
5 PF00045 - HerPhvul.007G27 not assigned.a (original description: pacid=37164734 transcript=Phvul.
6 PTHR35313:SlPhvul.008G00 Cell wall orgarexine patterning factor (NEF1) (original description: paci
7 PTHR35313:SlPhvul.008G00 Cell wall orgarexine patterning factor (NEF1) (original description: paci
8 PTHR35313:SlPhvul.008G00 Cell wall orgarexine patterning factor (NEF1) (original description: paci
9 PTHR35313:SlPhvul.008G00 Cell wall orgarexine patterning factor (NEF1) (original description: paci
10 PTHR35313:SlPhvul.008G00 Cell wall orgarexine patterning factor (NEF1) (original description: paci
11 PTHR35313:SlPhvul.008G00 Cell wall orgarexine patterning factor (NEF1) (original description: paci
12 KOG0211 - PrPhvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
13 KOG0211 - PrPhvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
14 KOG0211 - PrPhvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
15 KOG0211 - PrPhvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
16 KOG0211 - PrPhvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
17 KOG0211 - PrPhvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
18 KOG0211 - PrPhvul.008G00 not assigned.r no hits & (original description: pacid=37158928 transcri
19 K03131 - tran:Phvul.008G01 RNA biosynthcomponent TAF6 of TFIIId basal transcription regulation c
20 K03131 - tran:Phvul.008G01 RNA biosynthcomponent TAF6 of TFIIId basal transcription regulation c
21 PTHR13068//lPhvul.008G04 RNA biosynthtranscription factor (mTERF) (original description: pacid=
22 0 Phvul.008G06 not assigned.r no hits & (original description: pacid=37159335 transcri
23 0 Phvul.008G06 not assigned.r no hits & (original description: pacid=37159335 transcri
24 0 Phvul.008G06 not assigned.r no hits & (original description: pacid=37159335 transcri
25 0 Phvul.008G06 not assigned.r no hits & (original description: pacid=37159335 transcri
26 0 Phvul.008G06 not assigned.r no hits & (original description: pacid=37159335 transcri
27 KOG1947 - LePhvul.008G07 not assigned.r no hits & (original description: pacid=37157631 transcri
28 KOG1947 - LePhvul.008G07 not assigned.r no hits & (original description: pacid=37157631 transcri
29 KOG1947 - LePhvul.008G07 not assigned.r no hits & (original description: pacid=37157631 transcri
30 KOG1947 - LePhvul.008G07 not assigned.r no hits & (original description: pacid=37157631 transcri
31 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715
32 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715
33 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715
34 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715
35 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715
36 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715
37 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715
38 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715
39 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715
40 PF00069//PFCPhvul.008G09 Protein modif protein kinase (LRR-XII) (original description: pacid=3715
41 PTHR33103:SlPhvul.008G11 not assigned.r no hits & (original description: pacid=37158099 transcri
42 PTHR33103:SlPhvul.008G11 not assigned.r no hits & (original description: pacid=37158099 transcri
43 PTHR33103:SlPhvul.008G11 not assigned.r no hits & (original description: pacid=37159657 transcri
44 PTHR33103:SlPhvul.008G11 not assigned.r no hits & (original description: pacid=37161383 transcri
45 PTHR33103:SlPhvul.008G11 not assigned.r no hits & (original description: pacid=37161383 transcri
46 PTHR33103:SlPhvul.008G11 not assigned.r no hits & (original description: pacid=37161383 transcri
47 PTHR13683:SlPhvul.008G11 Protein home pepsin-type protease (original description: pacid=37158
48 PTHR13683:SlPhvul.008G11 Protein home pepsin-type protease (original description: pacid=37158
49 0 Phvul.008G15 not assigned.r no hits & (original description: pacid=37160418 transcri
50 0 Phvul.008G15 not assigned.r no hits & (original description: pacid=37160418 transcri
51 0 Phvul.008G15 not assigned.r no hits & (original description: pacid=37160418 transcri
52 0 Phvul.008G15 not assigned.r no hits & (original description: pacid=37160418 transcri
53 4.2.1.119 - EnPhvul.008G20 Lipid metaboli hydroxyacyl-ACP dehydratase (mtHD) (original descriptic
54 4.2.1.119 - EnPhvul.008G20 Lipid metaboli hydroxyacyl-ACP dehydratase (mtHD) (original descriptic
55 4.2.1.119 - EnPhvul.008G20 Lipid metaboli hydroxyacyl-ACP dehydratase (mtHD) (original descriptic
56
57
58
59
60

1
 2
 3 4.2.1.119 - EnPhvul.008G20Lipid metabol hydroxyacyl-ACP dehydratase (mtHD) (original descriptio
 4 0 Phvul.008G22 not assigned.r no hits & (original description: pacid=37161082 transcri
 5 0 Phvul.008G22 not assigned.r no hits & (original description: pacid=37161082 transcri
 6 0 Phvul.008G22 not assigned.r no hits & (original description: pacid=37161082 transcri
 7 0 Phvul.008G22 not assigned.r no hits & (original description: pacid=37161082 transcri
 8
 9 PTHR22950:SlPhvul.008G22Solute transp proline transporter (ProT) (original description: pacid=37
 10 PTHR22950:SlPhvul.008G22Solute transp proline transporter (ProT) (original description: pacid=37
 11 PTHR22950:SlPhvul.008G22Solute transp proline transporter (ProT) (original description: pacid=37
 12 PTHR22950:SlPhvul.008G22Solute transp proline transporter (ProT) (original description: pacid=37
 13 PTHR24012:SlPhvul.008G27 not assigned.a (original description: pacid=37160931 transcript=Phvul.
 14 PTHR24012:SlPhvul.008G27 not assigned.a (original description: pacid=37160931 transcript=Phvul.
 15 PTHR24012:SlPhvul.008G27 not assigned.a (original description: pacid=37160931 transcript=Phvul.
 16 K02259 - cytoPhvul.008G28Cellular respir component COX15 of cytochrome c oxidase assembly (o
 17 K02259 - cytoPhvul.008G28Cellular respir component COX15 of cytochrome c oxidase assembly (o
 18 PTHR10641:SlPhvul.009G10RNA biosynth transcription factor (MYB) (original description: pacid=37
 19 PTHR10972:SlPhvul.009G12 not assigned.a (original description: pacid=37148875 transcript=Phvul.
 20 PTHR10972:SlPhvul.009G12 not assigned.a (original description: pacid=37148875 transcript=Phvul.
 21 PTHR10972:SlPhvul.009G12 not assigned.a (original description: pacid=37148875 transcript=Phvul.
 22 PTHR10972:SlPhvul.009G12 not assigned.a (original description: pacid=37148875 transcript=Phvul.
 23 K08867 - WNkPhvul.009G17Protein modif protein kinase (MAP3K-WNK) (original description: pacid
 24 K08867 - WNkPhvul.009G17Protein modif protein kinase (MAP3K-WNK) (original description: pacid
 25 K08867 - WNkPhvul.009G17Protein modif protein kinase (MAP3K-WNK) (original description: pacid
 26 K08867 - WNkPhvul.009G17Protein modif protein kinase (MAP3K-WNK) (original description: pacid
 27 PTHR23421:SlPhvul.009G23Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=37
 28 PTHR23421:SlPhvul.009G23Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=37
 29 K13066 - caffPhvul.009G25Enzyme classii Enzyme classification.EC_2 transferases.EC_2.1 transfera
 30 K13066 - caffPhvul.009G25Enzyme classii Enzyme classification.EC_2 transferases.EC_2.1 transfera
 31 K13066 - caffPhvul.009G25Enzyme classii Enzyme classification.EC_2 transferases.EC_2.1 transfera
 32 K13066 - caffPhvul.009G25Enzyme classii Enzyme classification.EC_2 transferases.EC_2.1 transfera
 33 K17592 - sacsiPhvul.010G03 not assigned.a (original description: pacid=37143296 transcript=Phvul.
 34 K17592 - sacsiPhvul.010G03 not assigned.a (original description: pacid=37143296 transcript=Phvul.
 35 K17592 - sacsiPhvul.010G03 not assigned.a (original description: pacid=37143296 transcript=Phvul.
 36 K17592 - sacsiPhvul.010G03 not assigned.a (original description: pacid=37143296 transcript=Phvul.
 37 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 38 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 39 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 40 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 41 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 42 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 43 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 44 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 45 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 46 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 47 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 48 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 49 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 50 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 51 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 52 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 53 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 54 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 55 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 56 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 57 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 58 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 59 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
 60

1
2
3 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
4 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
5 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
6 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
7 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
8 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
9 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
10 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
11 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
12 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
13 PTHR23253:SlPhvul.010G04Protein biosyr component eIF4G of eIF4F mRNA unwinding complex (oi
14 PTHR12565:SlPhvul.010G07RNA biosynth transcription factor (bHLH) (original description: pacid=3
15 K13335 - peroPhvul.010G08not assigned.a (original description: pacid=37142487 transcript=Phvul.
16 K13335 - peroPhvul.010G08not assigned.a (original description: pacid=37142487 transcript=Phvul.
17 K13335 - peroPhvul.010G08not assigned.a (original description: pacid=37142487 transcript=Phvul.
18 K13335 - peroPhvul.010G08not assigned.a (original description: pacid=37142487 transcript=Phvul.
19 K13335 - peroPhvul.010G08not assigned.a (original description: pacid=37142487 transcript=Phvul.
20 K13335 - peroPhvul.010G08not assigned.a (original description: pacid=37142487 transcript=Phvul.
21 K13335 - peroPhvul.010G08not assigned.a (original description: pacid=37142487 transcript=Phvul.
22 K13335 - peroPhvul.010G08not assigned.a (original description: pacid=37142487 transcript=Phvul.
23 K13335 - peroPhvul.010G08not assigned.a (original description: pacid=37142487 transcript=Phvul.
24 K13335 - peroPhvul.010G08not assigned.a (original description: pacid=37142487 transcript=Phvul.
25 K13335 - peroPhvul.010G08not assigned.a (original description: pacid=37142487 transcript=Phvul.
26 K13335 - peroPhvul.010G08not assigned.a (original description: pacid=37142487 transcript=Phvul.
27 K13335 - peroPhvul.010G08not assigned.a (original description: pacid=37142487 transcript=Phvul.
28 1.13.11.58 - LiPhvul.010G13Enzyme classii Enzyme classification.EC_1 oxidoreductases.EC_1.13 oxi
29 1.13.11.58 - LiPhvul.010G13Enzyme classii Enzyme classification.EC_1 oxidoreductases.EC_1.13 oxi
30 1.13.11.58 - LiPhvul.010G13Enzyme classii Enzyme classification.EC_1 oxidoreductases.EC_1.13 oxi
31 1.13.11.58 - LiPhvul.010G13Enzyme classii Enzyme classification.EC_1 oxidoreductases.EC_1.13 oxi
32 K01537 - Ca2+Phvul.011G01Solute transp P2B-type calcium cation-transporting ATPase (ACA) (orig
33 K01537 - Ca2+Phvul.011G01Solute transp P2B-type calcium cation-transporting ATPase (ACA) (orig
34 K01537 - Ca2+Phvul.011G01Solute transp P2B-type calcium cation-transporting ATPase (ACA) (orig
35 K01537 - Ca2+Phvul.011G01Solute transp P2B-type calcium cation-transporting ATPase (ACA) (orig
36 K08873 - PI-3-Phvul.011G05Protein modif protein kinase (PIKK) (original description: pacid=371548
37 K08873 - PI-3-Phvul.011G05Protein modif protein kinase (PIKK) (original description: pacid=371548
38 K08873 - PI-3-Phvul.011G05Protein modif protein kinase (PIKK) (original description: pacid=371548
39 K08873 - PI-3-Phvul.011G05Protein modif protein kinase (PIKK) (original description: pacid=371548
40 PTHR14194:SlPhvul.011G06RNA biosynth TAC16 cofactor of plastid-encoded RNA polymerase (orig
41 PTHR14194:SlPhvul.011G06RNA biosynth TAC16 cofactor of plastid-encoded RNA polymerase (orig
42 PF05938 - PlaiPhvul.011G11not assigned.a (original description: pacid=37156233 transcript=Phvul.
43 PF05938 - PlaiPhvul.011G12not assigned.a (original description: pacid=37155659 transcript=Phvul.
44 0 Phvul.011G12not assigned.r no hits & (original description: pacid=37155251 transcri
45 0 Phvul.011G12not assigned.r no hits & (original description: pacid=37155251 transcri
46 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
47 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
48 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
49 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
50 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
51 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
52 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
53 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
54 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
55 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
56 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
57 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
58 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
59 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
60

3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
 3.4.19.5//3.5. Phvul.011G16Enzyme classii Putative threonine aspartase OS=Arabidopsis thaliana (s
 0 Phvul.011G20not assigned.r no hits & (original description: pacid=37156963 transcri
 0 Phvul.011G20not assigned.r no hits & (original description: pacid=37156963 transcri
 0 Phvul.011G20not assigned.r no hits & (original description: pacid=37156963 transcri
 0 Phvul.011G20not assigned.r no hits & (original description: pacid=37156963 transcri
 PTHR23076:SI Phvul.L00205: not assigned.ã (original description: pacid=37144324 transcript=Phvul.
 PTHR23076:SI Phvul.L00205: not assigned.ã (original description: pacid=37144324 transcript=Phvul.
 PTHR23076:SI Phvul.L00205: not assigned.ã (original description: pacid=37144324 transcript=Phvul.
 PTHR23076:SI Phvul.L00205: not assigned.ã (original description: pacid=37144324 transcript=Phvul.
 PTHR23076:SI Phvul.L00205: not assigned.ã (original description: pacid=37144324 transcript=Phvul.
 PTHR23076:SI Phvul.L00205: not assigned.ã (original description: pacid=37144324 transcript=Phvul.
 PTHR23076:SI Phvul.L00205: not assigned.ã (original description: pacid=37144324 transcript=Phvul.
 PTHR23076:SI Phvul.L00205: not assigned.ã (original description: pacid=37144324 transcript=Phvul.
 PTHR23076:SI Phvul.L00205: not assigned.ã (original description: pacid=37144324 transcript=Phvul.
 K12872 - pre-iPhvul.L00253:RNA processir component MAC5 of non-snRNP MOS4-associated comp
 K12872 - pre-iPhvul.L00253:RNA processir component MAC5 of non-snRNP MOS4-associated comp
 K12872 - pre-iPhvul.L00253:RNA processir component MAC5 of non-snRNP MOS4-associated comp
 PTHR11709//I Phvul.L00734:Cell wall orgar lignin laccase (original description: pacid=37178902 tran
 PTHR11695//I Phvul.008G00Enzyme classii 2-alkenal reductase (NADP(+)-dependent) OS=Nicotiana
 PTHR11695//I Phvul.008G00Enzyme classii 2-alkenal reductase (NADP(+)-dependent) OS=Nicotiana
 KOG0513 - Ca Phvul.001G02Lipid metaboli phospholipase A2 (pPLA2-II) (original description: pacid=
 KOG0513 - Ca Phvul.001G02Lipid metaboli phospholipase A2 (pPLA2-II) (original description: pacid=
 PTHR31471:SI Phvul.001G02 not assigned.r no hits & (original description: pacid=37167696 transcri
 PTHR31471:SI Phvul.001G02 not assigned.r no hits & (original description: pacid=37167696 transcri
 PTHR31471:SI Phvul.001G02 not assigned.r no hits & (original description: pacid=37167696 transcri
 PTHR31471:SI Phvul.001G02 not assigned.r no hits & (original description: pacid=37167696 transcri
 3.2.1.153 - Fr Phvul.001G03Carbohydrate acid beta-fructofuranosidase (CWIN) (original descriptio
 PTHR22166:SI Phvul.001G05Cell cycle orgã ER cisternae formation factor (LUNAPARK) (original desc
 PTHR22166:SI Phvul.001G05Cell cycle orgã ER cisternae formation factor (LUNAPARK) (original desc
 K12446 - L-arã Phvul.001G07Carbohydrate L-arabinose kinase (original description: pacid=37168452
 K12446 - L-arã Phvul.001G07Carbohydrate L-arabinose kinase (original description: pacid=37168452
 K01895 - acet Phvul.001G09Lipid metaboli acetyl-CoA synthetase (original description: pacid=37171
 K01895 - acet Phvul.001G09Lipid metaboli acetyl-CoA synthetase (original description: pacid=37171
 K12580 - CCR¿ Phvul.001G10RNA processir component NOT3/5 of mRNA deadenylation CCR4-NOT (¿
 K12580 - CCR¿ Phvul.001G10RNA processir component NOT3/5 of mRNA deadenylation CCR4-NOT (¿
 K12580 - CCR¿ Phvul.001G10RNA processir component NOT3/5 of mRNA deadenylation CCR4-NOT (¿
 K12580 - CCR¿ Phvul.001G10RNA processir component NOT3/5 of mRNA deadenylation CCR4-NOT (¿
 6.3.1.14 - Dip¿ Phvul.001G11Protein biosyr diphthamide synthetase (DPH6) (original description: pa
 6.3.1.14 - Dip¿ Phvul.001G11Protein biosyr diphthamide synthetase (DPH6) (original description: pa

1
2
3 PTHR22762//IPhvu.001G12 not assigned.ã (original description: pacid=37171176 transcript=Phvu.
4 PTHR22762//IPhvu.001G12 not assigned.ã (original description: pacid=37171176 transcript=Phvu.
5 PTHR23155//IPhvu.001G13 not assigned.ã (original description: pacid=37169278 transcript=Phvu.
6 PTHR23155//IPhvu.001G13 not assigned.ã (original description: pacid=37169278 transcript=Phvu.
7 PTHR23155//IPhvu.001G13 not assigned.ã (original description: pacid=37169278 transcript=Phvu.
8 PTHR23155//IPhvu.001G13 not assigned.ã (original description: pacid=37169278 transcript=Phvu.
9 PTHR23155//IPhvu.001G13 not assigned.ã (original description: pacid=37169278 transcript=Phvu.
10 PTHR23155//IPhvu.001G13 not assigned.ã (original description: pacid=37169278 transcript=Phvu.
11 PTHR23155//IPhvu.001G13 not assigned.ã (original description: pacid=37169278 transcript=Phvu.
12 PTHR23155//IPhvu.001G13 not assigned.ã (original description: pacid=37169278 transcript=Phvu.
13 PTHR23155//IPhvu.001G13 not assigned.ã (original description: pacid=37169278 transcript=Phvu.
14 PTHR23155//IPhvu.001G13 not assigned.ã (original description: pacid=37169278 transcript=Phvu.
15 PTHR23155//IPhvu.001G13 not assigned.ã (original description: pacid=37169278 transcript=Phvu.
16 PTHR31529:SIPhvu.001G15RNA biosynth transcription factor (AS2/LOB) (original description: paci
17 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3
18 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3
19 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3
20 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3
21 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3
22 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3
23 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3
24 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3
25 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3
26 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3
27 PF14379 - MY Phvu.001G16Nutrient uptal transcription factor (PHR1) (original description: pacid=3
28 2.4.1.67 - GalãPhvu.001G21Carbohydrate stachyose synthase (original description: pacid=3717114
29 2.4.1.67 - GalãPhvu.001G21Carbohydrate stachyose synthase (original description: pacid=3717114
30 PTHR23115:SIPhvu.001G22Protein biosyr IF-2 translation initiation factor (original description: pac
31 PTHR23115:SIPhvu.001G22Protein biosyr IF-2 translation initiation factor (original description: pac
32 PTHR23115:SIPhvu.001G22Protein biosyr IF-2 translation initiation factor (original description: pac
33 PTHR23115:SIPhvu.001G22Protein biosyr IF-2 translation initiation factor (original description: pac
34 PTHR23115:SIPhvu.001G22Protein biosyr IF-2 translation initiation factor (original description: pac
35 PTHR23083//IPhvu.002G01 not assigned.ã (original description: pacid=37176692 transcript=Phvu.
36 PTHR23083//IPhvu.002G01 not assigned.ã (original description: pacid=37176692 transcript=Phvu.
37 PTHR23083//IPhvu.002G01 not assigned.ã (original description: pacid=37176692 transcript=Phvu.
38 PTHR23083//IPhvu.002G01 not assigned.ã (original description: pacid=37176692 transcript=Phvu.
39 PF01535//PF1Phvu.002G04RNA processir RNA editing factor (YS1) (original description: pacid=371
40 PF01535//PF1Phvu.002G04RNA processir RNA editing factor (YS1) (original description: pacid=371
41 PF01535//PF1Phvu.002G04RNA processir RNA editing factor (YS1) (original description: pacid=371
42 PF01535//PF1Phvu.002G04RNA processir RNA editing factor (YS1) (original description: pacid=371
43 PF01535//PF1Phvu.002G04RNA processir RNA editing factor (YS1) (original description: pacid=371
44 PF01535//PF1Phvu.002G04RNA processir RNA editing factor (YS1) (original description: pacid=371
45 PF01535//PF1Phvu.002G04RNA processir RNA editing factor (YS1) (original description: pacid=371
46 PF13912 - C2I Phvu.002G05RNA biosynth C2H2 zinc finger transcription factor (original descriptio
47 PF13912 - C2I Phvu.002G05RNA biosynth C2H2 zinc finger transcription factor (original descriptio
48 PTHR31867:SIPhvu.002G15Cell wall orgar alpha-class expansin (original description: pacid=371767
49 PTHR31867:SIPhvu.002G15Cell wall orgar alpha-class expansin (original description: pacid=371767
50 PTHR31867:SIPhvu.002G15Cell wall orgar alpha-class expansin (original description: pacid=371767
51 PTHR31867:SIPhvu.002G15Cell wall orgar alpha-class expansin (original description: pacid=371767
52 PTHR31867:SIPhvu.002G15Cell wall orgar alpha-class expansin (original description: pacid=371767
53 PTHR31867:SIPhvu.002G15Cell wall orgar alpha-class expansin (original description: pacid=371767
54 1.1.1.133 - dT Phvu.002G15Carbohydrate UDP-L-rhamnose synthase (original description: pacid=3
55 PTHR22835//IPhvu.002G24 not assigned.ã (original description: pacid=37176697 transcript=Phvu.
56 PTHR22835//IPhvu.002G24 not assigned.ã (original description: pacid=37176697 transcript=Phvu.
57 PTHR22835//IPhvu.002G24 not assigned.ã (original description: pacid=37176697 transcript=Phvu.
58 PTHR22835//IPhvu.002G24 not assigned.ã (original description: pacid=37176697 transcript=Phvu.
59 PTHR22835//IPhvu.002G24 not assigned.ã (original description: pacid=37176697 transcript=Phvu.
60

1
2
3 PTHR22835//IPhvu.002G24not assigned.ã (original description: pacid=37176697 transcript=Phvu.
4 PTHR22870:SIPhvu.002G25not assigned.ã (original description: pacid=37177422 transcript=Phvu.
5 PTHR22870:SIPhvu.002G25not assigned.ã (original description: pacid=37177422 transcript=Phvu.
6 PTHR23315:SIPhvu.002G26Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (origi
7 PTHR11514:SIPhvu.002G29RNA biosynthetranscription factor (bHLH) (original description: pacid=3
8 PTHR11514:SIPhvu.002G29RNA biosynthetranscription factor (bHLH) (original description: pacid=3
9 PTHR23315:SIPhvu.003G02not assigned.r no hits & (original description: pacid=37144503 transcri
10 PTHR23315:SIPhvu.003G02not assigned.r no hits & (original description: pacid=37144503 transcri
11 3.2.1.177 - AlçPhvu.003G03Cell wall orgar 1,6-alpha-xylosidase (original description: pacid=371470
12 3.2.1.177 - AlçPhvu.003G03Cell wall orgar 1,6-alpha-xylosidase (original description: pacid=371470
13 3.2.1.177 - AlçPhvu.003G03Cell wall orgar 1,6-alpha-xylosidase (original description: pacid=371470
14 3.2.1.177 - AlçPhvu.003G03Cell wall orgar 1,6-alpha-xylosidase (original description: pacid=371470
15 PTHR31642:SIPhvu.003G05Lipid metabolicalcatalytic protein (CER2) (original description: pacid=3714
16 PTHR31642:SIPhvu.003G05Lipid metabolicalcatalytic protein (CER2) (original description: pacid=3714
17 PTHR31642:SIPhvu.003G05Lipid metabolicalcatalytic protein (CER2) (original description: pacid=3714
18 PTHR31642:SIPhvu.003G05Lipid metabolicalcatalytic protein (CER2) (original description: pacid=3714
19 PTHR10774//IPhvu.003G08not assigned.ã (original description: pacid=37146764 transcript=Phvu.
20 PTHR10774//IPhvu.003G08not assigned.ã (original description: pacid=37146764 transcript=Phvu.
21 K15108 - soluIPhvu.003G10Solute transpcsolute transporter (MTCC) (original description: pacid=3
22 K15108 - soluIPhvu.003G10Solute transpcsolute transporter (MTCC) (original description: pacid=3
23 K15108 - soluIPhvu.003G10Solute transpcsolute transporter (MTCC) (original description: pacid=3
24 K15108 - soluIPhvu.003G10Solute transpcsolute transporter (MTCC) (original description: pacid=3
25 PTHR16166:SIPhvu.003G11not assigned.r no hits & (original description: pacid=37145453 transcri
26 PTHR16166:SIPhvu.003G11not assigned.r no hits & (original description: pacid=37145453 transcri
27 PTHR16166:SIPhvu.003G11not assigned.r no hits & (original description: pacid=37145453 transcri
28 K18789 - xyloçPhvu.003G16Cell wall orgar xylogalacturonan xylosyltransferase (original description
29 K00753 - glyccPhvu.003G29Protein modif alpha-1,3-fucosyltransferase (original description: pacid=
30 K12386 - cystiPhvu.004G05not assigned.ã (original description: pacid=37163777 transcript=Phvu.
31 K02112 - F-tyçPhvu.004G12Photosynthesi subunit beta of peripheral CF1 subcomplex of ATP synth
32 K02112 - F-tyçPhvu.004G12Photosynthesi subunit beta of peripheral CF1 subcomplex of ATP synth
33 K02112 - F-tyçPhvu.004G12Photosynthesi subunit beta of peripheral CF1 subcomplex of ATP synth
34 K02112 - F-tyçPhvu.004G12Photosynthesi subunit beta of peripheral CF1 subcomplex of ATP synth
35 PTHR14445:SIPhvu.004G13not assigned.ã (original description: pacid=37163533 transcript=Phvu.
36 PTHR14445:SIPhvu.004G13not assigned.ã (original description: pacid=37163533 transcript=Phvu.
37 PTHR14445:SIPhvu.004G13not assigned.ã (original description: pacid=37163533 transcript=Phvu.
38 PTHR14445:SIPhvu.004G13not assigned.ã (original description: pacid=37163533 transcript=Phvu.
39 PTHR10438:SIPhvu.004G17Redox homeo atypical thioredoxin (ACHT) (original description: pacid=
40 PTHR10438:SIPhvu.004G17Redox homeo atypical thioredoxin (ACHT) (original description: pacid=
41 PF00651 - BTEPhvu.005G05not assigned.ã (original description: pacid=37154040 transcript=Phvu.
42 PF00651 - BTEPhvu.005G05not assigned.ã (original description: pacid=37154040 transcript=Phvu.
43 PF00954//PFPhvu.005G08Protein modif protein kinase (SD-1) (original description: pacid=371538
44 2.7.1.26 - RibcPhvu.005G09not assigned.ã (original description: pacid=37154603 transcript=Phvu.
45 PTHR31072:SIPhvu.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37
4 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37
5 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37
6 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37
7 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37
8 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37
9 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37
10 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37
11 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37
12 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37
13 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37
14 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37
15 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37
16 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37
17 PTHR31072:SIPhvul.005G09RNA biosynthetranscription factor (TCP) (original description: pacid=37
18 K01530 - phosPhvul.005G10Solute transpP4-type ATPase component ALA of phospholipid flippase
19 K01530 - phosPhvul.005G10Solute transpP4-type ATPase component ALA of phospholipid flippase
20 K01530 - phosPhvul.005G10Solute transpP4-type ATPase component ALA of phospholipid flippase
21 K01530 - phosPhvul.005G10Solute transpP4-type ATPase component ALA of phospholipid flippase
22 K01530 - phosPhvul.005G10Solute transpP4-type ATPase component ALA of phospholipid flippase
23 K01530 - phosPhvul.005G10Solute transpP4-type ATPase component ALA of phospholipid flippase
24 K01530 - phosPhvul.005G10Solute transpP4-type ATPase component ALA of phospholipid flippase
25 PTHR10593//IPhvul.005G13RNA biosynthC2H2 zinc finger transcription factor (original descriptor
26 PTHR10593//IPhvul.005G13RNA biosynthC2H2 zinc finger transcription factor (original descriptor
27 PTHR10593//IPhvul.005G13RNA biosynthC2H2 zinc finger transcription factor (original descriptor
28 PTHR10593//IPhvul.005G13RNA biosynthC2H2 zinc finger transcription factor (original descriptor
29 PTHR10593//IPhvul.005G13RNA biosynthC2H2 zinc finger transcription factor (original descriptor
30 K15918 - D-glPhvul.005G17Photosynthesiglycerate kinase (original description: pacid=37152247 tr
31 K15918 - D-glPhvul.005G17Photosynthesiglycerate kinase (original description: pacid=37152247 tr
32 K15918 - D-glPhvul.005G17Photosynthesiglycerate kinase (original description: pacid=37152247 tr
33 K15918 - D-glPhvul.005G17Photosynthesiglycerate kinase (original description: pacid=37152247 tr
34 K15918 - D-glPhvul.005G17Photosynthesiglycerate kinase (original description: pacid=37152247 tr
35 K15918 - D-glPhvul.005G17Photosynthesiglycerate kinase (original description: pacid=37152247 tr
36 0 Phvul.006G14not assigned.r no hits & (original description: pacid=37171334 transcri
37 0 Phvul.006G14not assigned.r no hits & (original description: pacid=37171334 transcri
38 0 Phvul.006G14not assigned.r no hits & (original description: pacid=37171334 transcri
39 0 Phvul.006G14not assigned.r no hits & (original description: pacid=37171334 transcri
40 0 Phvul.006G14not assigned.r no hits & (original description: pacid=37171334 transcri
41 K16296 - serirPhvul.006G16Protein home-serine carboxypeptidase (original description: pacid=371
42 K16296 - serirPhvul.006G16Protein home-serine carboxypeptidase (original description: pacid=371
43 K10758 - thiolPhvul.007G03Protein modif atypical quiescin sulfhydryl oxidase (QSOX) (original desc
44 K10758 - thiolPhvul.007G03Protein modif atypical quiescin sulfhydryl oxidase (QSOX) (original desc
45 K10758 - thiolPhvul.007G03Protein modif atypical quiescin sulfhydryl oxidase (QSOX) (original desc
46 K10758 - thiolPhvul.007G03Protein modif atypical quiescin sulfhydryl oxidase (QSOX) (original desc
47 K10758 - thiolPhvul.007G03Protein modif atypical quiescin sulfhydryl oxidase (QSOX) (original desc
48 K10758 - thiolPhvul.007G03Protein modif atypical quiescin sulfhydryl oxidase (QSOX) (original desc
49 PF13041 - PPFPhvul.007G06not assigned.a (original description: pacid=37164814 transcript=Phvul.i
50 PF13041 - PPFPhvul.007G06not assigned.a (original description: pacid=37164814 transcript=Phvul.i
51 PF13041 - PPFPhvul.007G06not assigned.a (original description: pacid=37164814 transcript=Phvul.i
52 PF13041 - PPFPhvul.007G06not assigned.a (original description: pacid=37164814 transcript=Phvul.i
53 PF13041 - PPFPhvul.007G06not assigned.a (original description: pacid=37164814 transcript=Phvul.i
54 PF13041 - PPFPhvul.007G06not assigned.a (original description: pacid=37164814 transcript=Phvul.i
55 PF13041 - PPFPhvul.007G06not assigned.a (original description: pacid=37164814 transcript=Phvul.i
56 PF13041 - PPFPhvul.007G06not assigned.a (original description: pacid=37164814 transcript=Phvul.i
57 PF13041 - PPFPhvul.007G06not assigned.a (original description: pacid=37164814 transcript=Phvul.i
58 PF13041 - PPFPhvul.007G06not assigned.a (original description: pacid=37164814 transcript=Phvul.i
59 PF13041 - PPFPhvul.007G06not assigned.a (original description: pacid=37164814 transcript=Phvul.i
60

1
2
3 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.
4 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.
5 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.
6 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.
7 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.
8 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.
9 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.
10 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.
11 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.
12 PF13041 - PPFPhvul.007G06not assigned.ã (original description: pacid=37164814 transcript=Phvul.
13 PF12646 - DorPhvul.007G09not assigned.r no hits & (original description: pacid=37167603 transcri
14 PTHR15856//IPhvul.007G11RNA biosynthePHD finger transcription factor (original description: paci
15 PTHR15856//IPhvul.007G11RNA biosynthePHD finger transcription factor (original description: paci
16 PTHR15856//IPhvul.007G11RNA biosynthePHD finger transcription factor (original description: paci
17 PTHR15856//IPhvul.007G11RNA biosynthePHD finger transcription factor (original description: paci
18 PTHR15856//IPhvul.007G11RNA biosynthePHD finger transcription factor (original description: paci
19 PTHR23257//IPhvul.007G18Protein modif protein kinase (MAP3K-RAF) (original description: pacid=
20 PTHR23257//IPhvul.007G18Protein modif protein kinase (MAP3K-RAF) (original description: pacid=
21 PTHR23315:SIPhvul.007G19not assigned.ã (original description: pacid=37164330 transcript=Phvul.
22 PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165
23 PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165
24 PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165
25 PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165
26 PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165
27 PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165
28 PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165
29 PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165
30 PTHR31707:SIPhvul.007G21Cell wall orgar pectin methylesterase (original description: pacid=37165
31 K10728 - topoPhvul.007G21Cell cycle orgacell cycle replicated DNA checkpoint protein (TopBP1) (o
32 K10728 - topoPhvul.007G21Cell cycle orgacell cycle replicated DNA checkpoint protein (TopBP1) (o
33 K10728 - topoPhvul.007G21Cell cycle orgacell cycle replicated DNA checkpoint protein (TopBP1) (o
34 K10728 - topoPhvul.007G21Cell cycle orgacell cycle replicated DNA checkpoint protein (TopBP1) (o
35 PTHR22912:SIPhvul.007G25Redox homeo NADPH-dependent thioredoxin reductase (original descr
36 PTHR27004:SIPhvul.008G04not assigned.ã (original description: pacid=37160665 transcript=Phvul.
37 PTHR27004:SIPhvul.008G04not assigned.ã (original description: pacid=37160665 transcript=Phvul.
38 PTHR10641//IPhvul.008G06RNA biosynthe transcription factor (MYB) (original description: pacid=37
39 PTHR10641//IPhvul.008G06RNA biosynthe transcription factor (MYB) (original description: pacid=37
40 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37159657 transcri
41 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37159657 transcri
42 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37159657 transcri
43 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37159657 transcri
44 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37161406 transcri
45 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37161406 transcri
46 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37161406 transcri
47 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37161406 transcri
48 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37161406 transcri
49 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37161406 transcri
50 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37161406 transcri
51 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37161406 transcri
52 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37161406 transcri
53 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37161406 transcri
54 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37161406 transcri
55 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37160139 transcri
56 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37160139 transcri
57 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37160139 transcri
58 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37160139 transcri
59 PTHR33103:SIPhvul.008G11not assigned.r no hits & (original description: pacid=37160139 transcri
60

1
2
3 PTHR22847//IPhvu.008G12RNA biosynthtranscriptional co-repressor (LUG) (original description: p
4 PTHR22847//IPhvu.008G12RNA biosynthtranscriptional co-repressor (LUG) (original description: p
5 PTHR22847//IPhvu.008G12RNA biosynthtranscriptional co-repressor (LUG) (original description: p
6 PTHR22847//IPhvu.008G12RNA biosynthtranscriptional co-repressor (LUG) (original description: p
7 PTHR10795//IPhvu.008G22Protein home protease (SBT4) (original description: pacid=37158609 tr
8 PTHR13301//IPhvu.008G27not assigned.ε (original description: pacid=37161159 transcript=Phvu.0
9 PTHR13301//IPhvu.008G27not assigned.ε (original description: pacid=37161159 transcript=Phvu.0
10 3.4.17.1 - CarIPhvu.009G01Protein home M14 carboxypeptidase (original description: pacid=3715
11 3.4.17.1 - CarIPhvu.009G01Protein home M14 carboxypeptidase (original description: pacid=3715
12 K08505 - protPhvu.009G03Vesicle trafficlSFT12 group Qc-type SNARE protein (original description
13 PTHR13878:SIPhvu.009G06Phytohormon cytokinin dehydrogenase (original description: pacid=37
14 PTHR13878:SIPhvu.009G06Phytohormon cytokinin dehydrogenase (original description: pacid=37
15 PTHR13878:SIPhvu.009G06Phytohormon cytokinin dehydrogenase (original description: pacid=37
16 PTHR13878:SIPhvu.009G06Phytohormon cytokinin dehydrogenase (original description: pacid=37
17 PTHR13878:SIPhvu.009G06Phytohormon cytokinin dehydrogenase (original description: pacid=37
18 PTHR13878:SIPhvu.009G06Phytohormon cytokinin dehydrogenase (original description: pacid=37
19 PTHR13878:SIPhvu.009G06Phytohormon cytokinin dehydrogenase (original description: pacid=37
20 PTHR13878:SIPhvu.009G06Phytohormon cytokinin dehydrogenase (original description: pacid=37
21 PTHR13878:SIPhvu.009G06Phytohormon cytokinin dehydrogenase (original description: pacid=37
22 PTHR13878:SIPhvu.009G06Phytohormon cytokinin dehydrogenase (original description: pacid=37
23 PTHR13878:SIPhvu.009G06Phytohormon cytokinin dehydrogenase (original description: pacid=37
24 PTHR13878:SIPhvu.009G06Phytohormon cytokinin dehydrogenase (original description: pacid=37
25 PTHR13878:SIPhvu.009G06Phytohormon cytokinin dehydrogenase (original description: pacid=37
26 PTHR23500:SIPhvu.009G11Solute transpmonosaccharide transporter (AZT) (original description:
27 PTHR23500:SIPhvu.009G11Solute transpmonosaccharide transporter (AZT) (original description:
28 0 Phvu.009G15not assigned.ε (original description: pacid=37149132 transcript=Phvu.0
29 0 Phvu.009G15not assigned.ε (original description: pacid=37149132 transcript=Phvu.0
30 0 Phvu.009G15not assigned.ε (original description: pacid=37149132 transcript=Phvu.0
31 0 Phvu.009G15not assigned.ε (original description: pacid=37149132 transcript=Phvu.0
32 PTHR31673:SIPhvu.009G20Cell wall orgar COB cellulose microfibrils and hemicellulose interaction
33 PTHR23421:SIPhvu.009G23Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=37
34 PTHR23421:SIPhvu.009G23Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=37
35 PTHR23421:SIPhvu.009G23Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=37
36 PTHR23421:SIPhvu.009G23Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=37
37 PTHR15371:SIPhvu.009G25not assigned.ε (original description: pacid=37151366 transcript=Phvu.0
38 PTHR15371:SIPhvu.009G25not assigned.ε (original description: pacid=37151366 transcript=Phvu.0
39 PTHR15371:SIPhvu.009G25not assigned.ε (original description: pacid=37151366 transcript=Phvu.0
40 PTHR15371:SIPhvu.009G25not assigned.ε (original description: pacid=37151366 transcript=Phvu.0
41 0 Phvu.010G02not assigned.r no hits & (original description: pacid=37143141 transcri
42 0 Phvu.010G02not assigned.r no hits & (original description: pacid=37143141 transcri
43 0 Phvu.010G02not assigned.r no hits & (original description: pacid=37143141 transcri
44 0 Phvu.010G02not assigned.r no hits & (original description: pacid=37143141 transcri
45 PF00931//PFCPhvu.010G02External stimu effector receptor (NLR) (original description: pacid=3714
46 PF00931//PFCPhvu.010G02External stimu effector receptor (NLR) (original description: pacid=3714
47 PF00931//PFCPhvu.010G02External stimu effector receptor (NLR) (original description: pacid=3714
48 PF00931//PFCPhvu.010G02External stimu effector receptor (NLR) (original description: pacid=3714
49 PTHR13902//IPhvu.010G06Protein modif protein kinase (MAP3K-WNK) (original description: pacid
50 PTHR13902//IPhvu.010G06Protein modif protein kinase (MAP3K-WNK) (original description: pacid
51
52
53
54
55
56
57
58
59
60

1
2
3 PTHR13902//IPhvu.010G06Protein modif protein kinase (MAP3K-WNK) (original description: pacid
4 PTHR13902//IPhvu.010G06Protein modif protein kinase (MAP3K-WNK) (original description: pacid
5 K13335 - peroPhvu.010G08not assigned.ã (original description: pacid=37142487 transcript=Phvu.0
6 K13335 - peroPhvu.010G08not assigned.ã (original description: pacid=37142487 transcript=Phvu.0
7 K13335 - peroPhvu.010G08not assigned.ã (original description: pacid=37142487 transcript=Phvu.0
8 K13335 - peroPhvu.010G08not assigned.ã (original description: pacid=37142487 transcript=Phvu.0
9 K13335 - peroPhvu.010G08not assigned.ã (original description: pacid=37142487 transcript=Phvu.0
10 K13335 - peroPhvu.010G08not assigned.ã (original description: pacid=37142487 transcript=Phvu.0
11 K13335 - peroPhvu.010G08not assigned.ã (original description: pacid=37142487 transcript=Phvu.0
12 K13335 - peroPhvu.010G08not assigned.ã (original description: pacid=37142487 transcript=Phvu.0
13 K13335 - peroPhvu.010G08not assigned.ã (original description: pacid=37142487 transcript=Phvu.0
14 K13335 - peroPhvu.010G08not assigned.ã (original description: pacid=37142487 transcript=Phvu.0
15 K13335 - peroPhvu.010G08not assigned.ã (original description: pacid=37142487 transcript=Phvu.0
16 2.5.1.72 - QuiiPhvu.010G09not assigned.ã (original description: pacid=37143242 transcript=Phvu.0
17 2.5.1.72 - QuiiPhvu.010G09not assigned.ã (original description: pacid=37143242 transcript=Phvu.0
18 2.5.1.72 - QuiiPhvu.010G09not assigned.ã (original description: pacid=37143242 transcript=Phvu.0
19 2.5.1.72 - QuiiPhvu.010G09not assigned.ã (original description: pacid=37143242 transcript=Phvu.0
20 2.5.1.72 - QuiiPhvu.010G09not assigned.ã (original description: pacid=37143242 transcript=Phvu.0
21 PTHR11200:SiPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or
22 PTHR11200:SiPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or
23 PTHR11200:SiPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or
24 PTHR11200:SiPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or
25 PTHR11200:SiPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or
26 PTHR11200:SiPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or
27 PTHR11200:SiPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or
28 PTHR11200:SiPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or
29 PTHR11200:SiPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or
30 PTHR11200:SiPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or
31 PTHR11200:SiPhvu.011G00Multi-process SAC-group-I inositol-polyphosphate 3,5-phosphatase (or
32 5.3.4.1 - ProtePhvu.011G00not assigned.ã (original description: pacid=37156678 transcript=Phvu.0
33 PF05678 - VQ Phvu.011G20External stim WRKY33-activating protein (SIB) (original description: pa
34 PF05678 - VQ Phvu.011G20External stim WRKY33-activating protein (SIB) (original description: pa
35 PF05678 - VQ Phvu.011G20External stim WRKY33-activating protein (SIB) (original description: pa
36 PF05678 - VQ Phvu.011G20External stim WRKY33-activating protein (SIB) (original description: pa
37 PF05678 - VQ Phvu.011G20External stim WRKY33-activating protein (SIB) (original description: pa
38 PTHR10774//IPhvu.L00167not assigned.ã (original description: pacid=37157494 transcript=Phvu.0
39 PTHR10774//IPhvu.L00167not assigned.ã (original description: pacid=37157494 transcript=Phvu.0
40 K12872 - pre-iPhvu.L00253RNA processir component MAC5 of non-snRNP MOS4-associated comp
41 K12872 - pre-iPhvu.L00253RNA processir component MAC5 of non-snRNP MOS4-associated comp
42 PTHR24089:SiPhvu.L00984:Solute transpc solute transporter (MTCC) (original description: pacid=37
43 PTHR24089:SiPhvu.L00984:Solute transpc solute transporter (MTCC) (original description: pacid=37
44 PTHR24089:SiPhvu.L00984:Solute transpc solute transporter (MTCC) (original description: pacid=37
45 PTHR24089:SiPhvu.L00984:Solute transpc solute transporter (MTCC) (original description: pacid=37
46 PTHR24089:SiPhvu.L00984:Solute transpc solute transporter (MTCC) (original description: pacid=37
47 PTHR24089:SiPhvu.L00984:Solute transpc solute transporter (MTCC) (original description: pacid=37
48 PTHR24089:SiPhvu.L00984:Solute transpc solute transporter (MTCC) (original description: pacid=37
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5 average heterodimer (original description: pacid=37176220 transcript=Phvul.002G267400.1 locus=Ph
6 average heterodimer (original description: pacid=37176220 transcript=Phvul.002G267400.1 locus=Ph
7 isation (original description: pacid=37176892 transcript=Phvul.002G071800.1 locus=Phvul.002G071
8 isation (original description: pacid=37176892 transcript=Phvul.002G071800.1 locus=Phvul.002G071
9 isation (original description: pacid=37176892 transcript=Phvul.002G071800.1 locus=Phvul.002G071
10 isation (original description: pacid=37176892 transcript=Phvul.002G071800.1 locus=Phvul.002G071
11 006G201700.1 locus=Phvul.006G201700 ID=Phvul.006G201700.1.v2.1 annot-version=v2.1) & Prote
12 pt=Phvul.009G057800.1 locus=Phvul.009G057800 ID=Phvul.009G057800.1.v2.1 annot-version=v2.1
13 pt=Phvul.009G057800.1 locus=Phvul.009G057800 ID=Phvul.009G057800.1.v2.1 annot-version=v2.1
14 009G086800.1 locus=Phvul.009G086800 ID=Phvul.009G086800.1.v2.1 annot-version=v2.1) & Trans
15 L42908 transcript=Phvul.010G116400.1 locus=Phvul.010G116400 ID=Phvul.010G116400.1.v2.1 ann
16 L42908 transcript=Phvul.010G116400.1 locus=Phvul.010G116400 ID=Phvul.010G116400.1.v2.1 ann
17 L42908 transcript=Phvul.010G116400.1 locus=Phvul.010G116400 ID=Phvul.010G116400.1.v2.1 ann
18 L42908 transcript=Phvul.010G116400.1 locus=Phvul.010G116400 ID=Phvul.010G116400.1.v2.1 ann
19 178944 transcript=Phvul.L009543.1 locus=Phvul.L009543 ID=Phvul.L009543.1.v2.1 annot-version=v
20 178944 transcript=Phvul.L009543.1 locus=Phvul.L009543 ID=Phvul.L009543.1.v2.1 annot-version=v
21 178944 transcript=Phvul.L009543.1 locus=Phvul.L009543 ID=Phvul.L009543.1.v2.1 annot-version=v
22 178944 transcript=Phvul.L009543.1 locus=Phvul.L009543 ID=Phvul.L009543.1.v2.1 annot-version=v
23 pacid=37170135 transcript=Phvul.001G077200.2 locus=Phvul.001G077200 ID=Phvul.001G077200.2
24 pacid=37170135 transcript=Phvul.001G077200.2 locus=Phvul.001G077200 ID=Phvul.001G077200.2
25 pacid=37170135 transcript=Phvul.001G077200.2 locus=Phvul.001G077200 ID=Phvul.001G077200.2
26 pacid=37170135 transcript=Phvul.001G077200.2 locus=Phvul.001G077200 ID=Phvul.001G077200.2
27 i4 transcript=Phvul.001G215300.2 locus=Phvul.001G215300 ID=Phvul.001G215300.2.v2.1 annot-vei
28 i4 transcript=Phvul.001G215300.2 locus=Phvul.001G215300 ID=Phvul.001G215300.2.v2.1 annot-vei
29 i4 transcript=Phvul.001G215300.2 locus=Phvul.001G215300 ID=Phvul.001G215300.2.v2.1 annot-vei
30 i4 transcript=Phvul.001G215300.2 locus=Phvul.001G215300 ID=Phvul.001G215300.2.v2.1 annot-vei
31 average heterodimer (original description: pacid=37176220 transcript=Phvul.002G267400.1 locus=Ph
32 average heterodimer (original description: pacid=37176220 transcript=Phvul.002G267400.1 locus=Ph
33 average heterodimer (original description: pacid=37176220 transcript=Phvul.002G267400.1 locus=Ph
34 average heterodimer (original description: pacid=37176220 transcript=Phvul.002G267400.1 locus=Ph
35 7175022 transcript=Phvul.002G281100.1 locus=Phvul.002G281100 ID=Phvul.002G281100.1.v2.1 an
36 7175022 transcript=Phvul.002G281100.1 locus=Phvul.002G281100 ID=Phvul.002G281100.1.v2.1 an
37 7175022 transcript=Phvul.002G281100.1 locus=Phvul.002G281100 ID=Phvul.002G281100.1.v2.1 an
38 7175022 transcript=Phvul.002G281100.1 locus=Phvul.002G281100 ID=Phvul.002G281100.1.v2.1 an
39 004G044900.1 locus=Phvul.004G044900 ID=Phvul.004G044900.1.v2.1 annot-version=v2.1) & Recep
40 pt=Phvul.006G158900.1 locus=Phvul.006G158900 ID=Phvul.006G158900.1.v2.1 annot-version=v2.1
41 pt=Phvul.008G071966.1 locus=Phvul.008G071966 ID=Phvul.008G071966.1.v2.1 annot-version=v2.1
42 pt=Phvul.008G071966.1 locus=Phvul.008G071966 ID=Phvul.008G071966.1.v2.1 annot-version=v2.1
43 pt=Phvul.008G071966.1 locus=Phvul.008G071966 ID=Phvul.008G071966.1.v2.1 annot-version=v2.1
44 pt=Phvul.008G071966.1 locus=Phvul.008G071966 ID=Phvul.008G071966.1.v2.1 annot-version=v2.1
45 pt=Phvul.008G110200.1 locus=Phvul.008G110200 ID=Phvul.008G110200.1.v2.1 annot-version=v2.1
46 pt=Phvul.008G110500.1 locus=Phvul.008G110500 ID=Phvul.008G110500.1.v2.1 annot-version=v2.1
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3 l=37174973 transcript=Phvul.002G304500.1 locus=Phvul.002G304500 ID=Phvul.002G304500.1.v2.1
4 pt=Phvul.003G103100.2 locus=Phvul.003G103100 ID=Phvul.003G103100.2.v2.1 annot-version=v2.1
5 pt=Phvul.003G103100.2 locus=Phvul.003G103100 ID=Phvul.003G103100.2.v2.1 annot-version=v2.1
6 004G044800.1 locus=Phvul.004G044800 ID=Phvul.004G044800.1.v2.1 annot-version=v2.1) & Recep
7 004G106000.1 locus=Phvul.004G106000 ID=Phvul.004G106000.1.v2.1 annot-version=v2.1) & Penta
8 description: pacid=37162620 transcript=Phvul.004G133400.1 locus=Phvul.004G133400 ID=Phvul.00
9 description: pacid=37162620 transcript=Phvul.004G133400.1 locus=Phvul.004G133400 ID=Phvul.00
10 37162268 transcript=Phvul.004G176700.1 locus=Phvul.004G176700 ID=Phvul.004G176700.1.v2.1 a
11 37162268 transcript=Phvul.004G176700.1 locus=Phvul.004G176700 ID=Phvul.004G176700.1.v2.1 a
12 37162268 transcript=Phvul.004G176700.1 locus=Phvul.004G176700 ID=Phvul.004G176700.1.v2.1 a
13 37162268 transcript=Phvul.004G176700.1 locus=Phvul.004G176700 ID=Phvul.004G176700.1.v2.1 a
14 pt=Phvul.005G087300.1 locus=Phvul.005G087300 ID=Phvul.005G087300.1.v2.1 annot-version=v2.1
15 pt=Phvul.005G116100.2 locus=Phvul.005G116100 ID=Phvul.005G116100.2.v2.1 annot-version=v2.1
16 pt=Phvul.005G116100.2 locus=Phvul.005G116100 ID=Phvul.005G116100.2.v2.1 annot-version=v2.1
17 pt=Phvul.005G116100.2 locus=Phvul.005G116100 ID=Phvul.005G116100.2.v2.1 annot-version=v2.1
18 pt=Phvul.005G116100.2 locus=Phvul.005G116100 ID=Phvul.005G116100.2.v2.1 annot-version=v2.1
19 iption co-activator complex (original description: pacid=37153200 transcript=Phvul.005G180200.1 l
20 iption co-activator complex (original description: pacid=37153200 transcript=Phvul.005G180200.1 l
21 /clinging complex (original description: pacid=37172334 transcript=Phvul.006G019800.1 locus=Phvul.0
22 /clinging complex (original description: pacid=37172334 transcript=Phvul.006G019800.1 locus=Phvul.0
23 /clinging complex (original description: pacid=37172334 transcript=Phvul.006G019800.1 locus=Phvul.0
24 /clinging complex (original description: pacid=37172334 transcript=Phvul.006G019800.1 locus=Phvul.0
25 :37172897 transcript=Phvul.006G067700.1 locus=Phvul.006G067700 ID=Phvul.006G067700.1.v2.1 ;
26 :37172897 transcript=Phvul.006G067700.1 locus=Phvul.006G067700 ID=Phvul.006G067700.1.v2.1 ;
27 :37172897 transcript=Phvul.006G067700.1 locus=Phvul.006G067700 ID=Phvul.006G067700.1.v2.1 ;
28 :37172897 transcript=Phvul.006G067700.1 locus=Phvul.006G067700 ID=Phvul.006G067700.1.v2.1 ;
29 pt=Phvul.006G106900.2 locus=Phvul.006G106900 ID=Phvul.006G106900.2.v2.1 annot-version=v2.1
30 pt=Phvul.006G106900.2 locus=Phvul.006G106900 ID=Phvul.006G106900.2.v2.1 annot-version=v2.1
31 pt=Phvul.006G137200.3 locus=Phvul.006G137200 ID=Phvul.006G137200.3.v2.1 annot-version=v2.1
32 pt=Phvul.006G137200.3 locus=Phvul.006G137200 ID=Phvul.006G137200.3.v2.1 annot-version=v2.1
33 d=37167252 transcript=Phvul.007G113800.1 locus=Phvul.007G113800 ID=Phvul.007G113800.1.v2.:
34 d=37167252 transcript=Phvul.007G113800.1 locus=Phvul.007G113800 ID=Phvul.007G113800.1.v2.:
35 sp|q949z1|pplr4_arath : 540.0) & Enzyme classification.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2
36 sp|q949z1|pplr4_arath : 540.0) & Enzyme classification.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2
37 pt=Phvul.007G219400.1 locus=Phvul.007G219400 ID=Phvul.007G219400.1.v2.1 annot-version=v2.1
38 pt=Phvul.007G219400.1 locus=Phvul.007G219400 ID=Phvul.007G219400.1.v2.1 annot-version=v2.1
39 pt=Phvul.008G071966.1 locus=Phvul.008G071966 ID=Phvul.008G071966.1.v2.1 annot-version=v2.1
40 pt=Phvul.008G071966.1 locus=Phvul.008G071966 ID=Phvul.008G071966.1.v2.1 annot-version=v2.1
41 pt=Phvul.008G107300.1 locus=Phvul.008G107300 ID=Phvul.008G107300.1.v2.1 annot-version=v2.1
42 pt=Phvul.008G107300.1 locus=Phvul.008G107300 ID=Phvul.008G107300.1.v2.1 annot-version=v2.1
43 oreductase acting on CH-OH group of donor(50.1.1 : 403.8) & Tropinone reductase homolog OS=Da
44 oreductase acting on CH-OH group of donor(50.1.1 : 403.8) & Tropinone reductase homolog OS=Da
45 008G257700.2 locus=Phvul.008G257700 ID=Phvul.008G257700.2.v2.1 annot-version=v2.1) & Cinna
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3 008G257700.2 locus=Phvul.008G257700 ID=Phvul.008G257700.2.v2.1 annot-version=v2.1) & Cinna
4 008G257700.2 locus=Phvul.008G257700 ID=Phvul.008G257700.2.v2.1 annot-version=v2.1) & Cinna
5 008G257700.2 locus=Phvul.008G257700 ID=Phvul.008G257700.2.v2.1 annot-version=v2.1) & Cinna
6 original description: pacid=37157587 transcript=Phvul.008G282700.1 locus=Phvul.008G282700 ID=P
7 008G289600.1 locus=Phvul.008G289600 ID=Phvul.008G289600.1.v2.1 annot-version=v2.1) & Trans
8 inal description: pacid=37151972 transcript=Phvul.009G127300.1 locus=Phvul.009G127300 ID=Phv
9 inal description: pacid=37151972 transcript=Phvul.009G127300.1 locus=Phvul.009G127300 ID=Phv
10 inal description: pacid=37151972 transcript=Phvul.009G127300.1 locus=Phvul.009G127300 ID=Phv
11 inal description: pacid=37151972 transcript=Phvul.009G127300.1 locus=Phvul.009G127300 ID=Phv
12 inal description: pacid=37151972 transcript=Phvul.009G127300.1 locus=Phvul.009G127300 ID=Phv
13 inal description: pacid=37151972 transcript=Phvul.009G127300.1 locus=Phvul.009G127300 ID=Phv
14 inal description: pacid=37151972 transcript=Phvul.009G127300.1 locus=Phvul.009G127300 ID=Phv
15 7151643 transcript=Phvul.009G160700.1 locus=Phvul.009G160700 ID=Phvul.009G160700.1.v2.1 an
16 7151643 transcript=Phvul.009G160700.1 locus=Phvul.009G160700 ID=Phvul.009G160700.1.v2.1 an
17 7151643 transcript=Phvul.009G160700.1 locus=Phvul.009G160700 ID=Phvul.009G160700.1.v2.1 an
18 7151643 transcript=Phvul.009G160700.1 locus=Phvul.009G160700 ID=Phvul.009G160700.1.v2.1 an
19 7151643 transcript=Phvul.009G160700.1 locus=Phvul.009G160700 ID=Phvul.009G160700.1.v2.1 an
20 010G064700.1 locus=Phvul.010G064700 ID=Phvul.010G064700.1.v2.1 annot-version=v2.1) & Putat
21 010G064700.1 locus=Phvul.010G064700 ID=Phvul.010G064700.1.v2.1 annot-version=v2.1) & Putat
22 010G064700.1 locus=Phvul.010G064700 ID=Phvul.010G064700.1.v2.1 annot-version=v2.1) & Putat
23 010G064700.1 locus=Phvul.010G064700 ID=Phvul.010G064700.1.v2.1 annot-version=v2.1) & Putat
24 010G064700.1 locus=Phvul.010G064700 ID=Phvul.010G064700.1.v2.1 annot-version=v2.1) & Putat
25 pt=Phvul.011G047100.1 locus=Phvul.011G047100 ID=Phvul.011G047100.1.v2.1 annot-version=v2.1
26 pt=Phvul.011G047100.1 locus=Phvul.011G047100 ID=Phvul.011G047100.1.v2.1 annot-version=v2.1
27 pt=Phvul.011G047100.1 locus=Phvul.011G047100 ID=Phvul.011G047100.1.v2.1 annot-version=v2.1
28 340 transcript=Phvul.011G050300.2 locus=Phvul.011G050300 ID=Phvul.011G050300.2.v2.1 annot-v
29 340 transcript=Phvul.011G050300.2 locus=Phvul.011G050300 ID=Phvul.011G050300.2.v2.1 annot-v
30 340 transcript=Phvul.011G050300.2 locus=Phvul.011G050300 ID=Phvul.011G050300.2.v2.1 annot-v
31 340 transcript=Phvul.011G050300.2 locus=Phvul.011G050300 ID=Phvul.011G050300.2.v2.1 annot-v
32 340 transcript=Phvul.011G050300.2 locus=Phvul.011G050300 ID=Phvul.011G050300.2.v2.1 annot-v
33 iscript=Phvul.L007343.1 locus=Phvul.L007343 ID=Phvul.L007343.1.v2.1 annot-version=v2.1) &
34 iscript=Phvul.L007343.1 locus=Phvul.L007343 ID=Phvul.L007343.1.v2.1 annot-version=v2.1) &
35 pt=Phvul.001G022700.1 locus=Phvul.001G022700 ID=Phvul.001G022700.1.v2.1 annot-version=v2.1
36 pt=Phvul.001G022700.1 locus=Phvul.001G022700 ID=Phvul.001G022700.1.v2.1 annot-version=v2.1
37 n: pacid=37171142 transcript=Phvul.001G036800.1 locus=Phvul.001G036800 ID=Phvul.001G036800
38 bonucleoprotein particle (snRNP) (original description: pacid=37171024 transcript=Phvul.001G1007
39 bonucleoprotein particle (snRNP) (original description: pacid=37171024 transcript=Phvul.001G1007
40 pt=Phvul.001G153600.2 locus=Phvul.001G153600 ID=Phvul.001G153600.2.v2.1 annot-version=v2.1
41 pt=Phvul.001G153600.2 locus=Phvul.001G153600 ID=Phvul.001G153600.2.v2.1 annot-version=v2.1
42 pt=Phvul.001G153600.2 locus=Phvul.001G153600 ID=Phvul.001G153600.2.v2.1 annot-version=v2.1
43 pt=Phvul.001G153600.2 locus=Phvul.001G153600 ID=Phvul.001G153600.2.v2.1 annot-version=v2.1
44 ption: pacid=37170160 transcript=Phvul.001G247000.1 locus=Phvul.001G247000 ID=Phvul.001G24
45 75333 transcript=Phvul.002G004100.1 locus=Phvul.002G004100 ID=Phvul.002G004100.1.v2.1 ann
46 002G013866.1 locus=Phvul.002G013866 ID=Phvul.002G013866.1.v2.1 annot-version=v2.1) & Suppi
47 002G013866.1 locus=Phvul.002G013866 ID=Phvul.002G013866.1.v2.1 annot-version=v2.1) & Suppi
48 pt=Phvul.002G212900.1 locus=Phvul.002G212900 ID=Phvul.002G212900.1.v2.1 annot-version=v2.1
49 002G253200.1 locus=Phvul.002G253200 ID=Phvul.002G253200.1.v2.1 annot-version=v2.1) & Ultra
50 002G253200.1 locus=Phvul.002G253200 ID=Phvul.002G253200.1.v2.1 annot-version=v2.1) & Ultra
51 original description: pacid=37147648 transcript=Phvul.003G029000.2 locus=Phvul.003G029000 ID=
52 original description: pacid=37147648 transcript=Phvul.003G029000.2 locus=Phvul.003G029000 ID=
53
54
55
56
57
58
59
60

1
2
3 =37147433 transcript=Phvul.003G087600.2 locus=Phvul.003G087600 ID=Phvul.003G087600.2.v2.1
4 =37147433 transcript=Phvul.003G087600.2 locus=Phvul.003G087600 ID=Phvul.003G087600.2.v2.1
5 =37147433 transcript=Phvul.003G087600.2 locus=Phvul.003G087600 ID=Phvul.003G087600.2.v2.1
6 =37147433 transcript=Phvul.003G087600.2 locus=Phvul.003G087600 ID=Phvul.003G087600.2.v2.1
7 =37147433 transcript=Phvul.003G087600.2 locus=Phvul.003G087600 ID=Phvul.003G087600.2.v2.1
8 =37147433 transcript=Phvul.003G087600.2 locus=Phvul.003G087600 ID=Phvul.003G087600.2.v2.1
9 =37147433 transcript=Phvul.003G087600.2 locus=Phvul.003G087600 ID=Phvul.003G087600.2.v2.1
10 =37147433 transcript=Phvul.003G087600.2 locus=Phvul.003G087600 ID=Phvul.003G087600.2.v2.1
11 =37147433 transcript=Phvul.003G087600.2 locus=Phvul.003G087600 ID=Phvul.003G087600.2.v2.1
12 =37147433 transcript=Phvul.003G087600.2 locus=Phvul.003G087600 ID=Phvul.003G087600.2.v2.1
13 =37147433 transcript=Phvul.003G087600.2 locus=Phvul.003G087600 ID=Phvul.003G087600.2.v2.1
14 7147137 transcript=Phvul.003G104200.1 locus=Phvul.003G104200 ID=Phvul.003G104200.1.v2.1 an
15 7147137 transcript=Phvul.003G104200.1 locus=Phvul.003G104200 ID=Phvul.003G104200.1.v2.1 an
16 ription: pacid=37147484 transcript=Phvul.003G141700.1 locus=Phvul.003G141700 ID=Phvul.003G1
17 ription: pacid=37147484 transcript=Phvul.003G141700.1 locus=Phvul.003G141700 ID=Phvul.003G1
18 limer (original description: pacid=37147450 transcript=Phvul.003G231500.1 locus=Phvul.003G2315
19 limer (original description: pacid=37147450 transcript=Phvul.003G231500.1 locus=Phvul.003G2315
20 limer (original description: pacid=37147450 transcript=Phvul.003G231500.1 locus=Phvul.003G2315
21 limer (original description: pacid=37147450 transcript=Phvul.003G231500.1 locus=Phvul.003G2315
22 003G294601.1 locus=Phvul.003G294601 ID=Phvul.003G294601.1.v2.1 annot-version=v2.1) & Polya
23 scription: pacid=37145147 transcript=Phvul.003G294800.4 locus=Phvul.003G294800 ID=Phvul.003G
24 scription: pacid=37145147 transcript=Phvul.003G294800.4 locus=Phvul.003G294800 ID=Phvul.003G
25 pt=Phvul.004G015500.1 locus=Phvul.004G015500 ID=Phvul.004G015500.1.v2.1 annot-version=v2.1
26 pt=Phvul.004G015500.1 locus=Phvul.004G015500 ID=Phvul.004G015500.1.v2.1 annot-version=v2.1
27 pt=Phvul.004G015500.1 locus=Phvul.004G015500 ID=Phvul.004G015500.1.v2.1 annot-version=v2.1
28 pt=Phvul.004G015500.1 locus=Phvul.004G015500 ID=Phvul.004G015500.1.v2.1 annot-version=v2.1
29 pt=Phvul.004G032100.1 locus=Phvul.004G032100 ID=Phvul.004G032100.1.v2.1 annot-version=v2.1
30 004G044900.1 locus=Phvul.004G044900 ID=Phvul.004G044900.1.v2.1 annot-version=v2.1) & Rece
31 004G044900.1 locus=Phvul.004G044900 ID=Phvul.004G044900.1.v2.1 annot-version=v2.1) & Rece
32 17162349 transcript=Phvul.004G163200.1 locus=Phvul.004G163200 ID=Phvul.004G163200.1.v2.1 ar
33 tyltransferase complex (original description: pacid=37154558 transcript=Phvul.005G010700.2 locus
34 :a (sp|q0ds59|c14b2_orysj : 99.8) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoredu
35 :a (sp|q0ds59|c14b2_orysj : 99.8) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoredu
36 :a (sp|q0ds59|c14b2_orysj : 99.8) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoredu
37 :a (sp|q0ds59|c14b2_orysj : 99.8) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoredu
38 :a (sp|q0ds59|c14b2_orysj : 99.8) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoredu
39 :a (sp|q0ds59|c14b2_orysj : 99.8) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoredu
40 :a (sp|q0ds59|c14b2_orysj : 99.8) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoredu
41 :a (sp|q0ds59|c14b2_orysj : 99.8) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoredu
42 :a (sp|q0ds59|c14b2_orysj : 99.8) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoredu
43 :a (sp|q0ds59|c14b2_orysj : 99.8) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoredu
44 :a (sp|q0ds59|c14b2_orysj : 99.8) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoredu
45 :a (sp|q0ds59|c14b2_orysj : 99.8) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoredu
46 :a (sp|q0ds59|c14b2_orysj : 99.8) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoredu
47 :a (sp|q0ds59|c14b2_orysj : 99.8) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoredu
48 :a (sp|q0ds59|c14b2_orysj : 99.8) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoredu
49 :a (sp|q0ds59|c14b2_orysj : 99.8) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoredu
50 :a (sp|q0ds59|c14b2_orysj : 99.8) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoredu
51 :ription: pacid=37152284 transcript=Phvul.005G081600.1 locus=Phvul.005G081600 ID=Phvul.005G
52 :ription: pacid=37152284 transcript=Phvul.005G081600.1 locus=Phvul.005G081600 ID=Phvul.005G
53 152450 transcript=Phvul.005G097200.6 locus=Phvul.005G097200 ID=Phvul.005G097200.6.v2.1 anr
54 152450 transcript=Phvul.005G097200.6 locus=Phvul.005G097200 ID=Phvul.005G097200.6.v2.1 anr
55 152450 transcript=Phvul.005G097200.6 locus=Phvul.005G097200 ID=Phvul.005G097200.6.v2.1 anr
56 152450 transcript=Phvul.005G097200.6 locus=Phvul.005G097200 ID=Phvul.005G097200.6.v2.1 anr
57 152450 transcript=Phvul.005G097200.6 locus=Phvul.005G097200 ID=Phvul.005G097200.6.v2.1 anr
58 152450 transcript=Phvul.005G097200.6 locus=Phvul.005G097200 ID=Phvul.005G097200.6.v2.1 anr
59 152450 transcript=Phvul.005G097200.6 locus=Phvul.005G097200 ID=Phvul.005G097200.6.v2.1 anr
60

1
2
3 152450 transcript=Phvul.005G097200.6 locus=Phvul.005G097200 ID=Phvul.005G097200.6.v2.1 anr
4 pt=Phvul.006G062000.1 locus=Phvul.006G062000 ID=Phvul.006G062000.1.v2.1 annot-version=v2.1
5 pt=Phvul.006G062000.1 locus=Phvul.006G062000 ID=Phvul.006G062000.1.v2.1 annot-version=v2.1
6 n: pacid=37171400 transcript=Phvul.006G130611.1 locus=Phvul.006G130611 ID=Phvul.006G13061
7 n: pacid=37171400 transcript=Phvul.006G130611.1 locus=Phvul.006G130611 ID=Phvul.006G13061
8 pt=Phvul.006G192200.4 locus=Phvul.006G192200 ID=Phvul.006G192200.4.v2.1 annot-version=v2.1
9 pt=Phvul.006G192200.4 locus=Phvul.006G192200 ID=Phvul.006G192200.4.v2.1 annot-version=v2.1
10 pt=Phvul.006G192200.4 locus=Phvul.006G192200 ID=Phvul.006G192200.4.v2.1 annot-version=v2.1
11 pt=Phvul.006G192200.4 locus=Phvul.006G192200 ID=Phvul.006G192200.4.v2.1 annot-version=v2.1
12 pt=Phvul.006G192200.4 locus=Phvul.006G192200 ID=Phvul.006G192200.4.v2.1 annot-version=v2.1
13 pt=Phvul.006G192200.4 locus=Phvul.006G192200 ID=Phvul.006G192200.4.v2.1 annot-version=v2.1
14 d=37166015 transcript=Phvul.007G058400.2 locus=Phvul.007G058400 ID=Phvul.007G058400.2.v2.:
15 d=37166015 transcript=Phvul.007G058400.2 locus=Phvul.007G058400 ID=Phvul.007G058400.2.v2.:
16 007G064700.1 locus=Phvul.007G064700 ID=Phvul.007G064700.1.v2.1 annot-version=v2.1) & Carbc
17 007G064700.1 locus=Phvul.007G064700 ID=Phvul.007G064700.1.v2.1 annot-version=v2.1) & Carbc
18 pt=Phvul.007G182300.2 locus=Phvul.007G182300 ID=Phvul.007G182300.2.v2.1 annot-version=v2.1
19 pt=Phvul.007G198500.1 locus=Phvul.007G198500 ID=Phvul.007G198500.1.v2.1 annot-version=v2.1
20 pt=Phvul.007G198500.1 locus=Phvul.007G198500 ID=Phvul.007G198500.1.v2.1 annot-version=v2.1
21 original description: pacid=37164911 transcript=Phvul.007G233800.2 locus=Phvul.007G233800 ID=Ph
22 iginal description: pacid=37164911 transcript=Phvul.007G233800.2 locus=Phvul.007G233800 ID=Ph
23 iginal description: pacid=37164911 transcript=Phvul.007G233800.2 locus=Phvul.007G233800 ID=Ph
24 iginal description: pacid=37164911 transcript=Phvul.007G233800.2 locus=Phvul.007G233800 ID=Ph
25 pt=Phvul.008G008300.6 locus=Phvul.008G008300 ID=Phvul.008G008300.6.v2.1 annot-version=v2.1
26 pt=Phvul.008G008300.6 locus=Phvul.008G008300 ID=Phvul.008G008300.6.v2.1 annot-version=v2.1
27 pt=Phvul.008G008300.6 locus=Phvul.008G008300 ID=Phvul.008G008300.6.v2.1 annot-version=v2.1
28 pt=Phvul.008G008300.6 locus=Phvul.008G008300 ID=Phvul.008G008300.6.v2.1 annot-version=v2.1
29 pt=Phvul.008G008300.6 locus=Phvul.008G008300 ID=Phvul.008G008300.6.v2.1 annot-version=v2.1
30 pt=Phvul.008G008300.6 locus=Phvul.008G008300 ID=Phvul.008G008300.6.v2.1 annot-version=v2.1
31 pt=Phvul.008G008300.6 locus=Phvul.008G008300 ID=Phvul.008G008300.6.v2.1 annot-version=v2.1
32 pt=Phvul.008G008300.6 locus=Phvul.008G008300 ID=Phvul.008G008300.6.v2.1 annot-version=v2.1
33 pt=Phvul.008G008300.6 locus=Phvul.008G008300 ID=Phvul.008G008300.6.v2.1 annot-version=v2.1
34 pt=Phvul.008G008300.6 locus=Phvul.008G008300 ID=Phvul.008G008300.6.v2.1 annot-version=v2.1
35 pt=Phvul.008G008300.6 locus=Phvul.008G008300 ID=Phvul.008G008300.6.v2.1 annot-version=v2.1
36 pt=Phvul.008G008300.6 locus=Phvul.008G008300 ID=Phvul.008G008300.6.v2.1 annot-version=v2.1
37 pt=Phvul.008G008300.6 locus=Phvul.008G008300 ID=Phvul.008G008300.6.v2.1 annot-version=v2.1
38 pt=Phvul.008G008300.6 locus=Phvul.008G008300 ID=Phvul.008G008300.6.v2.1 annot-version=v2.1
39 pt=Phvul.008G008300.6 locus=Phvul.008G008300 ID=Phvul.008G008300.6.v2.1 annot-version=v2.1
40 pt=Phvul.008G008300.6 locus=Phvul.008G008300 ID=Phvul.008G008300.6.v2.1 annot-version=v2.1
41 pt=Phvul.008G008300.6 locus=Phvul.008G008300 ID=Phvul.008G008300.6.v2.1 annot-version=v2.1
42 transcript=Phvul.008G009200.2 locus=Phvul.008G009200 ID=Phvul.008G009200.2.v2.1 annot-versi
43 transcript=Phvul.008G009200.2 locus=Phvul.008G009200 ID=Phvul.008G009200.2.v2.1 annot-versi
44 transcript=Phvul.008G009200.2 locus=Phvul.008G009200 ID=Phvul.008G009200.2.v2.1 annot-versi
45 transcript=Phvul.008G009200.2 locus=Phvul.008G009200 ID=Phvul.008G009200.2.v2.1 annot-versi
46 transcript=Phvul.008G009200.2 locus=Phvul.008G009200 ID=Phvul.008G009200.2.v2.1 annot-versi
47 id=37159912 transcript=Phvul.008G038300.1 locus=Phvul.008G038300 ID=Phvul.008G038300.1.v2.
48 id=37159912 transcript=Phvul.008G038300.1 locus=Phvul.008G038300 ID=Phvul.008G038300.1.v2.
49 57650 transcript=Phvul.008G093200.3 locus=Phvul.008G093200 ID=Phvul.008G093200.3.v2.1 anno
50 57650 transcript=Phvul.008G093200.3 locus=Phvul.008G093200 ID=Phvul.008G093200.3.v2.1 anno
51 57650 transcript=Phvul.008G093200.3 locus=Phvul.008G093200 ID=Phvul.008G093200.3.v2.1 anno
52 57650 transcript=Phvul.008G093200.3 locus=Phvul.008G093200 ID=Phvul.008G093200.3.v2.1 anno
53 57650 transcript=Phvul.008G093200.3 locus=Phvul.008G093200 ID=Phvul.008G093200.3.v2.1 anno
54 57650 transcript=Phvul.008G093200.3 locus=Phvul.008G093200 ID=Phvul.008G093200.3.v2.1 anno
55 57650 transcript=Phvul.008G093200.3 locus=Phvul.008G093200 ID=Phvul.008G093200.3.v2.1 anno
56 57650 transcript=Phvul.008G093200.3 locus=Phvul.008G093200 ID=Phvul.008G093200.3.v2.1 anno
57 57650 transcript=Phvul.008G093200.3 locus=Phvul.008G093200 ID=Phvul.008G093200.3.v2.1 anno
58 57650 transcript=Phvul.008G093200.3 locus=Phvul.008G093200 ID=Phvul.008G093200.3.v2.1 anno
59 7158726 transcript=Phvul.008G108800.2 locus=Phvul.008G108800 ID=Phvul.008G108800.2.v2.1 ar
60

1
2
3 pt=Phvul.001G102901.4 locus=Phvul.001G102901 ID=Phvul.001G102901.4.v2.1 annot-version=v2.1
4 pt=Phvul.001G102901.4 locus=Phvul.001G102901 ID=Phvul.001G102901.4.v2.1 annot-version=v2.1
5 pt=Phvul.001G102901.4 locus=Phvul.001G102901 ID=Phvul.001G102901.4.v2.1 annot-version=v2.1
6 pt=Phvul.001G102901.4 locus=Phvul.001G102901 ID=Phvul.001G102901.4.v2.1 annot-version=v2.1
7 pt=Phvul.001G102901.4 locus=Phvul.001G102901 ID=Phvul.001G102901.4.v2.1 annot-version=v2.1
8 pt=Phvul.001G102901.4 locus=Phvul.001G102901 ID=Phvul.001G102901.4.v2.1 annot-version=v2.1
9 pt=Phvul.001G102901.4 locus=Phvul.001G102901 ID=Phvul.001G102901.4.v2.1 annot-version=v2.1
10 pt=Phvul.001G102901.4 locus=Phvul.001G102901 ID=Phvul.001G102901.4.v2.1 annot-version=v2.1
11 pt=Phvul.001G102901.4 locus=Phvul.001G102901 ID=Phvul.001G102901.4.v2.1 annot-version=v2.1
12
13 description: pacid=37168948 transcript=Phvul.001G147800.2 locus=Phvul.001G147800 ID=Phvul.001G173900.1
14 001G173900.1 locus=Phvul.001G173900 ID=Phvul.001G173900.1.v2.1 annot-version=v2.1) & no de
15 001G173900.1 locus=Phvul.001G173900 ID=Phvul.001G173900.1.v2.1 annot-version=v2.1) & no de
16 001G173900.1 locus=Phvul.001G173900 ID=Phvul.001G173900.1.v2.1 annot-version=v2.1) & no de
17 001G173900.1 locus=Phvul.001G173900 ID=Phvul.001G173900.1.v2.1 annot-version=v2.1) & no de
18 001G173900.1 locus=Phvul.001G173900 ID=Phvul.001G173900.1.v2.1 annot-version=v2.1) & no de
19 pt=Phvul.001G179700.1 locus=Phvul.001G179700 ID=Phvul.001G179700.1.v2.1 annot-version=v2.1
20 pt=Phvul.001G179700.1 locus=Phvul.001G179700 ID=Phvul.001G179700.1.v2.1 annot-version=v2.1
21
22 original description: pacid=37169688 transcript=Phvul.001G200700.5 locus=Phvul.001G200700 ID=Phvul.001G260300.1
23 original description: pacid=37169688 transcript=Phvul.001G200700.5 locus=Phvul.001G200700 ID=Phvul.001G260300.1
24 original description: pacid=37169688 transcript=Phvul.001G200700.5 locus=Phvul.001G200700 ID=Phvul.001G260300.1
25 original description: pacid=37169688 transcript=Phvul.001G200700.5 locus=Phvul.001G200700 ID=Phvul.001G260300.1
26 original description: pacid=37169688 transcript=Phvul.001G200700.5 locus=Phvul.001G200700 ID=Phvul.001G260300.1
27 original description: pacid=37169688 transcript=Phvul.001G200700.5 locus=Phvul.001G200700 ID=Phvul.001G260300.1
28 original description: pacid=37169688 transcript=Phvul.001G200700.5 locus=Phvul.001G200700 ID=Phvul.001G260300.1
29 original description: pacid=37169688 transcript=Phvul.001G200700.5 locus=Phvul.001G200700 ID=Phvul.001G260300.1
30 original description: pacid=37169688 transcript=Phvul.001G200700.5 locus=Phvul.001G200700 ID=Phvul.001G260300.1
31 original description: pacid=37169688 transcript=Phvul.001G200700.5 locus=Phvul.001G200700 ID=Phvul.001G260300.1
32 001G260300.1 locus=Phvul.001G260300 ID=Phvul.001G260300.1.v2.1 annot-version=v2.1) & U-bo
33 aliana (sp|q9t003|asmt_arath : 299.0) & Enzyme classification.EC_2 transferases.EC_2.1 transferases
34 aliana (sp|q9t003|asmt_arath : 299.0) & Enzyme classification.EC_2 transferases.EC_2.1 transferases
35 ar : pacid=37175569 transcript=Phvul.002G058900.1 locus=Phvul.002G058900 ID=Phvul.002G058900.1
36 ar : pacid=37175569 transcript=Phvul.002G058900.1 locus=Phvul.002G058900 ID=Phvul.002G058900.1
37 9 transcript=Phvul.002G068200.1 locus=Phvul.002G068200 ID=Phvul.002G068200.1.v2.1 annot-ver
38 9 transcript=Phvul.002G068200.1 locus=Phvul.002G068200 ID=Phvul.002G068200.1.v2.1 annot-ver
39 9 transcript=Phvul.002G068200.1 locus=Phvul.002G068200 ID=Phvul.002G068200.1.v2.1 annot-ver
40 9 transcript=Phvul.002G068200.1 locus=Phvul.002G068200 ID=Phvul.002G068200.1.v2.1 annot-ver
41 9 transcript=Phvul.002G068200.1 locus=Phvul.002G068200 ID=Phvul.002G068200.1.v2.1 annot-ver
42 9 transcript=Phvul.002G068200.1 locus=Phvul.002G068200 ID=Phvul.002G068200.1.v2.1 annot-ver
43 37176681 transcript=Phvul.002G163400.1 locus=Phvul.002G163400 ID=Phvul.002G163400.1.v2.1 a
44 37176681 transcript=Phvul.002G163400.1 locus=Phvul.002G163400 ID=Phvul.002G163400.1.v2.1 a
45 on (original description: pacid=37174412 transcript=Phvul.002G165300.1 locus=Phvul.002G165300
46 on (original description: pacid=37174412 transcript=Phvul.002G165300.1 locus=Phvul.002G165300
47 on (original description: pacid=37174412 transcript=Phvul.002G165300.1 locus=Phvul.002G165300
48 on (original description: pacid=37174412 transcript=Phvul.002G165300.1 locus=Phvul.002G165300
49 on (original description: pacid=37174412 transcript=Phvul.002G165300.1 locus=Phvul.002G165300
50 on (original description: pacid=37174412 transcript=Phvul.002G165300.1 locus=Phvul.002G165300
51 on (original description: pacid=37174412 transcript=Phvul.002G165300.1 locus=Phvul.002G165300
52 on (original description: pacid=37175361 transcript=Phvul.002G216700.3 locus=Phvul.002G216700 ID=Phvul.002G2
53 on (original description: pacid=37175361 transcript=Phvul.002G216700.3 locus=Phvul.002G216700 ID=Phvul.002G2
54 on (original description: pacid=37175361 transcript=Phvul.002G216700.3 locus=Phvul.002G216700 ID=Phvul.002G2
55 on (original description: pacid=37175361 transcript=Phvul.002G216700.3 locus=Phvul.002G216700 ID=Phvul.002G2
56 on (original description: pacid=37175361 transcript=Phvul.002G216700.3 locus=Phvul.002G216700 ID=Phvul.002G2
57 002G243300.1 locus=Phvul.002G243300 ID=Phvul.002G243300.1.v2.1 annot-version=v2.1) & GD
58 002G243300.1 locus=Phvul.002G243300 ID=Phvul.002G243300.1.v2.1 annot-version=v2.1) & GD
59 002G243300.1 locus=Phvul.002G243300 ID=Phvul.002G243300.1.v2.1 annot-version=v2.1) & GD
60

1
2
3 003G247200.2 locus=Phvul.003G247200 ID=Phvul.003G247200.2.v2.1 annot-version=v2.1) & Probe
4 003G280100.2 locus=Phvul.003G280100 ID=Phvul.003G280100.2.v2.1 annot-version=v2.1) & Probe
5 003G280100.2 locus=Phvul.003G280100 ID=Phvul.003G280100.2.v2.1 annot-version=v2.1) & Probe
6 003G294601.1 locus=Phvul.003G294601 ID=Phvul.003G294601.1.v2.1 annot-version=v2.1) & Polya
7 003G294601.1 locus=Phvul.003G294601 ID=Phvul.003G294601.1.v2.1 annot-version=v2.1) & Polya
8 003G294601.1 locus=Phvul.003G294601 ID=Phvul.003G294601.1.v2.1 annot-version=v2.1) & Polya
9 003G294601.1 locus=Phvul.003G294601 ID=Phvul.003G294601.1.v2.1 annot-version=v2.1) & Polya
10 003G294601.1 locus=Phvul.003G294601 ID=Phvul.003G294601.1.v2.1 annot-version=v2.1) & Polya
11 003G294601.1 locus=Phvul.003G294601 ID=Phvul.003G294601.1.v2.1 annot-version=v2.1) & Polya
12
13 scription: pacid=37145147 transcript=Phvul.003G294800.4 locus=Phvul.003G294800 ID=Phvul.003G
14 scription: pacid=37145147 transcript=Phvul.003G294800.4 locus=Phvul.003G294800 ID=Phvul.003G
15 scription: pacid=37145147 transcript=Phvul.003G294800.4 locus=Phvul.003G294800 ID=Phvul.003G
16 scription: pacid=37145147 transcript=Phvul.003G294800.4 locus=Phvul.003G294800 ID=Phvul.003G
17 scription: pacid=37145147 transcript=Phvul.003G294800.4 locus=Phvul.003G294800 ID=Phvul.003G
18 scription: pacid=37145147 transcript=Phvul.003G294800.4 locus=Phvul.003G294800 ID=Phvul.003G
19 scription: pacid=37145147 transcript=Phvul.003G294800.4 locus=Phvul.003G294800 ID=Phvul.003G
20 scription: pacid=37145147 transcript=Phvul.003G294800.4 locus=Phvul.003G294800 ID=Phvul.003G
21 scription: pacid=37145147 transcript=Phvul.003G294800.4 locus=Phvul.003G294800 ID=Phvul.003G
22 scription: pacid=37145147 transcript=Phvul.003G294800.4 locus=Phvul.003G294800 ID=Phvul.003G
23 pt=Phvul.004G032100.1 locus=Phvul.004G032100 ID=Phvul.004G032100.1.v2.1 annot-version=v2.1
24 pt=Phvul.004G032100.1 locus=Phvul.004G032100 ID=Phvul.004G032100.1.v2.1 annot-version=v2.1
25 pt=Phvul.004G032100.1 locus=Phvul.004G032100 ID=Phvul.004G032100.1.v2.1 annot-version=v2.1
26 pt=Phvul.004G032100.1 locus=Phvul.004G032100 ID=Phvul.004G032100.1.v2.1 annot-version=v2.1
27 pt=Phvul.004G032100.1 locus=Phvul.004G032100 ID=Phvul.004G032100.1.v2.1 annot-version=v2.1
28 004G044800.1 locus=Phvul.004G044800 ID=Phvul.004G044800.1.v2.1 annot-version=v2.1) & Recep
29 004G044800.1 locus=Phvul.004G044800 ID=Phvul.004G044800.1.v2.1 annot-version=v2.1) & Recep
30 pt=Phvul.004G050550.1 locus=Phvul.004G050550 ID=Phvul.004G050550.1.v2.1 annot-version=v2.1
31 pt=Phvul.004G050550.1 locus=Phvul.004G050550 ID=Phvul.004G050550.1.v2.1 annot-version=v2.1
32 pt=Phvul.004G050550.1 locus=Phvul.004G050550 ID=Phvul.004G050550.1.v2.1 annot-version=v2.1
33 pt=Phvul.004G050550.1 locus=Phvul.004G050550 ID=Phvul.004G050550.1.v2.1 annot-version=v2.1
34 pt=Phvul.004G050550.1 locus=Phvul.004G050550 ID=Phvul.004G050550.1.v2.1 annot-version=v2.1
35 pt=Phvul.004G050550.1 locus=Phvul.004G050550 ID=Phvul.004G050550.1.v2.1 annot-version=v2.1
36 pt=Phvul.004G173101.1 locus=Phvul.004G173101 ID=Phvul.004G173101.1.v2.1 annot-version=v2.1
37 pt=Phvul.004G173101.1 locus=Phvul.004G173101 ID=Phvul.004G173101.1.v2.1 annot-version=v2.1
38 pt=Phvul.004G173101.1 locus=Phvul.004G173101 ID=Phvul.004G173101.1.v2.1 annot-version=v2.1
39 pt=Phvul.004G173101.1 locus=Phvul.004G173101 ID=Phvul.004G173101.1.v2.1 annot-version=v2.1
40 pt=Phvul.004G173101.1 locus=Phvul.004G173101 ID=Phvul.004G173101.1.v2.1 annot-version=v2.1
41
42 l transcript=Phvul.005G006400.1 locus=Phvul.005G006400 ID=Phvul.005G006400.1.v2.1 annot-vers
43 l transcript=Phvul.005G006400.1 locus=Phvul.005G006400 ID=Phvul.005G006400.1.v2.1 annot-vers
44 l transcript=Phvul.005G006400.1 locus=Phvul.005G006400 ID=Phvul.005G006400.1.v2.1 annot-vers
45 l transcript=Phvul.005G006400.1 locus=Phvul.005G006400 ID=Phvul.005G006400.1.v2.1 annot-vers
46 l transcript=Phvul.005G006400.1 locus=Phvul.005G006400 ID=Phvul.005G006400.1.v2.1 annot-vers
47 lator complex (original description: pacid=37153872 transcript=Phvul.005G014300.2 locus=Phvul.0
48 005G056400.1 locus=Phvul.005G056400 ID=Phvul.005G056400.1.v2.1 annot-version=v2.1) & BTB/f
49 ranscript=Phvul.005G095300.1 locus=Phvul.005G095300 ID=Phvul.005G095300.1.v2.1 annot-versic
50 pt=Phvul.005G100300.1 locus=Phvul.005G100300 ID=Phvul.005G100300.1.v2.1 annot-version=v2.1
51 pt=Phvul.005G116100.2 locus=Phvul.005G116100 ID=Phvul.005G116100.2.v2.1 annot-version=v2.1
52 pt=Phvul.005G116100.2 locus=Phvul.005G116100 ID=Phvul.005G116100.2.v2.1 annot-version=v2.1
53 pt=Phvul.005G116100.2 locus=Phvul.005G116100 ID=Phvul.005G116100.2.v2.1 annot-version=v2.1
54 pt=Phvul.005G116100.2 locus=Phvul.005G116100 ID=Phvul.005G116100.2.v2.1 annot-version=v2.1
55 pt=Phvul.005G116100.2 locus=Phvul.005G116100 ID=Phvul.005G116100.2.v2.1 annot-version=v2.1
56 pt=Phvul.005G116100.2 locus=Phvul.005G116100 ID=Phvul.005G116100.2.v2.1 annot-version=v2.1
57 pt=Phvul.005G116100.2 locus=Phvul.005G116100 ID=Phvul.005G116100.2.v2.1 annot-version=v2.1
58 pt=Phvul.005G116100.2 locus=Phvul.005G116100 ID=Phvul.005G116100.2.v2.1 annot-version=v2.1
59 pt=Phvul.005G116100.2 locus=Phvul.005G116100 ID=Phvul.005G116100.2.v2.1 annot-version=v2.1
60

1
2
3 on: pacid=37161546 transcript=Phvul.008G206400.6 locus=Phvul.008G206400 ID=Phvul.008G206400.1.v2.1
4 pt=Phvul.008G225900.1 locus=Phvul.008G225900 ID=Phvul.008G225900.1.v2.1 annot-version=v2.1
5 pt=Phvul.008G225900.1 locus=Phvul.008G225900 ID=Phvul.008G225900.1.v2.1 annot-version=v2.1
6 pt=Phvul.008G225900.1 locus=Phvul.008G225900 ID=Phvul.008G225900.1.v2.1 annot-version=v2.1
7 pt=Phvul.008G225900.1 locus=Phvul.008G225900 ID=Phvul.008G225900.1.v2.1 annot-version=v2.1
8 pt=Phvul.008G225900.1 locus=Phvul.008G225900 ID=Phvul.008G225900.1.v2.1 annot-version=v2.1
9
10 7160845 transcript=Phvul.008G227600.1 locus=Phvul.008G227600 ID=Phvul.008G227600.1.v2.1 an
11 7160845 transcript=Phvul.008G227600.1 locus=Phvul.008G227600 ID=Phvul.008G227600.1.v2.1 an
12 7160845 transcript=Phvul.008G227600.1 locus=Phvul.008G227600 ID=Phvul.008G227600.1.v2.1 an
13 7160845 transcript=Phvul.008G227600.1 locus=Phvul.008G227600 ID=Phvul.008G227600.1.v2.1 an
14 7160845 transcript=Phvul.008G227600.1 locus=Phvul.008G227600 ID=Phvul.008G227600.1.v2.1 an
15 008G274900.3 locus=Phvul.008G274900 ID=Phvul.008G274900.3.v2.1 annot-version=v2.1) & Heter
16 008G274900.3 locus=Phvul.008G274900 ID=Phvul.008G274900.3.v2.1 annot-version=v2.1) & Heter
17 008G274900.3 locus=Phvul.008G274900 ID=Phvul.008G274900.3.v2.1 annot-version=v2.1) & Heter
18 original description: pacid=37157587 transcript=Phvul.008G282700.1 locus=Phvul.008G282700 ID=P
19 original description: pacid=37157587 transcript=Phvul.008G282700.1 locus=Phvul.008G282700 ID=P
20 7152011 transcript=Phvul.009G106700.1 locus=Phvul.009G106700 ID=Phvul.009G106700.1.v2.1 an
21 009G121300.2 locus=Phvul.009G121300 ID=Phvul.009G121300.2.v2.1 annot-version=v2.1) & Oxyst
22 009G121300.2 locus=Phvul.009G121300 ID=Phvul.009G121300.2.v2.1 annot-version=v2.1) & Oxyst
23 009G121300.2 locus=Phvul.009G121300 ID=Phvul.009G121300.2.v2.1 annot-version=v2.1) & Oxyst
24 009G121300.2 locus=Phvul.009G121300 ID=Phvul.009G121300.2.v2.1 annot-version=v2.1) & Oxyst
25 009G121300.2 locus=Phvul.009G121300 ID=Phvul.009G121300.2.v2.1 annot-version=v2.1) & Oxyst
26 009G121300.2 locus=Phvul.009G121300 ID=Phvul.009G121300.2.v2.1 annot-version=v2.1) & Oxyst
27 009G121300.2 locus=Phvul.009G121300 ID=Phvul.009G121300.2.v2.1 annot-version=v2.1) & Oxyst
28 009G121300.2 locus=Phvul.009G121300 ID=Phvul.009G121300.2.v2.1 annot-version=v2.1) & Oxyst
29 009G121300.2 locus=Phvul.009G121300 ID=Phvul.009G121300.2.v2.1 annot-version=v2.1) & Oxyst
30 009G121300.2 locus=Phvul.009G121300 ID=Phvul.009G121300.2.v2.1 annot-version=v2.1) & Oxyst
31 009G121300.2 locus=Phvul.009G121300 ID=Phvul.009G121300.2.v2.1 annot-version=v2.1) & Oxyst
32 009G121300.2 locus=Phvul.009G121300 ID=Phvul.009G121300.2.v2.1 annot-version=v2.1) & Oxyst
33 009G121300.2 locus=Phvul.009G121300 ID=Phvul.009G121300.2.v2.1 annot-version=v2.1) & Oxyst
34 7151089 transcript=Phvul.009G232500.1 locus=Phvul.009G232500 ID=Phvul.009G232500.1.v2.1 an
35 7151089 transcript=Phvul.009G232500.1 locus=Phvul.009G232500 ID=Phvul.009G232500.1.v2.1 an
36 ase transferring one-carbon group(50.2.1 : 458.4) & Caffeic acid 3-O-methyltransferase 1 OS=Ocimu
37 ase transferring one-carbon group(50.2.1 : 458.4) & Caffeic acid 3-O-methyltransferase 1 OS=Ocimu
38 ase transferring one-carbon group(50.2.1 : 458.4) & Caffeic acid 3-O-methyltransferase 1 OS=Ocimu
39 ase transferring one-carbon group(50.2.1 : 458.4) & Caffeic acid 3-O-methyltransferase 1 OS=Ocimu
40 ase transferring one-carbon group(50.2.1 : 458.4) & Caffeic acid 3-O-methyltransferase 1 OS=Ocimu
41 ase transferring one-carbon group(50.2.1 : 458.4) & Caffeic acid 3-O-methyltransferase 1 OS=Ocimu
42 010G032400.1 locus=Phvul.010G032400 ID=Phvul.010G032400.1.v2.1 annot-version=v2.1) & no de
43 010G032400.1 locus=Phvul.010G032400 ID=Phvul.010G032400.1.v2.1 annot-version=v2.1) & no de
44 010G032400.1 locus=Phvul.010G032400 ID=Phvul.010G032400.1.v2.1 annot-version=v2.1) & no de
45 010G032400.1 locus=Phvul.010G032400 ID=Phvul.010G032400.1.v2.1 annot-version=v2.1) & no de
46 010G032400.1 locus=Phvul.010G032400 ID=Phvul.010G032400.1.v2.1 annot-version=v2.1) & no de
47 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
48 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
49 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
50 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
51 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
52 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
53 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
54 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
55 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
56 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
57 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
58 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
59 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
60

1
2
3 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
4 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
5 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
6 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
7 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
8 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
9 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
10 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
11 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
12 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
13 original description: pacid=37143150 transcript=Phvul.010G043700.9 locus=Phvul.010G043700 ID=P
14 }7142159 transcript=Phvul.010G070600.3 locus=Phvul.010G070600 ID=Phvul.010G070600.3.v2.1 at
15 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
16 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
17 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
18 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
19 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
20 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
21 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
22 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
23 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
24 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
25 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
26 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
27 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
28 doreductase acting on single donor with incorporation of molecular oxygen (oxygenase)(50.1.12 : 9
29 doreductase acting on single donor with incorporation of molecular oxygen (oxygenase)(50.1.12 : 9
30 doreductase acting on single donor with incorporation of molecular oxygen (oxygenase)(50.1.12 : 9
31 doreductase acting on single donor with incorporation of molecular oxygen (oxygenase)(50.1.12 : 9
32 doreductase acting on single donor with incorporation of molecular oxygen (oxygenase)(50.1.12 : 9
33 doreductase acting on single donor with incorporation of molecular oxygen (oxygenase)(50.1.12 : 9
34 ginal description: pacid=37155673 transcript=Phvul.011G013900.1 locus=Phvul.011G013900 ID=Phv
35 ginal description: pacid=37155673 transcript=Phvul.011G013900.1 locus=Phvul.011G013900 ID=Phv
36 ginal description: pacid=37155673 transcript=Phvul.011G013900.1 locus=Phvul.011G013900 ID=Phv
37 ginal description: pacid=37155673 transcript=Phvul.011G013900.1 locus=Phvul.011G013900 ID=Phv
38 ginal description: pacid=37155673 transcript=Phvul.011G013900.1 locus=Phvul.011G013900 ID=Phv
39 340 transcript=Phvul.011G050300.2 locus=Phvul.011G050300 ID=Phvul.011G050300.2.v2.1 annot-v
40 340 transcript=Phvul.011G050300.2 locus=Phvul.011G050300 ID=Phvul.011G050300.2.v2.1 annot-v
41 340 transcript=Phvul.011G050300.2 locus=Phvul.011G050300 ID=Phvul.011G050300.2.v2.1 annot-v
42 340 transcript=Phvul.011G050300.2 locus=Phvul.011G050300 ID=Phvul.011G050300.2.v2.1 annot-v
43 ginal description: pacid=37155940 transcript=Phvul.011G061600.1 locus=Phvul.011G061600 ID=Ph
44 ginal description: pacid=37155940 transcript=Phvul.011G061600.1 locus=Phvul.011G061600 ID=Ph
45 011G114700.1 locus=Phvul.011G114700 ID=Phvul.011G114700.1.v2.1 annot-version=v2.1) & S-pro
46 011G123000.1 locus=Phvul.011G123000 ID=Phvul.011G123000.1.v2.1 annot-version=v2.1) & S-pro
47 pt=Phvul.011G123701.1 locus=Phvul.011G123701 ID=Phvul.011G123701.1.v2.1 annot-version=v2.1
48 pt=Phvul.011G123701.1 locus=Phvul.011G123701 ID=Phvul.011G123701.1.v2.1 annot-version=v2.1
49 |p|o65268|tasp1_arath : 331.0) & Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting or
50 |p|o65268|tasp1_arath : 331.0) & Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting or
51 |p|o65268|tasp1_arath : 331.0) & Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting or
52 |p|o65268|tasp1_arath : 331.0) & Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting or
53 |p|o65268|tasp1_arath : 331.0) & Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting or
54 |p|o65268|tasp1_arath : 331.0) & Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting or
55 |p|o65268|tasp1_arath : 331.0) & Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting or
56 |p|o65268|tasp1_arath : 331.0) & Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting or
57 |p|o65268|tasp1_arath : 331.0) & Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting or
58 |p|o65268|tasp1_arath : 331.0) & Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting or
59 |p|o65268|tasp1_arath : 331.0) & Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting or
60

1
2
3 |p|o65268|tasp1_arath : 331.0) & Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting or
4 |p|o65268|tasp1_arath : 331.0) & Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting or
5 |p|o65268|tasp1_arath : 331.0) & Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting or
6 |p|o65268|tasp1_arath : 331.0) & Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting or
7 |p|o65268|tasp1_arath : 331.0) & Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting or
8 |p|o65268|tasp1_arath : 331.0) & Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting or
9 |p|o65268|tasp1_arath : 331.0) & Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting or
10 |p|o65268|tasp1_arath : 331.0) & Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting or
11 pt=Phvul.011G202700.1 locus=Phvul.011G202700 ID=Phvul.011G202700.1.v2.1 annot-version=v2.1
12 pt=Phvul.011G202700.1 locus=Phvul.011G202700 ID=Phvul.011G202700.1.v2.1 annot-version=v2.1
13 pt=Phvul.011G202700.1 locus=Phvul.011G202700 ID=Phvul.011G202700.1.v2.1 annot-version=v2.1
14 pt=Phvul.011G202700.1 locus=Phvul.011G202700 ID=Phvul.011G202700.1.v2.1 annot-version=v2.1
15 pt=Phvul.011G202700.1 locus=Phvul.011G202700 ID=Phvul.011G202700.1.v2.1 annot-version=v2.1
16 L002051.2 locus=Phvul.L002051 ID=Phvul.L002051.2.v2.1 annot-version=v2.1) & Probable inactive ,
17 L002051.2 locus=Phvul.L002051 ID=Phvul.L002051.2.v2.1 annot-version=v2.1) & Probable inactive ,
18 L002051.2 locus=Phvul.L002051 ID=Phvul.L002051.2.v2.1 annot-version=v2.1) & Probable inactive ,
19 L002051.2 locus=Phvul.L002051 ID=Phvul.L002051.2.v2.1 annot-version=v2.1) & Probable inactive ,
20 L002051.2 locus=Phvul.L002051 ID=Phvul.L002051.2.v2.1 annot-version=v2.1) & Probable inactive ,
21 L002051.2 locus=Phvul.L002051 ID=Phvul.L002051.2.v2.1 annot-version=v2.1) & Probable inactive ,
22 L002051.2 locus=Phvul.L002051 ID=Phvul.L002051.2.v2.1 annot-version=v2.1) & Probable inactive ,
23 L002051.2 locus=Phvul.L002051 ID=Phvul.L002051.2.v2.1 annot-version=v2.1) & Probable inactive ,
24 L002051.2 locus=Phvul.L002051 ID=Phvul.L002051.2.v2.1 annot-version=v2.1) & Probable inactive ,
25 L002051.2 locus=Phvul.L002051 ID=Phvul.L002051.2.v2.1 annot-version=v2.1) & Probable inactive ,
26 L002051.2 locus=Phvul.L002051 ID=Phvul.L002051.2.v2.1 annot-version=v2.1) & Probable inactive ,
27 |lex (original description: pacid=37157526 transcript=Phvul.L002537.1 locus=Phvul.L002537 ID=Phv
28 |lex (original description: pacid=37157526 transcript=Phvul.L002537.1 locus=Phvul.L002537 ID=Phv
29 |lex (original description: pacid=37157526 transcript=Phvul.L002537.1 locus=Phvul.L002537 ID=Phv
30 |script=Phvul.L007343.1 locus=Phvul.L007343 ID=Phvul.L007343.1.v2.1 annot-version=v2.1) &
31 tabacum (sp|q9sln8|dbr_tobac : 451.0) & Enzyme classification.EC_1 oxidoreductases.EC_1.3 oxid
32 tabacum (sp|q9sln8|dbr_tobac : 451.0) & Enzyme classification.EC_1 oxidoreductases.EC_1.3 oxid
33 =37167879 transcript=Phvul.001G020300.1 locus=Phvul.001G020300 ID=Phvul.001G020300.1.v2.1 ;
34 =37168006 transcript=Phvul.001G020350.1 locus=Phvul.001G020350 ID=Phvul.001G020350.1.v2.1 ;
35 pt=Phvul.001G022700.1 locus=Phvul.001G022700 ID=Phvul.001G022700.1.v2.1 annot-version=v2.1
36 pt=Phvul.001G022700.1 locus=Phvul.001G022700 ID=Phvul.001G022700.1.v2.1 annot-version=v2.1
37 pt=Phvul.001G022700.1 locus=Phvul.001G022700 ID=Phvul.001G022700.1.v2.1 annot-version=v2.1
38 pt=Phvul.001G022700.1 locus=Phvul.001G022700 ID=Phvul.001G022700.1.v2.1 annot-version=v2.1
39 n: pacid=37171142 transcript=Phvul.001G036800.1 locus=Phvul.001G036800 ID=Phvul.001G036800
40 :ription: pacid=37169604 transcript=Phvul.001G057800.1 locus=Phvul.001G057800 ID=Phvul.001G0
41 :ription: pacid=37169604 transcript=Phvul.001G057800.1 locus=Phvul.001G057800 ID=Phvul.001G0
42 2 transcript=Phvul.001G077700.1 locus=Phvul.001G077700 ID=Phvul.001G077700.1.v2.1 annot-ver
43 2 transcript=Phvul.001G077700.1 locus=Phvul.001G077700 ID=Phvul.001G077700.1.v2.1 annot-ver
44 1272 transcript=Phvul.001G097800.2 locus=Phvul.001G097800 ID=Phvul.001G097800.2.v2.1 annot-
45 1272 transcript=Phvul.001G097800.2 locus=Phvul.001G097800 ID=Phvul.001G097800.2.v2.1 annot-
46 complex (original description: pacid=37170938 transcript=Phvul.001G109300.2 locus=Phvul.001G10
47 complex (original description: pacid=37170938 transcript=Phvul.001G109300.2 locus=Phvul.001G10
48 complex (original description: pacid=37170938 transcript=Phvul.001G109300.2 locus=Phvul.001G10
49 complex (original description: pacid=37170938 transcript=Phvul.001G109300.2 locus=Phvul.001G10
50 cid=37170057 transcript=Phvul.001G114900.1 locus=Phvul.001G114900 ID=Phvul.001G114900.1.v
51 cid=37170057 transcript=Phvul.001G114900.1 locus=Phvul.001G114900 ID=Phvul.001G114900.1.v
52
53
54
55
56
57
58
59
60

1
2
3 002G243300.1 locus=Phvul.002G243300 ID=Phvul.002G243300.1.v2.1 annot-version=v2.1) & GDSL
4 002G253100.1 locus=Phvul.002G253100 ID=Phvul.002G253100.1.v2.1 annot-version=v2.1) & Ultrav
5 002G253100.1 locus=Phvul.002G253100 ID=Phvul.002G253100.1.v2.1 annot-version=v2.1) & Ultrav
6 inal description: pacid=37176498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.
7 }7176085 transcript=Phvul.002G290000.3 locus=Phvul.002G290000 ID=Phvul.002G290000.3.v2.1 an
8 }7176085 transcript=Phvul.002G290000.3 locus=Phvul.002G290000 ID=Phvul.002G290000.3.v2.1 an
9 pt=Phvul.003G022200.1 locus=Phvul.003G022200 ID=Phvul.003G022200.1.v2.1 annot-version=v2.1
10 pt=Phvul.003G022200.1 locus=Phvul.003G022200 ID=Phvul.003G022200.1.v2.1 annot-version=v2.1
11 }83 transcript=Phvul.003G035400.1 locus=Phvul.003G035400 ID=Phvul.003G035400.1.v2.1 annot-v
12 }83 transcript=Phvul.003G035400.1 locus=Phvul.003G035400 ID=Phvul.003G035400.1.v2.1 annot-v
13 }83 transcript=Phvul.003G035400.1 locus=Phvul.003G035400 ID=Phvul.003G035400.1.v2.1 annot-v
14 }83 transcript=Phvul.003G035400.1 locus=Phvul.003G035400 ID=Phvul.003G035400.1.v2.1 annot-v
15 45461 transcript=Phvul.003G050600.1 locus=Phvul.003G050600 ID=Phvul.003G050600.1.v2.1 anno
16 45461 transcript=Phvul.003G050600.1 locus=Phvul.003G050600 ID=Phvul.003G050600.1.v2.1 anno
17 45461 transcript=Phvul.003G050600.1 locus=Phvul.003G050600 ID=Phvul.003G050600.1.v2.1 anno
18 45461 transcript=Phvul.003G050600.1 locus=Phvul.003G050600 ID=Phvul.003G050600.1.v2.1 anno
19 003G088200.1 locus=Phvul.003G088200 ID=Phvul.003G088200.1.v2.1 annot-version=v2.1) & C2 an
20 003G088200.1 locus=Phvul.003G088200 ID=Phvul.003G088200.1.v2.1 annot-version=v2.1) & C2 an
21 7147137 transcript=Phvul.003G104200.1 locus=Phvul.003G104200 ID=Phvul.003G104200.1.v2.1 an
22 7147137 transcript=Phvul.003G104200.1 locus=Phvul.003G104200 ID=Phvul.003G104200.1.v2.1 an
23 7147137 transcript=Phvul.003G104200.1 locus=Phvul.003G104200 ID=Phvul.003G104200.1.v2.1 an
24 7147137 transcript=Phvul.003G104200.1 locus=Phvul.003G104200 ID=Phvul.003G104200.1.v2.1 an
25 pt=Phvul.003G119100.3 locus=Phvul.003G119100 ID=Phvul.003G119100.3.v2.1 annot-version=v2.1
26 pt=Phvul.003G119100.3 locus=Phvul.003G119100 ID=Phvul.003G119100.3.v2.1 annot-version=v2.1
27 pt=Phvul.003G119100.3 locus=Phvul.003G119100 ID=Phvul.003G119100.3.v2.1 annot-version=v2.1
28 i: pacid=37146945 transcript=Phvul.003G169700.1 locus=Phvul.003G169700 ID=Phvul.003G169700
29 =37144631 transcript=Phvul.003G292000.3 locus=Phvul.003G292000 ID=Phvul.003G292000.3.v2.1
30 004G058600.1 locus=Phvul.004G058600 ID=Phvul.004G058600.1.v2.1 annot-version=v2.1) & Cystir
31 ase complex (original description: pacid=37162257 transcript=Phvul.004G121666.1 locus=Phvul.00
32 ase complex (original description: pacid=37162257 transcript=Phvul.004G121666.1 locus=Phvul.00
33 ase complex (original description: pacid=37162257 transcript=Phvul.004G121666.1 locus=Phvul.00
34 ase complex (original description: pacid=37162257 transcript=Phvul.004G121666.1 locus=Phvul.00
35 004G133700.1 locus=Phvul.004G133700 ID=Phvul.004G133700.1.v2.1 annot-version=v2.1) & Unch:
36 004G133700.1 locus=Phvul.004G133700 ID=Phvul.004G133700.1.v2.1 annot-version=v2.1) & Unch:
37 004G133700.1 locus=Phvul.004G133700 ID=Phvul.004G133700.1.v2.1 annot-version=v2.1) & Unch:
38 004G133700.1 locus=Phvul.004G133700 ID=Phvul.004G133700.1.v2.1 annot-version=v2.1) & Unch:
39 37162268 transcript=Phvul.004G176700.1 locus=Phvul.004G176700 ID=Phvul.004G176700.1.v2.1 a
40 37162268 transcript=Phvul.004G176700.1 locus=Phvul.004G176700 ID=Phvul.004G176700.1.v2.1 a
41 005G056400.1 locus=Phvul.005G056400 ID=Phvul.005G056400.1.v2.1 annot-version=v2.1) & BTB/f
42 005G056400.1 locus=Phvul.005G056400 ID=Phvul.005G056400.1.v2.1 annot-version=v2.1) & BTB/f
43 816 transcript=Phvul.005G088800.1 locus=Phvul.005G088800 ID=Phvul.005G088800.1.v2.1 annot-v
44 005G095600.1 locus=Phvul.005G095600 ID=Phvul.005G095600.1.v2.1 annot-version=v2.1) & Bifun
45 152450 transcript=Phvul.005G097200.6 locus=Phvul.005G097200 ID=Phvul.005G097200.6.v2.1 anr
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3 pacid=37158953 transcript=Phvul.008G125400.2 locus=Phvul.008G125400 ID=Phvul.008G125400.2
4 pacid=37158953 transcript=Phvul.008G125400.2 locus=Phvul.008G125400 ID=Phvul.008G125400.2
5 pacid=37158953 transcript=Phvul.008G125400.2 locus=Phvul.008G125400 ID=Phvul.008G125400.2
6 pacid=37158953 transcript=Phvul.008G125400.2 locus=Phvul.008G125400 ID=Phvul.008G125400.2
7
8 ranscript=Phvul.008G229100.1 locus=Phvul.008G229100 ID=Phvul.008G229100.1.v2.1 annot-versio
9 008G279750.1 locus=Phvul.008G279750 ID=Phvul.008G279750.1.v2.1 annot-version=v2.1) & Cellul
10 008G279750.1 locus=Phvul.008G279750 ID=Phvul.008G279750.1.v2.1 annot-version=v2.1) & Cellul
11 i0212 transcript=Phvul.009G010800.1 locus=Phvul.009G010800 ID=Phvul.009G010800.1.v2.1 annot
12 i0212 transcript=Phvul.009G010800.1 locus=Phvul.009G010800 ID=Phvul.009G010800.1.v2.1 annot
13 r: pacid=37149708 transcript=Phvul.009G034800.1 locus=Phvul.009G034800 ID=Phvul.009G034800C
14 150988 transcript=Phvul.009G060200.2 locus=Phvul.009G060200 ID=Phvul.009G060200.2.v2.1 anr
15 150988 transcript=Phvul.009G060200.2 locus=Phvul.009G060200 ID=Phvul.009G060200.2.v2.1 anr
16 150988 transcript=Phvul.009G060200.2 locus=Phvul.009G060200 ID=Phvul.009G060200.2.v2.1 anr
17 150988 transcript=Phvul.009G060200.2 locus=Phvul.009G060200 ID=Phvul.009G060200.2.v2.1 anr
18 150988 transcript=Phvul.009G060200.2 locus=Phvul.009G060200 ID=Phvul.009G060200.2.v2.1 anr
19 150988 transcript=Phvul.009G060200.2 locus=Phvul.009G060200 ID=Phvul.009G060200.2.v2.1 anr
20 150988 transcript=Phvul.009G060200.2 locus=Phvul.009G060200 ID=Phvul.009G060200.2.v2.1 anr
21 150988 transcript=Phvul.009G060200.2 locus=Phvul.009G060200 ID=Phvul.009G060200.2.v2.1 anr
22 150988 transcript=Phvul.009G060200.2 locus=Phvul.009G060200 ID=Phvul.009G060200.2.v2.1 anr
23 150988 transcript=Phvul.009G060200.2 locus=Phvul.009G060200 ID=Phvul.009G060200.2.v2.1 anr
24 150988 transcript=Phvul.009G060200.2 locus=Phvul.009G060200 ID=Phvul.009G060200.2.v2.1 anr
25 150988 transcript=Phvul.009G060200.2 locus=Phvul.009G060200 ID=Phvul.009G060200.2.v2.1 anr
26 pacid=37150227 transcript=Phvul.009G115500.1 locus=Phvul.009G115500 ID=Phvul.009G115500.1
27 pacid=37150227 transcript=Phvul.009G115500.1 locus=Phvul.009G115500 ID=Phvul.009G115500.1
28 009G158700.1 locus=Phvul.009G158700 ID=Phvul.009G158700.1.v2.1 annot-version=v2.1) & Unch:
29 009G158700.1 locus=Phvul.009G158700 ID=Phvul.009G158700.1.v2.1 annot-version=v2.1) & Unch:
30 009G158700.1 locus=Phvul.009G158700 ID=Phvul.009G158700.1.v2.1 annot-version=v2.1) & Unch:
31 009G158700.1 locus=Phvul.009G158700 ID=Phvul.009G158700.1.v2.1 annot-version=v2.1) & Unch:
32 protein (original description: pacid=37151888 transcript=Phvul.009G203100.1 locus=Phvul.009G20
33 7151089 transcript=Phvul.009G232500.1 locus=Phvul.009G232500 ID=Phvul.009G232500.1.v2.1 an
34 7151089 transcript=Phvul.009G232500.1 locus=Phvul.009G232500 ID=Phvul.009G232500.1.v2.1 an
35 7151089 transcript=Phvul.009G232500.1 locus=Phvul.009G232500 ID=Phvul.009G232500.1.v2.1 an
36 7151089 transcript=Phvul.009G232500.1 locus=Phvul.009G232500 ID=Phvul.009G232500.1.v2.1 an
37 009G255100.2 locus=Phvul.009G255100 ID=Phvul.009G255100.2.v2.1 annot-version=v2.1) & Outer
38 009G255100.2 locus=Phvul.009G255100 ID=Phvul.009G255100.2.v2.1 annot-version=v2.1) & Outer
39 009G255100.2 locus=Phvul.009G255100 ID=Phvul.009G255100.2.v2.1 annot-version=v2.1) & Outer
40 009G255100.2 locus=Phvul.009G255100 ID=Phvul.009G255100.2.v2.1 annot-version=v2.1) & Outer
41 pt=Phvul.010G026500.1 locus=Phvul.010G026500 ID=Phvul.010G026500.1.v2.1 annot-version=v2.1
42 pt=Phvul.010G026500.1 locus=Phvul.010G026500 ID=Phvul.010G026500.1.v2.1 annot-version=v2.1
43 pt=Phvul.010G026500.1 locus=Phvul.010G026500 ID=Phvul.010G026500.1.v2.1 annot-version=v2.1
44 pt=Phvul.010G026500.1 locus=Phvul.010G026500 ID=Phvul.010G026500.1.v2.1 annot-version=v2.1
45 i3028 transcript=Phvul.010G028900.2 locus=Phvul.010G028900 ID=Phvul.010G028900.2.v2.1 anno
46 i3028 transcript=Phvul.010G028900.2 locus=Phvul.010G028900 ID=Phvul.010G028900.2.v2.1 anno
47 i3028 transcript=Phvul.010G028900.2 locus=Phvul.010G028900 ID=Phvul.010G028900.2.v2.1 anno
48 i3028 transcript=Phvul.010G028900.2 locus=Phvul.010G028900 ID=Phvul.010G028900.2.v2.1 anno
49 l=37142449 transcript=Phvul.010G067900.1 locus=Phvul.010G067900 ID=Phvul.010G067900.1.v2.1
50 l=37142449 transcript=Phvul.010G067900.1 locus=Phvul.010G067900 ID=Phvul.010G067900.1.v2.1
51
52
53
54
55
56
57
58
59
60

1
2
3 l=37142449 transcript=Phvul.010G067900.1 locus=Phvul.010G067900 ID=Phvul.010G067900.1.v2.1
4 l=37142449 transcript=Phvul.010G067900.1 locus=Phvul.010G067900 ID=Phvul.010G067900.1.v2.1
5 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
6 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
7 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
8 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
9 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
10 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
11 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
12 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
13 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
14 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
15 010G089200.2 locus=Phvul.010G089200 ID=Phvul.010G089200.2.v2.1 annot-version=v2.1) & Perox
16 010G094450.1 locus=Phvul.010G094450 ID=Phvul.010G094450.1.v2.1 annot-version=v2.1) & Quinc
17 010G094450.1 locus=Phvul.010G094450 ID=Phvul.010G094450.1.v2.1 annot-version=v2.1) & Quinc
18 010G094450.1 locus=Phvul.010G094450 ID=Phvul.010G094450.1.v2.1 annot-version=v2.1) & Quinc
19 010G094450.1 locus=Phvul.010G094450 ID=Phvul.010G094450.1.v2.1 annot-version=v2.1) & Quinc
20 010G094450.1 locus=Phvul.010G094450 ID=Phvul.010G094450.1.v2.1 annot-version=v2.1) & Quinc
21 010G094450.1 locus=Phvul.010G094450 ID=Phvul.010G094450.1.v2.1 annot-version=v2.1) & Quinc
22 original description: pacid=37156003 transcript=Phvul.011G001200.2 locus=Phvul.011G001200 ID=Ph
23 original description: pacid=37156003 transcript=Phvul.011G001200.2 locus=Phvul.011G001200 ID=Ph
24 original description: pacid=37156003 transcript=Phvul.011G001200.2 locus=Phvul.011G001200 ID=Ph
25 original description: pacid=37156003 transcript=Phvul.011G001200.2 locus=Phvul.011G001200 ID=Ph
26 original description: pacid=37156003 transcript=Phvul.011G001200.2 locus=Phvul.011G001200 ID=Ph
27 original description: pacid=37156003 transcript=Phvul.011G001200.2 locus=Phvul.011G001200 ID=Ph
28 original description: pacid=37156003 transcript=Phvul.011G001200.2 locus=Phvul.011G001200 ID=Ph
29 original description: pacid=37156003 transcript=Phvul.011G001200.2 locus=Phvul.011G001200 ID=Ph
30 original description: pacid=37156003 transcript=Phvul.011G001200.2 locus=Phvul.011G001200 ID=Ph
31 original description: pacid=37156003 transcript=Phvul.011G001200.2 locus=Phvul.011G001200 ID=Ph
32 011G004200.1 locus=Phvul.011G004200 ID=Phvul.011G004200.1.v2.1 annot-version=v2.1) & Prote
33 cid=37155891 transcript=Phvul.011G203450.1 locus=Phvul.011G203450 ID=Phvul.011G203450.1.v
34 cid=37155891 transcript=Phvul.011G203450.1 locus=Phvul.011G203450 ID=Phvul.011G203450.1.v
35 cid=37155891 transcript=Phvul.011G203450.1 locus=Phvul.011G203450 ID=Phvul.011G203450.1.v
36 cid=37155891 transcript=Phvul.011G203450.1 locus=Phvul.011G203450 ID=Phvul.011G203450.1.v
37 cid=37155891 transcript=Phvul.011G203450.1 locus=Phvul.011G203450 ID=Phvul.011G203450.1.v
38 cid=37155891 transcript=Phvul.011G203450.1 locus=Phvul.011G203450 ID=Phvul.011G203450.1.v
39 L001679.1 locus=Phvul.L001679 ID=Phvul.L001679.1.v2.1 annot-version=v2.1) & C2 and GRAM don
40 L001679.1 locus=Phvul.L001679 ID=Phvul.L001679.1.v2.1 annot-version=v2.1) & C2 and GRAM don
41 lex (original description: pacid=37157526 transcript=Phvul.L002537.1 locus=Phvul.L002537 ID=Phv
42 lex (original description: pacid=37157526 transcript=Phvul.L002537.1 locus=Phvul.L002537 ID=Phv
43 7179027 transcript=Phvul.L009843.2 locus=Phvul.L009843 ID=Phvul.L009843.2.v2.1 annot-version=
44 7179027 transcript=Phvul.L009843.2 locus=Phvul.L009843 ID=Phvul.L009843.2.v2.1 annot-version=
45 7179027 transcript=Phvul.L009843.2 locus=Phvul.L009843 ID=Phvul.L009843.2.v2.1 annot-version=
46 7179027 transcript=Phvul.L009843.2 locus=Phvul.L009843 ID=Phvul.L009843.2.v2.1 annot-version=
47 7179027 transcript=Phvul.L009843.2 locus=Phvul.L009843 ID=Phvul.L009843.2.v2.1 annot-version=
48 7179027 transcript=Phvul.L009843.2 locus=Phvul.L009843 ID=Phvul.L009843.2.v2.1 annot-version=
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5 vul.002G267400 ID=Phvul.002G267400.1.v2.1 annot-version=v2.1) &
6 vul.002G267400 ID=Phvul.002G267400.1.v2.1 annot-version=v2.1) &
7 l800 ID=Phvul.002G071800.1.v2.1 annot-version=v2.1) &
8 l800 ID=Phvul.002G071800.1.v2.1 annot-version=v2.1) &
9 l800 ID=Phvul.002G071800.1.v2.1 annot-version=v2.1) &
10 l800 ID=Phvul.002G071800.1.v2.1 annot-version=v2.1) &
11 l800 ID=Phvul.002G071800.1.v2.1 annot-version=v2.1) &
12 :in EXECUTER 1, chloroplastic OS=Arabidopsis thaliana (sp|q93yw0|exec1_arath : 424.0)
13 1)
14 1)
15 1)
16 :membrane 9 superfamily member 9 OS=Arabidopsis thaliana (sp|q9c5n2|tmn9_arath : 972.0)
17 ot-version=v2.1) &
18 ot-version=v2.1) &
19 ot-version=v2.1) &
20 ot-version=v2.1) &
21 ot-version=v2.1) &
22 .2.1) &
23 .2.1) &
24 .2.1) &
25 .2.1) &
26 .2.1) &
27 .2.1) &
28 !.v2.1 annot-version=v2.1) &
29 !.v2.1 annot-version=v2.1) &
30 !.v2.1 annot-version=v2.1) &
31 !.v2.1 annot-version=v2.1) &
32 rsion=v2.1) &
33 rsion=v2.1) &
34 rsion=v2.1) &
35 rsion=v2.1) &
36 rsion=v2.1) &
37 rsion=v2.1) &
38 rsion=v2.1) &
39 vul.002G267400 ID=Phvul.002G267400.1.v2.1 annot-version=v2.1) &
40 vul.002G267400 ID=Phvul.002G267400.1.v2.1 annot-version=v2.1) &
41 vul.002G267400 ID=Phvul.002G267400.1.v2.1 annot-version=v2.1) &
42 vul.002G267400 ID=Phvul.002G267400.1.v2.1 annot-version=v2.1) &
43 not-version=v2.1) &
44 not-version=v2.1) &
45 not-version=v2.1) &
46 not-version=v2.1) &
47 not-version=v2.1) &
48 not-version=v2.1) &
49 ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2_sollc : 499.0)
50 1)
51 1)
52 1)
53 1)
54 1)
55 1)
56 1)
57 1)
58 1)
59 1)
60

1
2
3 annot-version=v2.1) &
4 annot-version=v2.1) &
5 annot-version=v2.1) &
6 annot-version=v2.1) &
7 annot-version=v2.1) &
8 annot-version=v2.1) &
9 annot-version=v2.1) &
10 annot-version=v2.1) &
11 annot-version=v2.1) &
12 not-version=v2.1) &
13 not-version=v2.1) &
14 not-version=v2.1) &
15 not-version=v2.1) &
16 not-version=v2.1) &
17
18 1)
19 1)
20 1)
21 1)
22 1)
23 1)
24 0.8.v2.1 annot-version=v2.1) &
25 0.8.v2.1 annot-version=v2.1) &
26 0.8.v2.1 annot-version=v2.1) &
27 0.8.v2.1 annot-version=v2.1) &
28 0.8.v2.1 annot-version=v2.1) &
29 0.8.v2.1 annot-version=v2.1) &
30 0.8.v2.1 annot-version=v2.1) &
31 0.8.v2.1 annot-version=v2.1) &
32 0.8.v2.1 annot-version=v2.1) &
33 0.8.v2.1 annot-version=v2.1) &
34 0.8.v2.1 annot-version=v2.1) &
35 0.8.v2.1 annot-version=v2.1) &
36 0.8.v2.1 annot-version=v2.1) &
37 0.8.v2.1 annot-version=v2.1) &
38 0.8.v2.1 annot-version=v2.1) &
39 0.8.v2.1 annot-version=v2.1) &
40 0.8.v2.1 annot-version=v2.1) &
41 0.8.v2.1 annot-version=v2.1) &
42 0.8.v2.1 annot-version=v2.1) &
43 0.8.v2.1 annot-version=v2.1) &
44 0.8.v2.1 annot-version=v2.1) &
45 rsion=v2.1) &
46 rsion=v2.1) &
47
48 l800 ID=Phvul.002G071800.1.v2.1 annot-version=v2.1) &
49 l800 ID=Phvul.002G071800.1.v2.1 annot-version=v2.1) &
50
51 ..1 annot-version=v2.1) &
52 ..1 annot-version=v2.1) &
53 ..1 annot-version=v2.1) &
54 ..1 annot-version=v2.1) &
55 ..1 annot-version=v2.1) &
56 v2.1 annot-version=v2.1) &
57 v2.1 annot-version=v2.1) &
58 v2.1 annot-version=v2.1) &
59 v2.1 annot-version=v2.1) &
60

1
2
3 1 annot-version=v2.1) &
4 1)
5 1)
6 ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2_sollc : 539.0)
7 atricopeptide repeat-containing protein At4g21190 OS=Arabidopsis thaliana (sp|q8lg95|pp332_ara
8 4G133400.1.v2.1 annot-version=v2.1) &
9 4G133400.1.v2.1 annot-version=v2.1) &
10 annot-version=v2.1) &
11 annot-version=v2.1) &
12 annot-version=v2.1) &
13 annot-version=v2.1) &
14 1)
15 1)
16 1)
17 1)
18 locus=Phvul.005G180200 ID=Phvul.005G180200.1.v2.1 annot-version=v2.1) &
19 locus=Phvul.005G180200 ID=Phvul.005G180200.1.v2.1 annot-version=v2.1) &
20 06G019800 ID=Phvul.006G019800.1.v2.1 annot-version=v2.1) &
21 06G019800 ID=Phvul.006G019800.1.v2.1 annot-version=v2.1) &
22 06G019800 ID=Phvul.006G019800.1.v2.1 annot-version=v2.1) &
23 06G019800 ID=Phvul.006G019800.1.v2.1 annot-version=v2.1) &
24 annot-version=v2.1) &
25 annot-version=v2.1) &
26 annot-version=v2.1) &
27 annot-version=v2.1) &
28 1)
29 1)
30 1)
31 1)
32 1 annot-version=v2.1) &
33 1 annot-version=v2.1) &
34 : 205.1) (original description: pacid=37166776 transcript=Phvul.007G211400.1 locus=Phvul.007G21
35 : 205.1) (original description: pacid=37166776 transcript=Phvul.007G211400.1 locus=Phvul.007G21
36 1)
37 1)
38 1)
39 1)
40 1)
41 1)
42 1)
43 1)
44 1)
45 1)
46 1)
47 1)
48 1)
49 1)
50 1)
51 1)
52 1)
53 1)
54 1)
55 1)
56 1)
57 1)
58 1)
59 1)
60

1
 2
 3 amoyl-CoA reductase 1 OS=Arabidopsis thaliana (sp|q9s9n9|ccr1_arath : 214.0)
 4 amoyl-CoA reductase 1 OS=Arabidopsis thaliana (sp|q9s9n9|ccr1_arath : 214.0)
 5 amoyl-CoA reductase 1 OS=Arabidopsis thaliana (sp|q9s9n9|ccr1_arath : 214.0)
 6 Phvul.008G282700.1.v2.1 annot-version=v2.1) &
 7
 8 membrane 9 superfamily member 12 OS=Arabidopsis thaliana (sp|f4jre0|tmn12_arath : 1080.0)
 9 ul.009G127300.1.v2.1 annot-version=v2.1) &
 10 ul.009G127300.1.v2.1 annot-version=v2.1) &
 11 ul.009G127300.1.v2.1 annot-version=v2.1) &
 12 ul.009G127300.1.v2.1 annot-version=v2.1) &
 13 not-version=v2.1) &
 14 not-version=v2.1) &
 15 not-version=v2.1) &
 16 not-version=v2.1) &
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60

1
2
3 annot-version=v2.1) &
4 annot-version=v2.1) &
5 annot-version=v2.1) &
6 annot-version=v2.1) &
7 annot-version=v2.1) &
8 annot-version=v2.1) &
9 annot-version=v2.1) &
10 annot-version=v2.1) &
11 annot-version=v2.1) &
12 annot-version=v2.1) &
13 annot-version=v2.1) &
14 annot-version=v2.1) &
15 annot-version=v2.1) &
16 .41700.1.v2.1 annot-version=v2.1) &
17 .41700.1.v2.1 annot-version=v2.1) &
18 500 ID=Phvul.003G231500.1.v2.1 annot-version=v2.1) &
19 500 ID=Phvul.003G231500.1.v2.1 annot-version=v2.1) &
20 500 ID=Phvul.003G231500.1.v2.1 annot-version=v2.1) &
21 500 ID=Phvul.003G231500.1.v2.1 annot-version=v2.1) &
22 500 ID=Phvul.003G231500.1.v2.1 annot-version=v2.1) &
23 500 ID=Phvul.003G231500.1.v2.1 annot-version=v2.1) &
24 idenylate-binding protein RBP47B OS=Arabidopsis thaliana (sp|q0ww84|rb47b_arath : 97.4)
25 G294800.4.v2.1 annot-version=v2.1) &
26 G294800.4.v2.1 annot-version=v2.1) &
27
28 1)
29 1)
30 1)
31 1)
32 1)
33 1)
34 1)
35 ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2_sollc : 499.0)
36 ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2_sollc : 499.0)
37 annot-version=v2.1) &
38 :=Phvul.005G010700 ID=Phvul.005G010700.2.v2.1 annot-version=v2.1) &
39
40 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c
41 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c
42 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c
43 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c
44 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c
45 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c
46 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c
47 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c
48 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c
49 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c
50 ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (c
51 081600.1.v2.1 annot-version=v2.1) &
52 081600.1.v2.1 annot-version=v2.1) &
53 not-version=v2.1) &
54 not-version=v2.1) &
55 not-version=v2.1) &
56 not-version=v2.1) &
57 not-version=v2.1) &
58 not-version=v2.1) &
59 not-version=v2.1) &
60

1
2
3 not-version=v2.1) &
4 1)
5 1)
6 1)
7 l1.1.v2.1 annot-version=v2.1) &
8 l1.1.v2.1 annot-version=v2.1) &
9 1)
10 1)
11 1)
12 1)
13 1)
14 1)
15 1 annot-version=v2.1) &
16 1 annot-version=v2.1) &
17 xylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1_acter : 319.0)
18 xylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1_acter : 319.0)
19 1)
20 1)
21 1)
22 1)
23 1)
24 vl.007G233800.2.v2.1 annot-version=v2.1) &
25 vl.007G233800.2.v2.1 annot-version=v2.1) &
26 vl.007G233800.2.v2.1 annot-version=v2.1) &
27 vl.007G233800.2.v2.1 annot-version=v2.1) &
28 vl.007G233800.2.v2.1 annot-version=v2.1) &
29 1)
30 1)
31 1)
32 1)
33 1)
34 1)
35 1)
36 1)
37 1)
38 1)
39 1)
40 1)
41 1)
42 1)
43 ion=v2.1) &
44 ion=v2.1) &
45 ion=v2.1) &
46 ion=v2.1) &
47 ion=v2.1) &
48 .1 annot-version=v2.1) &
49 .1 annot-version=v2.1) &
50 rt-version=v2.1) &
51 rt-version=v2.1) &
52 rt-version=v2.1) &
53 rt-version=v2.1) &
54 rt-version=v2.1) &
55 rt-version=v2.1) &
56 rt-version=v2.1) &
57 rt-version=v2.1) &
58 rt-version=v2.1) &
59 nnot-version=v2.1) &
60

1
2
3 nnot-version=v2.1) &
4 nnot-version=v2.1) &
5 nnot-version=v2.1) &
6
7 1)
8 1)
9 1)
10 1)
11 1)
12 1)
13 1)
14 1)

15 aracterized protein At3g49140 OS=Arabidopsis thaliana (sp|q0wmn5|y3913_arath : 104.0)
16 ie(50.2.4 : 244.3) (original description: pacid=37159277 transcript=Phvul.008G290300.1 locus=Phvu
17 ie(50.2.4 : 244.3) (original description: pacid=37159277 transcript=Phvul.008G290300.1 locus=Phvu
18 ie(50.2.4 : 244.3) (original description: pacid=37159277 transcript=Phvul.008G290300.1 locus=Phvu
19 ie(50.2.4 : 244.3) (original description: pacid=37159277 transcript=Phvul.008G290300.1 locus=Phvu
20
21 not-version=v2.1) &
22 not-version=v2.1) &
23 2.1 annot-version=v2.1) &
24 2.1 annot-version=v2.1) &
25 2.1 annot-version=v2.1) &
26
27 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
28 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
29 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
30 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
31 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
32 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
33 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
34 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
35 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
36 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
37 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
38 not-version=v2.1) &
39 not-version=v2.1) &
40 not-version=v2.1) &
41 not-version=v2.1) &
42 not-version=v2.1) &
43 not-version=v2.1) &
44 not-version=v2.1) &
45 not-version=v2.1) &
46 not-version=v2.1) &
47 not-version=v2.1) &
48 not-version=v2.1) &
49 vul.010G048400.4.v2.1 annot-version=v2.1) &
50 vul.010G048400.4.v2.1 annot-version=v2.1) &
51 vul.010G048400.4.v2.1 annot-version=v2.1) &
52 vul.010G048400.4.v2.1 annot-version=v2.1) &
53 vul.010G048400.4.v2.1 annot-version=v2.1) &
54 vul.010G048400.4.v2.1 annot-version=v2.1) &
55 vul.010G048400.4.v2.1 annot-version=v2.1) &
56 vul.010G048400.4.v2.1 annot-version=v2.1) &
57 vul.010G048400.4.v2.1 annot-version=v2.1) &
58 vul.010G048400.4.v2.1 annot-version=v2.1) &
59 vul.010G048400.4.v2.1 annot-version=v2.1) &
60

1
2
3 vul.010G048400.4.v2.1 annot-version=v2.1) &
4 vul.010G048400.4.v2.1 annot-version=v2.1) &
5 vul.010G048400.4.v2.1 annot-version=v2.1) &
6 vul.010G048400.4.v2.1 annot-version=v2.1) &
7 vul.010G048400.4.v2.1 annot-version=v2.1) &
8 vul.010G048400.4.v2.1 annot-version=v2.1) &
9 vul.010G048400.4.v2.1 annot-version=v2.1) &
10 vul.010G048400.4.v2.1 annot-version=v2.1) &
11 vul.010G048400.4.v2.1 annot-version=v2.1) &
12 vul.010G048400.4.v2.1 annot-version=v2.1) &
13 ot-version=v2.1) &
14 ot-version=v2.1) &
15 ot-version=v2.1) &
16 ot-version=v2.1) &
17 1.v2.1 annot-version=v2.1) &
18 1.v2.1 annot-version=v2.1) &
19 1.v2.1 annot-version=v2.1) &
20 1.v2.1 annot-version=v2.1) &
21 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
22 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
23 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
24 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
25 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
26 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
27 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
28 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
29 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
30 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
31 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
32 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
33 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
34 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
35 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
36 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
37 de methionine sulfoxide reductase B1, chloroplastic OS=*Oryza sativa* subsp. *japonica* (sp|q0dc89|r
38 de methionine sulfoxide reductase B1, chloroplastic OS=*Oryza sativa* subsp. *japonica* (sp|q0dc89|r
39 de methionine sulfoxide reductase B1, chloroplastic OS=*Oryza sativa* subsp. *japonica* (sp|q0dc89|r
40 de methionine sulfoxide reductase B1, chloroplastic OS=*Oryza sativa* subsp. *japonica* (sp|q0dc89|r
41)200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
42)200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
43 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
44 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
45 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
46 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
47 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
48 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
49 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
50 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
51 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
52 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
53 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
54 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
55 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
56 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
57 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
58 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
59 1))200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
60

1
2
3 1)
4 1)
5 1)
6 1)
7 1)
8 1)
9 1)
10 1)
11 1)
12 1G147800.2.v2.1 annot-version=v2.1) &
13
14 description available(sp|q9zuu2|pxl2c_arath : 319.0)
15 description available(sp|q9zuu2|pxl2c_arath : 319.0)
16 description available(sp|q9zuu2|pxl2c_arath : 319.0)
17 description available(sp|q9zuu2|pxl2c_arath : 319.0)
18
19 1)
20 1)
21
22 hvul.001G200700.5.v2.1 annot-version=v2.1) &
23 hvul.001G200700.5.v2.1 annot-version=v2.1) &
24 hvul.001G200700.5.v2.1 annot-version=v2.1) &
25 hvul.001G200700.5.v2.1 annot-version=v2.1) &
26 hvul.001G200700.5.v2.1 annot-version=v2.1) &
27 hvul.001G200700.5.v2.1 annot-version=v2.1) &
28 hvul.001G200700.5.v2.1 annot-version=v2.1) &
29 hvul.001G200700.5.v2.1 annot-version=v2.1) &
30 hvul.001G200700.5.v2.1 annot-version=v2.1) &
31 hvul.001G200700.5.v2.1 annot-version=v2.1) &
32 x domain-containing protein 6 OS=Arabidopsis thaliana (sp|o48700|pub6_arath : 901.0)
33
34 ie transferring one-carbon group(50.2.1 : 212.4) (original description: pacid=37169062 transcript=Pl
35 ie transferring one-carbon group(50.2.1 : 212.4) (original description: pacid=37169062 transcript=Pl
36 J).1.v2.1 annot-version=v2.1) &
37 J).1.v2.1 annot-version=v2.1) &
38 rsion=v2.1) &
39 rsion=v2.1) &
40 rsion=v2.1) &
41 rsion=v2.1) &
42 rsion=v2.1) &
43 annot-version=v2.1) &
44 annot-version=v2.1) &
45 ID=Phvul.002G165300.1.v2.1 annot-version=v2.1) &
46 ID=Phvul.002G165300.1.v2.1 annot-version=v2.1) &
47 ID=Phvul.002G165300.1.v2.1 annot-version=v2.1) &
48 ID=Phvul.002G165300.1.v2.1 annot-version=v2.1) &
49
50 216700.3.v2.1 annot-version=v2.1) &
51 216700.3.v2.1 annot-version=v2.1) &
52 216700.3.v2.1 annot-version=v2.1) &
53 216700.3.v2.1 annot-version=v2.1) &
54
55 . esterase/lipase At1g29670 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 284.0)
56 . esterase/lipase At1g29670 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 284.0)
57
58
59
60

1
2
3 violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8_arath : 108.0)
4 violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8_arath : 108.0)
5 violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8_arath : 108.0)
6 violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8_arath : 108.0)
7
8 v2.1 annot-version=v2.1) &
9 v2.1 annot-version=v2.1) &
10 v2.1 annot-version=v2.1) &
11 v2.1 annot-version=v2.1) &
12 mycin-sensitive aminopeptidase OS=Arabidopsis thaliana (sp|q8h0s9|psa_arath : 805.0)
13 mycin-sensitive aminopeptidase OS=Arabidopsis thaliana (sp|q8h0s9|psa_arath : 805.0)
14 version=v2.1) &
15 version=v2.1) &
16 Phvul.002G320900 ID=Phvul.002G320900.1.v2.1 annot-version=v2.1) &
17 Phvul.002G320900 ID=Phvul.002G320900.1.v2.1 annot-version=v2.1) &
18 Phvul.002G320900 ID=Phvul.002G320900.1.v2.1 annot-version=v2.1) &
19 Phvul.002G320900 ID=Phvul.002G320900.1.v2.1 annot-version=v2.1) &
20 annot-version=v2.1) &
21 annot-version=v2.1) &
22 annot-version=v2.1) &
23 annot-version=v2.1) &
24 annot-version=v2.1) &
25 annot-version=v2.1) &
26 annot-version=v2.1) &
27 annot-version=v2.1) &
28 annot-version=v2.1) &
29 annot-version=v2.1) &
30 annot-version=v2.1) &
31 annot-version=v2.1) &
32 annot-version=v2.1) &
33 annot-version=v2.1) &
34 Phvul.003G032300.1.v2.1 annot-version=v2.1) &
35 Phvul.003G032300.1.v2.1 annot-version=v2.1) &
36 Phvul.003G057700 ID=Phvul.003G057700.1.v2.1 annot-version=v2.1) &
37 Phvul.003G057700 ID=Phvul.003G057700.1.v2.1 annot-version=v2.1) &
38
39
40
41
42
43
44
45
46
47
48
49
50
51 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42_arath : 431.0)
52 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42_arath : 431.0)
53 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42_arath : 431.0)
54 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42_arath : 431.0)
55 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42_arath : 431.0)
56 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42_arath : 431.0)
57 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42_arath : 431.0)
58 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42_arath : 431.0)
59 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42_arath : 431.0)
60

1
2
3 able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|dr142_arath : 431.0)
4 able methyltransferase PMT20 OS=Arabidopsis thaliana (sp|q9c6s7|pmtk_arath : 983.0)
5 able methyltransferase PMT20 OS=Arabidopsis thaliana (sp|q9c6s7|pmtk_arath : 983.0)
6 idenylate-binding protein RBP47B OS=Arabidopsis thaliana (sp|q0ww84|rb47b_arath : 97.4)
7 idenylate-binding protein RBP47B OS=Arabidopsis thaliana (sp|q0ww84|rb47b_arath : 97.4)
8 idenylate-binding protein RBP47B OS=Arabidopsis thaliana (sp|q0ww84|rb47b_arath : 97.4)
9 idenylate-binding protein RBP47B OS=Arabidopsis thaliana (sp|q0ww84|rb47b_arath : 97.4)
10 idenylate-binding protein RBP47B OS=Arabidopsis thaliana (sp|q0ww84|rb47b_arath : 97.4)
11 idenylate-binding protein RBP47B OS=Arabidopsis thaliana (sp|q0ww84|rb47b_arath : 97.4)
12 G294800.4.v2.1 annot-version=v2.1) &
13 G294800.4.v2.1 annot-version=v2.1) &
14 G294800.4.v2.1 annot-version=v2.1) &
15 G294800.4.v2.1 annot-version=v2.1) &
16 G294800.4.v2.1 annot-version=v2.1) &
17 G294800.4.v2.1 annot-version=v2.1) &
18 G294800.4.v2.1 annot-version=v2.1) &
19 G294800.4.v2.1 annot-version=v2.1) &
20 G294800.4.v2.1 annot-version=v2.1) &
21 G294800.4.v2.1 annot-version=v2.1) &
22 G294800.4.v2.1 annot-version=v2.1) &
23 1)
24 1)
25 1)
26 1)
27 1)
28 ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2_sollc : 539.0)
29 ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2_sollc : 539.0)
30 ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2_sollc : 539.0)
31 1)
32 1)
33 1)
34 1)
35 1)
36 1)
37 1)
38 1)
39 1)
40 1)
41 sion=v2.1) &
42 sion=v2.1) &
43 sion=v2.1) &
44 sion=v2.1) &
45 sion=v2.1) &
46 05G014300 ID=Phvul.005G014300.2.v2.1 annot-version=v2.1) &
47 POZ domain-containing protein At1g04390 OS=Arabidopsis thaliana (sp|p93820|y1439_arath : 760
48 on=v2.1) &
49 1)
50 1)
51 1)
52 1)
53 1)
54 1)
55 1)
56 1)
57 1)
58 1)
59 1)
60

1
2
3 1)
4 1)
5 1)
6 J.1.v2.1 annot-version=v2.1) &
7 J.1.v2.1 annot-version=v2.1) &
8) ID=Phvul.006G105800.1.v2.1 annot-version=v2.1) &
9 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp_arath : 80.
10 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp_arath : 80.
11 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp_arath : 80.
12 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp_arath : 80.
13 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp_arath : 80.
14 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp_arath : 80.
15 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp_arath : 80.
16 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp_arath : 80.
17 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp_arath : 80.
18 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp_arath : 80.
19 polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp_arath : 80.
20 rot-version=v2.1) &
21 rot-version=v2.1) &
22 rot-version=v2.1) &
23 rot-version=v2.1) &
24 rot-version=v2.1) &
25 rot-version=v2.1) &
26 rot-version=v2.1) &
27 rot-version=v2.1) &
28 rot-version=v2.1) &
29 rot-version=v2.1) &
30 rot-version=v2.1) &
31 1)
32 ot-version=v2.1) &
33 ot-version=v2.1) &
34 ot-version=v2.1) &
35 ot-version=v2.1) &
36 ot-version=v2.1) &
37)iquitin-protein ligase CSU1 OS=Arabidopsis thaliana (sp|q9sy88|csu1_arath : 419.0)
38)iquitin-protein ligase CSU1 OS=Arabidopsis thaliana (sp|q9sy88|csu1_arath : 419.0)
39 1)
40 1)
41 1)
42 1)
43 1)
44 1)
45 I.0.1.v2.1 annot-version=v2.1) &
46 I.0.1.v2.1 annot-version=v2.1) &
47 I.007G034000.2.v2.1 annot-version=v2.1) &
48 version=v2.1) &
49 version=v2.1) &
50 version=v2.1) &
51 version=v2.1) &
52 version=v2.1) &
53 version=v2.1) &
54 i6600.1.v2.1 annot-version=v2.1) &
55 i6600.1.v2.1 annot-version=v2.1) &
56 i6600.1.v2.1 annot-version=v2.1) &
57 i6600.1.v2.1 annot-version=v2.1) &
58 i6600.1.v2.1 annot-version=v2.1) &
59 i6600.1.v2.1 annot-version=v2.1) &
60

1
2
3 1 annot-version=v2.1) &
4 1 annot-version=v2.1) &
5 1 annot-version=v2.1) &
6 1 annot-version=v2.1) &
7 1 annot-version=v2.1) &
8 1 annot-version=v2.1) &
9 1 annot-version=v2.1) &
10 1 annot-version=v2.1) &
11 1 annot-version=v2.1) &
12 1 annot-version=v2.1) &
13 1 annot-version=v2.1) &
14 oxylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1_acter : 319.0)
15 oxylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1_acter : 319.0)
16 oxylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1_acter : 319.0)
17 oxylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1_acter : 319.0)
18 oxylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1_acter : 319.0)
19 oxylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1_acter : 319.0)
20 1.v2.1 annot-version=v2.1) &
21 1.v2.1 annot-version=v2.1) &
22 1.v2.1 annot-version=v2.1) &
23 1.v2.1 annot-version=v2.1) &
24 1.v2.1 annot-version=v2.1) &
25 1)
26 1)
27 1)
28 1)
29 1)
30 1)
31 1.v2.1 annot-version=v2.1) &
32 1.v2.1 annot-version=v2.1) &
33 1.v2.1 annot-version=v2.1) &
34 1.v2.1 annot-version=v2.1) &
35 1.v2.1 annot-version=v2.1) &
36 1)
37 1)
38 1)
39 1)
40 1)
41 1)
42 1)
43 1)
44 10.2.v2.1 annot-version=v2.1) &
45 10.2.v2.1 annot-version=v2.1) &
46 10.2.v2.1 annot-version=v2.1) &
47 10.2.v2.1 annot-version=v2.1) &
48 10.2.v2.1 annot-version=v2.1) &
49 10.2.v2.1 annot-version=v2.1) &
50 10.2.v2.1 annot-version=v2.1) &
51 10.2.v2.1 annot-version=v2.1) &
52 10.2.v2.1 annot-version=v2.1) &
53 10.2.v2.1 annot-version=v2.1) &
54 10.2.v2.1 annot-version=v2.1) &
55 -version=v2.1) &
56 nin-2 OS=Pisum sativum (sp|p08688|alb2_pea : 223.0)
57 nin-2 OS=Pisum sativum (sp|p08688|alb2_pea : 223.0)
58 nin-2 OS=Pisum sativum (sp|p08688|alb2_pea : 223.0)
59 nin-2 OS=Pisum sativum (sp|p08688|alb2_pea : 253.0)
60

1
2
3 min-2 OS=Pisum sativum (sp|p08688|alb2_pea : 253.0)
4 min-2 OS=Pisum sativum (sp|p08688|alb2_pea : 222.0)
5 min-2 OS=Pisum sativum (sp|p08688|alb2_pea : 222.0)
6
7 .1 annot-version=v2.1) &
8 .1 annot-version=v2.1) &
9 .1 annot-version=v2.1) &
10 .1 annot-version=v2.1) &
11 .1 annot-version=v2.1) &
12
13 1)
14 1)
15 1)
16 1)
17 1)
18 1)
19 12100 ID=Phvul.008G012100.2.v2.1 annot-version=v2.1) &
20 12100 ID=Phvul.008G012100.2.v2.1 annot-version=v2.1) &
21 annot-version=v2.1) &
22
23 1)
24 1)
25 1)
26 1)
27 1)
28 1)
29 1)
30 1)
31 1)
32 1)
33
34 it-version=v2.1) &
35 it-version=v2.1) &
36 it-version=v2.1) &
37 it-version=v2.1) &
38 it-version=v2.1) &
39 it-version=v2.1) &
40 it-version=v2.1) &
41
42 1)
43 1)
44 1)
45 1)
46 1)
47 1)
48 version=v2.1) &
49 version=v2.1) &
50
51 1)
52 1)
53 1)
54 1)
55 1)
56 00.6.v2.1 annot-version=v2.1) &
57 00.6.v2.1 annot-version=v2.1) &
58 00.6.v2.1 annot-version=v2.1) &
59
60

1
2
3 00.6.v2.1 annot-version=v2.1) &
4 1)
5 1)
6 1)
7 1)
8 1)
9
10 not-version=v2.1) &
11 not-version=v2.1) &
12 not-version=v2.1) &
13 not-version=v2.1) &
14
15 rogeneous nuclear ribonucleoprotein 1 OS=Arabidopsis thaliana (sp|q8w034|rnp1_arath : 211.0)
16 rogeneous nuclear ribonucleoprotein 1 OS=Arabidopsis thaliana (sp|q8w034|rnp1_arath : 211.0)
17 rogeneous nuclear ribonucleoprotein 1 OS=Arabidopsis thaliana (sp|q8w034|rnp1_arath : 211.0)
18
19 'hvul.008G282700.1.v2.1 annot-version=v2.1) &
20 'hvul.008G282700.1.v2.1 annot-version=v2.1) &
21
22 not-version=v2.1) &
23 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
24 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
25 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
26 terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
27
28 1 annot-version=v2.1) &
29 1 annot-version=v2.1) &
30 1 annot-version=v2.1) &
31 1 annot-version=v2.1) &
32
33 not-version=v2.1) &
34 not-version=v2.1) &
35
36 'm basilicum (sp|q9xgw0|comt1_ociba : 362.0) (original description: pacid=37151728 transcript=Pr
37 'm basilicum (sp|q9xgw0|comt1_ociba : 362.0) (original description: pacid=37151728 transcript=Pr
38 'm basilicum (sp|q9xgw0|comt1_ociba : 362.0) (original description: pacid=37151728 transcript=Pr
39 'm basilicum (sp|q9xgw0|comt1_ociba : 362.0) (original description: pacid=37151728 transcript=Pr
40
41 'escription available(sp|f4jts8|nov_arath : 150.0)
42 'escription available(sp|f4jts8|nov_arath : 150.0)
43 'escription available(sp|f4jts8|nov_arath : 150.0)
44 'escription available(sp|f4jts8|nov_arath : 150.0)
45 'escription available(sp|f4jts8|nov_arath : 150.0)
46
47 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
48 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
49 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
50 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
51 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
52 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
53 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
54 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
55 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
56 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
57 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
58 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
59 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
60

1
2
3 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
4 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
5 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
6 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
7 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
8 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
9 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
10 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
11 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
12 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
13 'hvul.010G043700.9.v2.1 annot-version=v2.1) &
14 nnot-version=v2.1) &
15 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)
16 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)
17 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)
18 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)
19 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)
20 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)
21 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)
22 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)
23 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)
24 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)
25 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)
26 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)
27 kisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)
28 |33.8) & Seed linoleate 9S-lipoxygenase OS=Glycine max (sp|p24095|loxx_soybn : 884.0) (original d
29 |33.8) & Seed linoleate 9S-lipoxygenase OS=Glycine max (sp|p24095|loxx_soybn : 884.0) (original d
30 |33.8) & Seed linoleate 9S-lipoxygenase OS=Glycine max (sp|p24095|loxx_soybn : 884.0) (original d
31 |33.8) & Seed linoleate 9S-lipoxygenase OS=Glycine max (sp|p24095|loxx_soybn : 884.0) (original d
32 |33.8) & Seed linoleate 9S-lipoxygenase OS=Glycine max (sp|p24095|loxx_soybn : 884.0) (original d
33 |33.8) & Seed linoleate 9S-lipoxygenase OS=Glycine max (sp|p24095|loxx_soybn : 884.0) (original d
34 /ul.011G013900.1.v2.1 annot-version=v2.1) &
35 /ul.011G013900.1.v2.1 annot-version=v2.1) &
36 /ul.011G013900.1.v2.1 annot-version=v2.1) &
37 /ul.011G013900.1.v2.1 annot-version=v2.1) &
38 /ul.011G013900.1.v2.1 annot-version=v2.1) &
39 /ersion=v2.1) &
40 /ersion=v2.1) &
41 /ersion=v2.1) &
42 /ersion=v2.1) &
43 /ersion=v2.1) &
44 vul.011G061600.1.v2.1 annot-version=v2.1) &
45 vul.011G061600.1.v2.1 annot-version=v2.1) &
46 tein homolog 5 OS=Arabidopsis thaliana (sp|o23020|sph5_arath : 90.5)
47 tein homolog 5 OS=Arabidopsis thaliana (sp|o23020|sph5_arath : 90.9)
48 1)
49 1)
50 1)
51 1)
52 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
53 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
54 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
55 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
56 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
57 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
58 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
59 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
60

1
2
3 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
4 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
5 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
6 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
7 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
8 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
9 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
10 n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01

11 1)
12 1)
13 1)
14 1)
15 1)

16 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi
17 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi
18 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi
19 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi
20 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi
21 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi
22 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi
23 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi
24 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi
25 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi
26 ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi
27 ul.L002537.1.v2.1 annot-version=v2.1) &
28 ul.L002537.1.v2.1 annot-version=v2.1) &
29 ul.L002537.1.v2.1 annot-version=v2.1) &
30 ul.L002537.1.v2.1 annot-version=v2.1) &
31

32 loreductase acting on CH-CH group of donor(50.1.3 : 281.4) (original description: pacid=37157789 tr
33 loreductase acting on CH-CH group of donor(50.1.3 : 281.4) (original description: pacid=37157789 tr
34 loreductase acting on CH-CH group of donor(50.1.3 : 281.4) (original description: pacid=37157789 tr
35 annot-version=v2.1) &
36 annot-version=v2.1) &
37

38 1)
39 1)
40 1)
41 1)
42

43 0.1.v2.1 annot-version=v2.1) &
44 J57800.1.v2.1 annot-version=v2.1) &
45 J57800.1.v2.1 annot-version=v2.1) &
46 sion=v2.1) &
47 sion=v2.1) &
48 sion=v2.1) &
49 -version=v2.1) &
50 -version=v2.1) &
51 09300 ID=Phvul.001G109300.2.v2.1 annot-version=v2.1) &
52 09300 ID=Phvul.001G109300.2.v2.1 annot-version=v2.1) &
53 09300 ID=Phvul.001G109300.2.v2.1 annot-version=v2.1) &
54 09300 ID=Phvul.001G109300.2.v2.1 annot-version=v2.1) &
55 09300 ID=Phvul.001G109300.2.v2.1 annot-version=v2.1) &
56 09300 ID=Phvul.001G109300.2.v2.1 annot-version=v2.1) &
57 2.1 annot-version=v2.1) &
58 2.1 annot-version=v2.1) &
59 2.1 annot-version=v2.1) &
60

1
 2
 3 α-glucosidase OS=Spinacia oleracea (sp|o04893|aglu_spiol : 80.9)
 4 α-glucosidase OS=Spinacia oleracea (sp|o04893|aglu_spiol : 80.9)
 5
 6 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 339.0)
 7 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 339.0)
 8 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 339.0)
 9 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 339.0)
 10 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 339.0)
 11 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 339.0)
 12 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 339.0)
 13 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 339.0)
 14 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 339.0)
 15 :ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 339.0)
 16 .1 annot-version=v2.1) &
 17 nnot-version=v2.1) &
 18 nnot-version=v2.1) &
 19 nnot-version=v2.1) &
 20 nnot-version=v2.1) &
 21 nnot-version=v2.1) &
 22 nnot-version=v2.1) &
 23 nnot-version=v2.1) &
 24 nnot-version=v2.1) &
 25 nnot-version=v2.1) &
 26 nnot-version=v2.1) &
 27 nnot-version=v2.1) &
 28 :rsion=v2.1) &
 29 :rsion=v2.1) &
 30
 31 2.1 annot-version=v2.1) &
 32 2.1 annot-version=v2.1) &
 33 2.1 annot-version=v2.1) &
 34 2.1 annot-version=v2.1) &
 35
 36 ressor of RPS4-RLD 1 OS=Arabidopsis thaliana (sp|f4js25|srfr1_arath : 275.0)
 37 ressor of RPS4-RLD 1 OS=Arabidopsis thaliana (sp|f4js25|srfr1_arath : 275.0)
 38 ressor of RPS4-RLD 1 OS=Arabidopsis thaliana (sp|f4js25|srfr1_arath : 275.0)
 39 ressor of RPS4-RLD 1 OS=Arabidopsis thaliana (sp|f4js25|srfr1_arath : 275.0)
 40
 41 ot-version=v2.1) &
 42 ot-version=v2.1) &
 43 ot-version=v2.1) &
 44 ot-version=v2.1) &
 45
 46 J.1.v2.1 annot-version=v2.1) &
 47 J.1.v2.1 annot-version=v2.1) &
 48
 49 ersion=v2.1) &
 50 ersion=v2.1) &
 51 ersion=v2.1) &
 52 ersion=v2.1) &
 53 ersion=v2.1) &
 54
 55 annot-version=v2.1) &
 56 . esterase/lipase At1g29670 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 284.0)
 57 . esterase/lipase At1g29670 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 284.0)
 58 . esterase/lipase At1g29670 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 284.0)
 59
 60

1
 2
 3 . esterase/lipase At1g29670 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 284.0)
 4 violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8_arath : 98.6)
 5 violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8_arath : 98.6)
 6 ul.002G262600.2.v2.1 annot-version=v2.1) &
 7 nnot-version=v2.1) &
 8 nnot-version=v2.1) &
 9 1)
 10 1)
 11 ersion=v2.1) &
 12 ersion=v2.1) &
 13 ersion=v2.1) &
 14 ersion=v2.1) &
 15 ersion=v2.1) &
 16 ersion=v2.1) &
 17 ersion=v2.1) &
 18 ersion=v2.1) &
 19 ersion=v2.1) &
 20 ersion=v2.1) &
 21 ersion=v2.1) &
 22 ersion=v2.1) &
 23 ersion=v2.1) &
 24 id GRAM domain-containing protein At1g03370 OS=Arabidopsis thaliana (sp|q9zvt9|c2gr1_arath : :
 25 id GRAM domain-containing protein At1g03370 OS=Arabidopsis thaliana (sp|q9zvt9|c2gr1_arath : :
 26 annot-version=v2.1) &
 27 annot-version=v2.1) &
 28 annot-version=v2.1) &
 29 annot-version=v2.1) &
 30 annot-version=v2.1) &
 31 1)
 32 1)
 33 1)
 34).1.v2.1 annot-version=v2.1) &
 35 annot-version=v2.1) &
 36 nosin homolog OS=Arabidopsis thaliana (sp|p57758|ctns_arath : 317.0)
 37 4G121666 ID=Phvul.004G121666.1.v2.1 annot-version=v2.1) &
 38 4G121666 ID=Phvul.004G121666.1.v2.1 annot-version=v2.1) &
 39 4G121666 ID=Phvul.004G121666.1.v2.1 annot-version=v2.1) &
 40 4G121666 ID=Phvul.004G121666.1.v2.1 annot-version=v2.1) &
 41 aracterized protein At5g08430 OS=Arabidopsis thaliana (sp|q9ft92|y5843_arath : 311.0)
 42 aracterized protein At5g08430 OS=Arabidopsis thaliana (sp|q9ft92|y5843_arath : 311.0)
 43 aracterized protein At5g08430 OS=Arabidopsis thaliana (sp|q9ft92|y5843_arath : 311.0)
 44 aracterized protein At5g08430 OS=Arabidopsis thaliana (sp|q9ft92|y5843_arath : 311.0)
 45 annot-version=v2.1) &
 46 annot-version=v2.1) &
 47 POZ domain-containing protein At1g04390 OS=Arabidopsis thaliana (sp|p93820|y1439_arath : 760
 48 POZ domain-containing protein At1g04390 OS=Arabidopsis thaliana (sp|p93820|y1439_arath : 760
 49 ersion=v2.1) &
 50 ctional riboflavin kinase/FMN phosphatase OS=Arabidopsis thaliana (sp|q84md8|fhyrk_arath : 248
 51 not-version=v2.1) &
 52
 53
 54
 55
 56
 57
 58
 59
 60

1
2
3 not-version=v2.1) &
4 not-version=v2.1) &
5 not-version=v2.1) &
6 not-version=v2.1) &
7 not-version=v2.1) &
8 not-version=v2.1) &
9 not-version=v2.1) &
10 not-version=v2.1) &
11 not-version=v2.1) &
12 not-version=v2.1) &
13 not-version=v2.1) &
14 not-version=v2.1) &
15 not-version=v2.1) &
16 not-version=v2.1) &
17
18 101400 ID=Phvul.005G101400.3.v2.1 annot-version=v2.1) &
19 101400 ID=Phvul.005G101400.3.v2.1 annot-version=v2.1) &
20 101400 ID=Phvul.005G101400.3.v2.1 annot-version=v2.1) &
21 101400 ID=Phvul.005G101400.3.v2.1 annot-version=v2.1) &
22 101400 ID=Phvul.005G101400.3.v2.1 annot-version=v2.1) &
23 101400 ID=Phvul.005G101400.3.v2.1 annot-version=v2.1) &
24 101400 ID=Phvul.005G101400.3.v2.1 annot-version=v2.1) &
25
26 J.1.v2.1 annot-version=v2.1) &
27 J.1.v2.1 annot-version=v2.1) &
28 J.1.v2.1 annot-version=v2.1) &
29 J.1.v2.1 annot-version=v2.1) &
30
31 n=v2.1) &
32 n=v2.1) &
33 n=v2.1) &
34 n=v2.1) &
35
36 1)
37 1)
38 1)
39 1)
40
41 ot-version=v2.1) &
42 ot-version=v2.1) &
43
44 035900.2.v2.1 annot-version=v2.1) &
45 035900.2.v2.1 annot-version=v2.1) &
46 035900.2.v2.1 annot-version=v2.1) &
47 035900.2.v2.1 annot-version=v2.1) &
48
49 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara**
50 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara**
51 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara**
52 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara**
53 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara**
54 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara**
55 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara**
56 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara**
57 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara**
58 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara**
59 **atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara**
60

1
2
3 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara
4 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara
5 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara
6 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara
7 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara
8 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara
9 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara
10 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara
11 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara
12 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara
13 atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara
14 1)

15 ..1 annot-version=v2.1) &

16 ..1 annot-version=v2.1) &

17 ..1 annot-version=v2.1) &

18 ..1 annot-version=v2.1) &

19 ..1 annot-version=v2.1) &

20 annot-version=v2.1) &

21 annot-version=v2.1) &

22 x domain-containing protein 3 OS=Arabidopsis thaliana (sp|q8gww5|pub3_arath : 647.0)

23 :-version=v2.1) &

24 :-version=v2.1) &

25 :-version=v2.1) &

26 :-version=v2.1) &

27 :-version=v2.1) &

28 :-version=v2.1) &

29 :-version=v2.1) &

30 Phvul.007G215300.1.v2.1 annot-version=v2.1) &

31 Phvul.007G215300.1.v2.1 annot-version=v2.1) &

32 Phvul.007G215300.1.v2.1 annot-version=v2.1) &

33 Phvul.007G215300.1.v2.1 annot-version=v2.1) &

34 51800.1.v2.1 annot-version=v2.1) &

35 ptor-like protein 6 OS=Arabidopsis thaliana (sp|q9c637|rlp6_arath : 408.0)

36 ptor-like protein 6 OS=Arabidopsis thaliana (sp|q9c637|rlp6_arath : 408.0)

37 inot-version=v2.1) &

38 inot-version=v2.1) &

39 1)

40 1)

41 1)

42 1)

43 1)

44 1)

45 1)

46 1)

47 1)

48 1)

49 1)

50 1)

51 1)

52 1)

53 1)

54 1)

55 1)

56 1)

57 1)

58 1)

59 1)

60 1)

1
2
3 ?v2.1 annot-version=v2.1) &
4 ?v2.1 annot-version=v2.1) &
5 ?v2.1 annot-version=v2.1) &
6 ?v2.1 annot-version=v2.1) &
7 ?v2.1 annot-version=v2.1) &
8 n=v2.1) &
9 lose synthase-like protein E6 OS=Oryza sativa subsp. japonica (sp|q651x6|csle6_orysj : 667.0)
10 lose synthase-like protein E6 OS=Oryza sativa subsp. japonica (sp|q651x6|csle6_orysj : 667.0)
11 t-version=v2.1) &
12 t-version=v2.1) &
13).1.v2.1 annot-version=v2.1) &
14 rot-version=v2.1) &
15 rot-version=v2.1) &
16 rot-version=v2.1) &
17 rot-version=v2.1) &
18 rot-version=v2.1) &
19 rot-version=v2.1) &
20 rot-version=v2.1) &
21 rot-version=v2.1) &
22 rot-version=v2.1) &
23 rot-version=v2.1) &
24 rot-version=v2.1) &
25 rot-version=v2.1) &
26 1.v2.1 annot-version=v2.1) &
27 1.v2.1 annot-version=v2.1) &
28 aracterized protein At4g14100 OS=Arabidopsis thaliana (sp|q67yc9|y4141_arath : 263.0)
29 aracterized protein At4g14100 OS=Arabidopsis thaliana (sp|q67yc9|y4141_arath : 263.0)
30 aracterized protein At4g14100 OS=Arabidopsis thaliana (sp|q67yc9|y4141_arath : 263.0)
31 aracterized protein At4g14100 OS=Arabidopsis thaliana (sp|q67yc9|y4141_arath : 263.0)
32 aracterized protein At4g14100 OS=Arabidopsis thaliana (sp|q67yc9|y4141_arath : 263.0)
33 13100 ID=Phvul.009G203100.1.v2.1 annot-version=v2.1) &
34 rot-version=v2.1) &
35 rot-version=v2.1) &
36 rot-version=v2.1) &
37 rot-version=v2.1) &
38 r envelope pore protein 16-2, chloroplastic OS=Arabidopsis thaliana (sp|q0wmz5|op162_arath : 18
39 r envelope pore protein 16-2, chloroplastic OS=Arabidopsis thaliana (sp|q0wmz5|op162_arath : 18
40 r envelope pore protein 16-2, chloroplastic OS=Arabidopsis thaliana (sp|q0wmz5|op162_arath : 18
41 r envelope pore protein 16-2, chloroplastic OS=Arabidopsis thaliana (sp|q0wmz5|op162_arath : 18
42 1)
43 1)
44 1)
45 1)
46 t-version=v2.1) &
47 t-version=v2.1) &
48 t-version=v2.1) &
49 t-version=v2.1) &
50 1 annot-version=v2.1) &
51 1 annot-version=v2.1) &
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1 annot-version=v2.1) &

1 annot-version=v2.1) &

xisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)

xisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)

xisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)

xisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)

xisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)

xisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)

xisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)

xisome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)

olinate synthase, chloroplastic OS=Arabidopsis thaliana (sp|q9fgs4|nada_arath : 152.0)

olinate synthase, chloroplastic OS=Arabidopsis thaliana (sp|q9fgs4|nada_arath : 152.0)

olinate synthase, chloroplastic OS=Arabidopsis thaliana (sp|q9fgs4|nada_arath : 152.0)

olinate synthase, chloroplastic OS=Arabidopsis thaliana (sp|q9fgs4|nada_arath : 152.0)

hvul.011G001200.2.v2.1 annot-version=v2.1) &

hvul.011G001200.2.v2.1 annot-version=v2.1) &

hvul.011G001200.2.v2.1 annot-version=v2.1) &

hvul.011G001200.2.v2.1 annot-version=v2.1) &

hvul.011G001200.2.v2.1 annot-version=v2.1) &

hvul.011G001200.2.v2.1 annot-version=v2.1) &

hvul.011G001200.2.v2.1 annot-version=v2.1) &

hvul.011G001200.2.v2.1 annot-version=v2.1) &

in ORANGE, chloroplastic OS=Arabidopsis thaliana (sp|q9fkf4|orang_arath : 453.0)

r2.1 annot-version=v2.1) &

r2.1 annot-version=v2.1) &

r2.1 annot-version=v2.1) &

r2.1 annot-version=v2.1) &

nain-containing protein At1g03370 OS=Arabidopsis thaliana (sp|q9zvt9|c2gr1_arath : 135.0)

nain-containing protein At1g03370 OS=Arabidopsis thaliana (sp|q9zvt9|c2gr1_arath : 135.0)

ul.L002537.1.v2.1 annot-version=v2.1) &

ul.L002537.1.v2.1 annot-version=v2.1) &

=v2.1) &

=v2.1) &

=v2.1) &

=v2.1) &

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

ith : 310.0)

Do not distribute

11400 ID=Phvul.007G211400.1.v2.1 annot-version=v2.1) &
11400 ID=Phvul.007G211400.1.v2.1 annot-version=v2.1) &

=Phvul.008G115900.1 locus=Phvul.008G115900 ID=Phvul.008G115900.1.v2.1 annot-version=v2.1) &
=Phvul.008G115900.1 locus=Phvul.008G115900 ID=Phvul.008G115900.1.v2.1 annot-version=v2.1) &

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

)
)
)
)

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

il.008G290300 ID=Phvul.008G290300.1.v2.1 annot-version=v2.1) &
il.008G290300 ID=Phvul.008G290300.1.v2.1 annot-version=v2.1) &
il.008G290300 ID=Phvul.008G290300.1.v2.1 annot-version=v2.1) &
il.008G290300 ID=Phvul.008G290300.1.v2.1 annot-version=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30 L1G160800.3 locus=Phvul.011G160800 ID=Phvul.011G160800.3.v2.1 annot-version=v2.1) &
31 L1G160800.3 locus=Phvul.011G160800 ID=Phvul.011G160800.3.v2.1 annot-version=v2.1) &
32 L1G160800.3 locus=Phvul.011G160800 ID=Phvul.011G160800.3.v2.1 annot-version=v2.1) &
33 L1G160800.3 locus=Phvul.011G160800 ID=Phvul.011G160800.3.v2.1 annot-version=v2.1) &
34 L1G160800.3 locus=Phvul.011G160800 ID=Phvul.011G160800.3.v2.1 annot-version=v2.1) &
35 L1G160800.3 locus=Phvul.011G160800 ID=Phvul.011G160800.3.v2.1 annot-version=v2.1) &
36 L1G160800.3 locus=Phvul.011G160800 ID=Phvul.011G160800.3.v2.1 annot-version=v2.1) &
37 nsrb1_orysj : 235.0)
38 nsrb1_orysj : 235.0)
39 nsrb1_orysj : 235.0)
40 nsrb1_orysj : 235.0)
41 nsrb1_orysj : 235.0)
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

hvu1.001G268700.1 locus=Phvu1.001G268700 ID=Phvu1.001G268700.1.v2.1 annot-version=v2.1) &
hvu1.001G268700.1 locus=Phvu1.001G268700 ID=Phvu1.001G268700.1.v2.1 annot-version=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

)
)
)
)
)
)
)
)
)

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

)

l.0)

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

.9)
.9)
.9)
.9)
.9)
.9)
.9)
.9)

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

hvvul.009G259000.1 locus=Phvvul.009G259000 ID=Phvvul.009G259000.1.v2.1 annot-version=v2.1) &
hvvul.009G259000.1 locus=Phvvul.009G259000 ID=Phvvul.009G259000.1.v2.1 annot-version=v2.1) &
hvvul.009G259000.1 locus=Phvvul.009G259000 ID=Phvvul.009G259000.1.v2.1 annot-version=v2.1) &
hvvul.009G259000.1 locus=Phvvul.009G259000 ID=Phvvul.009G259000.1.v2.1 annot-version=v2.1) &

1
2
3 L1G160800.3 locus=Phvul.011G160800 ID=Phvul.011G160800.3.v2.1 annot-version=v2.1) &
4 L1G160800.3 locus=Phvul.011G160800 ID=Phvul.011G160800.3.v2.1 annot-version=v2.1) &
5 L1G160800.3 locus=Phvul.011G160800 ID=Phvul.011G160800.3.v2.1 annot-version=v2.1) &
6 L1G160800.3 locus=Phvul.011G160800 ID=Phvul.011G160800.3.v2.1 annot-version=v2.1) &
7 L1G160800.3 locus=Phvul.011G160800 ID=Phvul.011G160800.3.v2.1 annot-version=v2.1) &
8 L1G160800.3 locus=Phvul.011G160800 ID=Phvul.011G160800.3.v2.1 annot-version=v2.1) &
9 L1G160800.3 locus=Phvul.011G160800 ID=Phvul.011G160800.3.v2.1 annot-version=v2.1) &
10 L1G160800.3 locus=Phvul.011G160800 ID=Phvul.011G160800.3.v2.1 annot-version=v2.1) &
11
12
13
14
15

16 i5_arath : 1349.0)
17 i5_arath : 1349.0)
18 i5_arath : 1349.0)
19 i5_arath : 1349.0)
20 i5_arath : 1349.0)
21 i5_arath : 1349.0)
22 i5_arath : 1349.0)
23 i5_arath : 1349.0)
24 i5_arath : 1349.0)
25 i5_arath : 1349.0)
26 i5_arath : 1349.0)
27
28
29
30
31

32 ranscript=Phvul.008G004400.1 locus=Phvul.008G004400 ID=Phvul.008G004400.1.v2.1 annot-versic
33 ranscript=Phvul.008G004400.1 locus=Phvul.008G004400 ID=Phvul.008G004400.1.v2.1 annot-versic
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1261.0)
1261.0)

.0)
.0)
.0)

Do not distribute

- 1
- 2
- 3 ith : 601.0)
- 4 ith : 601.0)
- 5 ith : 601.0)
- 6 ith : 601.0)
- 7 ith : 601.0)
- 8 ith : 601.0)
- 9 ith : 601.0)
- 10 ith : 601.0)
- 11 ith : 601.0)
- 12 ith : 601.0)
- 13 ith : 601.0)
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

:8.0)
:8.0)
:8.0)
:8.0)

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

&
&

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

0G135701.1.v2.1 annot-version=v2.1) &
0G135701.1.v2.1 annot-version=v2.1) &
0G135701.1.v2.1 annot-version=v2.1) &
0G135701.1.v2.1 annot-version=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

gn=v2.1) &
gn=v2.1) &

Do not distribute

| | miRNA_Acc. | Target_Acc. | Expectation | UPE\$ | miRNA_start | miRNA_end |
|----|--------------|--------------------|-------------|-------|-------------|-----------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | uagcuuaucağa | Phvul.004G023066.1 | 3 | -1 | 1 | 22 |
| 4 | uagcuuaucağa | Phvul.004G023066.1 | 3 | -1 | 1 | 22 |
| 5 | uagcuuaucağa | Phvul.004G023066.1 | 3 | -1 | 1 | 23 |
| 6 | uagcuuaucağa | Phvul.002G097400.1 | 3.5 | -1 | 1 | 22 |
| 7 | uagcuuaucağa | Phvul.002G097400.1 | 3.5 | -1 | 1 | 22 |
| 8 | uagcuuaucağa | Phvul.002G097400.1 | 3.5 | -1 | 1 | 23 |
| 9 | uagcuuaucağa | Phvul.002G097400.1 | 3.5 | -1 | 1 | 22 |
| 10 | uagcuuaucağa | Phvul.006G008480.2 | 3.5 | -1 | 1 | 22 |
| 11 | uagcuuaucağa | Phvul.006G008480.1 | 3.5 | -1 | 1 | 22 |
| 12 | uagcuuaucağa | Phvul.006G008480.2 | 3.5 | -1 | 1 | 22 |
| 13 | uagcuuaucağa | Phvul.006G008480.1 | 3.5 | -1 | 1 | 22 |
| 14 | uagcuuaucağa | Phvul.006G008480.2 | 3.5 | -1 | 1 | 22 |
| 15 | uagcuuaucağa | Phvul.006G008480.1 | 3.5 | -1 | 1 | 23 |
| 16 | uagcuuaucağa | Phvul.006G008480.2 | 3.5 | -1 | 1 | 23 |
| 17 | uagcuuaucağa | Phvul.006G008480.1 | 3.5 | -1 | 1 | 23 |
| 18 | uagcuuaucağa | Phvul.006G029000.1 | 3.5 | -1 | 1 | 22 |
| 19 | uagcuuaucağa | Phvul.006G029000.1 | 3.5 | -1 | 1 | 22 |
| 20 | uagcuuaucağa | Phvul.006G029000.1 | 3.5 | -1 | 1 | 22 |
| 21 | uagcuuaucağa | Phvul.006G110300.1 | 3.5 | -1 | 1 | 22 |
| 22 | uagcuuaucağa | Phvul.006G110300.1 | 3.5 | -1 | 1 | 22 |
| 23 | uagcuuaucağa | Phvul.006G110300.1 | 3.5 | -1 | 1 | 23 |
| 24 | uagcuuaucağa | Phvul.007G191600.1 | 3.5 | -1 | 1 | 22 |
| 25 | uagcuuaucağa | Phvul.007G191600.1 | 3.5 | -1 | 1 | 22 |
| 26 | uagcuuaucağa | Phvul.007G191600.1 | 3.5 | -1 | 1 | 23 |
| 27 | uagcuuaucağa | Phvul.001G070000.1 | 4 | -1 | 1 | 22 |
| 28 | uagcuuaucağa | Phvul.001G070000.1 | 4 | -1 | 1 | 22 |
| 29 | uagcuuaucağa | Phvul.001G070000.1 | 4 | -1 | 1 | 23 |
| 30 | uagcuuaucağa | Phvul.001G264600.2 | 4 | -1 | 1 | 22 |
| 31 | uagcuuaucağa | Phvul.001G264600.1 | 4 | -1 | 1 | 22 |
| 32 | uagcuuaucağa | Phvul.001G264600.2 | 4 | -1 | 1 | 22 |
| 33 | uagcuuaucağa | Phvul.001G264600.1 | 4 | -1 | 1 | 22 |
| 34 | uagcuuaucağa | Phvul.001G264600.2 | 4 | -1 | 1 | 22 |
| 35 | uagcuuaucağa | Phvul.001G264600.1 | 4 | -1 | 1 | 22 |
| 36 | uagcuuaucağa | Phvul.001G264600.2 | 4 | -1 | 1 | 23 |
| 37 | uagcuuaucağa | Phvul.001G264600.1 | 4 | -1 | 1 | 23 |
| 38 | uagcuuaucağa | Phvul.002G153500.1 | 4 | -1 | 1 | 22 |
| 39 | uagcuuaucağa | Phvul.002G153500.1 | 4 | -1 | 1 | 22 |
| 40 | uagcuuaucağa | Phvul.002G153500.1 | 4 | -1 | 1 | 23 |
| 41 | uagcuuaucağa | Phvul.003G092500.1 | 4 | -1 | 1 | 22 |
| 42 | uagcuuaucağa | Phvul.003G092500.1 | 4 | -1 | 1 | 22 |
| 43 | uagcuuaucağa | Phvul.004G000300.1 | 4 | -1 | 1 | 22 |
| 44 | uagcuuaucağa | Phvul.004G000300.1 | 4 | -1 | 1 | 22 |
| 45 | uagcuuaucağa | Phvul.004G000300.1 | 4 | -1 | 1 | 23 |
| 46 | uagcuuaucağa | Phvul.004G126100.1 | 4 | -1 | 1 | 22 |
| 47 | uagcuuaucağa | Phvul.004G126100.1 | 4 | -1 | 1 | 22 |
| 48 | uagcuuaucağa | Phvul.004G126100.1 | 4 | -1 | 1 | 23 |
| 49 | uagcuuaucağa | Phvul.005G063700.2 | 4 | -1 | 1 | 22 |
| 50 | uagcuuaucağa | Phvul.005G063700.1 | 4 | -1 | 1 | 22 |
| 51 | uagcuuaucağa | Phvul.005G063700.2 | 4 | -1 | 1 | 22 |
| 52 | uagcuuaucağa | Phvul.005G063700.1 | 4 | -1 | 1 | 22 |
| 53 | uagcuuaucağa | Phvul.005G063700.1 | 4 | -1 | 1 | 22 |
| 54 | uagcuuaucağa | Phvul.005G063700.2 | 4 | -1 | 1 | 22 |
| 55 | uagcuuaucağa | Phvul.005G063700.1 | 4 | -1 | 1 | 22 |
| 56 | uagcuuaucağa | Phvul.005G063700.2 | 4 | -1 | 1 | 22 |
| 57 | uagcuuaucağa | Phvul.005G063700.1 | 4 | -1 | 1 | 22 |
| 58 | uagcuuaucağa | Phvul.005G063700.2 | 4 | -1 | 1 | 22 |
| 59 | uagcuuaucağa | Phvul.005G063700.1 | 4 | -1 | 1 | 22 |
| 60 | uagcuuaucağa | Phvul.005G063700.1 | 4 | -1 | 1 | 22 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uagcuuaucağa Phvul.005G063700.2 | 4 | -1 | 1 | 23 |
| 3 | uagcuuaucağa Phvul.005G063700.1 | 4 | -1 | 1 | 23 |
| 4 | uagcuuaucağa Phvul.007G020600.1 | 4 | -1 | 1 | 22 |
| 5 | | | | | |
| 6 | uagcuuaucağa Phvul.007G020600.1 | 4 | -1 | 1 | 22 |
| 7 | uagcuuaucağa Phvul.007G020700.1 | 4 | -1 | 1 | 22 |
| 8 | uagcuuaucağa Phvul.007G020700.1 | 4 | -1 | 1 | 22 |
| 9 | | | | | |
| 10 | uagcuuaucağa Phvul.007G080800.1 | 4 | -1 | 1 | 22 |
| 11 | uagcuuaucağa Phvul.007G080800.1 | 4 | -1 | 1 | 22 |
| 12 | uagcuuaucağa Phvul.007G080800.1 | 4 | -1 | 1 | 23 |
| 13 | | | | | |
| 14 | uagcuuaucağa Phvul.007G254000.2 | 4 | -1 | 1 | 22 |
| 15 | uagcuuaucağa Phvul.007G254000.1 | 4 | -1 | 1 | 22 |
| 16 | uagcuuaucağa Phvul.007G254000.2 | 4 | -1 | 1 | 22 |
| 17 | | | | | |
| 18 | uagcuuaucağa Phvul.007G254000.1 | 4 | -1 | 1 | 22 |
| 19 | uagcuuaucağa Phvul.007G254000.2 | 4 | -1 | 1 | 23 |
| 20 | uagcuuaucağa Phvul.007G254000.1 | 4 | -1 | 1 | 23 |
| 21 | | | | | |
| 22 | uagcuuaucağa Phvul.008G212500.1 | 4 | -1 | 1 | 22 |
| 23 | uagcuuaucağa Phvul.008G212500.1 | 4 | -1 | 1 | 22 |
| 24 | uagcuuaucağa Phvul.008G212500.1 | 4 | -1 | 1 | 23 |
| 25 | | | | | |
| 26 | uagcuuaucağa Phvul.008G266300.1 | 4 | -1 | 1 | 22 |
| 27 | uagcuuaucağa Phvul.008G266300.1 | 4 | -1 | 1 | 22 |
| 28 | uagcuuaucağa Phvul.008G266300.1 | 4 | -1 | 1 | 23 |
| 29 | | | | | |
| 30 | uagcuuaucağa Phvul.011G002600.1 | 4 | -1 | 1 | 22 |
| 31 | uagcuuaucağa Phvul.011G002600.1 | 4 | -1 | 1 | 22 |
| 32 | uagcuuaucağa Phvul.011G002600.1 | 4 | -1 | 1 | 23 |
| 33 | | | | | |
| 34 | uagcuuaucağa Phvul.011G194501.1 | 4 | -1 | 1 | 22 |
| 35 | uagcuuaucağa Phvul.011G194501.1 | 4 | -1 | 1 | 22 |
| 36 | uagcuuaucağa Phvul.011G194501.1 | 4 | -1 | 1 | 23 |
| 37 | | | | | |
| 38 | uagcuuaucağa Phvul.L000308.2 | 4 | -1 | 1 | 22 |
| 39 | uagcuuaucağa Phvul.L000308.1 | 4 | -1 | 1 | 22 |
| 40 | uagcuuaucağa Phvul.L000308.2 | 4 | -1 | 1 | 22 |
| 41 | | | | | |
| 42 | uagcuuaucağa Phvul.L000308.1 | 4 | -1 | 1 | 22 |
| 43 | uagcuuaucağa Phvul.L000308.2 | 4 | -1 | 1 | 23 |
| 44 | uagcuuaucağa Phvul.L000308.1 | 4 | -1 | 1 | 23 |
| 45 | | | | | |
| 46 | uagcuuaucağa Phvul.001G021750.1 | 4.5 | -1 | 1 | 22 |
| 47 | uagcuuaucağa Phvul.001G021750.1 | 4.5 | -1 | 1 | 22 |
| 48 | uagcuuaucağa Phvul.001G021750.1 | 4.5 | -1 | 1 | 23 |
| 49 | | | | | |
| 50 | uagcuuaucağa Phvul.001G168600.1 | 4.5 | -1 | 1 | 22 |
| 51 | uagcuuaucağa Phvul.001G168600.1 | 4.5 | -1 | 1 | 22 |
| 52 | uagcuuaucağa Phvul.002G010100.1 | 4.5 | -1 | 1 | 22 |
| 53 | uagcuuaucağa Phvul.002G010100.1 | 4.5 | -1 | 1 | 22 |
| 54 | | | | | |
| 55 | uagcuuaucağa Phvul.002G010100.1 | 4.5 | -1 | 1 | 23 |
| 56 | uagcuuaucağa Phvul.002G149100.1 | 4.5 | -1 | 1 | 22 |
| 57 | uagcuuaucağa Phvul.002G149100.1 | 4.5 | -1 | 1 | 22 |
| 58 | | | | | |
| 59 | uagcuuaucağa Phvul.002G155200.1 | 4.5 | -1 | 1 | 22 |
| 60 | uagcuuaucağa Phvul.002G155200.1 | 4.5 | -1 | 1 | 22 |
| | uagcuuaucağa Phvul.002G211400.1 | 4.5 | -1 | 1 | 22 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uagcuuaucağa Phvul.002G211400.1 | 4.5 | -1 | 1 | 22 |
| 3 | uagcuuaucağa Phvul.002G211400.1 | 4.5 | -1 | 1 | 23 |
| 4 | uagcuuaucağa Phvul.003G069400.1 | 4.5 | -1 | 1 | 22 |
| 5 | uagcuuaucağa Phvul.003G069400.1 | 4.5 | -1 | 1 | 22 |
| 6 | uagcuuaucağa Phvul.003G141800.1 | 4.5 | -1 | 1 | 22 |
| 7 | uagcuuaucağa Phvul.003G141800.1 | 4.5 | -1 | 1 | 22 |
| 8 | uagcuuaucağa Phvul.003G141800.1 | 4.5 | -1 | 1 | 22 |
| 9 | uagcuuaucağa Phvul.003G141800.1 | 4.5 | -1 | 1 | 22 |
| 10 | uagcuuaucağa Phvul.003G141800.1 | 4.5 | -1 | 1 | 23 |
| 11 | uagcuuaucağa Phvul.003G239800.1 | 4.5 | -1 | 1 | 22 |
| 12 | uagcuuaucağa Phvul.003G239800.1 | 4.5 | -1 | 1 | 22 |
| 13 | uagcuuaucağa Phvul.003G239800.1 | 4.5 | -1 | 1 | 22 |
| 14 | uagcuuaucağa Phvul.003G239800.1 | 4.5 | -1 | 1 | 23 |
| 15 | uagcuuaucağa Phvul.004G053900.1 | 4.5 | -1 | 1 | 22 |
| 16 | uagcuuaucağa Phvul.004G053900.1 | 4.5 | -1 | 1 | 22 |
| 17 | uagcuuaucağa Phvul.004G053900.1 | 4.5 | -1 | 1 | 22 |
| 18 | uagcuuaucağa Phvul.004G157700.1 | 4.5 | -1 | 1 | 22 |
| 19 | uagcuuaucağa Phvul.004G157700.1 | 4.5 | -1 | 1 | 22 |
| 20 | uagcuuaucağa Phvul.004G157700.1 | 4.5 | -1 | 1 | 22 |
| 21 | uagcuuaucağa Phvul.004G157700.1 | 4.5 | -1 | 1 | 23 |
| 22 | uagcuuaucağa Phvul.004G177000.3 | 4.5 | -1 | 1 | 22 |
| 23 | uagcuuaucağa Phvul.004G177000.2 | 4.5 | -1 | 1 | 22 |
| 24 | uagcuuaucağa Phvul.004G177000.4 | 4.5 | -1 | 1 | 22 |
| 25 | uagcuuaucağa Phvul.004G177000.4 | 4.5 | -1 | 1 | 22 |
| 26 | uagcuuaucağa Phvul.004G177000.1 | 4.5 | -1 | 1 | 22 |
| 27 | uagcuuaucağa Phvul.004G177000.3 | 4.5 | -1 | 1 | 22 |
| 28 | uagcuuaucağa Phvul.004G177000.2 | 4.5 | -1 | 1 | 22 |
| 29 | uagcuuaucağa Phvul.004G177000.2 | 4.5 | -1 | 1 | 22 |
| 30 | uagcuuaucağa Phvul.004G177000.4 | 4.5 | -1 | 1 | 22 |
| 31 | uagcuuaucağa Phvul.004G177000.1 | 4.5 | -1 | 1 | 22 |
| 32 | uagcuuaucağa Phvul.004G177000.3 | 4.5 | -1 | 1 | 22 |
| 33 | uagcuuaucağa Phvul.004G177000.2 | 4.5 | -1 | 1 | 23 |
| 34 | uagcuuaucağa Phvul.004G177000.2 | 4.5 | -1 | 1 | 23 |
| 35 | uagcuuaucağa Phvul.004G177000.4 | 4.5 | -1 | 1 | 23 |
| 36 | uagcuuaucağa Phvul.004G177000.1 | 4.5 | -1 | 1 | 23 |
| 37 | uagcuuaucağa Phvul.004G177000.1 | 4.5 | -1 | 1 | 23 |
| 38 | uagcuuaucağa Phvul.006G103900.1 | 4.5 | -1 | 1 | 22 |
| 39 | uagcuuaucağa Phvul.006G103900.1 | 4.5 | -1 | 1 | 22 |
| 40 | uagcuuaucağa Phvul.006G103900.1 | 4.5 | -1 | 1 | 22 |
| 41 | uagcuuaucağa Phvul.006G103900.1 | 4.5 | -1 | 1 | 23 |
| 42 | uagcuuaucağa Phvul.006G158500.2 | 4.5 | -1 | 1 | 22 |
| 43 | uagcuuaucağa Phvul.006G158500.1 | 4.5 | -1 | 1 | 22 |
| 44 | uagcuuaucağa Phvul.006G158500.2 | 4.5 | -1 | 1 | 22 |
| 45 | uagcuuaucağa Phvul.006G158500.2 | 4.5 | -1 | 1 | 22 |
| 46 | uagcuuaucağa Phvul.006G158500.1 | 4.5 | -1 | 1 | 22 |
| 47 | uagcuuaucağa Phvul.006G158500.2 | 4.5 | -1 | 1 | 23 |
| 48 | uagcuuaucağa Phvul.006G158500.1 | 4.5 | -1 | 1 | 23 |
| 49 | uagcuuaucağa Phvul.006G158500.1 | 4.5 | -1 | 1 | 23 |
| 50 | uagcuuaucağa Phvul.007G054000.2 | 4.5 | -1 | 1 | 22 |
| 51 | uagcuuaucağa Phvul.007G054000.2 | 4.5 | -1 | 1 | 22 |
| 52 | uagcuuaucağa Phvul.007G054000.2 | 4.5 | -1 | 1 | 22 |
| 53 | uagcuuaucağa Phvul.007G054000.2 | 4.5 | -1 | 1 | 23 |
| 54 | uagcuuaucağa Phvul.007G154900.2 | 4.5 | -1 | 1 | 22 |
| 55 | uagcuuaucağa Phvul.007G154900.3 | 4.5 | -1 | 1 | 22 |
| 56 | uagcuuaucağa Phvul.007G154900.9 | 4.5 | -1 | 1 | 22 |
| 57 | uagcuuaucağa Phvul.007G154900.7 | 4.5 | -1 | 1 | 22 |
| 58 | uagcuuaucağa Phvul.007G154900.7 | 4.5 | -1 | 1 | 22 |
| 59 | uagcuuaucağa Phvul.007G154900.6 | 4.5 | -1 | 1 | 22 |
| 60 | uagcuuaucağa Phvul.007G154900.5 | 4.5 | -1 | 1 | 22 |
| | uagcuuaucağa Phvul.007G154900.8 | 4.5 | -1 | 1 | 22 |

| | | | | | |
|----|----------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uagcuuaucağa Phvul.007G154900.4 | 4.5 | -1 | 1 | 22 |
| 3 | uagcuuaucağa Phvul.007G154900.1 | 4.5 | -1 | 1 | 22 |
| 4 | uagcuuaucağa Phvul.007G154900.2 | 4.5 | -1 | 1 | 22 |
| 5 | | | | | |
| 6 | uagcuuaucağa Phvul.007G154900.3 | 4.5 | -1 | 1 | 22 |
| 7 | uagcuuaucağa Phvul.007G154900.9 | 4.5 | -1 | 1 | 22 |
| 8 | uagcuuaucağa Phvul.007G154900.7 | 4.5 | -1 | 1 | 22 |
| 9 | | | | | |
| 10 | uagcuuaucağa Phvul.007G154900.6 | 4.5 | -1 | 1 | 22 |
| 11 | uagcuuaucağa Phvul.007G154900.5 | 4.5 | -1 | 1 | 22 |
| 12 | uagcuuaucağa Phvul.007G154900.8 | 4.5 | -1 | 1 | 22 |
| 13 | | | | | |
| 14 | uagcuuaucağa Phvul.007G154900.4 | 4.5 | -1 | 1 | 22 |
| 15 | uagcuuaucağa Phvul.007G154900.1 | 4.5 | -1 | 1 | 22 |
| 16 | uagcuuaucağa Phvul.007G154900.15 | 4.5 | -1 | 1 | 22 |
| 17 | | | | | |
| 18 | uagcuuaucağa Phvul.007G154900.13 | 4.5 | -1 | 1 | 22 |
| 19 | uagcuuaucağa Phvul.007G154900.14 | 4.5 | -1 | 1 | 22 |
| 20 | uagcuuaucağa Phvul.007G154900.11 | 4.5 | -1 | 1 | 22 |
| 21 | | | | | |
| 22 | uagcuuaucağa Phvul.007G154900.12 | 4.5 | -1 | 1 | 22 |
| 23 | uagcuuaucağa Phvul.007G154900.10 | 4.5 | -1 | 1 | 22 |
| 24 | uagcuuaucağa Phvul.007G154900.15 | 4.5 | -1 | 1 | 22 |
| 25 | | | | | |
| 26 | uagcuuaucağa Phvul.007G154900.13 | 4.5 | -1 | 1 | 22 |
| 27 | uagcuuaucağa Phvul.007G154900.14 | 4.5 | -1 | 1 | 22 |
| 28 | uagcuuaucağa Phvul.007G154900.11 | 4.5 | -1 | 1 | 22 |
| 29 | | | | | |
| 30 | uagcuuaucağa Phvul.007G154900.12 | 4.5 | -1 | 1 | 22 |
| 31 | uagcuuaucağa Phvul.007G154900.10 | 4.5 | -1 | 1 | 22 |
| 32 | uagcuuaucağa Phvul.008G106500.1 | 4.5 | -1 | 1 | 22 |
| 33 | | | | | |
| 34 | uagcuuaucağa Phvul.008G106500.1 | 4.5 | -1 | 1 | 22 |
| 35 | uagcuuaucağa Phvul.009G021300.1 | 4.5 | -1 | 1 | 22 |
| 36 | uagcuuaucağa Phvul.009G021300.1 | 4.5 | -1 | 1 | 22 |
| 37 | | | | | |
| 38 | uagcuuaucağa Phvul.009G021300.1 | 4.5 | -1 | 1 | 23 |
| 39 | uagcuuaucağa Phvul.009G097000.1 | 4.5 | -1 | 1 | 22 |
| 40 | uagcuuaucağa Phvul.009G097000.2 | 4.5 | -1 | 1 | 22 |
| 41 | | | | | |
| 42 | uagcuuaucağa Phvul.009G097000.1 | 4.5 | -1 | 1 | 22 |
| 43 | uagcuuaucağa Phvul.009G097000.2 | 4.5 | -1 | 1 | 22 |
| 44 | uagcuuaucağa Phvul.009G122000.1 | 4.5 | -1 | 1 | 22 |
| 45 | uagcuuaucağa Phvul.009G122000.1 | 4.5 | -1 | 1 | 22 |
| 46 | | | | | |
| 47 | uagcuuaucağa Phvul.009G227900.2 | 4.5 | -1 | 1 | 22 |
| 48 | uagcuuaucağa Phvul.009G227900.3 | 4.5 | -1 | 1 | 22 |
| 49 | uagcuuaucağa Phvul.009G227900.1 | 4.5 | -1 | 1 | 22 |
| 50 | | | | | |
| 51 | uagcuuaucağa Phvul.009G227900.2 | 4.5 | -1 | 1 | 22 |
| 52 | uagcuuaucağa Phvul.009G227900.3 | 4.5 | -1 | 1 | 22 |
| 53 | uagcuuaucağa Phvul.009G227900.1 | 4.5 | -1 | 1 | 22 |
| 54 | | | | | |
| 55 | uagcuuaucağa Phvul.009G227900.2 | 4.5 | -1 | 1 | 23 |
| 56 | uagcuuaucağa Phvul.009G227900.3 | 4.5 | -1 | 1 | 23 |
| 57 | uagcuuaucağa Phvul.009G227900.1 | 4.5 | -1 | 1 | 23 |
| 58 | | | | | |
| 59 | uagcuuaucağa Phvul.010G159600.1 | 4.5 | -1 | 1 | 22 |
| 60 | uagcuuaucağa Phvul.010G159600.1 | 4.5 | -1 | 1 | 22 |
| | uagcuuaucağa Phvul.011G084000.1 | 4.5 | -1 | 1 | 22 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uagcuuaucağa Phvul.011G084000.1 | 4.5 | -1 | 1 | 22 |
| 3 | uagcuuaucağa Phvul.011G084000.1 | 4.5 | -1 | 1 | 23 |
| 4 | uagcuuaucağa Phvul.011G130500.1 | 4.5 | -1 | 1 | 22 |
| 5 | uagcuuaucağa Phvul.011G130500.1 | 4.5 | -1 | 1 | 22 |
| 6 | uagcuuaucağa Phvul.011G130500.1 | 4.5 | -1 | 1 | 22 |
| 7 | uagcuuaucağa Phvul.011G130500.1 | 4.5 | -1 | 1 | 23 |
| 8 | uagcuuaucağa Phvul.011G158500.1 | 4.5 | -1 | 1 | 22 |
| 9 | uagcuuaucağa Phvul.011G158500.1 | 4.5 | -1 | 1 | 22 |
| 10 | uagcuuaucağa Phvul.011G158500.1 | 4.5 | -1 | 1 | 22 |
| 11 | uagcuuaucağa Phvul.011G158500.1 | 4.5 | -1 | 1 | 23 |
| 12 | uagcuuaucağa Phvul.011G198100.1 | 4.5 | -1 | 1 | 22 |
| 13 | uagcuuaucağa Phvul.011G198100.1 | 4.5 | -1 | 1 | 22 |
| 14 | uagcuuaucağa Phvul.011G198100.1 | 4.5 | -1 | 1 | 22 |
| 15 | uagcuuaucağa Phvul.011G198100.1 | 4.5 | -1 | 1 | 23 |
| 16 | uagcuuaucağa Phvul.001G199500.1 | 5 | -1 | 1 | 22 |
| 17 | uagcuuaucağa Phvul.001G199500.1 | 5 | -1 | 1 | 22 |
| 18 | uagcuuaucağa Phvul.001G199500.1 | 5 | -1 | 1 | 22 |
| 19 | uagcuuaucağa Phvul.001G199500.1 | 5 | -1 | 1 | 23 |
| 20 | uagcuuaucağa Phvul.002G005300.2 | 5 | -1 | 1 | 22 |
| 21 | uagcuuaucağa Phvul.002G005300.1 | 5 | -1 | 1 | 22 |
| 22 | uagcuuaucağa Phvul.002G005300.1 | 5 | -1 | 1 | 22 |
| 23 | uagcuuaucağa Phvul.002G005300.2 | 5 | -1 | 1 | 22 |
| 24 | uagcuuaucağa Phvul.002G005300.1 | 5 | -1 | 1 | 22 |
| 25 | uagcuuaucağa Phvul.002G005300.2 | 5 | -1 | 1 | 23 |
| 26 | uagcuuaucağa Phvul.002G005300.1 | 5 | -1 | 1 | 23 |
| 27 | uagcuuaucağa Phvul.002G005300.1 | 5 | -1 | 1 | 22 |
| 28 | uagcuuaucağa Phvul.002G119100.1 | 5 | -1 | 1 | 22 |
| 29 | uagcuuaucağa Phvul.002G119100.1 | 5 | -1 | 1 | 22 |
| 30 | uagcuuaucağa Phvul.002G119100.1 | 5 | -1 | 1 | 23 |
| 31 | uagcuuaucağa Phvul.002G119100.1 | 5 | -1 | 1 | 22 |
| 32 | uagcuuaucağa Phvul.002G132700.1 | 5 | -1 | 1 | 22 |
| 33 | uagcuuaucağa Phvul.002G132700.1 | 5 | -1 | 1 | 22 |
| 34 | uagcuuaucağa Phvul.002G132700.1 | 5 | -1 | 1 | 23 |
| 35 | uagcuuaucağa Phvul.002G141000.2 | 5 | -1 | 1 | 22 |
| 36 | uagcuuaucağa Phvul.002G141000.1 | 5 | -1 | 1 | 22 |
| 37 | uagcuuaucağa Phvul.002G141000.1 | 5 | -1 | 1 | 22 |
| 38 | uagcuuaucağa Phvul.002G141000.2 | 5 | -1 | 1 | 22 |
| 39 | uagcuuaucağa Phvul.002G141000.1 | 5 | -1 | 1 | 22 |
| 40 | uagcuuaucağa Phvul.002G141000.1 | 5 | -1 | 1 | 22 |
| 41 | uagcuuaucağa Phvul.003G131900.1 | 5 | -1 | 1 | 22 |
| 42 | uagcuuaucağa Phvul.003G131900.1 | 5 | -1 | 1 | 22 |
| 43 | uagcuuaucağa Phvul.003G131900.1 | 5 | -1 | 1 | 23 |
| 44 | uagcuuaucağa Phvul.003G131900.1 | 5 | -1 | 1 | 23 |
| 45 | uagcuuaucağa Phvul.003G225700.1 | 5 | -1 | 1 | 23 |
| 46 | uagcuuaucağa Phvul.003G238000.1 | 5 | -1 | 1 | 22 |
| 47 | uagcuuaucağa Phvul.003G238000.1 | 5 | -1 | 1 | 22 |
| 48 | uagcuuaucağa Phvul.003G238000.1 | 5 | -1 | 1 | 22 |
| 49 | uagcuuaucağa Phvul.003G259300.1 | 5 | -1 | 1 | 22 |
| 50 | uagcuuaucağa Phvul.003G259300.1 | 5 | -1 | 1 | 22 |
| 51 | uagcuuaucağa Phvul.003G259300.1 | 5 | -1 | 1 | 23 |
| 52 | uagcuuaucağa Phvul.004G037700.1 | 5 | -1 | 1 | 22 |
| 53 | uagcuuaucağa Phvul.004G037700.3 | 5 | -1 | 1 | 22 |
| 54 | uagcuuaucağa Phvul.004G037700.2 | 5 | -1 | 1 | 22 |
| 55 | uagcuuaucağa Phvul.004G037700.1 | 5 | -1 | 1 | 22 |
| 56 | uagcuuaucağa Phvul.004G037700.3 | 5 | -1 | 1 | 22 |
| 57 | uagcuuaucağa Phvul.004G037700.2 | 5 | -1 | 1 | 22 |
| 58 | uagcuuaucağa Phvul.004G037700.1 | 5 | -1 | 1 | 22 |
| 59 | uagcuuaucağa Phvul.004G037700.2 | 5 | -1 | 1 | 22 |
| 60 | uagcuuaucağa Phvul.004G037700.1 | 5 | -1 | 1 | 23 |

| | | | | | |
|----|----------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uagcuuaucağa Phvul.004G037700.3 | 5 | -1 | 1 | 23 |
| 3 | uagcuuaucağa Phvul.004G037700.2 | 5 | -1 | 1 | 23 |
| 4 | uagcuuaucağa Phvul.004G089300.2 | 5 | -1 | 1 | 22 |
| 5 | uagcuuaucağa Phvul.004G089300.4 | 5 | -1 | 1 | 22 |
| 6 | uagcuuaucağa Phvul.004G089300.4 | 5 | -1 | 1 | 22 |
| 7 | uagcuuaucağa Phvul.004G089300.2 | 5 | -1 | 1 | 22 |
| 8 | uagcuuaucağa Phvul.004G089300.4 | 5 | -1 | 1 | 22 |
| 9 | uagcuuaucağa Phvul.004G089300.4 | 5 | -1 | 1 | 22 |
| 10 | uagcuuaucağa Phvul.004G089300.2 | 5 | -1 | 1 | 23 |
| 11 | uagcuuaucağa Phvul.004G089300.4 | 5 | -1 | 1 | 23 |
| 12 | uagcuuaucağa Phvul.004G174700.1 | 5 | -1 | 1 | 22 |
| 13 | uagcuuaucağa Phvul.004G174700.1 | 5 | -1 | 1 | 22 |
| 14 | uagcuuaucağa Phvul.004G174700.1 | 5 | -1 | 1 | 23 |
| 15 | uagcuuaucağa Phvul.005G125500.1 | 5 | -1 | 1 | 22 |
| 16 | uagcuuaucağa Phvul.005G125500.1 | 5 | -1 | 1 | 22 |
| 17 | uagcuuaucağa Phvul.005G125500.1 | 5 | -1 | 1 | 22 |
| 18 | uagcuuaucağa Phvul.006G044400.1 | 5 | -1 | 1 | 22 |
| 19 | uagcuuaucağa Phvul.006G044400.1 | 5 | -1 | 1 | 22 |
| 20 | uagcuuaucağa Phvul.006G044400.1 | 5 | -1 | 1 | 22 |
| 21 | uagcuuaucağa Phvul.006G044400.1 | 5 | -1 | 1 | 23 |
| 22 | uagcuuaucağa Phvul.007G072700.3 | 5 | -1 | 1 | 22 |
| 23 | uagcuuaucağa Phvul.007G072700.9 | 5 | -1 | 1 | 22 |
| 24 | uagcuuaucağa Phvul.007G072700.9 | 5 | -1 | 1 | 22 |
| 25 | uagcuuaucağa Phvul.007G072700.8 | 5 | -1 | 1 | 22 |
| 26 | uagcuuaucağa Phvul.007G072700.6 | 5 | -1 | 1 | 22 |
| 27 | uagcuuaucağa Phvul.007G072700.7 | 5 | -1 | 1 | 22 |
| 28 | uagcuuaucağa Phvul.007G072700.7 | 5 | -1 | 1 | 22 |
| 29 | uagcuuaucağa Phvul.007G072700.2 | 5 | -1 | 1 | 22 |
| 30 | uagcuuaucağa Phvul.007G072700.5 | 5 | -1 | 1 | 22 |
| 31 | uagcuuaucağa Phvul.007G072700.3 | 5 | -1 | 1 | 22 |
| 32 | uagcuuaucağa Phvul.007G072700.9 | 5 | -1 | 1 | 22 |
| 33 | uagcuuaucağa Phvul.007G072700.8 | 5 | -1 | 1 | 22 |
| 34 | uagcuuaucağa Phvul.007G072700.6 | 5 | -1 | 1 | 22 |
| 35 | uagcuuaucağa Phvul.007G072700.7 | 5 | -1 | 1 | 22 |
| 36 | uagcuuaucağa Phvul.007G072700.2 | 5 | -1 | 1 | 22 |
| 37 | uagcuuaucağa Phvul.007G072700.5 | 5 | -1 | 1 | 22 |
| 38 | uagcuuaucağa Phvul.007G072700.12 | 5 | -1 | 1 | 22 |
| 39 | uagcuuaucağa Phvul.007G072700.13 | 5 | -1 | 1 | 22 |
| 40 | uagcuuaucağa Phvul.007G072700.10 | 5 | -1 | 1 | 22 |
| 41 | uagcuuaucağa Phvul.007G072700.11 | 5 | -1 | 1 | 22 |
| 42 | uagcuuaucağa Phvul.007G072700.12 | 5 | -1 | 1 | 22 |
| 43 | uagcuuaucağa Phvul.007G072700.13 | 5 | -1 | 1 | 22 |
| 44 | uagcuuaucağa Phvul.007G072700.10 | 5 | -1 | 1 | 22 |
| 45 | uagcuuaucağa Phvul.007G072700.11 | 5 | -1 | 1 | 22 |
| 46 | uagcuuaucağa Phvul.007G072700.12 | 5 | -1 | 1 | 22 |
| 47 | uagcuuaucağa Phvul.007G072700.13 | 5 | -1 | 1 | 22 |
| 48 | uagcuuaucağa Phvul.007G072700.10 | 5 | -1 | 1 | 22 |
| 49 | uagcuuaucağa Phvul.007G072700.11 | 5 | -1 | 1 | 22 |
| 50 | uagcuuaucağa Phvul.007G215400.1 | 5 | -1 | 1 | 22 |
| 51 | uagcuuaucağa Phvul.007G215400.1 | 5 | -1 | 1 | 22 |
| 52 | uagcuuaucağa Phvul.007G215400.1 | 5 | -1 | 1 | 23 |
| 53 | uagcuuaucağa Phvul.007G249800.1 | 5 | -1 | 1 | 22 |
| 54 | uagcuuaucağa Phvul.007G249800.1 | 5 | -1 | 1 | 22 |
| 55 | uagcuuaucağa Phvul.007G249800.1 | 5 | -1 | 1 | 22 |
| 56 | uagcuuaucağa Phvul.007G249800.1 | 5 | -1 | 1 | 23 |
| 57 | uagcuuaucağa Phvul.008G074600.3 | 5 | -1 | 1 | 22 |
| 58 | uagcuuaucağa Phvul.008G074600.2 | 5 | -1 | 1 | 22 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uagcuuaucağa Phvul.008G074600.4 | 5 | -1 | 1 | 22 |
| 3 | uagcuuaucağa Phvul.008G074600.1 | 5 | -1 | 1 | 22 |
| 4 | uagcuuaucağa Phvul.008G074600.3 | 5 | -1 | 1 | 22 |
| 5 | | | | | |
| 6 | uagcuuaucağa Phvul.008G074600.2 | 5 | -1 | 1 | 22 |
| 7 | uagcuuaucağa Phvul.008G074600.4 | 5 | -1 | 1 | 22 |
| 8 | uagcuuaucağa Phvul.008G074600.1 | 5 | -1 | 1 | 22 |
| 9 | | | | | |
| 10 | uagcuuaucağa Phvul.008G123400.1 | 5 | -1 | 1 | 22 |
| 11 | uagcuuaucağa Phvul.008G123400.1 | 5 | -1 | 1 | 22 |
| 12 | uagcuuaucağa Phvul.008G129500.1 | 5 | -1 | 1 | 22 |
| 13 | uagcuuaucağa Phvul.008G129500.1 | 5 | -1 | 1 | 22 |
| 14 | uagcuuaucağa Phvul.008G129500.1 | 5 | -1 | 1 | 22 |
| 15 | uagcuuaucağa Phvul.008G129500.1 | 5 | -1 | 1 | 23 |
| 16 | uagcuuaucağa Phvul.008G164600.1 | 5 | -1 | 1 | 22 |
| 17 | uagcuuaucağa Phvul.008G164600.1 | 5 | -1 | 1 | 22 |
| 18 | uagcuuaucağa Phvul.008G164600.1 | 5 | -1 | 1 | 22 |
| 19 | uagcuuaucağa Phvul.008G164600.1 | 5 | -1 | 1 | 23 |
| 20 | uagcuuaucağa Phvul.008G225300.1 | 5 | -1 | 1 | 23 |
| 21 | uagcuuaucağa Phvul.008G230200.1 | 5 | -1 | 1 | 23 |
| 22 | uagcuuaucağa Phvul.008G230200.1 | 5 | -1 | 1 | 23 |
| 23 | uagcuuaucağa Phvul.009G030500.1 | 5 | -1 | 1 | 22 |
| 24 | uagcuuaucağa Phvul.009G030500.1 | 5 | -1 | 1 | 22 |
| 25 | uagcuuaucağa Phvul.009G030500.1 | 5 | -1 | 1 | 22 |
| 26 | uagcuuaucağa Phvul.009G030500.1 | 5 | -1 | 1 | 23 |
| 27 | uagcuuaucağa Phvul.009G099700.1 | 5 | -1 | 1 | 22 |
| 28 | uagcuuaucağa Phvul.009G099700.1 | 5 | -1 | 1 | 22 |
| 29 | uagcuuaucağa Phvul.009G099700.1 | 5 | -1 | 1 | 22 |
| 30 | uagcuuaucağa Phvul.009G099700.1 | 5 | -1 | 1 | 23 |
| 31 | uagcuuaucağa Phvul.009G233000.1 | 5 | -1 | 1 | 22 |
| 32 | uagcuuaucağa Phvul.009G233000.1 | 5 | -1 | 1 | 22 |
| 33 | uagcuuaucağa Phvul.009G233000.1 | 5 | -1 | 1 | 22 |
| 34 | uagcuuaucağa Phvul.009G233000.1 | 5 | -1 | 1 | 23 |
| 35 | uagcuuaucağa Phvul.010G021700.1 | 5 | -1 | 1 | 22 |
| 36 | uagcuuaucağa Phvul.010G021700.1 | 5 | -1 | 1 | 22 |
| 37 | uagcuuaucağa Phvul.010G021700.1 | 5 | -1 | 1 | 22 |
| 38 | uagcuuaucağa Phvul.010G021700.1 | 5 | -1 | 1 | 23 |
| 39 | uagcuuaucağa Phvul.010G104900.2 | 5 | -1 | 1 | 22 |
| 40 | uagcuuaucağa Phvul.010G104900.2 | 5 | -1 | 1 | 22 |
| 41 | uagcuuaucağa Phvul.010G104900.2 | 5 | -1 | 1 | 22 |
| 42 | uagcuuaucağa Phvul.010G104900.2 | 5 | -1 | 1 | 23 |
| 43 | uagcuuaucağa Phvul.010G129400.1 | 5 | -1 | 1 | 22 |
| 44 | uagcuuaucağa Phvul.010G129400.1 | 5 | -1 | 1 | 22 |
| 45 | uagcuuaucağa Phvul.010G129400.1 | 5 | -1 | 1 | 22 |
| 46 | uagcuuaucağa Phvul.010G129400.1 | 5 | -1 | 1 | 23 |
| 47 | uagcuuaucağa Phvul.010G157900.4 | 5 | -1 | 1 | 22 |
| 48 | uagcuuaucağa Phvul.010G157900.3 | 5 | -1 | 1 | 22 |
| 49 | uagcuuaucağa Phvul.010G157900.2 | 5 | -1 | 1 | 22 |
| 50 | uagcuuaucağa Phvul.010G157900.2 | 5 | -1 | 1 | 22 |
| 51 | uagcuuaucağa Phvul.010G157900.4 | 5 | -1 | 1 | 22 |
| 52 | uagcuuaucağa Phvul.010G157900.3 | 5 | -1 | 1 | 22 |
| 53 | uagcuuaucağa Phvul.010G157900.2 | 5 | -1 | 1 | 22 |
| 54 | uagcuuaucağa Phvul.010G157900.2 | 5 | -1 | 1 | 22 |
| 55 | uagcuuaucağa Phvul.010G157900.4 | 5 | -1 | 1 | 23 |
| 56 | uagcuuaucağa Phvul.010G157900.3 | 5 | -1 | 1 | 23 |
| 57 | uagcuuaucağa Phvul.010G157900.2 | 5 | -1 | 1 | 23 |
| 58 | uagcuuaucağa Phvul.010G157900.2 | 5 | -1 | 1 | 23 |
| 59 | uagcuuaucağa Phvul.011G006200.1 | 5 | -1 | 1 | 22 |
| 60 | uagcuuaucağa Phvul.011G006200.1 | 5 | -1 | 1 | 22 |
| | uagcuuaucağa Phvul.011G006200.1 | 5 | -1 | 1 | 23 |

| | | | | | | |
|----|--------------|--------------------|---|----|---|----|
| 1 | | | | | | |
| 2 | uagcuuaucağa | Phvul.011G161100.1 | 5 | -1 | 1 | 22 |
| 3 | uagcuuaucağa | Phvul.011G161100.1 | 5 | -1 | 1 | 22 |
| 4 | uagcuuaucağa | Phvul.011G161100.1 | 5 | -1 | 1 | 23 |
| 5 | | | | | | |
| 6 | uagcuuaucağa | Phvul.011G161900.1 | 5 | -1 | 1 | 22 |
| 7 | uagcuuaucağa | Phvul.011G161900.1 | 5 | -1 | 1 | 22 |
| 8 | | | | | | |
| 9 | | | | | | |
| 10 | | | | | | |
| 11 | | | | | | |
| 12 | | | | | | |
| 13 | | | | | | |
| 14 | | | | | | |
| 15 | | | | | | |
| 16 | | | | | | |
| 17 | | | | | | |
| 18 | | | | | | |
| 19 | | | | | | |
| 20 | | | | | | |
| 21 | | | | | | |
| 22 | | | | | | |
| 23 | | | | | | |
| 24 | | | | | | |
| 25 | | | | | | |
| 26 | | | | | | |
| 27 | | | | | | |
| 28 | | | | | | |
| 29 | | | | | | |
| 30 | | | | | | |
| 31 | | | | | | |
| 32 | | | | | | |
| 33 | | | | | | |
| 34 | | | | | | |
| 35 | | | | | | |
| 36 | | | | | | |
| 37 | | | | | | |
| 38 | | | | | | |
| 39 | | | | | | |
| 40 | | | | | | |
| 41 | | | | | | |
| 42 | | | | | | |
| 43 | | | | | | |
| 44 | | | | | | |
| 45 | | | | | | |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

Do not distribute

| Target_start | Target_end | miRNA_alignment | Target_alignment | Inhibition | Target_Desc. |
|--------------|------------|-----------------|------------------|-------------|--------------|
| 1193 | 1214 | UAGCUUAUC/ |:AGCACAUUG | Cleavage | pacid=371638 |
| 1193 | 1214 | UAGCUUAUC/ |:AGCACAUUG | Cleavage | pacid=371638 |
| 1192 | 1214 | UAGCUUAUC/ |:AAGCACAUUC | Cleavage | pacid=371638 |
| 1039 | 1060 | UAGCUUAUC/ |:UGAUGAUCA | Cleavage | pacid=371751 |
| 1039 | 1060 | UAGCUUAUC/ |:UGAUGAUCA | Cleavage | pacid=371751 |
| 1038 | 1060 | UAGCUUAUC/ |:CUGAUGAUC/ | Cleavage | pacid=371751 |
| 2781 | 2802 | UAGCUUAUC/ |:AGAACAUUU | Cleavage | pacid=371720 |
| 2784 | 2805 | UAGCUUAUC/ |:AGAACAUUU | Cleavage | pacid=371720 |
| 2781 | 2802 | UAGCUUAUC/ |:AGAACAUUU | Cleavage | pacid=371720 |
| 2784 | 2805 | UAGCUUAUC/ |:AGAACAUUU | Cleavage | pacid=371720 |
| 2780 | 2802 | UAGCUUAUC/ |:UAGAACAUI | Cleavage | pacid=371720 |
| 2783 | 2805 | UAGCUUAUC/ |:UAGAACAUI | Cleavage | pacid=371720 |
| 811 | 832 | UAGCUUAUC/ |:CCCUCUCAG | Cleavage | pacid=371735 |
| 811 | 832 | UAGCUUAUC/ |:CCCUCUCAG | Cleavage | pacid=371735 |
| 810 | 832 | UAGCUUAUC/ |:UCCUCCUCA | Cleavage | pacid=371735 |
| 1572 | 1594 | UAGCUUAUC/ |:UUGACAGUC/ | Cleavage | pacid=371722 |
| 1572 | 1594 | UAGCUUAUC/ |:UUGACAGUC/ | Cleavage | pacid=371722 |
| 1571 | 1594 | UAGCUUAUC/ |:UUUGACAGU | Cleavage | pacid=371722 |
| 3701 | 3722 | UAGCUUAUC/ |:UGAACAUC | Cleavage | pacid=371651 |
| 3701 | 3722 | UAGCUUAUC/ |:UGAACAUC | Cleavage | pacid=371651 |
| 3700 | 3722 | UAGCUUAUC/ |:UUGAACAUC/ | Cleavage | pacid=371651 |
| 263 | 284 | UAGCUUAUC/ |:UCCUAGUC | Translation | pacid=371681 |
| 263 | 284 | UAGCUUAUC/ |:UCCUAGUC | Translation | pacid=371681 |
| 262 | 284 | UAGCUUAUC/ |:CUCCUAGUC | Translation | pacid=371681 |
| 835 | 856 | UAGCUUAUC/ |:UCAACUGU | Cleavage | pacid=371688 |
| 871 | 892 | UAGCUUAUC/ |:UCAACUGU | Cleavage | pacid=371688 |
| 835 | 856 | UAGCUUAUC/ |:UCAACUGU | Cleavage | pacid=371688 |
| 871 | 892 | UAGCUUAUC/ |:UCAACUGU | Cleavage | pacid=371688 |
| 834 | 856 | UAGCUUAUC/ |:UCAAACUG | Cleavage | pacid=371688 |
| 870 | 892 | UAGCUUAUC/ |:UCAAACUG | Cleavage | pacid=371688 |
| 483 | 504 | UAGCUUAUC/ |:ACAACCUCAU | Cleavage | pacid=371764 |
| 483 | 504 | UAGCUUAUC/ |:ACAACCUCAU | Cleavage | pacid=371764 |
| 482 | 504 | UAGCUUAUC/ |:AACACCUCA | Cleavage | pacid=371764 |
| 2079 | 2100 | UAGCUUAUC/ |:UGCACAUC | Cleavage | pacid=371447 |
| 2079 | 2100 | UAGCUUAUC/ |:UGCACAUC | Cleavage | pacid=371447 |
| 1281 | 1302 | UAGCUUAUC/ |:AGUUCAUC | Cleavage | pacid=371616 |
| 1281 | 1302 | UAGCUUAUC/ |:AGUUCAUC | Cleavage | pacid=371616 |
| 1280 | 1302 | UAGCUUAUC/ |:CAGUUCAUC/ | Cleavage | pacid=371616 |
| 3452 | 3473 | UAGCUUAUC/ |:AUAACUUC | Cleavage | pacid=371630 |
| 3452 | 3473 | UAGCUUAUC/ |:AUAACUUC | Cleavage | pacid=371630 |
| 3451 | 3473 | UAGCUUAUC/ |:GAUAACUUC/ | Cleavage | pacid=371630 |
| 1823 | 1846 | UAGCUUAUC/ |:AUAACAUCCA | Cleavage | pacid=371529 |
| 1823 | 1846 | UAGCUUAUC/ |:AUAACAUCCA | Cleavage | pacid=371529 |
| 1823 | 1846 | UAGCUUAUC/ |:AUAACAUCCA | Cleavage | pacid=371529 |

| | | | |
|----|------|---------------------------------------|---------------------------|
| 1 | | | |
| 2 | 2296 | 2317 UAGCUUAUC/ :: : :::::GCAGAAACAC | Cleavage pacid=371754 |
| 3 | 2295 | 2317 UAGCUUAUC/ :: : :::::UGCAGAAAC/ | Cleavage pacid=371754 |
| 4 | 831 | 852 UAGCUUAUC/ ::::: :::::UAGUGAUCA | (Translation pacid=371478 |
| 5 | 831 | 852 UAGCUUAUC/ ::::: :::::UAGUGAUCA | (Translation pacid=371478 |
| 6 | 294 | 315 UAGCUUAUC/ ::::: :::::UGGACAUUG/ | Cleavage pacid=371458 |
| 7 | 294 | 315 UAGCUUAUC/ ::::: :::::UGGACAUUG/ | Cleavage pacid=371458 |
| 8 | 294 | 315 UAGCUUAUC/ ::::: :::::UGGACAUUG/ | Cleavage pacid=371458 |
| 9 | 293 | 315 UAGCUUAUC/ ::::: :::::GUGGACAUU | (Cleavage pacid=371458 |
| 10 | 125 | 146 UAGCUUAUC/ ::: :::::UGAGCACUG | (Cleavage pacid=371449 |
| 11 | 125 | 146 UAGCUUAUC/ ::: :::::UGAGCACUG | (Cleavage pacid=371449 |
| 12 | 125 | 146 UAGCUUAUC/ ::: :::::UGAGCACUG | (Cleavage pacid=371449 |
| 13 | 124 | 146 UAGCUUAUC/ ::: :::::AUGAGCACUC | Cleavage pacid=371449 |
| 14 | 780 | 801 UAGCUUAUC/ ::::: :::::UAGUGAUCA | (Translation pacid=371620 |
| 15 | 780 | 801 UAGCUUAUC/ ::::: :::::UAGUGAUCA | (Translation pacid=371620 |
| 16 | 780 | 801 UAGCUUAUC/ ::::: :::::UAGUGAUCA | (Translation pacid=371620 |
| 17 | 714 | 734 UAGCUUAUC/ ::: :::::ACAGCA-CAGI | Cleavage pacid=371638 |
| 18 | 714 | 734 UAGCUUAUC/ ::: :::::ACAGCA-CAGI | Cleavage pacid=371638 |
| 19 | 714 | 734 UAGCUUAUC/ ::: :::::ACAGCA-CAGI | Cleavage pacid=371638 |
| 20 | 713 | 734 UAGCUUAUC/ ::: :::::CACAGCA-CA | (Cleavage pacid=371638 |
| 21 | 1341 | 1362 UAGCUUAUC/ ::::: :::::UCGACACUG | (Cleavage pacid=371615 |
| 22 | 1258 | 1279 UAGCUUAUC/ ::::: :::::UCGACACUG | (Cleavage pacid=371615 |
| 23 | 1418 | 1439 UAGCUUAUC/ ::::: :::::UCGACACUG | (Cleavage pacid=371615 |
| 24 | 1418 | 1439 UAGCUUAUC/ ::::: :::::UCGACACUG | (Cleavage pacid=371615 |
| 25 | 1414 | 1435 UAGCUUAUC/ ::::: :::::UCGACACUG | (Cleavage pacid=371615 |
| 26 | 1414 | 1435 UAGCUUAUC/ ::::: :::::UCGACACUG | (Cleavage pacid=371615 |
| 27 | 1341 | 1362 UAGCUUAUC/ ::::: :::::UCGACACUG | (Cleavage pacid=371615 |
| 28 | 1258 | 1279 UAGCUUAUC/ ::::: :::::UCGACACUG | (Cleavage pacid=371615 |
| 29 | 1258 | 1279 UAGCUUAUC/ ::::: :::::UCGACACUG | (Cleavage pacid=371615 |
| 30 | 1418 | 1439 UAGCUUAUC/ ::::: :::::UCGACACUG | (Cleavage pacid=371615 |
| 31 | 1414 | 1435 UAGCUUAUC/ ::::: :::::UCGACACUG | (Cleavage pacid=371615 |
| 32 | 1340 | 1362 UAGCUUAUC/ ::::: :::::AUCGACACUC | (Cleavage pacid=371615 |
| 33 | 1257 | 1279 UAGCUUAUC/ ::::: :::::AUCGACACUC | (Cleavage pacid=371615 |
| 34 | 1257 | 1279 UAGCUUAUC/ ::::: :::::AUCGACACUC | (Cleavage pacid=371615 |
| 35 | 1417 | 1439 UAGCUUAUC/ ::::: :::::AUCGACACUC | (Cleavage pacid=371615 |
| 36 | 1413 | 1435 UAGCUUAUC/ ::::: :::::AUCGACACUC | (Cleavage pacid=371615 |
| 37 | 1969 | 1990 UAGCUUAUC/ ::: :::::GCACUAUCAC | Cleavage pacid=371732 |
| 38 | 1969 | 1990 UAGCUUAUC/ ::: :::::GCACUAUCAC | Cleavage pacid=371732 |
| 39 | 1969 | 1990 UAGCUUAUC/ ::: :::::GCACUAUCAC | Cleavage pacid=371732 |
| 40 | 1968 | 1990 UAGCUUAUC/ ::: :::::UGCACUAUC/ | Cleavage pacid=371732 |
| 41 | 441 | 462 UAGCUUAUC/ ::: :::::CCAAGAUCAU | Cleavage pacid=371725 |
| 42 | 441 | 462 UAGCUUAUC/ ::: :::::CCAAGAUCAU | Cleavage pacid=371725 |
| 43 | 671 | 692 UAGCUUAUC/ ::: :::::CCAAGAUCAU | Cleavage pacid=371725 |
| 44 | 441 | 462 UAGCUUAUC/ ::: :::::CCAAGAUCAU | Cleavage pacid=371725 |
| 45 | 671 | 692 UAGCUUAUC/ ::: :::::CCAAGAUCAU | Cleavage pacid=371725 |
| 46 | 671 | 692 UAGCUUAUC/ ::: :::::CCAAGAUCAU | Cleavage pacid=371725 |
| 47 | 440 | 462 UAGCUUAUC/ ::: :::::ACCAAGAUCA | Cleavage pacid=371725 |
| 48 | 670 | 692 UAGCUUAUC/ ::: :::::ACCAAGAUCA | Cleavage pacid=371725 |
| 49 | 454 | 475 UAGCUUAUC/ ::::: :::::UCAGCAUCG | (Translation pacid=371642 |
| 50 | 454 | 475 UAGCUUAUC/ ::::: :::::UCAGCAUCG | (Translation pacid=371642 |
| 51 | 454 | 475 UAGCUUAUC/ ::::: :::::UCAGCAUCG | (Translation pacid=371642 |
| 52 | 453 | 475 UAGCUUAUC/ ::::: :::::UUCAGCAUC | (Translation pacid=371642 |
| 53 | 1920 | 1941 UAGCUUAUC/ ::: :::::UGAGCAUAG | (Cleavage pacid=371663 |
| 54 | 1924 | 1945 UAGCUUAUC/ ::: :::::UGAGCAUAG | (Cleavage pacid=371663 |
| 55 | 1993 | 2014 UAGCUUAUC/ ::: :::::UGAGCAUAG | (Cleavage pacid=371663 |
| 56 | 1993 | 2014 UAGCUUAUC/ ::: :::::UGAGCAUAG | (Cleavage pacid=371663 |
| 57 | 2005 | 2026 UAGCUUAUC/ ::: :::::UGAGCAUAG | (Cleavage pacid=371663 |
| 58 | 2005 | 2026 UAGCUUAUC/ ::: :::::UGAGCAUAG | (Cleavage pacid=371663 |
| 59 | 2005 | 2026 UAGCUUAUC/ ::: :::::UGAGCAUAG | (Cleavage pacid=371663 |
| 60 | 2009 | 2030 UAGCUUAUC/ ::: :::::UGAGCAUAG | (Cleavage pacid=371663 |
| | 2009 | 2030 UAGCUUAUC/ ::: :::::UGAGCAUAG | (Cleavage pacid=371663 |

| | | | |
|----|------|---|--------------|
| 1 | | | |
| 2 | 2097 | 2118 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 3 | 2101 | 2122 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 4 | 1920 | 1941 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 5 | 1924 | 1945 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 6 | 1993 | 2014 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 7 | 2005 | 2026 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 8 | 2005 | 2026 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 9 | 2009 | 2030 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 10 | 2009 | 2030 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 11 | 2097 | 2118 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 12 | 2101 | 2122 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 13 | 1629 | 1650 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 14 | 1827 | 1848 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 15 | 1831 | 1852 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 16 | 1828 | 1849 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 17 | 1832 | 1853 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 18 | 1997 | 2018 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 19 | 1629 | 1650 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 20 | 1827 | 1848 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 21 | 1831 | 1852 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 22 | 1828 | 1849 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 23 | 1832 | 1853 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 24 | 1997 | 2018 UAGCUUAUC/ :::: :::: :::: ::::UGAGCAUAG(Cleavage | pacid=371663 |
| 25 | 1728 | 1749 UAGCUUAUC/ :::: :::: :::: ::::UCCAUAUGA(Cleavage | pacid=371580 |
| 26 | 1728 | 1749 UAGCUUAUC/ :::: :::: :::: ::::UCCAUAUGA(Cleavage | pacid=371580 |
| 27 | 1146 | 1167 UAGCUUAUC/ :::: :::: :::: ::::UCGUCAUCG(Cleavage | pacid=371506 |
| 28 | 1146 | 1167 UAGCUUAUC/ :::: :::: :::: ::::UCGUCAUCG(Cleavage | pacid=371506 |
| 29 | 1145 | 1167 UAGCUUAUC/ :::: :::: :::: ::::UUCGUCAUC(Cleavage | pacid=371506 |
| 30 | 750 | 771 UAGCUUAUC/ :::: :::: :::: ::::AAGACGUCAC(Cleavage | pacid=371507 |
| 31 | 751 | 772 UAGCUUAUC/ :::: :::: :::: ::::AAGACGUCAC(Cleavage | pacid=371507 |
| 32 | 750 | 771 UAGCUUAUC/ :::: :::: :::: ::::AAGACGUCAC(Cleavage | pacid=371507 |
| 33 | 751 | 772 UAGCUUAUC/ :::: :::: :::: ::::AAGACGUCAC(Cleavage | pacid=371507 |
| 34 | 786 | 807 UAGCUUAUC/ :::: :::: :::: ::::UAGUGAUCA(Translation | pacid=371493 |
| 35 | 786 | 807 UAGCUUAUC/ :::: :::: :::: ::::UAGUGAUCA(Translation | pacid=371493 |
| 36 | 2152 | 2173 UAGCUUAUC/ :::: :::: :::: ::::UCUGCAUCA(Cleavage | pacid=371502 |
| 37 | 2237 | 2258 UAGCUUAUC/ :::: :::: :::: ::::UCUGCAUCA(Cleavage | pacid=371502 |
| 38 | 2326 | 2347 UAGCUUAUC/ :::: :::: :::: ::::UCUGCAUCA(Cleavage | pacid=371502 |
| 39 | 2152 | 2173 UAGCUUAUC/ :::: :::: :::: ::::UCUGCAUCA(Cleavage | pacid=371502 |
| 40 | 2237 | 2258 UAGCUUAUC/ :::: :::: :::: ::::UCUGCAUCA(Cleavage | pacid=371502 |
| 41 | 2326 | 2347 UAGCUUAUC/ :::: :::: :::: ::::UCUGCAUCA(Cleavage | pacid=371502 |
| 42 | 2151 | 2173 UAGCUUAUC/ :::: :::: :::: ::::AUCUGCAUCA(Cleavage | pacid=371502 |
| 43 | 2236 | 2258 UAGCUUAUC/ :::: :::: :::: ::::AUCUGCAUCA(Cleavage | pacid=371502 |
| 44 | 2325 | 2347 UAGCUUAUC/ :::: :::: :::: ::::AUCUGCAUCA(Cleavage | pacid=371502 |
| 45 | 908 | 929 UAGCUUAUC/ :::: :::: :::: ::::GGAAAUAUA(Cleavage | pacid=371432 |
| 46 | 908 | 929 UAGCUUAUC/ :::: :::: :::: ::::GGAAAUAUA(Cleavage | pacid=371432 |
| 47 | 1518 | 1539 UAGCUUAUC/ :::: :::: :::: ::::CCAGCAUCUC(Cleavage | pacid=371552 |

| | | | | |
|----|------|------|---|--------------------------|
| 1 | | | | |
| 2 | 1518 | 1539 | UAGCUUAUC/ ::::: : ::: : :::::CCAGCAUCUC | Cleavage pacid=371552 |
| 3 | 1517 | 1539 | UAGCUUAUC/ ::::: : ::: : :::::ACCAGCAUCUC | Cleavage pacid=371552 |
| 4 | 752 | 773 | UAGCUUAUC/ ::::: : ::: : :::::UCAGGAGCAC | Translation pacid=371566 |
| 5 | 752 | 773 | UAGCUUAUC/ ::::: : ::: : :::::UCAGGAGCAC | Translation pacid=371566 |
| 6 | 751 | 773 | UAGCUUAUC/ ::::: : ::: : :::::CUCAGGAGCA | Translation pacid=371566 |
| 7 | 3 | 24 | UAGCUUAUC/ ::::: : ::: : :::::CACACAUCAU | Cleavage pacid=371555 |
| 8 | 3 | 24 | UAGCUUAUC/ ::::: : ::: : :::::CACACAUCAU | Cleavage pacid=371555 |
| 9 | 2 | 24 | UAGCUUAUC/ ::::: : ::: : :::::ACACAUCAU | Cleavage pacid=371555 |
| 10 | 2751 | 2772 | UAGCUUAUC/ ::::: : ::: : :::::UCUACAUGA | Translation pacid=371559 |
| 11 | 2751 | 2772 | UAGCUUAUC/ ::::: : ::: : :::::UCUACAUGA | Translation pacid=371559 |
| 12 | 2750 | 2772 | UAGCUUAUC/ ::::: : ::: : :::::GUCUACAUG | Translation pacid=371559 |
| 13 | 1565 | 1586 | UAGCUUAUC/ ::::: : ::: : :::::GCAGUGGCA | Cleavage pacid=371701 |
| 14 | 1565 | 1586 | UAGCUUAUC/ ::::: : ::: : :::::GCAGUGGCA | Cleavage pacid=371701 |
| 15 | 1564 | 1586 | UAGCUUAUC/ ::::: : ::: : :::::AGCAGUGGC | Cleavage pacid=371701 |
| 16 | 1691 | 1712 | UAGCUUAUC/ ::::: : ::: : :::::UUGGAAUUG | Cleavage pacid=371762 |
| 17 | 1829 | 1850 | UAGCUUAUC/ ::::: : ::: : :::::UUGGAAUUG | Cleavage pacid=371762 |
| 18 | 1691 | 1712 | UAGCUUAUC/ ::::: : ::: : :::::UUGGAAUUG | Cleavage pacid=371762 |
| 19 | 1829 | 1850 | UAGCUUAUC/ ::::: : ::: : :::::UUGGAAUUG | Cleavage pacid=371762 |
| 20 | 1690 | 1712 | UAGCUUAUC/ ::::: : ::: : :::::GUUGGAAUU | Cleavage pacid=371762 |
| 21 | 1828 | 1850 | UAGCUUAUC/ ::::: : ::: : :::::GUUGGAAUU | Cleavage pacid=371762 |
| 22 | 133 | 154 | UAGCUUAUC/ ::::: : ::: : :::::ACAACAUGA | Translation pacid=371760 |
| 23 | 133 | 154 | UAGCUUAUC/ ::::: : ::: : :::::ACAACAUGA | Translation pacid=371760 |
| 24 | 132 | 154 | UAGCUUAUC/ ::::: : ::: : :::::UACAACAUG | Translation pacid=371760 |
| 25 | 863 | 884 | UAGCUUAUC/ ::::: : ::: : :::::UUGGCUUCA | Cleavage pacid=371776 |
| 26 | 863 | 884 | UAGCUUAUC/ ::::: : ::: : :::::UUGGCUUCA | Cleavage pacid=371776 |
| 27 | 862 | 884 | UAGCUUAUC/ ::::: : ::: : :::::UUUGGCUUC | Cleavage pacid=371776 |
| 28 | 685 | 707 | UAGCUUAUC/ ::::: : ::: : :::::AUUUCAUCA | Translation pacid=371755 |
| 29 | 726 | 748 | UAGCUUAUC/ ::::: : ::: : :::::AUUUCAUCA | Translation pacid=371755 |
| 30 | 685 | 707 | UAGCUUAUC/ ::::: : ::: : :::::AUUUCAUCA | Translation pacid=371755 |
| 31 | 726 | 748 | UAGCUUAUC/ ::::: : ::: : :::::AUUUCAUCA | Translation pacid=371755 |
| 32 | 1047 | 1068 | UAGCUUAUC/ ::::: : ::: : :::::UUGACAUUG | Cleavage pacid=371444 |
| 33 | 1047 | 1068 | UAGCUUAUC/ ::::: : ::: : :::::UUGACAUUG | Cleavage pacid=371444 |
| 34 | 1046 | 1068 | UAGCUUAUC/ ::::: : ::: : :::::UUUGACAUU | Cleavage pacid=371444 |
| 35 | 768 | 790 | UAGCUUAUC/ ::::: : ::: : :::::GUCUACUUC | Translation pacid=371478 |
| 36 | 630 | 651 | UAGCUUAUC/ ::::: : ::: : :::::UCUGCAUCA | Cleavage pacid=371479 |
| 37 | 630 | 651 | UAGCUUAUC/ ::::: : ::: : :::::UCUGCAUCA | Cleavage pacid=371479 |
| 38 | 845 | 866 | UAGCUUAUC/ ::::: : ::: : :::::ACAACAUGA | Cleavage pacid=371457 |
| 39 | 845 | 866 | UAGCUUAUC/ ::::: : ::: : :::::ACAACAUGA | Cleavage pacid=371457 |
| 40 | 844 | 866 | UAGCUUAUC/ ::::: : ::: : :::::UACAACAUG | Cleavage pacid=371457 |
| 41 | 1335 | 1356 | UAGCUUAUC/ ::::: : ::: : :::::UUAACAUCC | Cleavage pacid=371619 |
| 42 | 1438 | 1459 | UAGCUUAUC/ ::::: : ::: : :::::UUAACAUCC | Cleavage pacid=371619 |
| 43 | 1523 | 1544 | UAGCUUAUC/ ::::: : ::: : :::::UUAACAUCC | Cleavage pacid=371619 |
| 44 | 1335 | 1356 | UAGCUUAUC/ ::::: : ::: : :::::UUAACAUCC | Cleavage pacid=371619 |
| 45 | 1438 | 1459 | UAGCUUAUC/ ::::: : ::: : :::::UUAACAUCC | Cleavage pacid=371619 |
| 46 | 1523 | 1544 | UAGCUUAUC/ ::::: : ::: : :::::UUAACAUCC | Cleavage pacid=371619 |
| 47 | 1334 | 1356 | UAGCUUAUC/ ::::: : ::: : :::::GUUAACAUC | Cleavage pacid=371619 |

| | | | | |
|----|------|--|----------|--------------|
| 1 | | | | |
| 2 | 1437 | 1459 UAGCUUAUC/:::..... :::: :::::GUUAACAUC | Cleavage | pacid=371619 |
| 3 | 1522 | 1544 UAGCUUAUC/:::..... :::: :::::GUUAACAUC | Cleavage | pacid=371619 |
| 4 | 1415 | 1436 UAGCUUAUC/.....:..... :::.....UUGGUGUUG | Cleavage | pacid=371625 |
| 5 | 1415 | 1436 UAGCUUAUC/.....:..... :::.....UUGGUGUUG | Cleavage | pacid=371625 |
| 6 | 1415 | 1436 UAGCUUAUC/.....:..... :::.....UUGGUGUUG | Cleavage | pacid=371625 |
| 7 | 1415 | 1436 UAGCUUAUC/.....:..... :::.....UUGGUGUUG | Cleavage | pacid=371625 |
| 8 | 1415 | 1436 UAGCUUAUC/.....:..... :::.....UUGGUGUUG | Cleavage | pacid=371625 |
| 9 | 1414 | 1436 UAGCUUAUC/.....:..... :::.....GUUGGUGUU | Cleavage | pacid=371625 |
| 10 | 1414 | 1436 UAGCUUAUC/.....:..... :::.....GUUGGUGUU | Cleavage | pacid=371625 |
| 11 | 1345 | 1366 UAGCUUAUC/ :::: : :::..... ::::GCAGCAACAC | Cleavage | pacid=371625 |
| 12 | 1345 | 1366 UAGCUUAUC/ :::: : :::..... ::::GCAGCAACAC | Cleavage | pacid=371625 |
| 13 | 1344 | 1366 UAGCUUAUC/ :::: : :::..... ::::AGCAGCAACA | Cleavage | pacid=371625 |
| 14 | 636 | 657 UAGCUUAUC/:::.....:..... : :UCCACAUCAG | Cleavage | pacid=371531 |
| 15 | 636 | 657 UAGCUUAUC/:::.....:..... : :UCCACAUCAG | Cleavage | pacid=371531 |
| 16 | 167 | 188 UAGCUUAUC/::: : : :.....:UCAAGAUUC | Cleavage | pacid=371718 |
| 17 | 167 | 188 UAGCUUAUC/::: : : :.....:UCAAGAUUC | Cleavage | pacid=371718 |
| 18 | 166 | 188 UAGCUUAUC/ :::: : : :.....:UUCAAGAUU | Cleavage | pacid=371718 |
| 19 | 606 | 627 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 20 | 709 | 730 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 21 | 721 | 742 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 22 | 736 | 757 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 23 | 741 | 762 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 24 | 849 | 870 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 25 | 895 | 916 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 26 | 606 | 627 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 27 | 709 | 730 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 28 | 721 | 742 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 29 | 736 | 757 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 30 | 741 | 762 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 31 | 849 | 870 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 32 | 895 | 916 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 33 | 471 | 492 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 34 | 652 | 673 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 35 | 744 | 765 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 36 | 1237 | 1258 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 37 | 471 | 492 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 38 | 652 | 673 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 39 | 744 | 765 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 40 | 1237 | 1258 UAGCUUAUC/ ::::: : : :.....:GAAACGUCG | Cleavage | pacid=371640 |
| 41 | 327 | 348 UAGCUUAUC/:..... : : :GCGGCAUCA | Cleavage | pacid=371657 |
| 42 | 327 | 348 UAGCUUAUC/:..... : : :GCGGCAUCA | Cleavage | pacid=371657 |
| 43 | 326 | 348 UAGCUUAUC/:..... : : :GCGGCAUCA | Cleavage | pacid=371657 |
| 44 | 1317 | 1338 UAGCUUAUC/.....:.....:.....: UUGAUUUU | Cleavage | pacid=371655 |
| 45 | 1317 | 1338 UAGCUUAUC/.....:.....:.....: UUGAUUUU | Cleavage | pacid=371655 |
| 46 | 1316 | 1338 UAGCUUAUC/:.....:.....:AUUGAUUU | Cleavage | pacid=371655 |
| 47 | 463 | 484 UAGCUUAUC/ ..: : :.....: AUAGAAGCA | Cleavage | pacid=371610 |
| 48 | 1712 | 1733 UAGCUUAUC/ ..: : :.....: AUAGAAGCA | Cleavage | pacid=371610 |

| | | | | | |
|----|------|--|-------------|--------------|--------------|
| 1 | | | | | |
| 2 | 3970 | 3991 UAGCUUAUC/ .. : | AUAGAAGCAC | Cleavage | pacid=371610 |
| 3 | 4017 | 4038 UAGCUUAUC/ .. : | AUAGAAGCAC | Cleavage | pacid=371610 |
| 4 | 463 | 484 UAGCUUAUC/ .. : | AUAGAAGCAC | Cleavage | pacid=371610 |
| 5 | 1712 | 1733 UAGCUUAUC/ .. : | AUAGAAGCAC | Cleavage | pacid=371610 |
| 6 | 3970 | 3991 UAGCUUAUC/ .. : | AUAGAAGCAC | Cleavage | pacid=371610 |
| 7 | 4017 | 4038 UAGCUUAUC/ .. : | AUAGAAGCAC | Cleavage | pacid=371610 |
| 8 | | | | | |
| 9 | | | | | |
| 10 | 1321 | 1342 UAGCUUAUC/ :.....: . :.:AAAUAUCAC | Cleavage | pacid=371593 | |
| 11 | 1321 | 1342 UAGCUUAUC/ :.....: . :.:AAAUAUCAC | Cleavage | pacid=371593 | |
| 12 | 1781 | 1802 UAGCUUAUC/:..... :: CUAGCAUCAC | Cleavage | pacid=371590 | |
| 13 | 1781 | 1802 UAGCUUAUC/:..... :: CUAGCAUCAC | Cleavage | pacid=371590 | |
| 14 | 1780 | 1802 UAGCUUAUC/:..... ::UCUAGCAUCAC | Cleavage | pacid=371590 | |
| 15 | 1544 | 1565 UAGCUUAUC/.....: :: :.....: UUGGUAUCU | Translation | pacid=371606 | |
| 16 | 1544 | 1565 UAGCUUAUC/.....: :: :.....: UUGGUAUCU | Translation | pacid=371606 | |
| 17 | 1543 | 1565 UAGCUUAUC/ :.....: :: :.....:AUUGGUAUCI | Translation | pacid=371606 | |
| 18 | 955 | 979 UAGCUUAUC/:: :... :.....: ::GUUCACAUUC | Cleavage | pacid=371603 | |
| 19 | 500 | 522 UAGCUUAUC/:: :... :.....: ::GUCCUAAUCAC | Cleavage | pacid=371593 | |
| 20 | 382 | 403 UAGCUUAUC/ :.....: :.....: . GAAACAUCAL | Cleavage | pacid=371512 | |
| 21 | 382 | 403 UAGCUUAUC/ :.....: :.....: . GAAACAUCAL | Cleavage | pacid=371512 | |
| 22 | 381 | 403 UAGCUUAUC/ :.....: :.....: . AGAAACAUCAC | Cleavage | pacid=371512 | |
| 23 | 5344 | 5365 UAGCUUAUC/ :.....: :.....: :: UGUUCAUCGAC | Cleavage | pacid=371485 | |
| 24 | 5344 | 5365 UAGCUUAUC/ :.....: :.....: :: UGUUCAUCGAC | Cleavage | pacid=371485 | |
| 25 | 5343 | 5365 UAGCUUAUC/ :.....: :.....: :: CUGUUCAUCAC | Cleavage | pacid=371485 | |
| 26 | 926 | 947 UAGCUUAUC/:.....: : : : : AUGACAUCAC | Cleavage | pacid=371519 | |
| 27 | 926 | 947 UAGCUUAUC/:.....: : : : : AUGACAUCAC | Cleavage | pacid=371519 | |
| 28 | 925 | 947 UAGCUUAUC/ :.....: :.....: : : : : GAUGACAUCAC | Cleavage | pacid=371519 | |
| 29 | 1319 | 1340 UAGCUUAUC/ :... :.....: :.....: ::ACAUAUAUCAC | Cleavage | pacid=371431 | |
| 30 | 1319 | 1340 UAGCUUAUC/ :... :.....: :.....: ::ACAUAUAUCAC | Cleavage | pacid=371431 | |
| 31 | 1318 | 1340 UAGCUUAUC/ :... :.....: :.....: ::AACAAUAUAUCAC | Cleavage | pacid=371431 | |
| 32 | 142 | 163 UAGCUUAUC/.....: :.....: : : : : UCGACAUCUC | Cleavage | pacid=371436 | |
| 33 | 142 | 163 UAGCUUAUC/.....: :.....: : : : : UCGACAUCUC | Cleavage | pacid=371436 | |
| 34 | 141 | 163 UAGCUUAUC/.....: :.....: : : : : GUCGACAUCUC | Cleavage | pacid=371436 | |
| 35 | 532 | 553 UAGCUUAUC/ :... :.....: : : : : .ACAACAACAG | Translation | pacid=371440 | |
| 36 | 532 | 553 UAGCUUAUC/ :... :.....: : : : : .ACAACAACAG | Translation | pacid=371440 | |
| 37 | 531 | 553 UAGCUUAUC/ :... :.....: : : : : .GACAACAACA | Translation | pacid=371440 | |
| 38 | 1994 | 2014 UAGCUUAUC/:: :... :.....: :.....: ::UCAG-AUCAG | Cleavage | pacid=371441 | |
| 39 | 2056 | 2076 UAGCUUAUC/:: :... :.....: :.....: ::UCAG-AUCAG | Cleavage | pacid=371441 | |
| 40 | 2070 | 2090 UAGCUUAUC/:: :... :.....: :.....: ::UCAG-AUCAG | Cleavage | pacid=371441 | |
| 41 | 1994 | 2014 UAGCUUAUC/:: :... :.....: :.....: ::UCAG-AUCAG | Cleavage | pacid=371441 | |
| 42 | 2056 | 2076 UAGCUUAUC/:: :... :.....: :.....: ::UCAG-AUCAG | Cleavage | pacid=371441 | |
| 43 | 2070 | 2090 UAGCUUAUC/:: :... :.....: :.....: ::UCAG-AUCAG | Cleavage | pacid=371441 | |
| 44 | 1993 | 2014 UAGCUUAUC/ :... :.....: :.....: ::AUCAG-AUCA | Cleavage | pacid=371441 | |
| 45 | 2055 | 2076 UAGCUUAUC/ :... :.....: :.....: ::AUCAG-AUCA | Cleavage | pacid=371441 | |
| 46 | 2069 | 2090 UAGCUUAUC/ :... :.....: :.....: ::AUCAG-AUCA | Cleavage | pacid=371441 | |
| 47 | 1207 | 1229 UAGCUUAUC/:: :.....: ::CUAAUAUCAC | Cleavage | pacid=371561 | |
| 48 | 1207 | 1229 UAGCUUAUC/:: :.....: ::CUAAUAUCAC | Cleavage | pacid=371561 | |
| 49 | 1206 | 1229 UAGCUUAUC/:: :.....: ::ACUAAUAUCAC | Cleavage | pacid=371561 | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | |
|-----|--|--------------|
| 470 | 491 UAGCUUAUC/::: :: ..: :::::::::::UCACCAAUGC Cleavage | pacid=371556 |
| 470 | 491 UAGCUUAUC/::: :: ..: :::::::::::UCACCAAUGC Cleavage | pacid=371556 |
| 469 | 491 UAGCUUAUC/ ::: :: ..: :::::::::::UUCACCAAUC Cleavage | pacid=371556 |
| 413 | 434 UAGCUUAUC/::: : ..: :::::::::::UCAUCUGUG(Cleavage | pacid=371568 |
| 413 | 434 UAGCUUAUC/::: : ..: :::::::::::UCAUCUGUG(Cleavage | pacid=371568 |

Do not distribute

| Multiplicity | Target_Acc. | ID | locusName | Pfam |
|--------------|--------------------|------------------|------------------|--------------|
| 1 | Phvul.004G023066.1 | Phvul.004G023066 | Phvul.004G023066 | PF00005,PF00 |
| 1 | Phvul.004G023066.1 | Phvul.004G023066 | Phvul.004G023066 | PF00005,PF00 |
| 1 | Phvul.004G023066.1 | Phvul.004G023066 | Phvul.004G023066 | PF00005,PF00 |
| 1 | Phvul.002G097400.1 | Phvul.002G097400 | Phvul.002G097400 | PF01193,PF01 |
| 1 | Phvul.002G097400.1 | Phvul.002G097400 | Phvul.002G097400 | PF01193,PF01 |
| 1 | Phvul.002G097400.1 | Phvul.002G097400 | Phvul.002G097400 | PF01193,PF01 |
| 1 | Phvul.006G008480.2 | Phvul.006G008480 | Phvul.006G008480 | PF00917,PF13 |
| 1 | Phvul.006G008480.1 | Phvul.006G008480 | Phvul.006G008480 | PF00917,PF13 |
| 1 | Phvul.006G008480.2 | Phvul.006G008480 | Phvul.006G008480 | PF00917,PF13 |
| 1 | Phvul.006G008480.1 | Phvul.006G008480 | Phvul.006G008480 | PF00917,PF13 |
| 1 | Phvul.006G008480.2 | Phvul.006G008480 | Phvul.006G008480 | PF00917,PF13 |
| 1 | Phvul.006G008480.1 | Phvul.006G008480 | Phvul.006G008480 | PF00917,PF13 |
| 1 | Phvul.006G029000.1 | Phvul.006G029000 | Phvul.006G029000 | PF08263,PF00 |
| 1 | Phvul.006G029000.1 | Phvul.006G029000 | Phvul.006G029000 | PF08263,PF00 |
| 1 | Phvul.006G029000.1 | Phvul.006G029000 | Phvul.006G029000 | PF08263,PF00 |
| 1 | Phvul.006G110300.1 | Phvul.006G110300 | Phvul.006G110300 | PF00153 |
| 1 | Phvul.006G110300.1 | Phvul.006G110300 | Phvul.006G110300 | PF00153 |
| 1 | Phvul.006G110300.1 | Phvul.006G110300 | Phvul.006G110300 | PF00153 |
| 1 | Phvul.007G191600.1 | Phvul.007G191600 | Phvul.007G191600 | PF00271,PF00 |
| 1 | Phvul.007G191600.1 | Phvul.007G191600 | Phvul.007G191600 | PF00271,PF00 |
| 1 | Phvul.007G191600.1 | Phvul.007G191600 | Phvul.007G191600 | PF00271,PF00 |
| 1 | Phvul.001G070000.1 | Phvul.001G070000 | Phvul.001G070000 | PF07714 |
| 1 | Phvul.001G070000.1 | Phvul.001G070000 | Phvul.001G070000 | PF07714 |
| 1 | Phvul.001G070000.1 | Phvul.001G070000 | Phvul.001G070000 | PF07714 |
| 1 | Phvul.001G264600.2 | Phvul.001G264600 | Phvul.001G264600 | PF01936 |
| 1 | Phvul.001G264600.1 | Phvul.001G264600 | Phvul.001G264600 | PF01936 |
| 1 | Phvul.001G264600.2 | Phvul.001G264600 | Phvul.001G264600 | PF01936 |
| 1 | Phvul.001G264600.1 | Phvul.001G264600 | Phvul.001G264600 | PF01936 |
| 1 | Phvul.001G264600.2 | Phvul.001G264600 | Phvul.001G264600 | PF01936 |
| 1 | Phvul.001G264600.1 | Phvul.001G264600 | Phvul.001G264600 | PF01936 |
| 1 | Phvul.002G153500.1 | Phvul.002G153500 | Phvul.002G153500 | PF04321 |
| 1 | Phvul.002G153500.1 | Phvul.002G153500 | Phvul.002G153500 | PF04321 |
| 1 | Phvul.002G153500.1 | Phvul.002G153500 | Phvul.002G153500 | PF04321 |
| 1 | Phvul.003G092500.1 | Phvul.003G092500 | Phvul.003G092500 | PF00403 |
| 1 | Phvul.003G092500.1 | Phvul.003G092500 | Phvul.003G092500 | PF00403 |
| 1 | Phvul.004G000300.1 | Phvul.004G000300 | Phvul.004G000300 | PF13180,PF13 |
| 1 | Phvul.004G000300.1 | Phvul.004G000300 | Phvul.004G000300 | PF13180,PF13 |
| 1 | Phvul.004G000300.1 | Phvul.004G000300 | Phvul.004G000300 | PF13180,PF13 |
| 1 | Phvul.004G126100.1 | Phvul.004G126100 | Phvul.004G126100 | PF08263,PF00 |
| 1 | Phvul.004G126100.1 | Phvul.004G126100 | Phvul.004G126100 | PF08263,PF00 |
| 1 | Phvul.004G126100.1 | Phvul.004G126100 | Phvul.004G126100 | PF08263,PF00 |
| 1 | Phvul.005G063700.2 | Phvul.005G063700 | Phvul.005G063700 | PF07714 |
| 1 | Phvul.005G063700.1 | Phvul.005G063700 | Phvul.005G063700 | PF07714 |
| 1 | Phvul.005G063700.2 | Phvul.005G063700 | Phvul.005G063700 | PF07714 |
| 1 | Phvul.005G063700.1 | Phvul.005G063700 | Phvul.005G063700 | PF07714 |

| | | | | |
|----|----------------------|------------------|------------------|--------------|
| 1 | | | | |
| 2 | 1 Phvul.005G063700.2 | Phvul.005G063700 | Phvul.005G063700 | PF07714 |
| 3 | 1 Phvul.005G063700.1 | Phvul.005G063700 | Phvul.005G063700 | PF07714 |
| 4 | 1 Phvul.007G020600.1 | Phvul.007G020600 | Phvul.007G020600 | PF00201 |
| 5 | | | | |
| 6 | 1 Phvul.007G020600.1 | Phvul.007G020600 | Phvul.007G020600 | PF00201 |
| 7 | 1 Phvul.007G020700.1 | Phvul.007G020700 | Phvul.007G020700 | PF00201 |
| 8 | 1 Phvul.007G020700.1 | Phvul.007G020700 | Phvul.007G020700 | PF00201 |
| 9 | | | | |
| 10 | 1 Phvul.007G080800.1 | Phvul.007G080800 | Phvul.007G080800 | PF03033 |
| 11 | 1 Phvul.007G080800.1 | Phvul.007G080800 | Phvul.007G080800 | PF03033 |
| 12 | 1 Phvul.007G080800.1 | Phvul.007G080800 | Phvul.007G080800 | PF03033 |
| 13 | | | | |
| 14 | 1 Phvul.007G254000.2 | Phvul.007G254000 | Phvul.007G254000 | PF00954,PF07 |
| 15 | 1 Phvul.007G254000.1 | Phvul.007G254000 | Phvul.007G254000 | PF00954,PF07 |
| 16 | 1 Phvul.007G254000.2 | Phvul.007G254000 | Phvul.007G254000 | PF00954,PF07 |
| 17 | | | | |
| 18 | 1 Phvul.007G254000.1 | Phvul.007G254000 | Phvul.007G254000 | PF00954,PF07 |
| 19 | 1 Phvul.007G254000.2 | Phvul.007G254000 | Phvul.007G254000 | PF00954,PF07 |
| 20 | 1 Phvul.007G254000.1 | Phvul.007G254000 | Phvul.007G254000 | PF00954,PF07 |
| 21 | | | | |
| 22 | 1 Phvul.008G212500.1 | Phvul.008G212500 | Phvul.008G212500 | PF01476,PF00 |
| 23 | 1 Phvul.008G212500.1 | Phvul.008G212500 | Phvul.008G212500 | PF01476,PF00 |
| 24 | 1 Phvul.008G212500.1 | Phvul.008G212500 | Phvul.008G212500 | PF01476,PF00 |
| 25 | | | | |
| 26 | 1 Phvul.008G266300.1 | Phvul.008G266300 | Phvul.008G266300 | PF16656,PF14 |
| 27 | 1 Phvul.008G266300.1 | Phvul.008G266300 | Phvul.008G266300 | PF16656,PF14 |
| 28 | 1 Phvul.008G266300.1 | Phvul.008G266300 | Phvul.008G266300 | PF16656,PF14 |
| 29 | | | | |
| 30 | 1 Phvul.011G002600.1 | Phvul.011G002600 | Phvul.011G002600 | 0 |
| 31 | 1 Phvul.011G002600.1 | Phvul.011G002600 | Phvul.011G002600 | 0 |
| 32 | 1 Phvul.011G002600.1 | Phvul.011G002600 | Phvul.011G002600 | 0 |
| 33 | | | | |
| 34 | 1 Phvul.011G194501.1 | Phvul.011G194501 | Phvul.011G194501 | PF01657 |
| 35 | 1 Phvul.011G194501.1 | Phvul.011G194501 | Phvul.011G194501 | PF01657 |
| 36 | 1 Phvul.011G194501.1 | Phvul.011G194501 | Phvul.011G194501 | PF01657 |
| 37 | | | | |
| 38 | 1 Phvul.L000308.2 | Phvul.L000308 | Phvul.L000308 | PF00847 |
| 39 | 1 Phvul.L000308.1 | Phvul.L000308 | Phvul.L000308 | PF00847 |
| 40 | 1 Phvul.L000308.2 | Phvul.L000308 | Phvul.L000308 | PF00847 |
| 41 | 1 Phvul.L000308.1 | Phvul.L000308 | Phvul.L000308 | PF00847 |
| 42 | | | | |
| 43 | 1 Phvul.L000308.2 | Phvul.L000308 | Phvul.L000308 | PF00847 |
| 44 | 1 Phvul.L000308.1 | Phvul.L000308 | Phvul.L000308 | PF00847 |
| 45 | | | | |
| 46 | 1 Phvul.001G021750.1 | Phvul.001G021750 | Phvul.001G021750 | PF00036 |
| 47 | 1 Phvul.001G021750.1 | Phvul.001G021750 | Phvul.001G021750 | PF00036 |
| 48 | 1 Phvul.001G021750.1 | Phvul.001G021750 | Phvul.001G021750 | PF00036 |
| 49 | 1 Phvul.001G168600.1 | Phvul.001G168600 | Phvul.001G168600 | PF12776 |
| 50 | | | | |
| 51 | 1 Phvul.001G168600.1 | Phvul.001G168600 | Phvul.001G168600 | PF12776 |
| 52 | 1 Phvul.002G010100.1 | Phvul.002G010100 | Phvul.002G010100 | PF10225 |
| 53 | 1 Phvul.002G010100.1 | Phvul.002G010100 | Phvul.002G010100 | PF10225 |
| 54 | | | | |
| 55 | 1 Phvul.002G010100.1 | Phvul.002G010100 | Phvul.002G010100 | PF10225 |
| 56 | 1 Phvul.002G149100.1 | Phvul.002G149100 | Phvul.002G149100 | PF12776 |
| 57 | 1 Phvul.002G149100.1 | Phvul.002G149100 | Phvul.002G149100 | PF12776 |
| 58 | | | | |
| 59 | 1 Phvul.002G155200.1 | Phvul.002G155200 | Phvul.002G155200 | PF02214 |
| 60 | 1 Phvul.002G155200.1 | Phvul.002G155200 | Phvul.002G155200 | PF02214 |
| | 1 Phvul.002G211400.1 | Phvul.002G211400 | Phvul.002G211400 | PF03000 |

| | | | | |
|----|----------------------|------------------|------------------|--------------|
| 1 | | | | |
| 2 | 1 Phvul.002G211400.1 | Phvul.002G211400 | Phvul.002G211400 | PF03000 |
| 3 | 1 Phvul.002G211400.1 | Phvul.002G211400 | Phvul.002G211400 | PF03000 |
| 4 | 1 Phvul.003G069400.1 | Phvul.003G069400 | Phvul.003G069400 | PF12776 |
| 5 | 1 Phvul.003G069400.1 | Phvul.003G069400 | Phvul.003G069400 | PF12776 |
| 6 | 1 Phvul.003G141800.1 | Phvul.003G141800 | Phvul.003G141800 | PF02225,PF06 |
| 7 | 1 Phvul.003G141800.1 | Phvul.003G141800 | Phvul.003G141800 | PF02225,PF06 |
| 8 | 1 Phvul.003G141800.1 | Phvul.003G141800 | Phvul.003G141800 | PF02225,PF06 |
| 9 | 1 Phvul.003G141800.1 | Phvul.003G141800 | Phvul.003G141800 | PF02225,PF06 |
| 10 | 1 Phvul.003G141800.1 | Phvul.003G141800 | Phvul.003G141800 | PF02225,PF06 |
| 11 | 1 Phvul.003G239800.1 | Phvul.003G239800 | Phvul.003G239800 | 0 |
| 12 | 1 Phvul.003G239800.1 | Phvul.003G239800 | Phvul.003G239800 | 0 |
| 13 | 1 Phvul.003G239800.1 | Phvul.003G239800 | Phvul.003G239800 | 0 |
| 14 | 1 Phvul.003G239800.1 | Phvul.003G239800 | Phvul.003G239800 | 0 |
| 15 | 1 Phvul.004G053900.1 | Phvul.004G053900 | Phvul.004G053900 | PF12776 |
| 16 | 1 Phvul.004G053900.1 | Phvul.004G053900 | Phvul.004G053900 | PF12776 |
| 17 | 1 Phvul.004G157700.1 | Phvul.004G157700 | Phvul.004G157700 | PF10496 |
| 18 | 1 Phvul.004G157700.1 | Phvul.004G157700 | Phvul.004G157700 | PF10496 |
| 19 | 1 Phvul.004G157700.1 | Phvul.004G157700 | Phvul.004G157700 | PF10496 |
| 20 | 1 Phvul.004G157700.1 | Phvul.004G157700 | Phvul.004G157700 | PF10496 |
| 21 | 1 Phvul.004G157700.1 | Phvul.004G157700 | Phvul.004G157700 | PF10496 |
| 22 | 1 Phvul.004G177000.3 | Phvul.004G177000 | Phvul.004G177000 | 0 |
| 23 | 1 Phvul.004G177000.2 | Phvul.004G177000 | Phvul.004G177000 | 0 |
| 24 | 1 Phvul.004G177000.4 | Phvul.004G177000 | Phvul.004G177000 | 0 |
| 25 | 1 Phvul.004G177000.1 | Phvul.004G177000 | Phvul.004G177000 | 0 |
| 26 | 1 Phvul.004G177000.1 | Phvul.004G177000 | Phvul.004G177000 | 0 |
| 27 | 1 Phvul.004G177000.3 | Phvul.004G177000 | Phvul.004G177000 | 0 |
| 28 | 1 Phvul.004G177000.2 | Phvul.004G177000 | Phvul.004G177000 | 0 |
| 29 | 1 Phvul.004G177000.4 | Phvul.004G177000 | Phvul.004G177000 | 0 |
| 30 | 1 Phvul.004G177000.4 | Phvul.004G177000 | Phvul.004G177000 | 0 |
| 31 | 1 Phvul.004G177000.1 | Phvul.004G177000 | Phvul.004G177000 | 0 |
| 32 | 1 Phvul.004G177000.3 | Phvul.004G177000 | Phvul.004G177000 | 0 |
| 33 | 1 Phvul.004G177000.2 | Phvul.004G177000 | Phvul.004G177000 | 0 |
| 34 | 1 Phvul.004G177000.2 | Phvul.004G177000 | Phvul.004G177000 | 0 |
| 35 | 1 Phvul.004G177000.4 | Phvul.004G177000 | Phvul.004G177000 | 0 |
| 36 | 1 Phvul.004G177000.1 | Phvul.004G177000 | Phvul.004G177000 | 0 |
| 37 | 1 Phvul.004G177000.1 | Phvul.004G177000 | Phvul.004G177000 | 0 |
| 38 | 1 Phvul.006G103900.1 | Phvul.006G103900 | Phvul.006G103900 | PF02736,PF00 |
| 39 | 1 Phvul.006G103900.1 | Phvul.006G103900 | Phvul.006G103900 | PF02736,PF00 |
| 40 | 1 Phvul.006G103900.1 | Phvul.006G103900 | Phvul.006G103900 | PF02736,PF00 |
| 41 | 1 Phvul.006G158500.2 | Phvul.006G158500 | Phvul.006G158500 | PF13920 |
| 42 | 1 Phvul.006G158500.1 | Phvul.006G158500 | Phvul.006G158500 | PF13920 |
| 43 | 1 Phvul.006G158500.1 | Phvul.006G158500 | Phvul.006G158500 | PF13920 |
| 44 | 1 Phvul.006G158500.2 | Phvul.006G158500 | Phvul.006G158500 | PF13920 |
| 45 | 1 Phvul.006G158500.1 | Phvul.006G158500 | Phvul.006G158500 | PF13920 |
| 46 | 1 Phvul.006G158500.1 | Phvul.006G158500 | Phvul.006G158500 | PF13920 |
| 47 | 1 Phvul.006G158500.2 | Phvul.006G158500 | Phvul.006G158500 | PF13920 |
| 48 | 1 Phvul.006G158500.1 | Phvul.006G158500 | Phvul.006G158500 | PF13920 |
| 49 | 1 Phvul.007G054000.2 | Phvul.007G054000 | Phvul.007G054000 | PF04851,PF14 |
| 50 | 1 Phvul.007G054000.2 | Phvul.007G054000 | Phvul.007G054000 | PF04851,PF14 |
| 51 | 1 Phvul.007G054000.2 | Phvul.007G054000 | Phvul.007G054000 | PF04851,PF14 |
| 52 | 1 Phvul.007G054000.2 | Phvul.007G054000 | Phvul.007G054000 | PF04851,PF14 |
| 53 | 1 Phvul.007G154900.2 | Phvul.007G154900 | Phvul.007G154900 | PF13921 |
| 54 | 1 Phvul.007G154900.3 | Phvul.007G154900 | Phvul.007G154900 | PF13921 |
| 55 | 1 Phvul.007G154900.3 | Phvul.007G154900 | Phvul.007G154900 | PF13921 |
| 56 | 1 Phvul.007G154900.9 | Phvul.007G154900 | Phvul.007G154900 | PF13921 |
| 57 | 1 Phvul.007G154900.7 | Phvul.007G154900 | Phvul.007G154900 | PF13921 |
| 58 | 1 Phvul.007G154900.6 | Phvul.007G154900 | Phvul.007G154900 | PF13921 |
| 59 | 1 Phvul.007G154900.6 | Phvul.007G154900 | Phvul.007G154900 | PF13921 |
| 60 | 1 Phvul.007G154900.5 | Phvul.007G154900 | Phvul.007G154900 | PF13921 |
| | 1 Phvul.007G154900.8 | Phvul.007G154900 | Phvul.007G154900 | PF13921 |

| | | | | |
|----|---|---------------------|-------------------|-------------------------------|
| 1 | | | | |
| 2 | 1 | Phvul.007G154900.4 | Phvul.007G154900 | Phvul.007G154900 PF13921 |
| 3 | 1 | Phvul.007G154900.1 | Phvul.007G154900 | Phvul.007G154900 PF13921 |
| 4 | 1 | Phvul.007G154900.2 | Phvul.007G154900 | Phvul.007G154900 PF13921 |
| 5 | 1 | Phvul.007G154900.3 | Phvul.007G154900 | Phvul.007G154900 PF13921 |
| 6 | 1 | Phvul.007G154900.9 | Phvul.007G154900 | Phvul.007G154900 PF13921 |
| 7 | 1 | Phvul.007G154900.7 | Phvul.007G154900 | Phvul.007G154900 PF13921 |
| 8 | 1 | Phvul.007G154900.6 | Phvul.007G154900 | Phvul.007G154900 PF13921 |
| 9 | 1 | Phvul.007G154900.5 | Phvul.007G154900 | Phvul.007G154900 PF13921 |
| 10 | 1 | Phvul.007G154900.8 | Phvul.007G154900 | Phvul.007G154900 PF13921 |
| 11 | 1 | Phvul.007G154900.4 | Phvul.007G154900 | Phvul.007G154900 PF13921 |
| 12 | 1 | Phvul.007G154900.1 | Phvul.007G154900 | Phvul.007G154900 PF13921 |
| 13 | 1 | Phvul.007G154900.15 | Phvul.007G154900. | Phvul.007G154900 PF13921 |
| 14 | 1 | Phvul.007G154900.13 | Phvul.007G154900. | Phvul.007G154900 PF13921 |
| 15 | 1 | Phvul.007G154900.14 | Phvul.007G154900. | Phvul.007G154900 PF13921 |
| 16 | 1 | Phvul.007G154900.11 | Phvul.007G154900. | Phvul.007G154900 PF13921 |
| 17 | 1 | Phvul.007G154900.12 | Phvul.007G154900. | Phvul.007G154900 PF13921 |
| 18 | 1 | Phvul.007G154900.10 | Phvul.007G154900. | Phvul.007G154900 PF13921 |
| 19 | 1 | Phvul.007G154900.15 | Phvul.007G154900. | Phvul.007G154900 PF13921 |
| 20 | 1 | Phvul.007G154900.13 | Phvul.007G154900. | Phvul.007G154900 PF13921 |
| 21 | 1 | Phvul.007G154900.14 | Phvul.007G154900. | Phvul.007G154900 PF13921 |
| 22 | 1 | Phvul.007G154900.11 | Phvul.007G154900. | Phvul.007G154900 PF13921 |
| 23 | 1 | Phvul.007G154900.12 | Phvul.007G154900. | Phvul.007G154900 PF13921 |
| 24 | 1 | Phvul.007G154900.10 | Phvul.007G154900. | Phvul.007G154900 PF13921 |
| 25 | 1 | Phvul.007G154900.15 | Phvul.007G154900. | Phvul.007G154900 PF13921 |
| 26 | 1 | Phvul.007G154900.13 | Phvul.007G154900. | Phvul.007G154900 PF13921 |
| 27 | 1 | Phvul.007G154900.14 | Phvul.007G154900. | Phvul.007G154900 PF13921 |
| 28 | 1 | Phvul.007G154900.11 | Phvul.007G154900. | Phvul.007G154900 PF13921 |
| 29 | 1 | Phvul.007G154900.12 | Phvul.007G154900. | Phvul.007G154900 PF13921 |
| 30 | 1 | Phvul.007G154900.10 | Phvul.007G154900. | Phvul.007G154900 PF13921 |
| 31 | 1 | Phvul.008G106500.1 | Phvul.008G106500 | Phvul.008G106500 PF08263,PF13 |
| 32 | 1 | Phvul.008G106500.1 | Phvul.008G106500 | Phvul.008G106500 PF08263,PF13 |
| 33 | 1 | Phvul.009G021300.1 | Phvul.009G021300 | Phvul.009G021300 PF01490 |
| 34 | 1 | Phvul.009G021300.1 | Phvul.009G021300 | Phvul.009G021300 PF01490 |
| 35 | 1 | Phvul.009G021300.1 | Phvul.009G021300 | Phvul.009G021300 PF01490 |
| 36 | 1 | Phvul.009G021300.1 | Phvul.009G021300 | Phvul.009G021300 PF01490 |
| 37 | 1 | Phvul.009G097000.1 | Phvul.009G097000 | Phvul.009G097000 PF09762 |
| 38 | 1 | Phvul.009G097000.2 | Phvul.009G097000 | Phvul.009G097000 PF09762 |
| 39 | 1 | Phvul.009G097000.1 | Phvul.009G097000 | Phvul.009G097000 PF09762 |
| 40 | 1 | Phvul.009G097000.2 | Phvul.009G097000 | Phvul.009G097000 PF09762 |
| 41 | 1 | Phvul.009G122000.1 | Phvul.009G122000 | Phvul.009G122000 PF12776 |
| 42 | 1 | Phvul.009G122000.1 | Phvul.009G122000 | Phvul.009G122000 PF12776 |
| 43 | 1 | Phvul.009G227900.2 | Phvul.009G227900 | Phvul.009G227900 PF03456,PF02 |
| 44 | 1 | Phvul.009G227900.3 | Phvul.009G227900 | Phvul.009G227900 PF03456,PF02 |
| 45 | 1 | Phvul.009G227900.1 | Phvul.009G227900 | Phvul.009G227900 PF03456,PF02 |
| 46 | 1 | Phvul.009G227900.2 | Phvul.009G227900 | Phvul.009G227900 PF03456,PF02 |
| 47 | 1 | Phvul.009G227900.3 | Phvul.009G227900 | Phvul.009G227900 PF03456,PF02 |
| 48 | 1 | Phvul.009G227900.1 | Phvul.009G227900 | Phvul.009G227900 PF03456,PF02 |
| 49 | 1 | Phvul.009G227900.2 | Phvul.009G227900 | Phvul.009G227900 PF03456,PF02 |
| 50 | 1 | Phvul.009G227900.3 | Phvul.009G227900 | Phvul.009G227900 PF03456,PF02 |
| 51 | 1 | Phvul.009G227900.1 | Phvul.009G227900 | Phvul.009G227900 PF03456,PF02 |
| 52 | 1 | Phvul.009G227900.2 | Phvul.009G227900 | Phvul.009G227900 PF03456,PF02 |
| 53 | 1 | Phvul.009G227900.3 | Phvul.009G227900 | Phvul.009G227900 PF03456,PF02 |
| 54 | 1 | Phvul.009G227900.1 | Phvul.009G227900 | Phvul.009G227900 PF03456,PF02 |
| 55 | 1 | Phvul.010G159600.1 | Phvul.010G159600 | Phvul.010G159600 PF03556 |
| 56 | 1 | Phvul.010G159600.1 | Phvul.010G159600 | Phvul.010G159600 PF03556 |
| 57 | 1 | Phvul.011G084000.1 | Phvul.011G084000 | Phvul.011G084000 PF12848,PF00 |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

| | | | | |
|----|----------------------|------------------|------------------|--------------|
| 1 | | | | |
| 2 | 1 Phvul.011G084000.1 | Phvul.011G084000 | Phvul.011G084000 | PF12848,PF00 |
| 3 | 1 Phvul.011G084000.1 | Phvul.011G084000 | Phvul.011G084000 | PF12848,PF00 |
| 4 | 1 Phvul.011G130500.1 | Phvul.011G130500 | Phvul.011G130500 | 0 |
| 5 | | | | |
| 6 | 1 Phvul.011G130500.1 | Phvul.011G130500 | Phvul.011G130500 | 0 |
| 7 | 1 Phvul.011G130500.1 | Phvul.011G130500 | Phvul.011G130500 | 0 |
| 8 | 1 Phvul.011G158500.1 | Phvul.011G158500 | Phvul.011G158500 | PF00201 |
| 9 | | | | |
| 10 | 1 Phvul.011G158500.1 | Phvul.011G158500 | Phvul.011G158500 | PF00201 |
| 11 | 1 Phvul.011G158500.1 | Phvul.011G158500 | Phvul.011G158500 | PF00201 |
| 12 | 1 Phvul.011G198100.1 | Phvul.011G198100 | Phvul.011G198100 | PF00931 |
| 13 | | | | |
| 14 | 1 Phvul.011G198100.1 | Phvul.011G198100 | Phvul.011G198100 | PF00931 |
| 15 | 1 Phvul.011G198100.1 | Phvul.011G198100 | Phvul.011G198100 | PF00931 |
| 16 | 1 Phvul.001G199500.1 | Phvul.001G199500 | Phvul.001G199500 | PF01805,PF04 |
| 17 | | | | |
| 18 | 1 Phvul.001G199500.1 | Phvul.001G199500 | Phvul.001G199500 | PF01805,PF04 |
| 19 | 1 Phvul.001G199500.1 | Phvul.001G199500 | Phvul.001G199500 | PF01805,PF04 |
| 20 | 1 Phvul.002G005300.2 | Phvul.002G005300 | Phvul.002G005300 | PF03372 |
| 21 | | | | |
| 22 | 1 Phvul.002G005300.1 | Phvul.002G005300 | Phvul.002G005300 | PF03372 |
| 23 | 1 Phvul.002G005300.2 | Phvul.002G005300 | Phvul.002G005300 | PF03372 |
| 24 | 1 Phvul.002G005300.1 | Phvul.002G005300 | Phvul.002G005300 | PF03372 |
| 25 | | | | |
| 26 | 1 Phvul.002G005300.2 | Phvul.002G005300 | Phvul.002G005300 | PF03372 |
| 27 | 1 Phvul.002G005300.1 | Phvul.002G005300 | Phvul.002G005300 | PF03372 |
| 28 | 1 Phvul.002G119100.1 | Phvul.002G119100 | Phvul.002G119100 | 0 |
| 29 | | | | |
| 30 | 1 Phvul.002G119100.1 | Phvul.002G119100 | Phvul.002G119100 | 0 |
| 31 | 1 Phvul.002G119100.1 | Phvul.002G119100 | Phvul.002G119100 | 0 |
| 32 | 1 Phvul.002G132700.1 | Phvul.002G132700 | Phvul.002G132700 | PF01632 |
| 33 | 1 Phvul.002G132700.1 | Phvul.002G132700 | Phvul.002G132700 | PF01632 |
| 34 | 1 Phvul.002G132700.1 | Phvul.002G132700 | Phvul.002G132700 | PF01632 |
| 35 | 1 Phvul.002G132700.1 | Phvul.002G132700 | Phvul.002G132700 | PF01632 |
| 36 | 1 Phvul.002G141000.2 | Phvul.002G141000 | Phvul.002G141000 | 0 |
| 37 | 1 Phvul.002G141000.1 | Phvul.002G141000 | Phvul.002G141000 | 0 |
| 38 | | | | |
| 39 | 1 Phvul.002G141000.2 | Phvul.002G141000 | Phvul.002G141000 | 0 |
| 40 | 1 Phvul.002G141000.1 | Phvul.002G141000 | Phvul.002G141000 | 0 |
| 41 | | | | |
| 42 | 1 Phvul.003G131900.1 | Phvul.003G131900 | Phvul.003G131900 | PF08612 |
| 43 | 1 Phvul.003G131900.1 | Phvul.003G131900 | Phvul.003G131900 | PF08612 |
| 44 | 1 Phvul.003G131900.1 | Phvul.003G131900 | Phvul.003G131900 | PF08612 |
| 45 | 1 Phvul.003G225700.1 | Phvul.003G225700 | Phvul.003G225700 | PF00324 |
| 46 | | | | |
| 47 | 1 Phvul.003G238000.1 | Phvul.003G238000 | Phvul.003G238000 | PF13371,PF13 |
| 48 | 1 Phvul.003G238000.1 | Phvul.003G238000 | Phvul.003G238000 | PF13371,PF13 |
| 49 | 1 Phvul.003G259300.1 | Phvul.003G259300 | Phvul.003G259300 | PF07798 |
| 50 | | | | |
| 51 | 1 Phvul.003G259300.1 | Phvul.003G259300 | Phvul.003G259300 | PF07798 |
| 52 | 1 Phvul.003G259300.1 | Phvul.003G259300 | Phvul.003G259300 | PF07798 |
| 53 | 1 Phvul.004G037700.1 | Phvul.004G037700 | Phvul.004G037700 | PF03634 |
| 54 | | | | |
| 55 | 1 Phvul.004G037700.3 | Phvul.004G037700 | Phvul.004G037700 | PF03634 |
| 56 | 1 Phvul.004G037700.2 | Phvul.004G037700 | Phvul.004G037700 | PF03634 |
| 57 | 1 Phvul.004G037700.1 | Phvul.004G037700 | Phvul.004G037700 | PF03634 |
| 58 | | | | |
| 59 | 1 Phvul.004G037700.3 | Phvul.004G037700 | Phvul.004G037700 | PF03634 |
| 60 | 1 Phvul.004G037700.2 | Phvul.004G037700 | Phvul.004G037700 | PF03634 |
| | 1 Phvul.004G037700.1 | Phvul.004G037700 | Phvul.004G037700 | PF03634 |

| | | | | |
|----|---|---------------------|------------------|-------------------------------|
| 1 | | | | |
| 2 | 1 | Phvul.004G037700.3 | Phvul.004G037700 | Phvul.004G037700 PF03634 |
| 3 | 1 | Phvul.004G037700.2 | Phvul.004G037700 | Phvul.004G037700 PF03634 |
| 4 | 1 | Phvul.004G089300.2 | Phvul.004G089300 | Phvul.004G089300 PF03372 |
| 5 | 1 | Phvul.004G089300.4 | Phvul.004G089300 | Phvul.004G089300 PF03372 |
| 6 | 1 | Phvul.004G089300.2 | Phvul.004G089300 | Phvul.004G089300 PF03372 |
| 7 | 1 | Phvul.004G089300.4 | Phvul.004G089300 | Phvul.004G089300 PF03372 |
| 8 | 1 | Phvul.004G089300.2 | Phvul.004G089300 | Phvul.004G089300 PF03372 |
| 9 | 1 | Phvul.004G089300.4 | Phvul.004G089300 | Phvul.004G089300 PF03372 |
| 10 | 1 | Phvul.004G089300.2 | Phvul.004G089300 | Phvul.004G089300 PF03372 |
| 11 | 1 | Phvul.004G089300.4 | Phvul.004G089300 | Phvul.004G089300 PF03372 |
| 12 | 1 | Phvul.004G174700.1 | Phvul.004G174700 | Phvul.004G174700 PF03485,PF05 |
| 13 | 1 | Phvul.004G174700.1 | Phvul.004G174700 | Phvul.004G174700 PF03485,PF05 |
| 14 | 1 | Phvul.004G174700.1 | Phvul.004G174700 | Phvul.004G174700 PF03485,PF05 |
| 15 | 1 | Phvul.005G125500.1 | Phvul.005G125500 | Phvul.005G125500 PF03015,PF07 |
| 16 | 1 | Phvul.005G125500.1 | Phvul.005G125500 | Phvul.005G125500 PF03015,PF07 |
| 17 | 1 | Phvul.006G044400.1 | Phvul.006G044400 | Phvul.006G044400 PF05739,PF09 |
| 18 | 1 | Phvul.006G044400.1 | Phvul.006G044400 | Phvul.006G044400 PF05739,PF09 |
| 19 | 1 | Phvul.006G044400.1 | Phvul.006G044400 | Phvul.006G044400 PF05739,PF09 |
| 20 | 1 | Phvul.007G072700.3 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 21 | 1 | Phvul.007G072700.9 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 22 | 1 | Phvul.007G072700.8 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 23 | 1 | Phvul.007G072700.6 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 24 | 1 | Phvul.007G072700.7 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 25 | 1 | Phvul.007G072700.2 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 26 | 1 | Phvul.007G072700.5 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 27 | 1 | Phvul.007G072700.3 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 28 | 1 | Phvul.007G072700.9 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 29 | 1 | Phvul.007G072700.8 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 30 | 1 | Phvul.007G072700.6 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 31 | 1 | Phvul.007G072700.7 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 32 | 1 | Phvul.007G072700.2 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 33 | 1 | Phvul.007G072700.5 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 34 | 1 | Phvul.007G072700.3 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 35 | 1 | Phvul.007G072700.9 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 36 | 1 | Phvul.007G072700.8 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 37 | 1 | Phvul.007G072700.6 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 38 | 1 | Phvul.007G072700.7 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 39 | 1 | Phvul.007G072700.2 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 40 | 1 | Phvul.007G072700.5 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 41 | 1 | Phvul.007G072700.12 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 42 | 1 | Phvul.007G072700.13 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 43 | 1 | Phvul.007G072700.10 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 44 | 1 | Phvul.007G072700.11 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 45 | 1 | Phvul.007G072700.12 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 46 | 1 | Phvul.007G072700.13 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 47 | 1 | Phvul.007G072700.10 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 48 | 1 | Phvul.007G072700.11 | Phvul.007G072700 | Phvul.007G072700 PF02902 |
| 49 | 1 | Phvul.007G215400.1 | Phvul.007G215400 | Phvul.007G215400 PF13664 |
| 50 | 1 | Phvul.007G215400.1 | Phvul.007G215400 | Phvul.007G215400 PF13664 |
| 51 | 1 | Phvul.007G215400.1 | Phvul.007G215400 | Phvul.007G215400 PF13664 |
| 52 | 1 | Phvul.007G249800.1 | Phvul.007G249800 | Phvul.007G249800 PF00149 |
| 53 | 1 | Phvul.007G249800.1 | Phvul.007G249800 | Phvul.007G249800 PF00149 |
| 54 | 1 | Phvul.007G249800.1 | Phvul.007G249800 | Phvul.007G249800 PF00149 |
| 55 | 1 | Phvul.008G074600.3 | Phvul.008G074600 | Phvul.008G074600 PF00400,PF14 |
| 56 | 1 | Phvul.008G074600.2 | Phvul.008G074600 | Phvul.008G074600 PF00400,PF14 |

| | | | | |
|----|----------------------|------------------|------------------|--------------|
| 1 | | | | |
| 2 | 1 Phvul.008G074600.4 | Phvul.008G074600 | Phvul.008G074600 | PF00400,PF14 |
| 3 | 1 Phvul.008G074600.1 | Phvul.008G074600 | Phvul.008G074600 | PF00400,PF14 |
| 4 | 1 Phvul.008G074600.3 | Phvul.008G074600 | Phvul.008G074600 | PF00400,PF14 |
| 5 | 1 Phvul.008G074600.2 | Phvul.008G074600 | Phvul.008G074600 | PF00400,PF14 |
| 6 | 1 Phvul.008G074600.4 | Phvul.008G074600 | Phvul.008G074600 | PF00400,PF14 |
| 7 | 1 Phvul.008G074600.1 | Phvul.008G074600 | Phvul.008G074600 | PF00400,PF14 |
| 8 | 1 Phvul.008G074600.1 | Phvul.008G074600 | Phvul.008G074600 | PF00400,PF14 |
| 9 | 1 Phvul.008G123400.1 | Phvul.008G123400 | Phvul.008G123400 | PF00646 |
| 10 | 1 Phvul.008G123400.1 | Phvul.008G123400 | Phvul.008G123400 | PF00646 |
| 11 | 1 Phvul.008G129500.1 | Phvul.008G129500 | Phvul.008G129500 | PF04851,PF02 |
| 12 | 1 Phvul.008G129500.1 | Phvul.008G129500 | Phvul.008G129500 | PF04851,PF02 |
| 13 | 1 Phvul.008G129500.1 | Phvul.008G129500 | Phvul.008G129500 | PF04851,PF02 |
| 14 | 1 Phvul.008G164600.1 | Phvul.008G164600 | Phvul.008G164600 | PF13855,PF12 |
| 15 | 1 Phvul.008G164600.1 | Phvul.008G164600 | Phvul.008G164600 | PF13855,PF12 |
| 16 | 1 Phvul.008G164600.1 | Phvul.008G164600 | Phvul.008G164600 | PF13855,PF12 |
| 17 | 1 Phvul.008G225300.1 | Phvul.008G225300 | Phvul.008G225300 | PF01490 |
| 18 | 1 Phvul.008G230200.1 | Phvul.008G230200 | Phvul.008G230200 | PF04893 |
| 19 | 1 Phvul.009G030500.1 | Phvul.009G030500 | Phvul.009G030500 | PF07690 |
| 20 | 1 Phvul.009G030500.1 | Phvul.009G030500 | Phvul.009G030500 | PF07690 |
| 21 | 1 Phvul.009G030500.1 | Phvul.009G030500 | Phvul.009G030500 | PF07690 |
| 22 | 1 Phvul.009G099700.1 | Phvul.009G099700 | Phvul.009G099700 | 0 |
| 23 | 1 Phvul.009G099700.1 | Phvul.009G099700 | Phvul.009G099700 | 0 |
| 24 | 1 Phvul.009G099700.1 | Phvul.009G099700 | Phvul.009G099700 | 0 |
| 25 | 1 Phvul.009G233000.1 | Phvul.009G233000 | Phvul.009G233000 | PF04178 |
| 26 | 1 Phvul.009G233000.1 | Phvul.009G233000 | Phvul.009G233000 | PF04178 |
| 27 | 1 Phvul.009G233000.1 | Phvul.009G233000 | Phvul.009G233000 | PF04178 |
| 28 | 1 Phvul.010G021700.1 | Phvul.010G021700 | Phvul.010G021700 | 0 |
| 29 | 1 Phvul.010G021700.1 | Phvul.010G021700 | Phvul.010G021700 | 0 |
| 30 | 1 Phvul.010G021700.1 | Phvul.010G021700 | Phvul.010G021700 | 0 |
| 31 | 1 Phvul.010G104900.2 | Phvul.010G104900 | Phvul.010G104900 | PF02548 |
| 32 | 1 Phvul.010G104900.2 | Phvul.010G104900 | Phvul.010G104900 | PF02548 |
| 33 | 1 Phvul.010G104900.2 | Phvul.010G104900 | Phvul.010G104900 | PF02548 |
| 34 | 1 Phvul.010G129400.1 | Phvul.010G129400 | Phvul.010G129400 | PF03514 |
| 35 | 1 Phvul.010G129400.1 | Phvul.010G129400 | Phvul.010G129400 | PF03514 |
| 36 | 1 Phvul.010G129400.1 | Phvul.010G129400 | Phvul.010G129400 | PF03514 |
| 37 | 1 Phvul.010G157900.4 | Phvul.010G157900 | Phvul.010G157900 | PF16987 |
| 38 | 1 Phvul.010G157900.3 | Phvul.010G157900 | Phvul.010G157900 | PF16987 |
| 39 | 1 Phvul.010G157900.2 | Phvul.010G157900 | Phvul.010G157900 | PF16987 |
| 40 | 1 Phvul.010G157900.4 | Phvul.010G157900 | Phvul.010G157900 | PF16987 |
| 41 | 1 Phvul.010G157900.3 | Phvul.010G157900 | Phvul.010G157900 | PF16987 |
| 42 | 1 Phvul.010G157900.2 | Phvul.010G157900 | Phvul.010G157900 | PF16987 |
| 43 | 1 Phvul.010G157900.4 | Phvul.010G157900 | Phvul.010G157900 | PF16987 |
| 44 | 1 Phvul.010G157900.3 | Phvul.010G157900 | Phvul.010G157900 | PF16987 |
| 45 | 1 Phvul.010G157900.2 | Phvul.010G157900 | Phvul.010G157900 | PF16987 |
| 46 | 1 Phvul.011G006200.1 | Phvul.011G006200 | Phvul.011G006200 | PF01399 |
| 47 | 1 Phvul.011G006200.1 | Phvul.011G006200 | Phvul.011G006200 | PF01399 |
| 48 | 1 Phvul.011G006200.1 | Phvul.011G006200 | Phvul.011G006200 | PF01399 |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | |
|----------------------|------------------|------------------|---------|
| 1 Phvul.011G161100.1 | Phvul.011G161100 | Phvul.011G161100 | PF00067 |
| 1 Phvul.011G161100.1 | Phvul.011G161100 | Phvul.011G161100 | PF00067 |
| 1 Phvul.011G161100.1 | Phvul.011G161100 | Phvul.011G161100 | PF00067 |
| 1 Phvul.011G161900.1 | Phvul.011G161900 | Phvul.011G161900 | PF00067 |
| 1 Phvul.011G161900.1 | Phvul.011G161900 | Phvul.011G161900 | PF00067 |

Do not distribute

| 1 | Panther | KOG | KEGG | KOG | GO | Best-hit-arabi-arabi-symbol |
|----|--------------------------|---------|-------------|----------|----------------|-----------------------------|
| 2 | PTHR24221,P ⁻ | KOG0058 | 3.6.3.44 | | 0 GO:0016887,C | AT3G28345.1 0 |
| 3 | PTHR24221,P ⁻ | KOG0058 | 3.6.3.44 | | 0 GO:0016887,C | AT3G28345.1 0 |
| 4 | PTHR24221,P ⁻ | KOG0058 | 3.6.3.44 | | 0 GO:0016887,C | AT3G28345.1 0 |
| 5 | PTHR24221,P ⁻ | KOG0058 | 3.6.3.44 | | 0 GO:0016887,C | AT3G28345.1 0 |
| 6 | PTHR11800 | KOG1522 | 2.7.7.6 | K03011 | GO:0046983,C | AT2G15430.1 NRPB3,NRPD3 |
| 7 | PTHR11800 | KOG1522 | 2.7.7.6 | K03011 | GO:0046983,C | AT2G15430.1 NRPB3,NRPD3 |
| 8 | PTHR11800 | KOG1522 | 2.7.7.6 | K03011 | GO:0046983,C | AT2G15430.1 NRPB3,NRPD3 |
| 9 | PTHR11800 | KOG1522 | 2.7.7.6 | K03011 | GO:0046983,C | AT2G15430.1 NRPB3,NRPD3 |
| 10 | PTHR24006,P ⁻ | | 0 3.4.19.12 | K11838 | GO:0005515 | AT5G06600.2 UBP12 |
| 11 | PTHR24006,P ⁻ | | 0 3.4.19.12 | K11838 | GO:0005515 | AT5G06600.2 UBP12 |
| 12 | PTHR24006,P ⁻ | | 0 3.4.19.12 | K11838 | GO:0005515 | AT5G06600.2 UBP12 |
| 13 | PTHR24006,P ⁻ | | 0 3.4.19.12 | K11838 | GO:0005515 | AT5G06600.2 UBP12 |
| 14 | PTHR24006,P ⁻ | | 0 3.4.19.12 | K11838 | GO:0005515 | AT5G06600.2 UBP12 |
| 15 | PTHR24006,P ⁻ | | 0 3.4.19.12 | K11838 | GO:0005515 | AT5G06600.2 UBP12 |
| 16 | PTHR24006,P ⁻ | | 0 3.4.19.12 | K11838 | GO:0005515 | AT5G06600.2 UBP12 |
| 17 | PTHR24006,P ⁻ | | 0 3.4.19.12 | K11838 | GO:0005515 | AT5G06600.2 UBP12 |
| 18 | PTHR24006,P ⁻ | | 0 3.4.19.12 | K11838 | GO:0005515 | AT5G06600.2 UBP12 |
| 19 | PTHR27000,P ⁻ | KOG1187 | 2.7.11.1 | | 0 GO:0005515,C | AT4G20270.1 BAM3 |
| 20 | PTHR27000,P ⁻ | KOG1187 | 2.7.11.1 | | 0 GO:0005515,C | AT4G20270.1 BAM3 |
| 21 | PTHR27000,P ⁻ | KOG1187 | 2.7.11.1 | | 0 GO:0005515,C | AT4G20270.1 BAM3 |
| 22 | PTHR27000,P ⁻ | KOG1187 | 2.7.11.1 | | 0 GO:0005515,C | AT4G20270.1 BAM3 |
| 23 | PTHR24089,P ⁻ | KOG0761 | | 0 K15119 | | 0 AT2G46320.1 0 |
| 24 | PTHR24089,P ⁻ | KOG0761 | | 0 K15119 | | 0 AT2G46320.1 0 |
| 25 | PTHR24089,P ⁻ | KOG0761 | | 0 K15119 | | 0 AT2G46320.1 0 |
| 26 | PTHR24089,P ⁻ | KOG0761 | | 0 K15119 | | 0 AT2G46320.1 0 |
| 27 | PTHR10799,P ⁻ | | 0 3.6.4.12 | K10841 | GO:0005524 | AT2G18760.1 CHR8 |
| 28 | PTHR10799,P ⁻ | | 0 3.6.4.12 | K10841 | GO:0005524 | AT2G18760.1 CHR8 |
| 29 | PTHR10799,P ⁻ | | 0 3.6.4.12 | K10841 | GO:0005524 | AT2G18760.1 CHR8 |
| 30 | PTHR10799,P ⁻ | | 0 3.6.4.12 | K10841 | GO:0005524 | AT2G18760.1 CHR8 |
| 31 | PTHR27009,P ⁻ | KOG1187 | 3.1.4.46 | | 0 GO:0006468,C | AT5G38260.1 0 |
| 32 | PTHR27009,P ⁻ | KOG1187 | 3.1.4.46 | | 0 GO:0006468,C | AT5G38260.1 0 |
| 33 | PTHR27009,P ⁻ | KOG1187 | 3.1.4.46 | | 0 GO:0006468,C | AT5G38260.1 0 |
| 34 | PTHR27009,P ⁻ | KOG1187 | 3.1.4.46 | | 0 GO:0006468,C | AT5G38260.1 0 |
| 35 | PTHR35744,P ⁻ | | 0 | 0 | 0 | 0 AT4G12240.1 0 |
| 36 | PTHR35744,P ⁻ | | 0 | 0 | 0 | 0 AT4G12240.1 0 |
| 37 | PTHR35744,P ⁻ | | 0 | 0 | 0 | 0 AT4G12240.1 0 |
| 38 | PTHR35744,P ⁻ | | 0 | 0 | 0 | 0 AT4G12240.1 0 |
| 39 | PTHR35744,P ⁻ | | 0 | 0 | 0 | 0 AT4G12240.1 0 |
| 40 | PTHR35744,P ⁻ | | 0 | 0 | 0 | 0 AT4G12240.1 0 |
| 41 | PTHR35744,P ⁻ | | 0 | 0 | 0 | 0 AT4G12240.1 0 |
| 42 | PTHR35744,P ⁻ | | 0 | 0 | 0 | 0 AT4G12240.1 0 |
| 43 | PTHR10366,P ⁻ | | 0 1.1.1.133 | K12451 | | 0 AT1G63000.1 NRS/ER,UER1 |
| 44 | PTHR10366,P ⁻ | | 0 1.1.1.133 | K12451 | | 0 AT1G63000.1 NRS/ER,UER1 |
| 45 | PTHR10366,P ⁻ | | 0 1.1.1.133 | K12451 | | 0 AT1G63000.1 NRS/ER,UER1 |
| 46 | PTHR10366,P ⁻ | | 0 1.1.1.133 | K12451 | | 0 AT1G63000.1 NRS/ER,UER1 |
| 47 | PTHR22814,P ⁻ | KOG1603 | | 0 | 0 GO:0046872,C | AT5G19090.2 0 |
| 48 | PTHR22814,P ⁻ | KOG1603 | | 0 | 0 GO:0046872,C | AT5G19090.2 0 |
| 49 | PTHR22939,P ⁻ | KOG1320 | 3.4.21.107 | | 0 GO:0005515 | AT5G36950.1 DegP10 |
| 50 | PTHR22939,P ⁻ | KOG1320 | 3.4.21.107 | | 0 GO:0005515 | AT5G36950.1 DegP10 |
| 51 | PTHR22939,P ⁻ | KOG1320 | 3.4.21.107 | | 0 GO:0005515 | AT5G36950.1 DegP10 |
| 52 | PTHR22939,P ⁻ | KOG1320 | 3.4.21.107 | | 0 GO:0005515 | AT5G36950.1 DegP10 |
| 53 | PTHR27000,P ⁻ | KOG1187 | 2.7.11.1 | | 0 GO:0005515,C | AT5G62230.1 ERL1 |
| 54 | PTHR27000,P ⁻ | KOG1187 | 2.7.11.1 | | 0 GO:0005515,C | AT5G62230.1 ERL1 |
| 55 | PTHR27000,P ⁻ | KOG1187 | 2.7.11.1 | | 0 GO:0005515,C | AT5G62230.1 ERL1 |
| 56 | PTHR27000,P ⁻ | KOG1187 | 2.7.11.1 | | 0 GO:0005515,C | AT5G62230.1 ERL1 |
| 57 | PTHR22967,P ⁻ | KOG1989 | 2.7.11.1 | K08853 | GO:0006468,C | AT2G32850.2 0 |
| 58 | PTHR22967,P ⁻ | KOG1989 | 2.7.11.1 | K08853 | GO:0006468,C | AT2G32850.2 0 |
| 59 | PTHR22967,P ⁻ | KOG1989 | 2.7.11.1 | K08853 | GO:0006468,C | AT2G32850.2 0 |
| 60 | PTHR22967,P ⁻ | KOG1989 | 2.7.11.1 | K08853 | GO:0006468,C | AT2G32850.2 0 |

| | | | | | | |
|----|----------------------------------|-------------|----------|----------------|--------------------------|---|
| 1 | | | | | | |
| 2 | PTHR22967,P ⁻ KOG1989 | 2.7.11.1 | K08853 | GO:0006468,C | AT2G32850.2 | 0 |
| 3 | PTHR22967,P ⁻ KOG1989 | 2.7.11.1 | K08853 | GO:0006468,C | AT2G32850.2 | 0 |
| 4 | PTHR11926,P ⁻ KOG1192 | 2.4.1.272 | | 0 GO:0016758,C | AT2G15480.2 UGT73B5 | |
| 5 | | | | | | |
| 6 | PTHR11926,P ⁻ KOG1192 | 2.4.1.272 | | 0 GO:0016758,C | AT2G15480.2 UGT73B5 | |
| 7 | PTHR11926,P ⁻ KOG1192 | 2.4.1.272 | | 0 GO:0016758,C | AT2G15480.2 UGT73B5 | |
| 8 | PTHR11926,P ⁻ KOG1192 | 2.4.1.272 | | 0 GO:0016758,C | AT2G15480.2 UGT73B5 | |
| 9 | | | | | | |
| 10 | PTHR11926,P ⁻ | 0 2.4.1.173 | | 0 GO:0030259,C | AT1G43620.2 TT15,UGT80B | |
| 11 | PTHR11926,P ⁻ | 0 2.4.1.173 | | 0 GO:0030259,C | AT1G43620.2 TT15,UGT80B | |
| 12 | PTHR11926,P ⁻ | 0 2.4.1.173 | | 0 GO:0030259,C | AT1G43620.2 TT15,UGT80B | |
| 13 | | | | | | |
| 14 | PTHR27002,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0048544,C | AT2G41890.1 | 0 |
| 15 | PTHR27002,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0048544,C | AT2G41890.1 | 0 |
| 16 | PTHR27002,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0048544,C | AT2G41890.1 | 0 |
| 17 | | | | | | |
| 18 | PTHR27002,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0048544,C | AT2G41890.1 | 0 |
| 19 | PTHR27002,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0048544,C | AT2G41890.1 | 0 |
| 20 | PTHR27002,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0048544,C | AT2G41890.1 | 0 |
| 21 | | | | | | |
| 22 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0006468,C | AT2G33580.1 | 0 |
| 23 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0006468,C | AT2G33580.1 | 0 |
| 24 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0006468,C | AT2G33580.1 | 0 |
| 25 | | | | | | |
| 26 | PTHR22953,P ⁻ KOG1378 | 3.1.3.2 | | 0 GO:0016787 | AT3G20500.1 ATPAP18,PAP | |
| 27 | PTHR22953,P ⁻ KOG1378 | 3.1.3.2 | | 0 GO:0016787 | AT3G20500.1 ATPAP18,PAP | |
| 28 | PTHR22953,P ⁻ KOG1378 | 3.1.3.2 | | 0 GO:0016787 | AT3G20500.1 ATPAP18,PAP | |
| 29 | | | | | | |
| 30 | PTHR36356,P ⁻ | 0 | 0 | 0 | AT2G44870.1 | 0 |
| 31 | PTHR36356,P ⁻ | 0 | 0 | 0 | AT2G44870.1 | 0 |
| 32 | PTHR36356,P ⁻ | 0 | 0 | 0 | AT2G44870.1 | 0 |
| 33 | | | | | | |
| 34 | PTHR32411 | 0 | 0 | 0 | AT4G05200.1 CRK25 | |
| 35 | PTHR32411 | 0 | 0 | 0 | AT4G05200.1 CRK25 | |
| 36 | PTHR32411 | 0 | 0 | 0 | AT4G05200.1 CRK25 | |
| 37 | | | | | | |
| 38 | PTHR32467,P ⁻ | 0 | 0 K09284 | GO:0006355,C | AT2G28550.1 RAP2.7,TOE1 | |
| 39 | PTHR32467,P ⁻ | 0 | 0 K09284 | GO:0006355,C | AT2G28550.1 RAP2.7,TOE1 | |
| 40 | PTHR32467,P ⁻ | 0 | 0 K09284 | GO:0006355,C | AT2G28550.1 RAP2.7,TOE1 | |
| 41 | PTHR32467,P ⁻ | 0 | 0 K09284 | GO:0006355,C | AT2G28550.1 RAP2.7,TOE1 | |
| 42 | PTHR32467,P ⁻ | 0 | 0 K09284 | GO:0006355,C | AT2G28550.1 RAP2.7,TOE1 | |
| 43 | PTHR32467,P ⁻ | 0 | 0 K09284 | GO:0006355,C | AT2G28550.1 RAP2.7,TOE1 | |
| 44 | PTHR32467,P ⁻ | 0 | 0 K09284 | GO:0006355,C | AT2G28550.1 RAP2.7,TOE1 | |
| 45 | | | | | | |
| 46 | 0 | 0 | 0 | 0 GO:0005509 | 0 | 0 |
| 47 | 0 | 0 | 0 | 0 GO:0005509 | 0 | 0 |
| 48 | 0 | 0 | 0 | 0 GO:0005509 | 0 | 0 |
| 49 | | | | | | |
| 50 | PTHR31704,P ⁻ | 0 | 0 | 0 | AT4G02550.1 | 0 |
| 51 | PTHR31704,P ⁻ | 0 | 0 | 0 | AT4G02550.1 | 0 |
| 52 | PTHR31587,P ⁻ | 0 | 0 | 0 | AT5G67610.1 | 0 |
| 53 | PTHR31587,P ⁻ | 0 | 0 | 0 | AT5G67610.1 | 0 |
| 54 | PTHR31587,P ⁻ | 0 | 0 | 0 | AT5G67610.1 | 0 |
| 55 | PTHR31587,P ⁻ | 0 | 0 | 0 | AT5G67610.1 | 0 |
| 56 | PTHR31704,P ⁻ | 0 | 0 | 0 | AT4G02210.2 | 0 |
| 57 | PTHR31704,P ⁻ | 0 | 0 | 0 | AT4G02210.2 | 0 |
| 58 | | | | | | |
| 59 | PTHR11145 KOG2714 | | 0 | 0 GO:0051260 | AT3G09030.1 | 0 |
| 60 | PTHR11145 KOG2714 | | 0 | 0 GO:0051260 | AT3G09030.1 | 0 |
| | PTHR32370,P ⁻ | 0 | 0 | 0 GO:0016567 | AT5G64330.1 JK218,NPH3,R | |

| | | | | | |
|----|----------------------------------|-------------|----------|---------------------------------------|---|
| 1 | | | | | |
| 2 | PTHR32370,P ⁻ | 0 | 0 | 0 GO:0016567 AT5G64330.1 JK218,NPH3,R | |
| 3 | PTHR32370,P ⁻ | 0 | 0 | 0 GO:0016567 AT5G64330.1 JK218,NPH3,R | |
| 4 | PTHR31704,P ⁻ | 0 | 0 | 0 0 AT4G02550.1 | 0 |
| 5 | PTHR31704,P ⁻ | 0 | 0 | 0 0 AT4G02550.1 | 0 |
| 6 | PTHR31704,P ⁻ | 0 | 0 | 0 0 AT4G02550.1 | 0 |
| 7 | PTHR10795,P ⁻ | 0 3.4.21.25 | | 0 GO:0016020,C AT2G19170.1 SLP3 | |
| 8 | PTHR10795,P ⁻ | 0 3.4.21.25 | | 0 GO:0016020,C AT2G19170.1 SLP3 | |
| 9 | PTHR10795,P ⁻ | 0 3.4.21.25 | | 0 GO:0016020,C AT2G19170.1 SLP3 | |
| 10 | PTHR10795,P ⁻ | 0 3.4.21.25 | | 0 GO:0016020,C AT2G19170.1 SLP3 | |
| 11 | PTHR34663,P ⁻ | 0 | 0 | 0 0 AT2G23270.1 | 0 |
| 12 | PTHR34663,P ⁻ | 0 | 0 | 0 0 AT2G23270.1 | 0 |
| 13 | PTHR34663,P ⁻ | 0 | 0 | 0 0 AT2G23270.1 | 0 |
| 14 | PTHR34663,P ⁻ | 0 | 0 | 0 0 AT2G23270.1 | 0 |
| 15 | PTHR31704,P ⁻ | 0 | 0 | 0 0 AT4G02550.1 | 0 |
| 16 | PTHR31704,P ⁻ | 0 | 0 | 0 0 AT4G02550.1 | 0 |
| 17 | PTHR31704,P ⁻ | 0 | 0 | 0 0 AT4G02550.1 | 0 |
| 18 | PTHR15959,P ⁻ KOG3894 | | 0 K08492 | 0 AT1G51740.1 ATSYP81,ATUI | |
| 19 | PTHR15959,P ⁻ KOG3894 | | 0 K08492 | 0 AT1G51740.1 ATSYP81,ATUI | |
| 20 | PTHR15959,P ⁻ KOG3894 | | 0 K08492 | 0 AT1G51740.1 ATSYP81,ATUI | |
| 21 | PTHR10302,P ⁻ | 0 | 0 | 0 GO:0006260,C AT4G20010.1 OSB2,PTAC9 | |
| 22 | PTHR10302,P ⁻ | 0 | 0 | 0 GO:0006260,C AT4G20010.1 OSB2,PTAC9 | |
| 23 | PTHR10302,P ⁻ | 0 | 0 | 0 GO:0006260,C AT4G20010.1 OSB2,PTAC9 | |
| 24 | PTHR10302,P ⁻ | 0 | 0 | 0 GO:0006260,C AT4G20010.1 OSB2,PTAC9 | |
| 25 | PTHR10302,P ⁻ | 0 | 0 | 0 GO:0006260,C AT4G20010.1 OSB2,PTAC9 | |
| 26 | PTHR10302,P ⁻ | 0 | 0 | 0 GO:0006260,C AT4G20010.1 OSB2,PTAC9 | |
| 27 | PTHR10302,P ⁻ | 0 | 0 | 0 GO:0006260,C AT4G20010.1 OSB2,PTAC9 | |
| 28 | PTHR10302,P ⁻ | 0 | 0 | 0 GO:0006260,C AT4G20010.1 OSB2,PTAC9 | |
| 29 | PTHR10302,P ⁻ | 0 | 0 | 0 GO:0006260,C AT4G20010.1 OSB2,PTAC9 | |
| 30 | PTHR10302,P ⁻ | 0 | 0 | 0 GO:0006260,C AT4G20010.1 OSB2,PTAC9 | |
| 31 | PTHR10302,P ⁻ | 0 | 0 | 0 GO:0006260,C AT4G20010.1 OSB2,PTAC9 | |
| 32 | PTHR10302,P ⁻ | 0 | 0 | 0 GO:0006260,C AT4G20010.1 OSB2,PTAC9 | |
| 33 | PTHR10302,P ⁻ | 0 | 0 | 0 GO:0006260,C AT4G20010.1 OSB2,PTAC9 | |
| 34 | PTHR10302,P ⁻ | 0 | 0 | 0 GO:0006260,C AT4G20010.1 OSB2,PTAC9 | |
| 35 | PTHR10302,P ⁻ | 0 | 0 | 0 GO:0006260,C AT4G20010.1 OSB2,PTAC9 | |
| 36 | PTHR10302,P ⁻ | 0 | 0 | 0 GO:0006260,C AT4G20010.1 OSB2,PTAC9 | |
| 37 | PTHR10302,P ⁻ | 0 | 0 | 0 GO:0006260,C AT4G20010.1 OSB2,PTAC9 | |
| 38 | PTHR13140,P ⁻ | 0 3.6.4.1 | K10357 | GO:0016459,C AT1G54560.1 ATXIE,XIE | |
| 39 | PTHR13140,P ⁻ | 0 3.6.4.1 | K10357 | GO:0016459,C AT1G54560.1 ATXIE,XIE | |
| 40 | PTHR13140,P ⁻ | 0 3.6.4.1 | K10357 | GO:0016459,C AT1G54560.1 ATXIE,XIE | |
| 41 | PTHR10044,P ⁻ KOG4172 | | 0 | 0 0 AT4G03000.2 | 0 |
| 42 | PTHR10044,P ⁻ KOG4172 | | 0 | 0 0 AT4G03000.2 | 0 |
| 43 | PTHR10044,P ⁻ KOG4172 | | 0 | 0 0 AT4G03000.2 | 0 |
| 44 | PTHR10044,P ⁻ KOG4172 | | 0 | 0 0 AT4G03000.2 | 0 |
| 45 | PTHR10044,P ⁻ KOG4172 | | 0 | 0 0 AT4G03000.2 | 0 |
| 46 | PTHR10044,P ⁻ KOG4172 | | 0 | 0 0 AT4G03000.2 | 0 |
| 47 | PTHR10044,P ⁻ KOG4172 | | 0 | 0 0 AT4G03000.2 | 0 |
| 48 | PTHR10044,P ⁻ KOG4172 | | 0 | 0 0 AT4G03000.2 | 0 |
| 49 | PTHR10799,P ⁻ | 0 3.6.4.12 | K11647 | GO:0016787,C AT3G06010.1 ATCHR12 | |
| 50 | PTHR10799,P ⁻ | 0 3.6.4.12 | K11647 | GO:0016787,C AT3G06010.1 ATCHR12 | |
| 51 | PTHR10799,P ⁻ | 0 3.6.4.12 | K11647 | GO:0016787,C AT3G06010.1 ATCHR12 | |
| 52 | PTHR10799,P ⁻ | 0 3.6.4.12 | K11647 | GO:0016787,C AT3G06010.1 ATCHR12 | |
| 53 | PTHR10641,P ⁻ | 0 | 0 | 0 0 AT5G41020.1 | 0 |
| 54 | PTHR10641,P ⁻ | 0 | 0 | 0 0 AT5G41020.1 | 0 |
| 55 | PTHR10641,P ⁻ | 0 | 0 | 0 0 AT5G41020.1 | 0 |
| 56 | PTHR10641,P ⁻ | 0 | 0 | 0 0 AT5G41020.1 | 0 |
| 57 | PTHR10641,P ⁻ | 0 | 0 | 0 0 AT5G41020.1 | 0 |
| 58 | PTHR10641,P ⁻ | 0 | 0 | 0 0 AT5G41020.1 | 0 |
| 59 | PTHR10641,P ⁻ | 0 | 0 | 0 0 AT5G41020.1 | 0 |
| 60 | PTHR10641,P ⁻ | 0 | 0 | 0 0 AT5G41020.1 | 0 |
| | PTHR10641,P ⁻ | 0 | 0 | 0 0 AT5G41020.1 | 0 |

| | | | | | | |
|----|----------------------------------|-----------|----------|---|-------------------------------------|---|
| 1 | | | | | | |
| 2 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 3 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 4 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 5 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 6 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 7 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 8 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 9 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 10 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 11 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 12 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 13 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 14 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 15 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 16 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 17 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 18 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 19 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 20 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 21 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 22 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 23 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 24 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 25 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 26 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 27 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 28 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 29 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 30 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 31 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT5G41020.1 | 0 |
| 32 | PTHR27000,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0005515,(AT4G08850.1 | 0 |
| 33 | PTHR27000,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0005515,(AT4G08850.1 | 0 |
| 34 | | | | | | |
| 35 | PTHR22950,P ⁻ KOG1303 | | 0 | 0 | 0 AT1G47670.1 | 0 |
| 36 | PTHR22950,P ⁻ KOG1303 | | 0 | 0 | 0 AT1G47670.1 | 0 |
| 37 | PTHR22950,P ⁻ KOG1303 | | 0 | 0 | 0 AT1G47670.1 | 0 |
| 38 | | | | | | |
| 39 | PTHR16441 | 0 | 0 | 0 | 0 AT4G32560.1 | 0 |
| 40 | PTHR16441 | 0 | 0 | 0 | 0 AT4G32560.1 | 0 |
| 41 | PTHR16441 | 0 | 0 | 0 | 0 AT4G32560.1 | 0 |
| 42 | PTHR16441 | 0 | 0 | 0 | 0 AT4G32560.1 | 0 |
| 43 | PTHR16441 | 0 | 0 | 0 | 0 AT4G32560.1 | 0 |
| 44 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 AT2G24960.2 | 0 |
| 45 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 AT2G24960.2 | 0 |
| 46 | | | | | | |
| 47 | PTHR15288,P ⁻ | 0 | 0 | 0 | 0 AT5G35560.1 | 0 |
| 48 | PTHR15288,P ⁻ | 0 | 0 | 0 | 0 AT5G35560.1 | 0 |
| 49 | PTHR15288,P ⁻ | 0 | 0 | 0 | 0 AT5G35560.1 | 0 |
| 50 | PTHR15288,P ⁻ | 0 | 0 | 0 | 0 AT5G35560.1 | 0 |
| 51 | PTHR15288,P ⁻ | 0 | 0 | 0 | 0 AT5G35560.1 | 0 |
| 52 | PTHR15288,P ⁻ | 0 | 0 | 0 | 0 AT5G35560.1 | 0 |
| 53 | PTHR15288,P ⁻ | 0 | 0 | 0 | 0 AT5G35560.1 | 0 |
| 54 | PTHR15288,P ⁻ | 0 | 0 | 0 | 0 AT5G35560.1 | 0 |
| 55 | PTHR15288,P ⁻ | 0 | 0 | 0 | 0 AT5G35560.1 | 0 |
| 56 | PTHR15288,P ⁻ | 0 | 0 | 0 | 0 AT5G35560.1 | 0 |
| 57 | PTHR15288,P ⁻ | 0 | 0 | 0 | 0 AT5G35560.1 | 0 |
| 58 | | | | | | |
| 59 | PTHR12281,P ⁻ | 0 | 0 K17824 | | 0 AT1G15860.2 | 0 |
| 60 | PTHR12281,P ⁻ | 0 | 0 K17824 | | 0 AT1G15860.2 | 0 |
| | PTHR19211,P ⁻ | 0 3.6.1.3 | K06185 | | GO:0016887,(AT5G60790.1 ATGCN1,GCN: | |

| | | | | | | | | |
|----|----------------------------------|-------------|----------|----------------|---------------|---------------|---|--|
| 1 | | | | | | | | |
| 2 | PTHR19211,P ⁻ | 0 3.6.1.3 | K06185 | GO:0016887,C | AT5G60790.1 | ATGCN1,GCN: | | |
| 3 | PTHR19211,P ⁻ | 0 3.6.1.3 | K06185 | GO:0016887,C | AT5G60790.1 | ATGCN1,GCN: | | |
| 4 | PTHR34118,P ⁻ | 0 | 0 K02116 | | 0 AT2G31040.1 | | 0 | |
| 5 | | | | | | | | |
| 6 | PTHR34118,P ⁻ | 0 | 0 K02116 | | 0 AT2G31040.1 | | 0 | |
| 7 | PTHR34118,P ⁻ | 0 | 0 K02116 | | 0 AT2G31040.1 | | 0 | |
| 8 | | | | | | | | |
| 9 | PTHR11926,P ⁻ | 0 2.4.1.324 | | 0 GO:0016758,C | AT1G22380.1 | AtUGT85A3,U | | |
| 10 | PTHR11926,P ⁻ | 0 2.4.1.324 | | 0 GO:0016758,C | AT1G22380.1 | AtUGT85A3,U | | |
| 11 | PTHR11926,P ⁻ | 0 2.4.1.324 | | 0 GO:0016758,C | AT1G22380.1 | AtUGT85A3,U | | |
| 12 | | | | | | | | |
| 13 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14460.1 | | 0 | |
| 14 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14460.1 | | 0 | |
| 15 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14460.1 | | 0 | |
| 16 | PTHR12323 KOG0007 | | 0 | 0 GO:0006396,C | AT4G31200.3 | | 0 | |
| 17 | | | | | | | | |
| 18 | PTHR12323 KOG0007 | | 0 | 0 GO:0006396,C | AT4G31200.3 | | 0 | |
| 19 | PTHR12323 KOG0007 | | 0 | 0 GO:0006396,C | AT4G31200.3 | | 0 | |
| 20 | | | | | | | | |
| 21 | PTHR11200,P ⁻ KOG0565 | 3.1.3.56 | | 0 | 0 AT4G18010.2 | 5PTASE2,AT5F | | |
| 22 | PTHR11200,P ⁻ KOG0565 | 3.1.3.56 | | 0 | 0 AT4G18010.2 | 5PTASE2,AT5F | | |
| 23 | PTHR11200,P ⁻ KOG0565 | 3.1.3.56 | | 0 | 0 AT4G18010.2 | 5PTASE2,AT5F | | |
| 24 | PTHR11200,P ⁻ KOG0565 | 3.1.3.56 | | 0 | 0 AT4G18010.2 | 5PTASE2,AT5F | | |
| 25 | PTHR11200,P ⁻ KOG0565 | 3.1.3.56 | | 0 | 0 AT4G18010.2 | 5PTASE2,AT5F | | |
| 26 | PTHR11200,P ⁻ KOG0565 | 3.1.3.56 | | 0 | 0 AT4G18010.2 | 5PTASE2,AT5F | | |
| 27 | PTHR11200,P ⁻ KOG0565 | 3.1.3.56 | | 0 | 0 AT4G18010.2 | 5PTASE2,AT5F | | |
| 28 | | | | | | | | |
| 29 | PTHR34996,P ⁻ | 0 | 0 | 0 | 0 | 0 | 0 | |
| 30 | PTHR34996,P ⁻ | 0 | 0 | 0 | 0 | 0 | 0 | |
| 31 | PTHR34996,P ⁻ | 0 | 0 | 0 | 0 | 0 | 0 | |
| 32 | | | | | | | | |
| 33 | PTHR36400 | 0 | 0 | 0 GO:0006412,C | AT5G45590.1 | | 0 | |
| 34 | PTHR36400 | 0 | 0 | 0 GO:0006412,C | AT5G45590.1 | | 0 | |
| 35 | PTHR36400 | 0 | 0 | 0 GO:0006412,C | AT5G45590.1 | | 0 | |
| 36 | | 0 | 0 | 0 | 0 | 0 | 0 | |
| 37 | | 0 | 0 | 0 | 0 | 0 | 0 | |
| 38 | | 0 | 0 | 0 | 0 | 0 | 0 | |
| 39 | | 0 | 0 | 0 | 0 | 0 | 0 | |
| 40 | | 0 | 0 | 0 | 0 | 0 | 0 | |
| 41 | | | | | | | | |
| 42 | PTHR12465 | 0 | 0 K13528 | GO:0016592,C | AT2G28230.1 | | 0 | |
| 43 | PTHR12465 | 0 | 0 K13528 | GO:0016592,C | AT2G28230.1 | | 0 | |
| 44 | PTHR12465 | 0 | 0 K13528 | GO:0016592,C | AT2G28230.1 | | 0 | |
| 45 | | | | | | | | |
| 46 | PTHR11785,P ⁻ KOG1286 | | 0 | 0 GO:0055085,C | AT5G04770.1 | ATCAT6,CAT6 | | |
| 47 | PTHR23083,P ⁻ KOG0548 | | 0 | 0 | 0 AT4G37460.1 | SRFR1 | | |
| 48 | PTHR23083,P ⁻ KOG0548 | | 0 | 0 | 0 AT4G37460.1 | SRFR1 | | |
| 49 | PTHR14360,P ⁻ KOG3156 | | 0 | 0 | 0 AT2G16460.1 | | 0 | |
| 50 | | | | | | | | |
| 51 | PTHR14360,P ⁻ KOG3156 | | 0 | 0 | 0 AT2G16460.1 | | 0 | |
| 52 | PTHR14360,P ⁻ KOG3156 | | 0 | 0 | 0 AT2G16460.1 | | 0 | |
| 53 | | | | | | | | |
| 54 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G02150.2 | PTF1,TCP13,TI | | |
| 55 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G02150.2 | PTF1,TCP13,TI | | |
| 56 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G02150.2 | PTF1,TCP13,TI | | |
| 57 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G02150.2 | PTF1,TCP13,TI | | |
| 58 | | | | | | | | |
| 59 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G02150.2 | PTF1,TCP13,TI | | |
| 60 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G02150.2 | PTF1,TCP13,TI | | |
| | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 AT3G02150.2 | PTF1,TCP13,TI | | |

| | | | | | | |
|----|----------------------------------|----------------|----------|---|---|-------------------------------------|
| 1 | | | | | | |
| 2 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 | AT3G02150.2 PTF1,TCP13,TI |
| 3 | PTHR31072,P ⁻ | 0 | 0 | 0 | 0 | AT3G02150.2 PTF1,TCP13,TI |
| 4 | PTHR11200,P ⁻ KOG0565 | 3.1.3.56 | | 0 | 0 | AT1G71710.1 |
| 5 | | | | | | 0 |
| 6 | PTHR11200,P ⁻ KOG0565 | 3.1.3.56 | | 0 | 0 | AT1G71710.1 |
| 7 | | | | | | 0 |
| 8 | PTHR11200,P ⁻ KOG0565 | 3.1.3.56 | | 0 | 0 | AT1G71710.1 |
| 9 | | | | | | 0 |
| 10 | PTHR11200,P ⁻ KOG0565 | 3.1.3.56 | | 0 | 0 | AT1G71710.1 |
| 11 | | | | | | 0 |
| 12 | PTHR11956,P ⁻ | 0 6.1.1.19 | K01887 | | | GO:0006420,(AT4G26300.1 emb1027 |
| 13 | | | | | | |
| 14 | PTHR11956,P ⁻ | 0 6.1.1.19 | K01887 | | | GO:0006420,(AT4G26300.1 emb1027 |
| 15 | | | | | | |
| 16 | PTHR11956,P ⁻ | 0 6.1.1.19 | K01887 | | | GO:0006420,(AT4G26300.1 emb1027 |
| 17 | | | | | | |
| 18 | PTHR11011,P ⁻ KOG1221 | 1.2.1.50,1.2.1 | K13356 | | | GO:0080019 AT4G33790.1 CER4,FAR3,G7 |
| 19 | | | | | | |
| 20 | PTHR11011,P ⁻ KOG1221 | 1.2.1.50,1.2.1 | K13356 | | | GO:0080019 AT4G33790.1 CER4,FAR3,G7 |
| 21 | | | | | | |
| 22 | PTHR19957,P ⁻ KOG3202 | | 0 K08498 | | | GO:0005515,(AT1G28490.1 ATSYP61,OSM |
| 23 | | | | | | |
| 24 | PTHR19957,P ⁻ KOG3202 | | 0 K08498 | | | GO:0005515,(AT1G28490.1 ATSYP61,OSM |
| 25 | | | | | | |
| 26 | PTHR19957,P ⁻ KOG3202 | | 0 K08498 | | | GO:0005515,(AT1G28490.1 ATSYP61,OSM |
| 27 | | | | | | |
| 28 | PTHR12606,P ⁻ KOG3246 | 3.4.22.68 | | 0 | | GO:0008234,(AT4G00690.1 ULP1B |
| 29 | | | | | | |
| 30 | PTHR12606,P ⁻ KOG3246 | 3.4.22.68 | | 0 | | GO:0008234,(AT4G00690.1 ULP1B |
| 31 | | | | | | |
| 32 | PTHR12606,P ⁻ KOG3246 | 3.4.22.68 | | 0 | | GO:0008234,(AT4G00690.1 ULP1B |
| 33 | | | | | | |
| 34 | PTHR12606,P ⁻ KOG3246 | 3.4.22.68 | | 0 | | GO:0008234,(AT4G00690.1 ULP1B |
| 35 | | | | | | |
| 36 | PTHR12606,P ⁻ KOG3246 | 3.4.22.68 | | 0 | | GO:0008234,(AT4G00690.1 ULP1B |
| 37 | | | | | | |
| 38 | PTHR12606,P ⁻ KOG3246 | 3.4.22.68 | | 0 | | GO:0008234,(AT4G00690.1 ULP1B |
| 39 | | | | | | |
| 40 | PTHR12606,P ⁻ KOG3246 | 3.4.22.68 | | 0 | | GO:0008234,(AT4G00690.1 ULP1B |
| 41 | | | | | | |
| 42 | PTHR12606,P ⁻ KOG3246 | 3.4.22.68 | | 0 | | GO:0008234,(AT4G00690.1 ULP1B |
| 43 | | | | | | |
| 44 | PTHR12606,P ⁻ KOG3246 | 3.4.22.68 | | 0 | | GO:0008234,(AT4G00690.1 ULP1B |
| 45 | | | | | | |
| 46 | PTHR12606,P ⁻ KOG3246 | 3.4.22.68 | | 0 | | GO:0008234,(AT4G00690.1 ULP1B |
| 47 | | | | | | |
| 48 | PTHR12606,P ⁻ KOG3246 | 3.4.22.68 | | 0 | | GO:0008234,(AT4G00690.1 ULP1B |
| 49 | | | | | | |
| 50 | PTHR12606,P ⁻ KOG3246 | 3.4.22.68 | | 0 | | GO:0008234,(AT4G00690.1 ULP1B |
| 51 | | | | | | |
| 52 | PTHR12606,P ⁻ KOG3246 | 3.4.22.68 | | 0 | | GO:0008234,(AT4G00690.1 ULP1B |
| 53 | | | | | | |
| 54 | PTHR23241,P ⁻ KOG2886 | | 0 | 0 | 0 | AT3G62580.1 |
| 55 | | | | | | |
| 56 | PTHR23241,P ⁻ KOG2886 | | 0 | 0 | 0 | AT3G62580.1 |
| 57 | | | | | | |
| 58 | PTHR23241,P ⁻ KOG2886 | | 0 | 0 | 0 | AT3G62580.1 |
| 59 | | | | | | |
| 60 | PTHR32440,P ⁻ KOG1432 | | 0 | 0 | 0 | GO:0016787 AT3G10150.1 ATPAP16,PAP |
| 61 | | | | | | |
| 62 | PTHR32440,P ⁻ KOG1432 | | 0 | 0 | 0 | GO:0016787 AT3G10150.1 ATPAP16,PAP |
| 63 | | | | | | |
| 64 | PTHR32440,P ⁻ KOG1432 | | 0 | 0 | 0 | GO:0016787 AT3G10150.1 ATPAP16,PAP |
| 65 | | | | | | |
| 66 | PTHR13743,P ⁻ | 0 | 0 | 0 | 0 | GO:0005515 AT2G45540.1 |
| 67 | | | | | | |
| 68 | PTHR13743,P ⁻ | 0 | 0 | 0 | 0 | GO:0005515 AT2G45540.1 |
| 69 | | | | | | |

| | | | | | | | | |
|----|----------------------------------|----------|----------|--------------|-------------|--------------|-------------------------|---|
| 1 | | | | | | | | |
| 2 | PTHR13743,P ⁻ | 0 | 0 | 0 | GO:0005515 | AT2G45540.1 | 0 | |
| 3 | PTHR13743,P ⁻ | 0 | 0 | 0 | GO:0005515 | AT2G45540.1 | 0 | |
| 4 | PTHR13743,P ⁻ | 0 | 0 | 0 | GO:0005515 | AT2G45540.1 | 0 | |
| 5 | PTHR13743,P ⁻ | 0 | 0 | 0 | GO:0005515 | AT2G45540.1 | 0 | |
| 6 | PTHR13743,P ⁻ | 0 | 0 | 0 | GO:0005515 | AT2G45540.1 | 0 | |
| 7 | PTHR13743,P ⁻ | 0 | 0 | 0 | GO:0005515 | AT2G45540.1 | 0 | |
| 8 | PTHR13743,P ⁻ | 0 | 0 | 0 | GO:0005515 | AT2G45540.1 | 0 | |
| 9 | PTHR32133,P ⁻ | 0 | 0 | 0 | GO:0005515 | AT3G24760.1 | 0 | |
| 10 | PTHR32133,P ⁻ | 0 | 0 | 0 | GO:0005515 | AT3G24760.1 | 0 | |
| 11 | PTHR32133,P ⁻ | 0 | 0 | 0 | GO:0005515 | AT3G24760.1 | 0 | |
| 12 | PTHR14950,P ⁻ KOG0701 | 3.1.26.3 | K11592 | GO:0016787,C | AT3G03300.3 | ATDCL2,DCL2 | | |
| 13 | PTHR14950,P ⁻ KOG0701 | 3.1.26.3 | K11592 | GO:0016787,C | AT3G03300.3 | ATDCL2,DCL2 | | |
| 14 | PTHR14950,P ⁻ KOG0701 | 3.1.26.3 | K11592 | GO:0016787,C | AT3G03300.3 | ATDCL2,DCL2 | | |
| 15 | PTHR14950,P ⁻ KOG0701 | 3.1.26.3 | K11592 | GO:0016787,C | AT3G03300.3 | ATDCL2,DCL2 | | |
| 16 | PTHR27003,P ⁻ | 0 | 2.7.11.1 | 0 | GO:0005515 | AT1G05700.1 | 0 | |
| 17 | PTHR27003,P ⁻ | 0 | 2.7.11.1 | 0 | GO:0005515 | AT1G05700.1 | 0 | |
| 18 | PTHR27003,P ⁻ | 0 | 2.7.11.1 | 0 | GO:0005515 | AT1G05700.1 | 0 | |
| 19 | PTHR27003,P ⁻ | 0 | 2.7.11.1 | 0 | GO:0005515 | AT1G05700.1 | 0 | |
| 20 | PTHR22950,P ⁻ KOG1303 | | 0 | K13946 | | 0 | AT2G38120.1 AUX1,MAP1,P | |
| 21 | PTHR12822,P ⁻ KOG3114 | | 0 | | 0 | GO:0016020 | AT2G39805.1 | 0 |
| 22 | PTHR12822,P ⁻ KOG3114 | | 0 | | 0 | GO:0016020 | AT2G39805.1 | 0 |
| 23 | PTHR23500,P ⁻ KOG0254 | | 0 | | 0 | GO:0055085,C | AT1G34580.1 | 0 |
| 24 | PTHR23500,P ⁻ KOG0254 | | 0 | | 0 | GO:0055085,C | AT1G34580.1 | 0 |
| 25 | PTHR23500,P ⁻ KOG0254 | | 0 | | 0 | GO:0055085,C | AT1G34580.1 | 0 |
| 26 | PTHR23500,P ⁻ KOG0254 | | 0 | | 0 | GO:0055085,C | AT1G34580.1 | 0 |
| 27 | PTHR13129,P ⁻ | 0 | 0 | K11789 | | 0 | AT4G31160.1 DCAF1 | |
| 28 | PTHR13129,P ⁻ | 0 | 0 | K11789 | | 0 | AT4G31160.1 DCAF1 | |
| 29 | PTHR13129,P ⁻ | 0 | 0 | K11789 | | 0 | AT4G31160.1 DCAF1 | |
| 30 | PTHR13129,P ⁻ | 0 | 0 | K11789 | | 0 | AT4G31160.1 DCAF1 | |
| 31 | PTHR21493,P ⁻ KOG1743 | | 0 | | 0 | GO:0016192 | AT3G49420.1 | 0 |
| 32 | PTHR21493,P ⁻ KOG1743 | | 0 | | 0 | GO:0016192 | AT3G49420.1 | 0 |
| 33 | PTHR21493,P ⁻ KOG1743 | | 0 | | 0 | GO:0016192 | AT3G49420.1 | 0 |
| 34 | PTHR21493,P ⁻ KOG1743 | | 0 | | 0 | GO:0016192 | AT3G49420.1 | 0 |
| 35 | PTHR31851,P ⁻ | 0 | 0 | 0 | 0 | AT4G27860.1 | | 0 |
| 36 | PTHR31851,P ⁻ | 0 | 0 | 0 | 0 | AT4G27860.1 | | 0 |
| 37 | PTHR31851,P ⁻ | 0 | 0 | 0 | 0 | AT4G27860.1 | | 0 |
| 38 | PTHR31851,P ⁻ | 0 | 0 | 0 | 0 | AT4G27860.1 | | 0 |
| 39 | PTHR20881 KOG2949 | 2.1.2.11 | K00606 | GO:0015940,C | AT3G61530.1 | PANB2 | | |
| 40 | PTHR20881 KOG2949 | 2.1.2.11 | K00606 | GO:0015940,C | AT3G61530.1 | PANB2 | | |
| 41 | PTHR20881 KOG2949 | 2.1.2.11 | K00606 | GO:0015940,C | AT3G61530.1 | PANB2 | | |
| 42 | PTHR20881 KOG2949 | 2.1.2.11 | K00606 | GO:0015940,C | AT3G61530.1 | PANB2 | | |
| 43 | PTHR31636,P ⁻ | 0 | 0 | 0 | 0 | AT3G13840.1 | | 0 |
| 44 | PTHR31636,P ⁻ | 0 | 0 | 0 | 0 | AT3G13840.1 | | 0 |
| 45 | PTHR31636,P ⁻ | 0 | 0 | 0 | 0 | AT3G13840.1 | | 0 |
| 46 | PTHR31636,P ⁻ | 0 | 0 | 0 | 0 | AT3G13840.1 | | 0 |
| 47 | PTHR33137,P ⁻ | 0 | 0 | K14972 | | 0 | AT1G15780.1 | 0 |
| 48 | PTHR33137,P ⁻ | 0 | 0 | K14972 | | 0 | AT1G15780.1 | 0 |
| 49 | PTHR33137,P ⁻ | 0 | 0 | K14972 | | 0 | AT1G15780.1 | 0 |
| 50 | PTHR33137,P ⁻ | 0 | 0 | K14972 | | 0 | AT1G15780.1 | 0 |
| 51 | PTHR33137,P ⁻ | 0 | 0 | K14972 | | 0 | AT1G15780.1 | 0 |
| 52 | PTHR33137,P ⁻ | 0 | 0 | K14972 | | 0 | AT1G15780.1 | 0 |
| 53 | PTHR33137,P ⁻ | 0 | 0 | K14972 | | 0 | AT1G15780.1 | 0 |
| 54 | PTHR33137,P ⁻ | 0 | 0 | K14972 | | 0 | AT1G15780.1 | 0 |
| 55 | PTHR33137,P ⁻ | 0 | 0 | K14972 | | 0 | AT1G15780.1 | 0 |
| 56 | PTHR33137,P ⁻ | 0 | 0 | K14972 | | 0 | AT1G15780.1 | 0 |
| 57 | PTHR33137,P ⁻ | 0 | 0 | K14972 | | 0 | AT1G15780.1 | 0 |
| 58 | PTHR33137,P ⁻ | 0 | 0 | K14972 | | 0 | AT1G15780.1 | 0 |
| 59 | PTHR10855 KOG1497 | | 0 | K12178 | GO:0005515 | AT5G42970.1 | ATS4,COP14,C | |
| 60 | PTHR10855 KOG1497 | | 0 | K12178 | GO:0005515 | AT5G42970.1 | ATS4,COP14,C | |
| | PTHR10855 KOG1497 | | 0 | K12178 | GO:0005515 | AT5G42970.1 | ATS4,COP14,C | |

| | | | |
|----|----------------------------------|-------------|-------------------------------------|
| 1 | | | |
| 2 | PTHR24282,P ⁻ KOG0157 | 1.14.13.173 | 0 GO:0055114,C AT3G14690.1 CYP72A15 |
| 3 | PTHR24282,P ⁻ KOG0157 | 1.14.13.173 | 0 GO:0055114,C AT3G14690.1 CYP72A15 |
| 4 | PTHR24282,P ⁻ KOG0157 | 1.14.13.173 | 0 GO:0055114,C AT3G14690.1 CYP72A15 |
| 5 | | | |
| 6 | PTHR24282,P ⁻ KOG0159 | 1.14.13.173 | 0 GO:0055114,C AT3G14690.1 CYP72A15 |
| 7 | PTHR24282,P ⁻ KOG0159 | 1.14.13.173 | 0 GO:0055114,C AT3G14690.1 CYP72A15 |
| 8 | | | |
| 9 | | | |
| 10 | | | |
| 11 | | | |
| 12 | | | |
| 13 | | | |
| 14 | | | |
| 15 | | | |
| 16 | | | |
| 17 | | | |
| 18 | | | |
| 19 | | | |
| 20 | | | |
| 21 | | | |
| 22 | | | |
| 23 | | | |
| 24 | | | |
| 25 | | | |
| 26 | | | |
| 27 | | | |
| 28 | | | |
| 29 | | | |
| 30 | | | |
| 31 | | | |
| 32 | | | |
| 33 | | | |
| 34 | | | |
| 35 | | | |
| 36 | | | |
| 37 | | | |
| 38 | | | |
| 39 | | | |
| 40 | | | |
| 41 | | | |
| 42 | | | |
| 43 | | | |
| 44 | | | |
| 45 | | | |
| 46 | | | |
| 47 | | | |
| 48 | | | |
| 49 | | | |
| 50 | | | |
| 51 | | | |
| 52 | | | |
| 53 | | | |
| 54 | | | |
| 55 | | | |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

Do not distribute

| arabi-defline | ID | Annot_defline | IDENTIFIER | NAME | DESCRIPTION |
|---------------------------------|----------------------|---------------|--------------|---------------|------------------|
| ABC transporter family protei | Phvul.004G02 | PTHR24221:SF | Phvul.004G02 | Solute transp | subfamily ABC |
| ABC transporter family protei | Phvul.004G02 | PTHR24221:SF | Phvul.004G02 | Solute transp | subfamily ABC |
| ABC transporter family protei | Phvul.004G02 | PTHR24221:SF | Phvul.004G02 | Solute transp | subfamily ABC |
| DNA-directed RNA polymerase | Phvul.002G09K03011 | - DNA | Phvul.002G09 | RNA biosynth | subunit 3 of R |
| DNA-directed RNA polymerase | Phvul.002G09K03011 | - DNA | Phvul.002G09 | RNA biosynth | subunit 3 of R |
| DNA-directed RNA polymerase | Phvul.002G09K03011 | - DNA | Phvul.002G09 | RNA biosynth | subunit 3 of R |
| ubiquitin-specific protease 12 | Phvul.006G00K11838 | - ubiq | Phvul.006G00 | Protein home | deubiquitinas |
| ubiquitin-specific protease 12 | Phvul.006G00K11838 | - ubiq | Phvul.006G00 | Protein home | deubiquitinas |
| ubiquitin-specific protease 12 | Phvul.006G00K11838 | - ubiq | Phvul.006G00 | Protein home | deubiquitinas |
| ubiquitin-specific protease 12 | Phvul.006G00K11838 | - ubiq | Phvul.006G00 | Protein home | deubiquitinas |
| ubiquitin-specific protease 12 | Phvul.006G00K11838 | - ubiq | Phvul.006G00 | Protein home | deubiquitinas |
| ubiquitin-specific protease 12 | Phvul.006G00K11838 | - ubiq | Phvul.006G00 | Protein home | deubiquitinas |
| Leucine-rich receptor-like prot | Phvul.006G02 | PTHR27000:SF | Phvul.006G02 | Protein modif | protein kinase |
| Leucine-rich receptor-like prot | Phvul.006G02 | PTHR27000:SF | Phvul.006G02 | Protein modif | protein kinase |
| Leucine-rich receptor-like prot | Phvul.006G02 | PTHR27000:SF | Phvul.006G02 | Protein modif | protein kinase |
| Mitochondrial substrate carri | Phvul.006G11K15119 | - solut | Phvul.006G11 | Solute transp | solute transp |
| Mitochondrial substrate carri | Phvul.006G11K15119 | - solut | Phvul.006G11 | Solute transp | solute transp |
| Mitochondrial substrate carri | Phvul.006G11K15119 | - solut | Phvul.006G11 | Solute transp | solute transp |
| chromatin remodeling 8 | Phvul.007G19K10841 | - DNA | Phvul.007G19 | DNA damage | DNA repair pr |
| chromatin remodeling 8 | Phvul.007G19K10841 | - DNA | Phvul.007G19 | DNA damage | DNA repair pr |
| chromatin remodeling 8 | Phvul.007G19K10841 | - DNA | Phvul.007G19 | DNA damage | DNA repair pr |
| Protein kinase superfamily prc | Phvul.001G07 | PTHR27009:SF | Phvul.001G07 | Enzyme classi | Rust resistanc |
| Protein kinase superfamily prc | Phvul.001G07 | PTHR27009:SF | Phvul.001G07 | Enzyme classi | Rust resistanc |
| Protein kinase superfamily prc | Phvul.001G07 | PTHR27009:SF | Phvul.001G07 | Enzyme classi | Rust resistanc |
| zinc finger (C2H2 type) family | Phvul.001G26 | PTHR35744:SF | Phvul.001G26 | RNA biosynth | C2H2 zinc fing |
| zinc finger (C2H2 type) family | Phvul.001G26 | PTHR35744:SF | Phvul.001G26 | RNA biosynth | C2H2 zinc fing |
| zinc finger (C2H2 type) family | Phvul.001G26 | PTHR35744:SF | Phvul.001G26 | RNA biosynth | C2H2 zinc fing |
| zinc finger (C2H2 type) family | Phvul.001G26 | PTHR35744:SF | Phvul.001G26 | RNA biosynth | C2H2 zinc fing |
| zinc finger (C2H2 type) family | Phvul.001G26 | PTHR35744:SF | Phvul.001G26 | RNA biosynth | C2H2 zinc fing |
| zinc finger (C2H2 type) family | Phvul.001G26 | PTHR35744:SF | Phvul.001G26 | RNA biosynth | C2H2 zinc fing |
| nucleotide-rhamnose synthas | Phvul.002G15.1.1.133 | - dT | Phvul.002G15 | Carbohydrate | UDP-L-rhamn |
| nucleotide-rhamnose synthas | Phvul.002G15.1.1.133 | - dT | Phvul.002G15 | Carbohydrate | UDP-L-rhamn |
| nucleotide-rhamnose synthas | Phvul.002G15.1.1.133 | - dT | Phvul.002G15 | Carbohydrate | UDP-L-rhamn |
| Heavy metal transport/detoxif | Phvul.003G09 | PTHR22814:SF | Phvul.003G09 | not assigned. | α (original desc |
| Heavy metal transport/detoxif | Phvul.003G09 | PTHR22814:SF | Phvul.003G09 | not assigned. | α (original desc |
| DegP protease 10 | Phvul.004G00 | PTHR22939:SF | Phvul.004G00 | Protein home | protease (Deg |
| DegP protease 10 | Phvul.004G00 | PTHR22939:SF | Phvul.004G00 | Protein home | protease (Deg |
| DegP protease 10 | Phvul.004G00 | PTHR22939:SF | Phvul.004G00 | Protein home | protease (Deg |
| ERECTA-like 1 | Phvul.004G12 | PTHR27000:SF | Phvul.004G12 | Protein modif | protein kinase |
| ERECTA-like 1 | Phvul.004G12 | PTHR27000:SF | Phvul.004G12 | Protein modif | protein kinase |
| ERECTA-like 1 | Phvul.004G12 | PTHR27000:SF | Phvul.004G12 | Protein modif | protein kinase |
| Protein kinase superfamily prc | Phvul.005G06K08853 | - AP2- | Phvul.005G06 | Protein modif | protein kinase |
| Protein kinase superfamily prc | Phvul.005G06K08853 | - AP2- | Phvul.005G06 | Protein modif | protein kinase |
| Protein kinase superfamily prc | Phvul.005G06K08853 | - AP2- | Phvul.005G06 | Protein modif | protein kinase |
| Protein kinase superfamily prc | Phvul.005G06K08853 | - AP2- | Phvul.005G06 | Protein modif | protein kinase |

1 Protein kinase superfamily prcPhvul.005G06K08853 - AP2-Phvul.005G06Protein modif protein kinase
2 Protein kinase superfamily prcPhvul.005G06K08853 - AP2-Phvul.005G06Protein modif protein kinase
3 UDP-glucosyl transferase 73B⁵Phvul.007G02PTHR11926//IPhvul.007G02Enzyme classi Soyasapogenc
4 UDP-glucosyl transferase 73B⁵Phvul.007G02PTHR11926//IPhvul.007G02Enzyme classi Soyasapogenc
5 UDP-glucosyl transferase 73B⁵Phvul.007G02PTHR11926//IPhvul.007G02Enzyme classi Soyasapogenc
6 UDP-glucosyl transferase 73B⁵Phvul.007G02PTHR11926//IPhvul.007G02Enzyme classi Soyasapogenc
7 UDP-Glycosyltransferase supe Phvul.007G08PTHR11926:SIPhvul.007G08Lipid metaboli UDP-glucose:s
8 UDP-Glycosyltransferase supe Phvul.007G08PTHR11926:SIPhvul.007G08Lipid metaboli UDP-glucose:s
9 UDP-Glycosyltransferase supe Phvul.007G08PTHR11926:SIPhvul.007G08Lipid metaboli UDP-glucose:s
10 curculin-like (mannose-bindingPhvul.007G25PTHR27002:SIPhvul.007G25Protein modif protein kinase
11 curculin-like (mannose-bindingPhvul.007G25PTHR27002:SIPhvul.007G25Protein modif protein kinase
12 curculin-like (mannose-bindingPhvul.007G25PTHR27002:SIPhvul.007G25Protein modif protein kinase
13 curculin-like (mannose-bindingPhvul.007G25PTHR27002:SIPhvul.007G25Protein modif protein kinase
14 curculin-like (mannose-bindingPhvul.007G25PTHR27002:SIPhvul.007G25Protein modif protein kinase
15 curculin-like (mannose-bindingPhvul.007G25PTHR27002:SIPhvul.007G25Protein modif protein kinase
16 curculin-like (mannose-bindingPhvul.007G25PTHR27002:SIPhvul.007G25Protein modif protein kinase
17 curculin-like (mannose-bindingPhvul.007G25PTHR27002:SIPhvul.007G25Protein modif protein kinase
18 curculin-like (mannose-bindingPhvul.007G25PTHR27002:SIPhvul.007G25Protein modif protein kinase
19 Protein kinase superfamily prcPhvul.008G21PTHR27001:SIPhvul.008G21External stimu LysM receptor
20 Protein kinase superfamily prcPhvul.008G21PTHR27001:SIPhvul.008G21External stimu LysM receptor
21 Protein kinase superfamily prcPhvul.008G21PTHR27001:SIPhvul.008G21External stimu LysM receptor
22 purple acid phosphatase 18 Phvul.008G26PTHR22953:SIPhvul.008G26not assigned.a (original desc
23 purple acid phosphatase 18 Phvul.008G26PTHR22953:SIPhvul.008G26not assigned.a (original desc
24 purple acid phosphatase 18 Phvul.008G26PTHR22953:SIPhvul.008G26not assigned.a (original desc
25 0 Phvul.011G00PTHR36356:SIPhvul.011G00not assigned.r no hits & (orig
26 0 Phvul.011G00PTHR36356:SIPhvul.011G00not assigned.r no hits & (orig
27 0 Phvul.011G00PTHR36356:SIPhvul.011G00not assigned.r no hits & (orig
28 cysteine-rich RLK (RECEPTOR-IPhvul.011G19PF01657 - SaltPhvul.011G19not assigned.a (original desc
29 cysteine-rich RLK (RECEPTOR-IPhvul.011G19PF01657 - SaltPhvul.011G19not assigned.a (original desc
30 cysteine-rich RLK (RECEPTOR-IPhvul.011G19PF01657 - SaltPhvul.011G19not assigned.a (original desc
31 related to AP2.7 Phvul.L00030{PTHR32467:SIPhvul.L00030{RNA biosynthtranscription f
32 related to AP2.7 Phvul.L00030{PTHR32467:SIPhvul.L00030{RNA biosynthtranscription f
33 related to AP2.7 Phvul.L00030{PTHR32467:SIPhvul.L00030{RNA biosynthtranscription f
34 related to AP2.7 Phvul.L00030{PTHR32467:SIPhvul.L00030{RNA biosynthtranscription f
35 related to AP2.7 Phvul.L00030{PTHR32467:SIPhvul.L00030{RNA biosynthtranscription f
36 related to AP2.7 Phvul.L00030{PTHR32467:SIPhvul.L00030{RNA biosynthtranscription f
37 0 Phvul.001G02PF00036 - EF IPhvul.001G02not assigned.r no hits & (orig
38 0 Phvul.001G02PF00036 - EF IPhvul.001G02not assigned.r no hits & (orig
39 0 Phvul.001G02PF00036 - EF IPhvul.001G02not assigned.r no hits & (orig
40 0 Phvul.001G16PF12776 - MyPhvul.001G16not assigned.r no hits & (orig
41 0 Phvul.001G16PF12776 - MyPhvul.001G16not assigned.r no hits & (orig
42 Uncharacterized conserved prPhvul.002G01PF10225 - UncPhvul.002G01not assigned.r no hits & (orig
43 Uncharacterized conserved prPhvul.002G01PF10225 - UncPhvul.002G01not assigned.r no hits & (orig
44 Uncharacterized conserved prPhvul.002G01PF10225 - UncPhvul.002G01not assigned.r no hits & (orig
45 0 Phvul.002G14PF12776 - MyPhvul.002G14not assigned.r no hits & (orig
46 0 Phvul.002G14PF12776 - MyPhvul.002G14not assigned.r no hits & (orig
47 BTB/POZ domain-containing pPhvul.002G15PTHR11145 - Phvul.002G15not assigned.a (original desc
48 BTB/POZ domain-containing pPhvul.002G15PTHR11145 - Phvul.002G15not assigned.a (original desc
49 Phototropic-responsive NPH3 Phvul.002G21PTHR32370:SIPhvul.002G21Protein home component NI

1 Phototropic-responsive NPH3 Phvul.002G21 PTHR32370:SlPhvul.002G21 Protein home component N
2 Phototropic-responsive NPH3 Phvul.002G21 PTHR32370:SlPhvul.002G21 Protein home component N
3
4 0 Phvul.003G06 PF12776 - MyPhvul.003G06 not assigned.r no hits & (orig
5 0 Phvul.003G06 PF12776 - MyPhvul.003G06 not assigned.r no hits & (orig
6 subtilisin-like serine protease :Phvul.003G14 PTHR10795:SlPhvul.003G14 Protein home protease (SBT
7 subtilisin-like serine protease :Phvul.003G14 PTHR10795:SlPhvul.003G14 Protein home protease (SBT
8 subtilisin-like serine protease :Phvul.003G14 PTHR10795:SlPhvul.003G14 Protein home protease (SBT
9
10 0 0 0 Phvul.003G23 Phytohormon PIP/PIPL precu
11 0 0 0 Phvul.003G23 Phytohormon PIP/PIPL precu
12 0 0 0 Phvul.003G23 Phytohormon PIP/PIPL precu
13 0 Phvul.004G05 PF12776 - MyPhvul.004G05 not assigned.r no hits & (orig
14 0 Phvul.004G05 PF12776 - MyPhvul.004G05 not assigned.r no hits & (orig
15
16 syntaxin of plants 81 Phvul.004G15 K08492 - synt:Phvul.004G15 Vesicle trafficl SYP8-group Q
17 syntaxin of plants 81 Phvul.004G15 K08492 - synt:Phvul.004G15 Vesicle trafficl SYP8-group Q
18 syntaxin of plants 81 Phvul.004G15 K08492 - synt:Phvul.004G15 Vesicle trafficl SYP8-group Q
19
20 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynth TAC9 cofactor
21 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynth TAC9 cofactor
22 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynth TAC9 cofactor
23 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynth TAC9 cofactor
24 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynth TAC9 cofactor
25 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynth TAC9 cofactor
26 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynth TAC9 cofactor
27 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynth TAC9 cofactor
28 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynth TAC9 cofactor
29 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynth TAC9 cofactor
30 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynth TAC9 cofactor
31 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynth TAC9 cofactor
32 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynth TAC9 cofactor
33 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynth TAC9 cofactor
34 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynth TAC9 cofactor
35 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynth TAC9 cofactor
36 plastid transcriptionally active Phvul.004G17 PTHR10302:SlPhvul.004G17 RNA biosynth TAC9 cofactor
37 Myosin family protein with DilPhvul.006G10 PTHR13140:SlPhvul.006G10 Cytoskeleton class XI myosin
38 Myosin family protein with DilPhvul.006G10 PTHR13140:SlPhvul.006G10 Cytoskeleton class XI myosin
39 Myosin family protein with DilPhvul.006G10 PTHR13140:SlPhvul.006G10 Cytoskeleton class XI myosin
40 RING/U-box superfamily protePhvul.006G15 PTHR10044:SlPhvul.006G15 not assigned.a (original desc
41 RING/U-box superfamily protePhvul.006G15 PTHR10044:SlPhvul.006G15 not assigned.a (original desc
42 RING/U-box superfamily protePhvul.006G15 PTHR10044:SlPhvul.006G15 not assigned.a (original desc
43 RING/U-box superfamily protePhvul.006G15 PTHR10044:SlPhvul.006G15 not assigned.a (original desc
44 RING/U-box superfamily protePhvul.006G15 PTHR10044:SlPhvul.006G15 not assigned.a (original desc
45 RING/U-box superfamily protePhvul.006G15 PTHR10044:SlPhvul.006G15 not assigned.a (original desc
46 RING/U-box superfamily protePhvul.006G15 PTHR10044:SlPhvul.006G15 not assigned.a (original desc
47 RING/U-box superfamily protePhvul.006G15 PTHR10044:SlPhvul.006G15 not assigned.a (original desc
48 Homeotic gene regulator Phvul.007G05 PTHR10799:SlPhvul.007G05 Chromatin org chromatin ren
49 Homeotic gene regulator Phvul.007G05 PTHR10799:SlPhvul.007G05 Chromatin org chromatin ren
50 Homeotic gene regulator Phvul.007G05 PTHR10799:SlPhvul.007G05 Chromatin org chromatin ren
51 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
52 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
53 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
54 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
55 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
56 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
57 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
58 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
59 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
60 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f

1 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
2 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
3 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
4 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
5 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
6 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
7 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
8 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
9 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
10 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
11 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
12 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
13 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
14 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
15 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
16 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
17 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
18 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
19 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
20 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
21 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
22 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
23 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
24 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
25 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
26 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
27 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
28 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
29 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
30 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
31 myb family transcription factoPhvul.007G15 PTHR10641:SlPhvul.007G15 RNA biosynth transcription f
32 Leucine-rich repeat receptor-liPhvul.008G10 PF00069//PF0Phvul.008G10 Protein modif protein kinase
33 Leucine-rich repeat receptor-liPhvul.008G10 PF00069//PF0Phvul.008G10 Protein modif protein kinase
34 Transmembrane amino acid trPhvul.009G02 PTHR22950//IPhvu.009G02 Solute transp amino acid tra
35 Transmembrane amino acid trPhvul.009G02 PTHR22950//IPhvu.009G02 Solute transp amino acid tra
36 Transmembrane amino acid trPhvul.009G02 PTHR22950//IPhvu.009G02 Solute transp amino acid tra
37 paramyosin-related Phvul.009G09 PTHR16441 - IPhvu.009G09 not assigned.r no hits & (orig
38 paramyosin-related Phvul.009G09 PTHR16441 - IPhvu.009G09 not assigned.r no hits & (orig
39 paramyosin-related Phvul.009G09 PTHR16441 - IPhvu.009G09 not assigned.r no hits & (orig
40 paramyosin-related Phvul.009G09 PTHR16441 - IPhvu.009G09 not assigned.r no hits & (orig
41 0 Phvul.009G12 PF12776 - MyPhvul.009G12 not assigned.r no hits & (orig
42 0 Phvul.009G12 PF12776 - MyPhvul.009G12 not assigned.r no hits & (orig
43 DENN (AEX-3) domain-containPhvul.009G22 PTHR15288:SlPhvul.009G22 not assigned.r no hits & (orig
44 DENN (AEX-3) domain-containPhvul.009G22 PTHR15288:SlPhvul.009G22 not assigned.r no hits & (orig
45 DENN (AEX-3) domain-containPhvul.009G22 PTHR15288:SlPhvul.009G22 not assigned.r no hits & (orig
46 DENN (AEX-3) domain-containPhvul.009G22 PTHR15288:SlPhvul.009G22 not assigned.r no hits & (orig
47 DENN (AEX-3) domain-containPhvul.009G22 PTHR15288:SlPhvul.009G22 not assigned.r no hits & (orig
48 DENN (AEX-3) domain-containPhvul.009G22 PTHR15288:SlPhvul.009G22 not assigned.r no hits & (orig
49 DENN (AEX-3) domain-containPhvul.009G22 PTHR15288:SlPhvul.009G22 not assigned.r no hits & (orig
50 DENN (AEX-3) domain-containPhvul.009G22 PTHR15288:SlPhvul.009G22 not assigned.r no hits & (orig
51 DENN (AEX-3) domain-containPhvul.009G22 PTHR15288:SlPhvul.009G22 not assigned.r no hits & (orig
52 DENN (AEX-3) domain-containPhvul.009G22 PTHR15288:SlPhvul.009G22 not assigned.r no hits & (orig
53 DENN (AEX-3) domain-containPhvul.009G22 PTHR15288:SlPhvul.009G22 not assigned.r no hits & (orig
54 DENN (AEX-3) domain-containPhvul.009G22 PTHR15288:SlPhvul.009G22 not assigned.r no hits & (orig
55 Domain of unknown function iPhvul.010G15 PTHR12281:SlPhvul.010G15 not assigned.r no hits & (orig
56 Domain of unknown function iPhvul.010G15 PTHR12281:SlPhvul.010G15 not assigned.r no hits & (orig
57 ABC transporter family proteirPhvul.011G08 K06185 - ATP-Phvul.011G08 not assigned.r (original desc
58
59
60

1 ABC transporter family proteiPhvul.011G08K06185 - ATP-Phvul.011G08not assigned.a (original desc
2 ABC transporter family proteiPhvul.011G08K06185 - ATP-Phvul.011G08not assigned.a (original desc
3 ATP synthase protein I -relatePhvul.011G13K02116 - ATP Phvul.011G13Photosynthes CGL160 factor
4 ATP synthase protein I -relatePhvul.011G13K02116 - ATP Phvul.011G13Photosynthes CGL160 factor
5 ATP synthase protein I -relatePhvul.011G13K02116 - ATP Phvul.011G13Photosynthes CGL160 factor
6 UDP-glucosyl transferase 85A:Phvul.011G15PTHR11926:SFPhvul.011G15Enzyme classi Linamarin syn
7 UDP-glucosyl transferase 85A:Phvul.011G15PTHR11926:SFPhvul.011G15Enzyme classi Linamarin syn
8 UDP-glucosyl transferase 85A:Phvul.011G15PTHR11926:SFPhvul.011G15Enzyme classi Linamarin syn
9 LRR and NB-ARC domains-coniPhvul.011G19PTHR23155//IPhvul.011G19not assigned.a (original desc
10 LRR and NB-ARC domains-coniPhvul.011G19PTHR23155//IPhvul.011G19not assigned.a (original desc
11 LRR and NB-ARC domains-coniPhvul.011G19PTHR23155//IPhvul.011G19not assigned.a (original desc
12 SWAP (Suppressor-of-White-APhvul.001G19PTHR12323 - (Phvul.001G19not assigned.r no hits & (orig
13 SWAP (Suppressor-of-White-APhvul.001G19PTHR12323 - (Phvul.001G19not assigned.r no hits & (orig
14 SWAP (Suppressor-of-White-APhvul.001G19PTHR12323 - (Phvul.001G19not assigned.r no hits & (orig
15 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol
16 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol
17 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol
18 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol
19 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol
20 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol
21 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol
22 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol
23 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol
24 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol
25 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol
26 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol
27 myo-inositol polyphosphate 5-Phvul.002G00PTHR11200:SFPhvul.002G00Multi-process type-I inositol
28 0 0 0 Phvul.002G11not assigned.r no hits & (orig
29 0 0 0 Phvul.002G11not assigned.r no hits & (orig
30 0 0 0 Phvul.002G11not assigned.r no hits & (orig
31 Ribosomal protein L35 Phvul.002G13PF01632 - RibPhvul.002G13not assigned.r no hits & (orig
32 Ribosomal protein L35 Phvul.002G13PF01632 - RibPhvul.002G13not assigned.r no hits & (orig
33 Ribosomal protein L35 Phvul.002G13PF01632 - RibPhvul.002G13not assigned.r no hits & (orig
34 Ribosomal protein L35 Phvul.002G13PF01632 - RibPhvul.002G13not assigned.r no hits & (orig
35 Ribosomal protein L35 Phvul.002G13PF01632 - RibPhvul.002G13not assigned.r no hits & (orig
36 0 0 0 Phvul.002G14not assigned.r no hits & (orig
37 0 0 0 Phvul.002G14not assigned.r no hits & (orig
38 0 0 0 Phvul.002G14not assigned.r no hits & (orig
39 0 0 0 Phvul.002G14not assigned.r no hits & (orig
40 0 0 0 Phvul.002G14not assigned.r no hits & (orig
41 TATA-binding related factor (TPhvul.003G13K13528 - medPhvul.003G13RNA biosynthe component M
42 TATA-binding related factor (TPhvul.003G13K13528 - medPhvul.003G13RNA biosynthe component M
43 TATA-binding related factor (TPhvul.003G13K13528 - medPhvul.003G13RNA biosynthe component M
44 cationic amino acid transportePhvul.003G22PTHR11785//IPhvul.003G22Solute transpccationic aminc
45 Tetratricopeptide repeat (TPRPhvul.003G23PF13371//PF1Phvul.003G23not assigned.a (original desc
46 Tetratricopeptide repeat (TPRPhvul.003G23PF13371//PF1Phvul.003G23not assigned.a (original desc
47 Protein of unknown function (Phvul.003G25PTHR14360:SFPhvul.003G25not assigned.r no hits & (orig
48 Protein of unknown function (Phvul.003G25PTHR14360:SFPhvul.003G25not assigned.r no hits & (orig
49 Protein of unknown function (Phvul.003G25PTHR14360:SFPhvul.003G25not assigned.r no hits & (orig
50 plastid transcription factor 1 Phvul.004G03PTHR31072:SFPhvul.004G03RNA biosynthe transcription f
51 plastid transcription factor 1 Phvul.004G03PTHR31072:SFPhvul.004G03RNA biosynthe transcription f
52 plastid transcription factor 1 Phvul.004G03PTHR31072:SFPhvul.004G03RNA biosynthe transcription f
53 plastid transcription factor 1 Phvul.004G03PTHR31072:SFPhvul.004G03RNA biosynthe transcription f
54 plastid transcription factor 1 Phvul.004G03PTHR31072:SFPhvul.004G03RNA biosynthe transcription f
55 plastid transcription factor 1 Phvul.004G03PTHR31072:SFPhvul.004G03RNA biosynthe transcription f
56 plastid transcription factor 1 Phvul.004G03PTHR31072:SFPhvul.004G03RNA biosynthe transcription f
57 plastid transcription factor 1 Phvul.004G03PTHR31072:SFPhvul.004G03RNA biosynthe transcription f
58 plastid transcription factor 1 Phvul.004G03PTHR31072:SFPhvul.004G03RNA biosynthe transcription f
59 plastid transcription factor 1 Phvul.004G03PTHR31072:SFPhvul.004G03RNA biosynthe transcription f
60 plastid transcription factor 1 Phvul.004G03PTHR31072:SFPhvul.004G03RNA biosynthe transcription f

1
2 plastid transcription factor 1 Phvul.004G03 PTHR31072:SlPhvul.004G03 RNA biosynth transcription f
3 plastid transcription factor 1 Phvul.004G03 PTHR31072:SlPhvul.004G03 RNA biosynth transcription f
4 DNase I-like superfamily prote Phvul.004G08 PTHR11200:SlPhvul.004G08 Multi-process type-I inositol
5 DNase I-like superfamily prote Phvul.004G08 PTHR11200:SlPhvul.004G08 Multi-process type-I inositol
6 DNase I-like superfamily prote Phvul.004G08 PTHR11200:SlPhvul.004G08 Multi-process type-I inositol
7 DNase I-like superfamily prote Phvul.004G08 PTHR11200:SlPhvul.004G08 Multi-process type-I inositol
8 DNase I-like superfamily prote Phvul.004G08 PTHR11200:SlPhvul.004G08 Multi-process type-I inositol
9 DNase I-like superfamily prote Phvul.004G08 PTHR11200:SlPhvul.004G08 Multi-process type-I inositol
10 DNase I-like superfamily prote Phvul.004G08 PTHR11200:SlPhvul.004G08 Multi-process type-I inositol
11 DNase I-like superfamily prote Phvul.004G08 PTHR11200:SlPhvul.004G08 Multi-process type-I inositol
12 Arginyl-tRNA synthetase, class Phvul.004G17 K01887 - argir Phvul.004G17 Protein biosyr arginine-tRNA
13 Arginyl-tRNA synthetase, class Phvul.004G17 K01887 - argir Phvul.004G17 Protein biosyr arginine-tRNA
14 Arginyl-tRNA synthetase, class Phvul.004G17 K01887 - argir Phvul.004G17 Protein biosyr arginine-tRNA
15 Arginyl-tRNA synthetase, class Phvul.004G17 K01887 - argir Phvul.004G17 Protein biosyr arginine-tRNA
16 Jojoba acyl CoA reductase-rel Phvul.005G121.2.1.50//1.2. Phvul.005G12 Cell wall orgar acyl CoA redu
17 Jojoba acyl CoA reductase-rel Phvul.005G121.2.1.50//1.2. Phvul.005G12 Cell wall orgar acyl CoA redu
18 Jojoba acyl CoA reductase-rel Phvul.005G121.2.1.50//1.2. Phvul.005G12 Cell wall orgar acyl CoA redu
19 syntaxin of plants 61 Phvul.006G04 K08498 - synt; Phvul.006G04 Vesicle trafficl SYP6 group Qc
20 syntaxin of plants 61 Phvul.006G04 K08498 - synt; Phvul.006G04 Vesicle trafficl SYP6 group Qc
21 syntaxin of plants 61 Phvul.006G04 K08498 - synt; Phvul.006G04 Vesicle trafficl SYP6 group Qc
22 syntaxin of plants 61 Phvul.006G04 K08498 - synt; Phvul.006G04 Vesicle trafficl SYP6 group Qc
23 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
24 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
25 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
26 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
27 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
28 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
29 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
30 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
31 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
32 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
33 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
34 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
35 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
36 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
37 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
38 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
39 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
40 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
41 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
42 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
43 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
44 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
45 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
46 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
47 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
48 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
49 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
50 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
51 UB-like protease 1B Phvul.007G07 PTHR12606:SlPhvul.007G07 not assigned.r no hits & (orig
52 Late embryogenesis abundant Phvul.007G21 PTHR23241//I Phvul.007G21 not assigned.r no hits & (orig
53 Late embryogenesis abundant Phvul.007G21 PTHR23241//I Phvul.007G21 not assigned.r no hits & (orig
54 Late embryogenesis abundant Phvul.007G21 PTHR23241//I Phvul.007G21 not assigned.r no hits & (orig
55 Late embryogenesis abundant Phvul.007G21 PTHR23241//I Phvul.007G21 not assigned.r no hits & (orig
56 purple acid phosphatase 16 Phvul.007G24 PTHR32440:SlPhvul.007G24 not assigned.a (original desc
57 purple acid phosphatase 16 Phvul.007G24 PTHR32440:SlPhvul.007G24 not assigned.a (original desc
58 purple acid phosphatase 16 Phvul.007G24 PTHR32440:SlPhvul.007G24 not assigned.a (original desc
59 purple acid phosphatase 16 Phvul.007G24 PTHR32440:SlPhvul.007G24 not assigned.a (original desc
60 WD-40 repeat family protein /Phvul.008G07 PF00400//PF0 Phvul.008G07 not assigned.a (original desc
WD-40 repeat family protein /Phvul.008G07 PF00400//PF0 Phvul.008G07 not assigned.a (original desc

1 WD-40 repeat family protein /Phvul.008G07PF00400//PF0Phvul.008G07not assigned.α (original desc
 2 WD-40 repeat family protein /Phvul.008G07PF00400//PF0Phvul.008G07not assigned.α (original desc
 3 WD-40 repeat family protein /Phvul.008G07PF00400//PF0Phvul.008G07not assigned.α (original desc
 4 WD-40 repeat family protein /Phvul.008G07PF00400//PF0Phvul.008G07not assigned.α (original desc
 5 WD-40 repeat family protein /Phvul.008G07PF00400//PF0Phvul.008G07not assigned.α (original desc
 6 WD-40 repeat family protein /Phvul.008G07PF00400//PF0Phvul.008G07not assigned.α (original desc
 7 WD-40 repeat family protein /Phvul.008G07PF00400//PF0Phvul.008G07not assigned.α (original desc
 8 WD-40 repeat family protein /Phvul.008G07PF00400//PF0Phvul.008G07not assigned.α (original desc
 9 Galactose oxidase/kelch repezPhvul.008G12PF00646 - F-bPhvul.008G12Protein home component FE
 10 Galactose oxidase/kelch repezPhvul.008G12PF00646 - F-bPhvul.008G12Protein home component FE
 11 dicer-like 2 Phvul.008G12K11592 - endcPhvul.008G12not assigned.α (original desc
 12 dicer-like 2 Phvul.008G12K11592 - endcPhvul.008G12not assigned.α (original desc
 13 dicer-like 2 Phvul.008G12K11592 - endcPhvul.008G12not assigned.α (original desc
 14 Leucine-rich repeat transmemPhvul.008G16PF12819//PF1Phvul.008G16not assigned.α (original desc
 15 Leucine-rich repeat transmemPhvul.008G16PF12819//PF1Phvul.008G16not assigned.α (original desc
 16 Leucine-rich repeat transmemPhvul.008G16PF12819//PF1Phvul.008G16not assigned.α (original desc
 17 Transmembrane amino acid trPhvul.008G22PTHR22950//IPhvu.008G22Solute transpcauxin transpo
 18 Integral membrane Yip1 familPhvul.008G23PTHR12822:SIPhvul.008G23not assigned.r no hits & (orig
 19 Major facilitator superfamily pPhvul.009G03PTHR23500:SIPhvul.009G03Solute transpmonosacchari
 20 Major facilitator superfamily pPhvul.009G03PTHR23500:SIPhvul.009G03Solute transpmonosacchari
 21 Major facilitator superfamily pPhvul.009G03PTHR23500:SIPhvul.009G03Solute transpmonosacchari
 22 DDB1-CUL4 associated factor :Phvul.009G09K11789 - HIV- Phvul.009G09not assigned.α (original desc
 23 DDB1-CUL4 associated factor :Phvul.009G09K11789 - HIV- Phvul.009G09not assigned.α (original desc
 24 DDB1-CUL4 associated factor :Phvul.009G09K11789 - HIV- Phvul.009G09not assigned.α (original desc
 25 Got1/Sft2-like vescicle transpcPhvul.009G23PTHR21493:SIPhvul.009G23not assigned.α (original desc
 26 Got1/Sft2-like vescicle transpcPhvul.009G23PTHR21493:SIPhvul.009G23not assigned.α (original desc
 27 Got1/Sft2-like vescicle transpcPhvul.009G23PTHR21493:SIPhvul.009G23not assigned.α (original desc
 28 vacuolar iron transporter (VIT)Phvul.010G02PTHR31851:SIPhvul.010G02Solute transpmetal cation t
 29 vacuolar iron transporter (VIT)Phvul.010G02PTHR31851:SIPhvul.010G02Solute transpmetal cation t
 30 vacuolar iron transporter (VIT)Phvul.010G02PTHR31851:SIPhvul.010G02Solute transpmetal cation t
 31 Phosphoenolpyruvate carboxyPhvul.010G102.1.2.11 - 3-mPhvul.010G10Coenzyme me ketopantoate
 32 Phosphoenolpyruvate carboxyPhvul.010G102.1.2.11 - 3-mPhvul.010G10Coenzyme me ketopantoate
 33 Phosphoenolpyruvate carboxyPhvul.010G102.1.2.11 - 3-mPhvul.010G10Coenzyme me ketopantoate
 34 GRAS family transcription factPhvul.010G12PTHR31636:SIPhvul.010G12External stim component N:
 35 GRAS family transcription factPhvul.010G12PTHR31636:SIPhvul.010G12External stim component N:
 36 GRAS family transcription factPhvul.010G12PTHR31636:SIPhvul.010G12External stim component N:
 37 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M
 38 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M
 39 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M
 40 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M
 41 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M
 42 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M
 43 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M
 44 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M
 45 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M
 46 0 Phvul.010G15K14972 - PAX-Phvul.010G15RNA biosynth component M
 47 Proteasome component (PCI) Phvul.011G00K12178 - COPPhvul.011G00Protein home component C:
 48 Proteasome component (PCI) Phvul.011G00K12178 - COPPhvul.011G00Protein home component C:
 49 Proteasome component (PCI) Phvul.011G00K12178 - COPPhvul.011G00Protein home component C:

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

cytochrome P450, family 72, sPhvul.011G161.14.13.173 - Phvul.011G16Enzyme classif 11-oxo-beta-a
cytochrome P450, family 72, sPhvul.011G161.14.13.173 - Phvul.011G16Enzyme classif 11-oxo-beta-a
cytochrome P450, family 72, sPhvul.011G161.14.13.173 - Phvul.011G16Enzyme classif 11-oxo-beta-a
cytochrome P450, family 72, sPhvul.011G16KOG0159 - CyPhvul.011G16Enzyme classif 11-oxo-beta-a
cytochrome P450, family 72, sPhvul.011G16KOG0159 - CyPhvul.011G16Enzyme classif 11-oxo-beta-a

Do not distribute

1
2
3 CB transporter (original description: pacid=37163835 transcript=Phvul.004G023066.1 locus=Phvul.0
4 CB transporter (original description: pacid=37163835 transcript=Phvul.004G023066.1 locus=Phvul.0
5 CB transporter (original description: pacid=37163835 transcript=Phvul.004G023066.1 locus=Phvul.0
6
7 :NA polymerase (original description: pacid=37175101 transcript=Phvul.002G097400.1 locus=Phvul.
8 :NA polymerase (original description: pacid=37175101 transcript=Phvul.002G097400.1 locus=Phvul.
9 :NA polymerase (original description: pacid=37175101 transcript=Phvul.002G097400.1 locus=Phvul.
10 :NA polymerase (original description: pacid=37175101 transcript=Phvul.002G097400.1 locus=Phvul.
11 e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0C
12 e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0C
13 e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0C
14 e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0C
15 e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0C
16 e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0C
17 e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0C
18 e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0C
19 ð (LRR-XI) (original description: pacid=37173573 transcript=Phvul.006G029000.1 locus=Phvul.006G0
20 ð (LRR-XI) (original description: pacid=37173573 transcript=Phvul.006G029000.1 locus=Phvul.006G0
21 ð (LRR-XI) (original description: pacid=37173573 transcript=Phvul.006G029000.1 locus=Phvul.006G0
22 ð (LRR-XI) (original description: pacid=37173573 transcript=Phvul.006G029000.1 locus=Phvul.006G0
23 rter (MTCC) (original description: pacid=37172256 transcript=Phvul.006G110300.1 locus=Phvul.00
24 rter (MTCC) (original description: pacid=37172256 transcript=Phvul.006G110300.1 locus=Phvul.00
25 rter (MTCC) (original description: pacid=37172256 transcript=Phvul.006G110300.1 locus=Phvul.00
26
27 **rotein (CSB) (original description: pacid=37165162 transcript=Phvul.007G191600.1 locus=Phvul.007G**
28 **rotein (CSB) (original description: pacid=37165162 transcript=Phvul.007G191600.1 locus=Phvul.007G**
29 **rotein (CSB) (original description: pacid=37165162 transcript=Phvul.007G191600.1 locus=Phvul.007G**
30
31 :e kinase Lr10 OS=Triticum aestivum (sp|p93604|lrk10_wheat : 383.0) & Enzyme classification.EC_2
32 :e kinase Lr10 OS=Triticum aestivum (sp|p93604|lrk10_wheat : 383.0) & Enzyme classification.EC_2
33 :e kinase Lr10 OS=Triticum aestivum (sp|p93604|lrk10_wheat : 383.0) & Enzyme classification.EC_2
34
35 rger transcription factor (original description: pacid=37168889 transcript=Phvul.001G264600.2 locus:
36 rger transcription factor (original description: pacid=37168889 transcript=Phvul.001G264600.2 locus:
37 rger transcription factor (original description: pacid=37168889 transcript=Phvul.001G264600.2 locus:
38 rger transcription factor (original description: pacid=37168889 transcript=Phvul.001G264600.2 locus:
39 rger transcription factor (original description: pacid=37168889 transcript=Phvul.001G264600.2 locus:
40 rger transcription factor (original description: pacid=37168889 transcript=Phvul.001G264600.2 locus:
41 rger transcription factor (original description: pacid=37168889 transcript=Phvul.001G264600.2 locus:
42
43 ose synthase (original description: pacid=37176460 transcript=Phvul.002G153500.1 locus=Phvul.00
44 ose synthase (original description: pacid=37176460 transcript=Phvul.002G153500.1 locus=Phvul.00
45 ose synthase (original description: pacid=37176460 transcript=Phvul.002G153500.1 locus=Phvul.00
46
47 :ription: pacid=37144799 transcript=Phvul.003G092500.1 locus=Phvul.003G092500 ID=Phvul.003GC
48 :ription: pacid=37144799 transcript=Phvul.003G092500.1 locus=Phvul.003G092500 ID=Phvul.003GC
49 } (original description: pacid=37161689 transcript=Phvul.004G000300.1 locus=Phvul.004G000300 |
50 } (original description: pacid=37161689 transcript=Phvul.004G000300.1 locus=Phvul.004G000300 |
51 } (original description: pacid=37161689 transcript=Phvul.004G000300.1 locus=Phvul.004G000300 |
52 } (original description: pacid=37161689 transcript=Phvul.004G000300.1 locus=Phvul.004G000300 |
53 ð (LRR-XIIIb) (original description: pacid=37163092 transcript=Phvul.004G126100.1 locus=Phvul.004
54 ð (LRR-XIIIb) (original description: pacid=37163092 transcript=Phvul.004G126100.1 locus=Phvul.004
55 ð (LRR-XIIIb) (original description: pacid=37163092 transcript=Phvul.004G126100.1 locus=Phvul.004
56 ð (NAK) (original description: pacid=37152911 transcript=Phvul.005G063700.2 locus=Phvul.005G063
57 ð (NAK) (original description: pacid=37152911 transcript=Phvul.005G063700.2 locus=Phvul.005G063
58 ð (NAK) (original description: pacid=37152911 transcript=Phvul.005G063700.2 locus=Phvul.005G063
59 ð (NAK) (original description: pacid=37152911 transcript=Phvul.005G063700.2 locus=Phvul.005G063
60 ð (NAK) (original description: pacid=37152911 transcript=Phvul.005G063700.2 locus=Phvul.005G063

1
2 ε (NAK) (original description: pacid=37152911 transcript=Phvul.005G063700.2 locus=Phvul.005G063700.2
3 ε (NAK) (original description: pacid=37152911 transcript=Phvul.005G063700.2 locus=Phvul.005G063700.2
4 α B glucuronide galactosyltransferase OS=Glycine max (sp|d4q9z4|sgt2_soybn : 540.0) & Enzyme C
5 α B glucuronide galactosyltransferase OS=Glycine max (sp|d4q9z4|sgt2_soybn : 540.0) & Enzyme C
6 α B glucuronide galactosyltransferase OS=Glycine max (sp|d4q9z4|sgt2_soybn : 554.0) & Enzyme C
7 α B glucuronide galactosyltransferase OS=Glycine max (sp|d4q9z4|sgt2_soybn : 554.0) & Enzyme C
8
9
10 sterol glucosyltransferase (original description: pacid=37167623 transcript=Phvul.007G080800.2 locus=Phvul.007G080800.2
11 sterol glucosyltransferase (original description: pacid=37167623 transcript=Phvul.007G080800.2 locus=Phvul.007G080800.2
12 sterol glucosyltransferase (original description: pacid=37167623 transcript=Phvul.007G080800.2 locus=Phvul.007G080800.2
13
14 ε (SD-2) (original description: pacid=37166958 transcript=Phvul.007G254000.2 locus=Phvul.007G254000.2
15 ε (SD-2) (original description: pacid=37166958 transcript=Phvul.007G254000.2 locus=Phvul.007G254000.2
16 ε (SD-2) (original description: pacid=37166958 transcript=Phvul.007G254000.2 locus=Phvul.007G254000.2
17 ε (SD-2) (original description: pacid=37166958 transcript=Phvul.007G254000.2 locus=Phvul.007G254000.2
18 ε (SD-2) (original description: pacid=37166958 transcript=Phvul.007G254000.2 locus=Phvul.007G254000.2
19 ε (SD-2) (original description: pacid=37166958 transcript=Phvul.007G254000.2 locus=Phvul.007G254000.2
20 ε (SD-2) (original description: pacid=37166958 transcript=Phvul.007G254000.2 locus=Phvul.007G254000.2
21
22 r kinase (NFR1/LYK3) (original description: pacid=37159081 transcript=Phvul.008G212500.1 locus=Phvul.008G212500.1
23 r kinase (NFR1/LYK3) (original description: pacid=37159081 transcript=Phvul.008G212500.1 locus=Phvul.008G212500.1
24 r kinase (NFR1/LYK3) (original description: pacid=37159081 transcript=Phvul.008G212500.1 locus=Phvul.008G212500.1
25
26 ription: pacid=37158281 transcript=Phvul.008G266300.1 locus=Phvul.008G266300 ID=Phvul.008G266300
27 ription: pacid=37158281 transcript=Phvul.008G266300.1 locus=Phvul.008G266300 ID=Phvul.008G266300
28 ription: pacid=37158281 transcript=Phvul.008G266300.1 locus=Phvul.008G266300 ID=Phvul.008G266300
29
30 ginal description: pacid=37155004 transcript=Phvul.011G002600.1 locus=Phvul.011G002600 ID=Phvul.011G002600
31 ginal description: pacid=37155004 transcript=Phvul.011G002600.1 locus=Phvul.011G002600 ID=Phvul.011G002600
32 ginal description: pacid=37155004 transcript=Phvul.011G002600.1 locus=Phvul.011G002600 ID=Phvul.011G002600
33
34 ription: pacid=37155693 transcript=Phvul.011G194501.1 locus=Phvul.011G194501 ID=Phvul.011G194501
35 ription: pacid=37155693 transcript=Phvul.011G194501.1 locus=Phvul.011G194501 ID=Phvul.011G194501
36 ription: pacid=37155693 transcript=Phvul.011G194501.1 locus=Phvul.011G194501 ID=Phvul.011G194501
37
38 factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308.2
39 factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308.2
40 factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308.2
41 factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308.2
42 factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308.2
43 factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308.2
44 factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308.2
45
46 ginal description: pacid=37170232 transcript=Phvul.001G021750.1 locus=Phvul.001G021750 ID=Phvul.001G021750
47 ginal description: pacid=37170232 transcript=Phvul.001G021750.1 locus=Phvul.001G021750 ID=Phvul.001G021750
48 ginal description: pacid=37170232 transcript=Phvul.001G021750.1 locus=Phvul.001G021750 ID=Phvul.001G021750
49
50 ginal description: pacid=37169040 transcript=Phvul.001G168600.1 locus=Phvul.001G168600 ID=Phvul.001G168600
51 ginal description: pacid=37169040 transcript=Phvul.001G168600.1 locus=Phvul.001G168600 ID=Phvul.001G168600
52 ginal description: pacid=37176961 transcript=Phvul.002G010100.1 locus=Phvul.002G010100 ID=Phvul.002G010100
53 ginal description: pacid=37176961 transcript=Phvul.002G010100.1 locus=Phvul.002G010100 ID=Phvul.002G010100
54 ginal description: pacid=37176961 transcript=Phvul.002G010100.1 locus=Phvul.002G010100 ID=Phvul.002G010100
55
56 ginal description: pacid=37174417 transcript=Phvul.002G149100.1 locus=Phvul.002G149100 ID=Phvul.002G149100
57 ginal description: pacid=37174417 transcript=Phvul.002G149100.1 locus=Phvul.002G149100 ID=Phvul.002G149100
58
59 ription: pacid=37174540 transcript=Phvul.002G155200.1 locus=Phvul.002G155200 ID=Phvul.002G155200
60 ription: pacid=37174540 transcript=Phvul.002G155200.1 locus=Phvul.002G155200 ID=Phvul.002G155200
PH3 of CUL3-BTB E3 ubiquitin ligase complex (original description: pacid=37175454 transcript=Phvul.002G155200.1 locus=Phvul.002G155200 ID=Phvul.002G155200

1 PH3 of CUL3-BTB E3 ubiquitin ligase complex (original description: pacid=37175454 transcript=Phvu
2 PH3 of CUL3-BTB E3 ubiquitin ligase complex (original description: pacid=37175454 transcript=Phvu
3 ginal description: pacid=37147834 transcript=Phvul.003G069400.1 locus=Phvul.003G069400 ID=Ph
4 ginal description: pacid=37147834 transcript=Phvul.003G069400.1 locus=Phvul.003G069400 ID=Ph
5 '2) (original description: pacid=37145836 transcript=Phvul.003G141800.1 locus=Phvul.003G141800
6 '2) (original description: pacid=37145836 transcript=Phvul.003G141800.1 locus=Phvul.003G141800
7 '2) (original description: pacid=37145836 transcript=Phvul.003G141800.1 locus=Phvul.003G141800
8 '2) (original description: pacid=37145836 transcript=Phvul.003G141800.1 locus=Phvul.003G141800
9 '2) (original description: pacid=37145836 transcript=Phvul.003G141800.1 locus=Phvul.003G141800
10 cursor polypeptide (original description: pacid=37144932 transcript=Phvul.003G239800.1 locus=Phvu
11 cursor polypeptide (original description: pacid=37144932 transcript=Phvul.003G239800.1 locus=Phvu
12 cursor polypeptide (original description: pacid=37144932 transcript=Phvul.003G239800.1 locus=Phvu
13 ginal description: pacid=37162038 transcript=Phvul.004G053900.1 locus=Phvul.004G053900 ID=Ph
14 ginal description: pacid=37162038 transcript=Phvul.004G053900.1 locus=Phvul.004G053900 ID=Ph
15 a-type SNARE component (original description: pacid=37163883 transcript=Phvul.004G157700.1 lo
16 a-type SNARE component (original description: pacid=37163883 transcript=Phvul.004G157700.1 lo
17 a-type SNARE component (original description: pacid=37163883 transcript=Phvul.004G157700.1 lo
18 ' of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
19 ' of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
20 ' of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
21 ' of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
22 ' of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
23 ' of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
24 ' of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
25 ' of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
26 ' of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
27 ' of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
28 ' of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
29 ' of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
30 ' of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
31 ' of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
32 ' of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
33 ' of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
34 ' of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
35 ' of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
36 ' of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
37 n microfilament-based motor protein (original description: pacid=37173217 transcript=Phvul.006G:
38 n microfilament-based motor protein (original description: pacid=37173217 transcript=Phvul.006G:
39 n microfilament-based motor protein (original description: pacid=37173217 transcript=Phvul.006G:
40 :ription: pacid=37172535 transcript=Phvul.006G158500.2 locus=Phvul.006G158500 ID=Phvul.006G1
41 :ription: pacid=37172535 transcript=Phvul.006G158500.2 locus=Phvul.006G158500 ID=Phvul.006G1
42 :ription: pacid=37172535 transcript=Phvul.006G158500.2 locus=Phvul.006G158500 ID=Phvul.006G1
43 :ription: pacid=37172535 transcript=Phvul.006G158500.2 locus=Phvul.006G158500 ID=Phvul.006G1
44 :ription: pacid=37172535 transcript=Phvul.006G158500.2 locus=Phvul.006G158500 ID=Phvul.006G1
45 :ription: pacid=37172535 transcript=Phvul.006G158500.2 locus=Phvul.006G158500 ID=Phvul.006G1
46 :ription: pacid=37172535 transcript=Phvul.006G158500.2 locus=Phvul.006G158500 ID=Phvul.006G1
47 :ription: pacid=37172535 transcript=Phvul.006G158500.2 locus=Phvul.006G158500 ID=Phvul.006G1
48 :ription: pacid=37172535 transcript=Phvul.006G158500.2 locus=Phvul.006G158500 ID=Phvul.006G1
49 nodeling factor (Snf2) (original description: pacid=37164242 transcript=Phvul.007G054000.2 locus=
50 nodeling factor (Snf2) (original description: pacid=37164242 transcript=Phvul.007G054000.2 locus=
51 factor (MYB-related) (original description: pacid=37166322 transcript=Phvul.007G154900.9 locus=P
52 factor (MYB-related) (original description: pacid=37166322 transcript=Phvul.007G154900.9 locus=P
53 factor (MYB-related) (original description: pacid=37166322 transcript=Phvul.007G154900.9 locus=P
54 factor (MYB-related) (original description: pacid=37166322 transcript=Phvul.007G154900.9 locus=P
55 factor (MYB-related) (original description: pacid=37166322 transcript=Phvul.007G154900.9 locus=P
56 factor (MYB-related) (original description: pacid=37166322 transcript=Phvul.007G154900.9 locus=P
57 factor (MYB-related) (original description: pacid=37166322 transcript=Phvul.007G154900.9 locus=P
58 factor (MYB-related) (original description: pacid=37166322 transcript=Phvul.007G154900.9 locus=P
59 factor (MYB-related) (original description: pacid=37166322 transcript=Phvul.007G154900.9 locus=P
60 factor (MYB-related) (original description: pacid=37166322 transcript=Phvul.007G154900.9 locus=P

1
2 :ription: pacid=37161055 transcript=Phvul.008G074600.4 locus=Phvul.008G074600 ID=Phvul.008GC
3 :ription: pacid=37161055 transcript=Phvul.008G074600.4 locus=Phvul.008G074600 ID=Phvul.008GC
4 :ription: pacid=37161055 transcript=Phvul.008G074600.4 locus=Phvul.008G074600 ID=Phvul.008GC
5 :ription: pacid=37161055 transcript=Phvul.008G074600.4 locus=Phvul.008G074600 ID=Phvul.008GC
6 :ription: pacid=37161055 transcript=Phvul.008G074600.4 locus=Phvul.008G074600 ID=Phvul.008GC
7 :ription: pacid=37161055 transcript=Phvul.008G074600.4 locus=Phvul.008G074600 ID=Phvul.008GC
8 :ription: pacid=37161055 transcript=Phvul.008G074600.4 locus=Phvul.008G074600 ID=Phvul.008GC
9
10 BX of SCF E3 ubiquitin ligase complex (original description: pacid=37159322 transcript=Phvul.008G1
11 BX of SCF E3 ubiquitin ligase complex (original description: pacid=37159322 transcript=Phvul.008G1
12 :ription: pacid=37159091 transcript=Phvul.008G129500.1 locus=Phvul.008G129500 ID=Phvul.008G1
13 :ription: pacid=37159091 transcript=Phvul.008G129500.1 locus=Phvul.008G129500 ID=Phvul.008G1
14 :ription: pacid=37159091 transcript=Phvul.008G129500.1 locus=Phvul.008G129500 ID=Phvul.008G1
15 :ription: pacid=37159091 transcript=Phvul.008G129500.1 locus=Phvul.008G129500 ID=Phvul.008G1
16 :ription: pacid=37160650 transcript=Phvul.008G164600.1 locus=Phvul.008G164600 ID=Phvul.008G1
17 :ription: pacid=37160650 transcript=Phvul.008G164600.1 locus=Phvul.008G164600 ID=Phvul.008G1
18 :ription: pacid=37160650 transcript=Phvul.008G164600.1 locus=Phvul.008G164600 ID=Phvul.008G1
19 :ription: pacid=37160650 transcript=Phvul.008G164600.1 locus=Phvul.008G164600 ID=Phvul.008G1
20 rter (AUX/LAX) (original description: pacid=37160317 transcript=Phvul.008G225300.1 locus=Phvul.(
21 ginal description: pacid=37159379 transcript=Phvul.008G230200.1 locus=Phvul.008G230200 ID=Ph
22 ide transporter (STP) (original description: pacid=37151241 transcript=Phvul.009G030500.1 locus=P
23 ide transporter (STP) (original description: pacid=37151241 transcript=Phvul.009G030500.1 locus=P
24 ide transporter (STP) (original description: pacid=37151241 transcript=Phvul.009G030500.1 locus=P
25 ide transporter (STP) (original description: pacid=37151241 transcript=Phvul.009G030500.1 locus=P
26 :ription: pacid=37148543 transcript=Phvul.009G099700.1 locus=Phvul.009G099700 ID=Phvul.009GC
27 :ription: pacid=37148543 transcript=Phvul.009G099700.1 locus=Phvul.009G099700 ID=Phvul.009GC
28 :ription: pacid=37148543 transcript=Phvul.009G099700.1 locus=Phvul.009G099700 ID=Phvul.009GC
29 :ription: pacid=37148543 transcript=Phvul.009G099700.1 locus=Phvul.009G099700 ID=Phvul.009GC
30 :ription: pacid=37151970 transcript=Phvul.009G233000.1 locus=Phvul.009G233000 ID=Phvul.009G2
31 :ription: pacid=37151970 transcript=Phvul.009G233000.1 locus=Phvul.009G233000 ID=Phvul.009G2
32 :ription: pacid=37151970 transcript=Phvul.009G233000.1 locus=Phvul.009G233000 ID=Phvul.009G2
33 :ription: pacid=37151970 transcript=Phvul.009G233000.1 locus=Phvul.009G233000 ID=Phvul.009G2
34 :ription: pacid=37151970 transcript=Phvul.009G233000.1 locus=Phvul.009G233000 ID=Phvul.009G2
35 ransporter (MEB) (original description: pacid=37143191 transcript=Phvul.010G021700.1 locus=Phv
36 ransporter (MEB) (original description: pacid=37143191 transcript=Phvul.010G021700.1 locus=Phv
37 ransporter (MEB) (original description: pacid=37143191 transcript=Phvul.010G021700.1 locus=Phv
38 hydroxymethyltransferase (original description: pacid=37143671 transcript=Phvul.010G104900.2 l
39 hydroxymethyltransferase (original description: pacid=37143671 transcript=Phvul.010G104900.2 l
40 hydroxymethyltransferase (original description: pacid=37143671 transcript=Phvul.010G104900.2 l
41 SP1 of NSP1-NSP2 nodulation initiation complex (original description: pacid=37144086 transcript=P
42 SP1 of NSP1-NSP2 nodulation initiation complex (original description: pacid=37144086 transcript=P
43 SP1 of NSP1-NSP2 nodulation initiation complex (original description: pacid=37144086 transcript=P
44 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**
45 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**
46 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**
47 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**
48 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**
49 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**
50 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**
51 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**
52 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**
53 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**
54 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**
55 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**
56 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**
57 **IED15 of tail module of MEDIATOR transcription co-activator complex (original description: pacid=3**
58 SN4 of COP9 signalosome complex (original description: pacid=37156177 transcript=Phvul.011G006
59 SN4 of COP9 signalosome complex (original description: pacid=37156177 transcript=Phvul.011G006
60 SN4 of COP9 signalosome complex (original description: pacid=37156177 transcript=Phvul.011G006

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

αmyrin 30-oxidase OS=Glycyrrhiza uralensis (sp|h1a988|c7254_glyur : 671.0) & Enzyme classificatio
αmyrin 30-oxidase OS=Glycyrrhiza uralensis (sp|h1a988|c7254_glyur : 671.0) & Enzyme classificatio
αmyrin 30-oxidase OS=Glycyrrhiza uralensis (sp|h1a988|c7254_glyur : 671.0) & Enzyme classificatio
αmyrin 30-oxidase OS=Glycyrrhiza uralensis (sp|h1a988|c7254_glyur : 483.0) & Enzyme classificatio
αmyrin 30-oxidase OS=Glycyrrhiza uralensis (sp|h1a988|c7254_glyur : 483.0) & Enzyme classificatio

Do not distribute

1
2
3 I04G023066 ID=Phvul.004G023066.1.v2.1 annot-version=v2.1) &
4 I04G023066 ID=Phvul.004G023066.1.v2.1 annot-version=v2.1) &
5 I04G023066 ID=Phvul.004G023066.1.v2.1 annot-version=v2.1) &
6 .002G097400 ID=Phvul.002G097400.1.v2.1 annot-version=v2.1) &
7 .002G097400 ID=Phvul.002G097400.1.v2.1 annot-version=v2.1) &
8 .002G097400 ID=Phvul.002G097400.1.v2.1 annot-version=v2.1) &
9 .002G097400 ID=Phvul.002G097400.1.v2.1 annot-version=v2.1) &
10 .002G097400 ID=Phvul.002G097400.1.v2.1 annot-version=v2.1) &
11 J6G008480 ID=Phvul.006G008480.2.v2.1 annot-version=v2.1) &
12 J6G008480 ID=Phvul.006G008480.2.v2.1 annot-version=v2.1) &
13 J6G008480 ID=Phvul.006G008480.2.v2.1 annot-version=v2.1) &
14 J6G008480 ID=Phvul.006G008480.2.v2.1 annot-version=v2.1) &
15 J6G008480 ID=Phvul.006G008480.2.v2.1 annot-version=v2.1) &
16 J6G008480 ID=Phvul.006G008480.2.v2.1 annot-version=v2.1) &
17 J6G008480 ID=Phvul.006G008480.2.v2.1 annot-version=v2.1) &
18 J6G008480 ID=Phvul.006G008480.2.v2.1 annot-version=v2.1) &
19 J29000 ID=Phvul.006G029000.1.v2.1 annot-version=v2.1) &
20 J29000 ID=Phvul.006G029000.1.v2.1 annot-version=v2.1) &
21 J29000 ID=Phvul.006G029000.1.v2.1 annot-version=v2.1) &
22 J29000 ID=Phvul.006G029000.1.v2.1 annot-version=v2.1) &
23 6G110300 ID=Phvul.006G110300.1.v2.1 annot-version=v2.1) &
24 6G110300 ID=Phvul.006G110300.1.v2.1 annot-version=v2.1) &
25 6G110300 ID=Phvul.006G110300.1.v2.1 annot-version=v2.1) &
26 6G110300 ID=Phvul.006G110300.1.v2.1 annot-version=v2.1) &
27 G191600 ID=Phvul.007G191600.1.v2.1 annot-version=v2.1) &
28 G191600 ID=Phvul.007G191600.1.v2.1 annot-version=v2.1) &
29 G191600 ID=Phvul.007G191600.1.v2.1 annot-version=v2.1) &
30 G191600 ID=Phvul.007G191600.1.v2.1 annot-version=v2.1) &
31 ? transferases.EC_2.7 transferase transferring phosphorus-containing group(50.2.7 : 125.6) (original
32 ? transferases.EC_2.7 transferase transferring phosphorus-containing group(50.2.7 : 125.6) (original
33 ? transferases.EC_2.7 transferase transferring phosphorus-containing group(50.2.7 : 125.6) (original
34 ? transferases.EC_2.7 transferase transferring phosphorus-containing group(50.2.7 : 125.6) (original
35 =Phvul.001G264600 ID=Phvul.001G264600.2.v2.1 annot-version=v2.1) &
36 =Phvul.001G264600 ID=Phvul.001G264600.2.v2.1 annot-version=v2.1) &
37 =Phvul.001G264600 ID=Phvul.001G264600.2.v2.1 annot-version=v2.1) &
38 =Phvul.001G264600 ID=Phvul.001G264600.2.v2.1 annot-version=v2.1) &
39 =Phvul.001G264600 ID=Phvul.001G264600.2.v2.1 annot-version=v2.1) &
40 =Phvul.001G264600 ID=Phvul.001G264600.2.v2.1 annot-version=v2.1) &
41 =Phvul.001G264600 ID=Phvul.001G264600.2.v2.1 annot-version=v2.1) &
42 =Phvul.001G264600 ID=Phvul.001G264600.2.v2.1 annot-version=v2.1) &
43 I2G153500 ID=Phvul.002G153500.1.v2.1 annot-version=v2.1) &
44 I2G153500 ID=Phvul.002G153500.1.v2.1 annot-version=v2.1) &
45 I2G153500 ID=Phvul.002G153500.1.v2.1 annot-version=v2.1) &
46 I92500.1.v2.1 annot-version=v2.1) & Heavy metal-associated isoprenylated plant protein 33 OS=Ar
47 I92500.1.v2.1 annot-version=v2.1) & Heavy metal-associated isoprenylated plant protein 33 OS=Ar
48 I92500.1.v2.1 annot-version=v2.1) & Heavy metal-associated isoprenylated plant protein 33 OS=Ar
49 D=Phvul.004G000300.1.v2.1 annot-version=v2.1) &
50 D=Phvul.004G000300.1.v2.1 annot-version=v2.1) &
51 D=Phvul.004G000300.1.v2.1 annot-version=v2.1) &
52 D=Phvul.004G000300.1.v2.1 annot-version=v2.1) &
53 .G126100 ID=Phvul.004G126100.1.v2.1 annot-version=v2.1) &
54 .G126100 ID=Phvul.004G126100.1.v2.1 annot-version=v2.1) &
55 .G126100 ID=Phvul.004G126100.1.v2.1 annot-version=v2.1) &
56 .G126100 ID=Phvul.004G126100.1.v2.1 annot-version=v2.1) &
57 3700 ID=Phvul.005G063700.2.v2.1 annot-version=v2.1) &
58 3700 ID=Phvul.005G063700.2.v2.1 annot-version=v2.1) &
59 3700 ID=Phvul.005G063700.2.v2.1 annot-version=v2.1) &
60 3700 ID=Phvul.005G063700.2.v2.1 annot-version=v2.1) &

1 3700 ID=Phvul.005G063700.2.v2.1 annot-version=v2.1) &
2 3700 ID=Phvul.005G063700.2.v2.1 annot-version=v2.1) &
3 3700 ID=Phvul.005G063700.2.v2.1 annot-version=v2.1) &
4 :lassification.EC_2 transferases.EC_2.4 glycosyltransferase(50.2.4 : 149.1) (original description: pacic
5 :lassification.EC_2 transferases.EC_2.4 glycosyltransferase(50.2.4 : 149.1) (original description: pacic
6 :lassification.EC_2 transferases.EC_2.4 glycosyltransferase(50.2.4 : 144.7) (original description: pacic
7 :lassification.EC_2 transferases.EC_2.4 glycosyltransferase(50.2.4 : 144.7) (original description: pacic
8 :lassification.EC_2 transferases.EC_2.4 glycosyltransferase(50.2.4 : 144.7) (original description: pacic
9 cus=Phvul.007G080800 ID=Phvul.007G080800.2.v2.1 annot-version=v2.1) &
10 cus=Phvul.007G080800 ID=Phvul.007G080800.2.v2.1 annot-version=v2.1) &
11 cus=Phvul.007G080800 ID=Phvul.007G080800.2.v2.1 annot-version=v2.1) &
12 cus=Phvul.007G080800 ID=Phvul.007G080800.2.v2.1 annot-version=v2.1) &
13 4000 ID=Phvul.007G254000.2.v2.1 annot-version=v2.1) &
14 4000 ID=Phvul.007G254000.2.v2.1 annot-version=v2.1) &
15 4000 ID=Phvul.007G254000.2.v2.1 annot-version=v2.1) &
16 4000 ID=Phvul.007G254000.2.v2.1 annot-version=v2.1) &
17 4000 ID=Phvul.007G254000.2.v2.1 annot-version=v2.1) &
18 4000 ID=Phvul.007G254000.2.v2.1 annot-version=v2.1) &
19 4000 ID=Phvul.007G254000.2.v2.1 annot-version=v2.1) &
20 4000 ID=Phvul.007G254000.2.v2.1 annot-version=v2.1) &
21 4000 ID=Phvul.007G254000.2.v2.1 annot-version=v2.1) &
22 Phvul.008G212500 ID=Phvul.008G212500.1.v2.1 annot-version=v2.1) &
23 Phvul.008G212500 ID=Phvul.008G212500.1.v2.1 annot-version=v2.1) &
24 Phvul.008G212500 ID=Phvul.008G212500.1.v2.1 annot-version=v2.1) &
25 266300.1.v2.1 annot-version=v2.1) & Purple acid phosphatase 18 OS=Arabidopsis thaliana (sp|q9lju
26 266300.1.v2.1 annot-version=v2.1) & Purple acid phosphatase 18 OS=Arabidopsis thaliana (sp|q9lju
27 266300.1.v2.1 annot-version=v2.1) & Purple acid phosphatase 18 OS=Arabidopsis thaliana (sp|q9lju
28 266300.1.v2.1 annot-version=v2.1) & Purple acid phosphatase 18 OS=Arabidopsis thaliana (sp|q9lju
29 vul.011G002600.1.v2.1 annot-version=v2.1)
30 vul.011G002600.1.v2.1 annot-version=v2.1)
31 vul.011G002600.1.v2.1 annot-version=v2.1)
32 vul.011G002600.1.v2.1 annot-version=v2.1)
33 194501.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protein kinase 25 OS=Arabidopsis t
34 194501.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protein kinase 25 OS=Arabidopsis t
35 194501.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protein kinase 25 OS=Arabidopsis t
36 8 ID=Phvul.L000308.2.v2.1 annot-version=v2.1) &
37 8 ID=Phvul.L000308.2.v2.1 annot-version=v2.1) &
38 8 ID=Phvul.L000308.2.v2.1 annot-version=v2.1) &
39 8 ID=Phvul.L000308.2.v2.1 annot-version=v2.1) &
40 8 ID=Phvul.L000308.2.v2.1 annot-version=v2.1) &
41 8 ID=Phvul.L000308.2.v2.1 annot-version=v2.1) &
42 8 ID=Phvul.L000308.2.v2.1 annot-version=v2.1) &
43 8 ID=Phvul.L000308.2.v2.1 annot-version=v2.1) &
44 8 ID=Phvul.L000308.2.v2.1 annot-version=v2.1) &
45 vul.001G021750.1.v2.1 annot-version=v2.1)
46 vul.001G021750.1.v2.1 annot-version=v2.1)
47 vul.001G021750.1.v2.1 annot-version=v2.1)
48 vul.001G021750.1.v2.1 annot-version=v2.1)
49 vul.001G168600.1.v2.1 annot-version=v2.1)
50 vul.001G168600.1.v2.1 annot-version=v2.1)
51 vul.002G010100.1.v2.1 annot-version=v2.1)
52 vul.002G010100.1.v2.1 annot-version=v2.1)
53 vul.002G010100.1.v2.1 annot-version=v2.1)
54 vul.002G010100.1.v2.1 annot-version=v2.1)
55 vul.002G149100.1.v2.1 annot-version=v2.1)
56 vul.002G149100.1.v2.1 annot-version=v2.1)
57 vul.002G149100.1.v2.1 annot-version=v2.1)
58 155200.1.v2.1 annot-version=v2.1) & BTB/POZ domain-containing protein At3g09030 OS=Arabidops
59 155200.1.v2.1 annot-version=v2.1) & BTB/POZ domain-containing protein At3g09030 OS=Arabidops
60 vl.002G211400.1 locus=Phvul.002G211400 ID=Phvul.002G211400.1.v2.1 annot-version=v2.1) &

1
2 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
3 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
4 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
5 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
6 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
7 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
8 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
9 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
10 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
11 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
12 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
13 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
14 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
15 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
16 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
17 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
18 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
19 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
20 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
21 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
22 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
23 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
24 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
25 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
26 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
27 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
28 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
29 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
30 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
31 'hvul.007G154900 ID=Phvul.007G154900.9.v2.1 annot-version=v2.1) &
32 106500 ID=Phvul.008G106500.1.v2.1 annot-version=v2.1) &
33 106500 ID=Phvul.008G106500.1.v2.1 annot-version=v2.1) &
34 009G021300 ID=Phvul.009G021300.1.v2.1 annot-version=v2.1) &
35 009G021300 ID=Phvul.009G021300.1.v2.1 annot-version=v2.1) &
36 009G021300 ID=Phvul.009G021300.1.v2.1 annot-version=v2.1) &
37 009G021300 ID=Phvul.009G021300.1.v2.1 annot-version=v2.1) &
38 vul.009G097000.2.v2.1 annot-version=v2.1)
39 vul.009G097000.2.v2.1 annot-version=v2.1)
40 vul.009G097000.2.v2.1 annot-version=v2.1)
41 vul.009G097000.2.v2.1 annot-version=v2.1)
42 vul.009G097000.2.v2.1 annot-version=v2.1)
43 vul.009G122000.1.v2.1 annot-version=v2.1)
44 vul.009G122000.1.v2.1 annot-version=v2.1)
45 vul.009G122000.1.v2.1 annot-version=v2.1)
46 vul.009G227900.3.v2.1 annot-version=v2.1)
47 vul.009G227900.3.v2.1 annot-version=v2.1)
48 vul.009G227900.3.v2.1 annot-version=v2.1)
49 vul.009G227900.3.v2.1 annot-version=v2.1)
50 vul.009G227900.3.v2.1 annot-version=v2.1)
51 vul.009G227900.3.v2.1 annot-version=v2.1)
52 vul.009G227900.3.v2.1 annot-version=v2.1)
53 vul.009G227900.3.v2.1 annot-version=v2.1)
54 vul.009G227900.3.v2.1 annot-version=v2.1)
55 vul.009G227900.3.v2.1 annot-version=v2.1)
56 vul.009G227900.3.v2.1 annot-version=v2.1)
57 vul.009G227900.3.v2.1 annot-version=v2.1)
58 vul.010G159600.1.v2.1 annot-version=v2.1)
59 vul.010G159600.1.v2.1 annot-version=v2.1)
60 J84000.1.v2.1 annot-version=v2.1) & ABC transporter F family member 1 OS=Arabidopsis thaliana (;

1
2 J84000.1.v2.1 annot-version=v2.1) & ABC transporter F family member 1 OS=Arabidopsis thaliana (;
3 J84000.1.v2.1 annot-version=v2.1) & ABC transporter F family member 1 OS=Arabidopsis thaliana (;
4 vl.011G130500.1 locus=Phvul.011G130500 ID=Phvul.011G130500.1.v2.1 annot-version=v2.1) &
5 vl.011G130500.1 locus=Phvul.011G130500 ID=Phvul.011G130500.1.v2.1 annot-version=v2.1) &
6 vl.011G130500.1 locus=Phvul.011G130500 ID=Phvul.011G130500.1.v2.1 annot-version=v2.1) &
7 sferases.EC_2.4 glycosyltransferase(50.2.4 : 237.6) (original description: pacid=37155521 transcript
8 sferases.EC_2.4 glycosyltransferase(50.2.4 : 237.6) (original description: pacid=37155521 transcript
9 sferases.EC_2.4 glycosyltransferase(50.2.4 : 237.6) (original description: pacid=37155521 transcript
10 198100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13-like protein 1 OS=Arabidop:
11 198100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13-like protein 1 OS=Arabidop:
12 198100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13-like protein 1 OS=Arabidop:
13 vl.001G199500.1.v2.1 annot-version=v2.1)
14 vl.001G199500.1.v2.1 annot-version=v2.1)
15 vl.001G199500.1.v2.1 annot-version=v2.1)
16 0.2 locus=Phvul.002G005300 ID=Phvul.002G005300.2.v2.1 annot-version=v2.1) &
17 0.2 locus=Phvul.002G005300 ID=Phvul.002G005300.2.v2.1 annot-version=v2.1) &
18 0.2 locus=Phvul.002G005300 ID=Phvul.002G005300.2.v2.1 annot-version=v2.1) &
19 0.2 locus=Phvul.002G005300 ID=Phvul.002G005300.2.v2.1 annot-version=v2.1) &
20 0.2 locus=Phvul.002G005300 ID=Phvul.002G005300.2.v2.1 annot-version=v2.1) &
21 vl.002G119100.1.v2.1 annot-version=v2.1)
22 vl.002G119100.1.v2.1 annot-version=v2.1)
23 vl.002G119100.1.v2.1 annot-version=v2.1)
24 vl.002G132700.1.v2.1 annot-version=v2.1)
25 vl.002G132700.1.v2.1 annot-version=v2.1)
26 vl.002G132700.1.v2.1 annot-version=v2.1)
27 vl.002G141000.2.v2.1 annot-version=v2.1)
28 vl.002G141000.2.v2.1 annot-version=v2.1)
29 vl.002G141000.2.v2.1 annot-version=v2.1)
30 vl.002G141000.2.v2.1 annot-version=v2.1)
31 =37144465 transcript=Phvul.003G131900.1 locus=Phvul.003G131900 ID=Phvul.003G131900.1.v2.1
32 =37144465 transcript=Phvul.003G131900.1 locus=Phvul.003G131900 ID=Phvul.003G131900.1.v2.1
33 =37144465 transcript=Phvul.003G131900.1 locus=Phvul.003G131900 ID=Phvul.003G131900.1.v2.1
34 is=Phvul.003G225700 ID=Phvul.003G225700.1.v2.1 annot-version=v2.1) &
35 238000.1.v2.1 annot-version=v2.1) & Suppressor of RPS4-RLD 1 OS=Arabidopsis thaliana (sp|f4js25|
36 238000.1.v2.1 annot-version=v2.1) & Suppressor of RPS4-RLD 1 OS=Arabidopsis thaliana (sp|f4js25|
37 vl.003G259300.1.v2.1 annot-version=v2.1)
38 vl.003G259300.1.v2.1 annot-version=v2.1)
39 vl.003G259300.1.v2.1 annot-version=v2.1)
40 vl.003G259300.1.v2.1 annot-version=v2.1)
41 vl.003G259300.1.v2.1 annot-version=v2.1)
42 vl.003G259300.1.v2.1 annot-version=v2.1)
43 vl.003G259300.1.v2.1 annot-version=v2.1)
44 vl.003G259300.1.v2.1 annot-version=v2.1)
45 vl.003G259300.1.v2.1 annot-version=v2.1)
46 vl.003G259300.1.v2.1 annot-version=v2.1)
47 vl.003G259300.1.v2.1 annot-version=v2.1)
48 vl.003G259300.1.v2.1 annot-version=v2.1)
49 vl.003G259300.1.v2.1 annot-version=v2.1)
50 vl.003G259300.1.v2.1 annot-version=v2.1)
51 vl.003G259300.1.v2.1 annot-version=v2.1)
52 vl.003G259300.1.v2.1 annot-version=v2.1)
53 vl.003G259300.1.v2.1 annot-version=v2.1)
54 vl.003G259300.1.v2.1 annot-version=v2.1)
55 vl.003G259300.1.v2.1 annot-version=v2.1)
56 vl.003G259300.1.v2.1 annot-version=v2.1)
57 vl.003G259300.1.v2.1 annot-version=v2.1)
58 vl.003G259300.1.v2.1 annot-version=v2.1)
59 vl.003G259300.1.v2.1 annot-version=v2.1)
60 vl.003G259300.1.v2.1 annot-version=v2.1)

1 :G037700 ID=Phvul.004G037700.3.v2.1 annot-version=v2.1) &
2 :G037700 ID=Phvul.004G037700.3.v2.1 annot-version=v2.1) &
3 :G037700 ID=Phvul.004G037700.3.v2.1 annot-version=v2.1) &
4 0.4 locus=Phvul.004G089300 ID=Phvul.004G089300.4.v2.1 annot-version=v2.1) &
5 0.4 locus=Phvul.004G089300 ID=Phvul.004G089300.4.v2.1 annot-version=v2.1) &
6 0.4 locus=Phvul.004G089300 ID=Phvul.004G089300.4.v2.1 annot-version=v2.1) &
7 0.4 locus=Phvul.004G089300 ID=Phvul.004G089300.4.v2.1 annot-version=v2.1) &
8 0.4 locus=Phvul.004G089300 ID=Phvul.004G089300.4.v2.1 annot-version=v2.1) &
9 0.4 locus=Phvul.004G089300 ID=Phvul.004G089300.4.v2.1 annot-version=v2.1) &
10 0.4 locus=Phvul.004G089300 ID=Phvul.004G089300.4.v2.1 annot-version=v2.1) &
11 0.4 locus=Phvul.004G089300 ID=Phvul.004G089300.4.v2.1 annot-version=v2.1) &
12 1700 ID=Phvul.004G174700.1.v2.1 annot-version=v2.1) &
13 1700 ID=Phvul.004G174700.1.v2.1 annot-version=v2.1) &
14 1700 ID=Phvul.004G174700.1.v2.1 annot-version=v2.1) &
15 500 ID=Phvul.005G125500.1.v2.1 annot-version=v2.1) &
16 500 ID=Phvul.005G125500.1.v2.1 annot-version=v2.1) &
17 500 ID=Phvul.005G125500.1.v2.1 annot-version=v2.1) &
18 Phvul.006G044400 ID=Phvul.006G044400.1.v2.1 annot-version=v2.1) &
19 Phvul.006G044400 ID=Phvul.006G044400.1.v2.1 annot-version=v2.1) &
20 Phvul.006G044400 ID=Phvul.006G044400.1.v2.1 annot-version=v2.1) &
21 Phvul.006G044400 ID=Phvul.006G044400.1.v2.1 annot-version=v2.1) &
22 Phvul.006G044400 ID=Phvul.006G044400.1.v2.1 annot-version=v2.1) &
23 vul.007G072700.9.v2.1 annot-version=v2.1)
24 vul.007G072700.9.v2.1 annot-version=v2.1)
25 vul.007G072700.9.v2.1 annot-version=v2.1)
26 vul.007G072700.9.v2.1 annot-version=v2.1)
27 vul.007G072700.9.v2.1 annot-version=v2.1)
28 vul.007G072700.9.v2.1 annot-version=v2.1)
29 vul.007G072700.9.v2.1 annot-version=v2.1)
30 vul.007G072700.9.v2.1 annot-version=v2.1)
31 vul.007G072700.9.v2.1 annot-version=v2.1)
32 vul.007G072700.9.v2.1 annot-version=v2.1)
33 vul.007G072700.9.v2.1 annot-version=v2.1)
34 vul.007G072700.9.v2.1 annot-version=v2.1)
35 vul.007G072700.9.v2.1 annot-version=v2.1)
36 vul.007G072700.9.v2.1 annot-version=v2.1)
37 vul.007G072700.9.v2.1 annot-version=v2.1)
38 vul.007G072700.9.v2.1 annot-version=v2.1)
39 vul.007G072700.9.v2.1 annot-version=v2.1)
40 vul.007G072700.9.v2.1 annot-version=v2.1)
41 vul.007G072700.9.v2.1 annot-version=v2.1)
42 vul.007G072700.9.v2.1 annot-version=v2.1)
43 vul.007G072700.9.v2.1 annot-version=v2.1)
44 vul.007G072700.9.v2.1 annot-version=v2.1)
45 vul.007G072700.9.v2.1 annot-version=v2.1)
46 vul.007G072700.9.v2.1 annot-version=v2.1)
47 vul.007G072700.9.v2.1 annot-version=v2.1)
48 vul.007G072700.9.v2.1 annot-version=v2.1)
49 vul.007G072700.9.v2.1 annot-version=v2.1)
50 vul.007G072700.9.v2.1 annot-version=v2.1)
51 vul.007G072700.9.v2.1 annot-version=v2.1)
52 vul.007G215400.1.v2.1 annot-version=v2.1)
53 vul.007G215400.1.v2.1 annot-version=v2.1)
54 vul.007G215400.1.v2.1 annot-version=v2.1)
55 vul.007G215400.1.v2.1 annot-version=v2.1)
56 249800.1.v2.1 annot-version=v2.1) & Probable inactive purple acid phosphatase 16 OS=Arabidopsis
57 249800.1.v2.1 annot-version=v2.1) & Probable inactive purple acid phosphatase 16 OS=Arabidopsis
58 249800.1.v2.1 annot-version=v2.1) & Probable inactive purple acid phosphatase 16 OS=Arabidopsis
59 J74600.4.v2.1 annot-version=v2.1) & BEACH domain-containing protein C2 OS=Arabidopsis thaliana
60 J74600.4.v2.1 annot-version=v2.1) & BEACH domain-containing protein C2 OS=Arabidopsis thaliana

1 074600.4.v2.1 annot-version=v2.1) & BEACH domain-containing protein C2 OS=Arabidopsis thaliana
2 074600.4.v2.1 annot-version=v2.1) & BEACH domain-containing protein C2 OS=Arabidopsis thaliana
3 074600.4.v2.1 annot-version=v2.1) & BEACH domain-containing protein C2 OS=Arabidopsis thaliana
4 074600.4.v2.1 annot-version=v2.1) & BEACH domain-containing protein C2 OS=Arabidopsis thaliana
5 074600.4.v2.1 annot-version=v2.1) & BEACH domain-containing protein C2 OS=Arabidopsis thaliana
6 074600.4.v2.1 annot-version=v2.1) & BEACH domain-containing protein C2 OS=Arabidopsis thaliana
7 074600.4.v2.1 annot-version=v2.1) & BEACH domain-containing protein C2 OS=Arabidopsis thaliana
8 074600.4.v2.1 annot-version=v2.1) & BEACH domain-containing protein C2 OS=Arabidopsis thaliana
9
10 123400.1 locus=Phvul.008G123400 ID=Phvul.008G123400.1.v2.1 annot-version=v2.1) &
11 123400.1 locus=Phvul.008G123400 ID=Phvul.008G123400.1.v2.1 annot-version=v2.1) &
12 129500.1.v2.1 annot-version=v2.1) & Endoribonuclease Dicer homolog 2 OS=Arabidopsis thaliana (s
13 129500.1.v2.1 annot-version=v2.1) & Endoribonuclease Dicer homolog 2 OS=Arabidopsis thaliana (s
14 129500.1.v2.1 annot-version=v2.1) & Endoribonuclease Dicer homolog 2 OS=Arabidopsis thaliana (s
15 164600.1.v2.1 annot-version=v2.1) & Probable LRR receptor-like serine/threonine-protein kinase At
16 164600.1.v2.1 annot-version=v2.1) & Probable LRR receptor-like serine/threonine-protein kinase At
17 164600.1.v2.1 annot-version=v2.1) & Probable LRR receptor-like serine/threonine-protein kinase At
18 008G225300 ID=Phvul.008G225300.1.v2.1 annot-version=v2.1) &
19
20
21
22
23 Phvul.009G030500 ID=Phvul.009G030500.1.v2.1 annot-version=v2.1) &
24 Phvul.009G030500 ID=Phvul.009G030500.1.v2.1 annot-version=v2.1) &
25 Phvul.009G030500 ID=Phvul.009G030500.1.v2.1 annot-version=v2.1) &
26
27 099700.1.v2.1 annot-version=v2.1) & DDB1- and CUL4-associated factor homolog 1 OS=Arabidopsis
28 099700.1.v2.1 annot-version=v2.1) & DDB1- and CUL4-associated factor homolog 1 OS=Arabidopsis
29 099700.1.v2.1 annot-version=v2.1) & DDB1- and CUL4-associated factor homolog 1 OS=Arabidopsis
30 233000.1.v2.1 annot-version=v2.1) & Vesicle transport protein GOT1 OS=Arabidopsis thaliana (sp|q
31 233000.1.v2.1 annot-version=v2.1) & Vesicle transport protein GOT1 OS=Arabidopsis thaliana (sp|q
32 233000.1.v2.1 annot-version=v2.1) & Vesicle transport protein GOT1 OS=Arabidopsis thaliana (sp|q
33
34
35 ul.010G021700 ID=Phvul.010G021700.1.v2.1 annot-version=v2.1) &
36 ul.010G021700 ID=Phvul.010G021700.1.v2.1 annot-version=v2.1) &
37 ul.010G021700 ID=Phvul.010G021700.1.v2.1 annot-version=v2.1) &
38
39 locus=Phvul.010G104900 ID=Phvul.010G104900.2.v2.1 annot-version=v2.1) &
40 locus=Phvul.010G104900 ID=Phvul.010G104900.2.v2.1 annot-version=v2.1) &
41 locus=Phvul.010G104900 ID=Phvul.010G104900.2.v2.1 annot-version=v2.1) &
42
43 Phvul.010G129400.1 locus=Phvul.010G129400 ID=Phvul.010G129400.1.v2.1 annot-version=v2.1) &
44 Phvul.010G129400.1 locus=Phvul.010G129400 ID=Phvul.010G129400.1.v2.1 annot-version=v2.1) &
45 Phvul.010G129400.1 locus=Phvul.010G129400 ID=Phvul.010G129400.1.v2.1 annot-version=v2.1) &
46
47 07144174 transcript=Phvul.010G157900.4 locus=Phvul.010G157900 ID=Phvul.010G157900.4.v2.1 ar
48 07144174 transcript=Phvul.010G157900.4 locus=Phvul.010G157900 ID=Phvul.010G157900.4.v2.1 ar
49 07144174 transcript=Phvul.010G157900.4 locus=Phvul.010G157900 ID=Phvul.010G157900.4.v2.1 ar
50 07144174 transcript=Phvul.010G157900.4 locus=Phvul.010G157900 ID=Phvul.010G157900.4.v2.1 ar
51 07144174 transcript=Phvul.010G157900.4 locus=Phvul.010G157900 ID=Phvul.010G157900.4.v2.1 ar
52 07144174 transcript=Phvul.010G157900.4 locus=Phvul.010G157900 ID=Phvul.010G157900.4.v2.1 ar
53 07144174 transcript=Phvul.010G157900.4 locus=Phvul.010G157900 ID=Phvul.010G157900.4.v2.1 ar
54 07144174 transcript=Phvul.010G157900.4 locus=Phvul.010G157900 ID=Phvul.010G157900.4.v2.1 ar
55 07144174 transcript=Phvul.010G157900.4 locus=Phvul.010G157900 ID=Phvul.010G157900.4.v2.1 ar
56 07144174 transcript=Phvul.010G157900.4 locus=Phvul.010G157900 ID=Phvul.010G157900.4.v2.1 ar
57 07144174 transcript=Phvul.010G157900.4 locus=Phvul.010G157900 ID=Phvul.010G157900.4.v2.1 ar
58
59 5200.1 locus=Phvul.011G006200 ID=Phvul.011G006200.1.v2.1 annot-version=v2.1) &
60 5200.1 locus=Phvul.011G006200 ID=Phvul.011G006200.1.v2.1 annot-version=v2.1) &
5200.1 locus=Phvul.011G006200 ID=Phvul.011G006200.1.v2.1 annot-version=v2.1) &

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

n.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with incorporation or redu
n.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with incorporation or redu
n.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with incorporation or redu
n.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with incorporation or redu
n.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with incorporation or redu

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

I description: pacid=37168185 transcript=Phvul.001G070000.1 locus=Phvul.001G070000 ID=Phvul.C
I description: pacid=37168185 transcript=Phvul.001G070000.1 locus=Phvul.001G070000 ID=Phvul.C
I description: pacid=37168185 transcript=Phvul.001G070000.1 locus=Phvul.001G070000 ID=Phvul.C

abidopsis thaliana (sp|f4jzl7|hip33_arath : 120.0)
abidopsis thaliana (sp|f4jzl7|hip33_arath : 120.0)

1
2
3
4 d=37166010 transcript=Phvul.007G020600.1 locus=Phvul.007G020600 ID=Phvul.007G020600.1.v2.:
5 d=37166010 transcript=Phvul.007G020600.1 locus=Phvul.007G020600 ID=Phvul.007G020600.1.v2.:
6 d=37164227 transcript=Phvul.007G020700.1 locus=Phvul.007G020700 ID=Phvul.007G020700.1.v2.:
7 d=37164227 transcript=Phvul.007G020700.1 locus=Phvul.007G020700 ID=Phvul.007G020700.1.v2.:
8
9

10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26 i7|ppa18_arath : 655.0)
27 i7|ppa18_arath : 655.0)
28 i7|ppa18_arath : 655.0)
29
30

31
32
33 :haliana (sp|q9m0x5|crk25_arath : 142.0)
34 :haliana (sp|q9m0x5|crk25_arath : 142.0)
35 :haliana (sp|q9m0x5|crk25_arath : 142.0)
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57

58 sis thaliana (sp|q9s7r7|y3903_arath : 505.0)
59 sis thaliana (sp|q9s7r7|y3903_arath : 505.0)
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

aliana (sp|q0wpj7|rf298_arath : 405.0)
aliana (sp|q0wpj7|rf298_arath : 405.0)
aliana (sp|q0wpj7|rf298_arath : 405.0)
aliana (sp|q0wpj7|rf298_arath : 405.0)
aliana (sp|q0wpj7|rf298_arath : 405.0)
aliana (sp|q0wpj7|rf298_arath : 405.0)

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2 sp|q9fjh6|ab1f_arath : 941.0)

3 sp|q9fjh6|ab1f_arath : 941.0)
4
5
6
7

8 :=Phvul.011G158500.1 locus=Phvul.011G158500 ID=Phvul.011G158500.1.v2.1 annot-version=v2.1)

9 :=Phvul.011G158500.1 locus=Phvul.011G158500 ID=Phvul.011G158500.1.v2.1 annot-version=v2.1)

10 :=Phvul.011G158500.1 locus=Phvul.011G158500 ID=Phvul.011G158500.1.v2.1 annot-version=v2.1)

11 sis thaliana (sp|q9lrr4|r13l1_arath : 526.0)

12 sis thaliana (sp|q9lrr4|r13l1_arath : 526.0)

13 sis thaliana (sp|q9lrr4|r13l1_arath : 526.0)
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40

41 annot-version=v2.1) &

42 annot-version=v2.1) &

43 annot-version=v2.1) &

44 |srfr1_arath : 1278.0)

45 |srfr1_arath : 1278.0)
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55

Do not distribute

. thaliana (sp|q9sr79|ppa16_arath : 484.0)
. thaliana (sp|q9sr79|ppa16_arath : 484.0)
. thaliana (sp|q9sr79|ppa16_arath : 484.0)
 (sp|f4ig73|bchc2_arath : 2405.0)
 (sp|f4ig73|bchc2_arath : 2405.0)

1
2 1 (sp|f4ig73|bchc2_arath : 2405.0)
3 1 (sp|f4ig73|bchc2_arath : 2405.0)
4 1 (sp|f4ig73|bchc2_arath : 2405.0)
5 1 (sp|f4ig73|bchc2_arath : 2405.0)
6 1 (sp|f4ig73|bchc2_arath : 2405.0)
7 1 (sp|f4ig73|bchc2_arath : 2405.0)
8 1 (sp|f4ig73|bchc2_arath : 2405.0)
9

10
11
12 sp|q3ebc8|dcl2_arath : 1293.0)
13 sp|q3ebc8|dcl2_arath : 1293.0)
14 sp|q3ebc8|dcl2_arath : 1293.0)
15 t1g05700 OS=Arabidopsis thaliana (sp|c0lgd6|y1570_arath : 285.0)
16 t1g05700 OS=Arabidopsis thaliana (sp|c0lgd6|y1570_arath : 285.0)
17 t1g05700 OS=Arabidopsis thaliana (sp|c0lgd6|y1570_arath : 285.0)
18
19
20
21
22
23
24
25

26
27 . thaliana (sp|q9m086|dcaf1_arath : 1457.0)
28 . thaliana (sp|q9m086|dcaf1_arath : 1457.0)
29 . thaliana (sp|q9m086|dcaf1_arath : 1457.0)
30 |6nmm1|got1_arath : 139.0)
31 |6nmm1|got1_arath : 139.0)
32 |6nmm1|got1_arath : 139.0)
33 |6nmm1|got1_arath : 139.0)
34
35
36
37
38
39
40
41
42
43
44
45

46 nnot-version=v2.1) &
47 nnot-version=v2.1) &
48 nnot-version=v2.1) &
49 nnot-version=v2.1) &
50 nnot-version=v2.1) &
51 nnot-version=v2.1) &
52 nnot-version=v2.1) &
53 nnot-version=v2.1) &
54 nnot-version=v2.1) &
55 nnot-version=v2.1) &
56 nnot-version=v2.1) &
57 nnot-version=v2.1) &
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

action of molecular oxygen(50.1.13 : 128.5) (original description: pacid=37155695 transcript=Phvul.
action of molecular oxygen(50.1.13 : 128.5) (original description: pacid=37155695 transcript=Phvul.
action of molecular oxygen(50.1.13 : 128.5) (original description: pacid=37155695 transcript=Phvul.
action of molecular oxygen(50.1.13 : 91.0) (original description: pacid=37156825 transcript=Phvul.O:
action of molecular oxygen(50.1.13 : 91.0) (original description: pacid=37156825 transcript=Phvul.O:

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

J01G070000.1.v2.1 annot-version=v2.1) &
J01G070000.1.v2.1 annot-version=v2.1) &
J01G070000.1.v2.1 annot-version=v2.1) &

Do not distribute

1
2
3
4 1 annot-version=v2.1) &
5 1 annot-version=v2.1) &
6 1 annot-version=v2.1) &
7 1 annot-version=v2.1) &
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

&
&
&

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2 011G161100.1 locus=Phvul.011G161100 ID=Phvul.011G161100.1.v2.1 annot-version=v2.1) &
3 011G161100.1 locus=Phvul.011G161100 ID=Phvul.011G161100.1.v2.1 annot-version=v2.1) &
4 011G161100.1 locus=Phvul.011G161100 ID=Phvul.011G161100.1.v2.1 annot-version=v2.1) &
5 11G161900.1 locus=Phvul.011G161900 ID=Phvul.011G161900.1.v2.1 annot-version=v2.1) &
6 11G161900.1 locus=Phvul.011G161900 ID=Phvul.011G161900.1.v2.1 annot-version=v2.1) &
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

| | miRNA_Acc. | Target_Acc. | Expectation | UPE\$ | miRNA_start | miRNA_end |
|----|--------------|--------------------|-------------|-------|-------------|-----------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 4 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 5 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 6 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 7 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 8 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 9 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 10 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 11 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 12 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 13 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 14 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 15 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 16 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 17 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 18 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 19 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 20 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 21 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 22 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 23 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 24 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 25 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 26 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 27 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 28 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 29 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 30 | uaaucugcaucc | Phvul.001G094400.1 | 1 | -1 | 1 | 21 |
| 31 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc | Phvul.001G035800.1 | 2.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc | Phvul.004G099600.1 | 3 | -1 | 1 | 21 |
| 60 | uaaucugcaucc | Phvul.004G099600.1 | 3 | -1 | 1 | 21 |
| | uaaucugcaucc | Phvul.004G099600.1 | 3 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.009G186300.1 | 3 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.009G186300.1 | 3 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.009G186300.1 | 3 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.009G186300.1 | 3 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.009G186300.1 | 3 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.009G186300.1 | 3 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.009G186300.1 | 3 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.009G186300.1 | 3 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.009G186300.1 | 3 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.009G186300.1 | 3 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.009G186300.1 | 3 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.009G186300.1 | 3 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.009G186300.1 | 3 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.009G186300.1 | 3 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.009G186300.1 | 3 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.009G186300.1 | 3 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.009G186300.1 | 3 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.009G186300.1 | 3 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.001G057100.4 | 3.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.001G057100.3 | 3.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.001G057100.2 | 3.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.001G057100.1 | 3.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.001G172700.2 | 3.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.001G172700.3 | 3.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.001G172700.4 | 3.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.001G172700.1 | 3.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.002G150900.1 | 3.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.002G150900.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.003G098100.1 | 3.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.003G098100.2 | 3.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.003G098100.1 | 3.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.003G098100.2 | 3.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.003G098100.2 | 3.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.003G098100.1 | 3.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.003G098100.2 | 3.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.003G098100.1 | 3.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.003G098100.1 | 3.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.003G098100.2 | 3.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.003G098100.1 | 3.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.003G098100.2 | 3.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.003G098100.2 | 3.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.003G098100.1 | 3.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.003G221800.2 | 3.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.005G045433.1 | 3.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.005G045433.1 | 3.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.005G045433.1 | 3.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.005G045433.1 | 3.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.005G045433.1 | 3.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.005G045433.1 | 3.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.005G045433.1 | 3.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.005G045433.1 | 3.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.005G045433.1 | 3.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.005G045433.1 | 3.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.005G045433.1 | 3.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.005G045433.1 | 3.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.005G045433.1 | 3.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.005G045433.1 | 3.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.005G045433.1 | 3.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.005G045433.1 | 3.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.005G045433.1 | 3.5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.005G045433.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.007G025200.1 | 3.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.007G025200.1 | 3.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.007G025200.1 | 3.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.007G025200.1 | 3.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.007G102900.1 | 3.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.007G143100.6 | 3.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.007G143100.1 | 3.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.007G143100.4 | 3.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.007G143100.7 | 3.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.007G143100.5 | 3.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.007G143100.3 | 3.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.007G168500.1 | 3.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.008G076450.3 | 3.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.008G132450.3 | 3.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.008G132450.2 | 3.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.008G132450.1 | 3.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.008G149406.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.010G070400.1 | 3.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.002G013866.1 | 4 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.002G032300.2 | 4 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.002G032300.1 | 4 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.002G047100.2 | 4 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.002G047100.4 | 4 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.002G047100.5 | 4 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.002G047100.1 | 4 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.002G047100.3 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.002G325500.1 | 4 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.002G325500.1 | 4 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.002G325500.1 | 4 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.002G325500.1 | 4 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.002G325500.1 | 4 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.002G325500.1 | 4 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.002G325500.1 | 4 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.002G325500.1 | 4 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.002G325500.1 | 4 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.002G325500.1 | 4 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.002G325500.1 | 4 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.002G325500.1 | 4 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.002G325500.1 | 4 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.002G325500.1 | 4 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.002G325500.1 | 4 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.002G325500.1 | 4 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.002G325500.1 | 4 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.002G325500.1 | 4 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.003G241500.1 | 4 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.003G241500.2 | 4 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.004G137100.2 | 4 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.007G235300.1 | 4 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.007G242700.1 | 4 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.008G039800.5 | 4 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.008G039800.4 | 4 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.008G263100.1 | 4 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.009G040600.1 | 4 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.009G040600.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.003G192900.1 | 4.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.003G192900.2 | 4.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.003G192900.1 | 4.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.003G192900.2 | 4.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.003G192900.2 | 4.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.003G192900.1 | 4.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.003G192900.2 | 4.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.003G192900.1 | 4.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.003G192900.1 | 4.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.003G192900.2 | 4.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.003G192900.1 | 4.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.003G192900.2 | 4.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.003G192900.2 | 4.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.003G192900.1 | 4.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.003G192900.2 | 4.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.003G192900.2 | 4.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.003G192900.1 | 4.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.003G192900.2 | 4.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.003G192900.1 | 4.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.003G192900.1 | 4.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.003G192900.2 | 4.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.005G089300.1 | 4.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.005G115200.1 | 4.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.005G157700.4 | 4.5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.005G157700.3 | 4.5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.005G157700.2 | 4.5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.005G157700.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.007G243700.3 | 4.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.007G243700.2 | 4.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.007G243700.1 | 4.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.007G243700.4 | 4.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.008G048900.1 | 4.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.008G048900.1 | 4.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.008G048900.1 | 4.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.008G048900.1 | 4.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.008G048900.1 | 4.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.008G048900.1 | 4.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.008G048900.1 | 4.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.008G048900.1 | 4.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.008G048900.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.008G230300.1 | 4.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.008G230300.1 | 4.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.008G230300.1 | 4.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.008G230300.1 | 4.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.008G230300.1 | 4.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.008G230300.1 | 4.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.008G230300.1 | 4.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.008G230300.1 | 4.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.008G230300.1 | 4.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.008G230300.1 | 4.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.008G230300.1 | 4.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.008G230300.1 | 4.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.008G274500.1 | 4.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.008G289400.4 | 4.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.008G289400.3 | 4.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.008G289400.2 | 4.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.008G289400.1 | 4.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.009G142100.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.011G213500.1 | 4.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.011G213500.1 | 4.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.011G213500.1 | 4.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.011G213500.1 | 4.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.011G213500.1 | 4.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.011G213500.1 | 4.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.011G213500.1 | 4.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.011G213500.1 | 4.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|------|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.L002946.1 | 4.5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.L002946.2 | 4.5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.L002946.3 | 4.5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.002G141800.1 | 4.75 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.001G062700.2 | 5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.002G025200.1 | 5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.002G025200.1 | 5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.002G025200.1 | 5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.002G025200.1 | 5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.002G025200.1 | 5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.002G025200.1 | 5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.002G025200.1 | 5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.002G025200.1 | 5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.002G025200.1 | 5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.002G025200.1 | 5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.002G025200.1 | 5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.002G025200.1 | 5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.002G025200.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.002G057600.1 | 5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.002G057600.1 | 5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.002G057600.1 | 5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.002G057600.1 | 5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.002G057600.1 | 5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.002G057600.1 | 5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.002G057600.1 | 5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.002G057600.1 | 5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.002G057600.1 | 5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.002G098000.1 | 5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.002G098000.3 | 5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.002G162800.2 | 5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.002G162800.1 | 5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.002G228000.2 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.003G128600.1 | 5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.003G135700.1 | 5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.003G151600.4 | 5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.003G151600.3 | 5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.003G217800.1 | 5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.003G217800.1 | 5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.003G217800.1 | 5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.003G217800.1 | 5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.003G217800.1 | 5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.003G217800.1 | 5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.003G217800.1 | 5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.003G217800.1 | 5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.003G217800.1 | 5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.003G217800.1 | 5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.003G217800.1 | 5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.003G217800.1 | 5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.003G217800.1 | 5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.003G217800.1 | 5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.003G217800.1 | 5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.003G217800.1 | 5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.003G217800.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.009G147000.1 | 5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.009G147000.1 | 5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.009G147000.1 | 5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.009G147000.1 | 5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.009G147000.1 | 5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.009G147000.1 | 5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.009G175900.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.009G175900.2 | 5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.009G207500.2 | 5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.009G207500.1 | 5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.009G219300.1 | 5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.009G219300.1 | 5 | -1 | 1 | 21 |
| | uaaucugcaucc Phvul.009G219300.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.011G091400.1 | 5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.011G091400.1 | 5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.011G091400.1 | 5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.011G091400.1 | 5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.011G091400.1 | 5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.011G091400.1 | 5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.011G091400.1 | 5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.011G091400.1 | 5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.011G091400.1 | 5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.011G091400.1 | 5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.011G091400.1 | 5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.011G091400.1 | 5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.011G091400.1 | 5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.011G091400.1 | 5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.011G091400.1 | 5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.011G091400.1 | 5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.011G091400.1 | 5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.011G091400.1 | 5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 43 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 44 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 45 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 46 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 47 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 48 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 49 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 50 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 51 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 52 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 53 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 54 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 55 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 56 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 57 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 58 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 59 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 60 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 3 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 4 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 5 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 6 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 7 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 8 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 9 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 10 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 11 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 12 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 13 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 14 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 15 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 16 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 17 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 18 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 19 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 20 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 21 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 22 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 23 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 24 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 25 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 26 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 27 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 28 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 29 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 30 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 31 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 32 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 33 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 34 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 35 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 36 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 37 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 38 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 39 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 40 | uaaucugcaucc Phvul.L002060.2 | 5 | -1 | 1 | 21 |
| 41 | uaaucugcaucc Phvul.L002060.1 | 5 | -1 | 1 | 21 |
| 42 | uaaucugcaucc Phvul.L002060.3 | 5 | -1 | 1 | 21 |
| 43 | | | | | |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|-----|----------------|---------|--------------------|--------------|
| 1 | | | | | |
| 2 | 575 | 595 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 3 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 4 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 5 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 6 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 7 | 575 | 595 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 8 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 9 | | | | | |
| 10 | 575 | 595 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 11 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 12 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 13 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 14 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 15 | 575 | 595 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 16 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 17 | | | | | |
| 18 | 575 | 595 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 19 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 20 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 21 | | | | | |
| 22 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 23 | 575 | 595 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 24 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 25 | | | | | |
| 26 | 575 | 595 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 27 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 28 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 29 | | | | | |
| 30 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 31 | 575 | 595 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 32 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 33 | | | | | |
| 34 | 575 | 595 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 35 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 36 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 37 | | | | | |
| 38 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 39 | 575 | 595 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 40 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 41 | | | | | |
| 42 | 575 | 595 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 43 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 44 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 45 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 46 | | | | | |
| 47 | 575 | 595 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 48 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 49 | | | | | |
| 50 | 575 | 595 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 51 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 52 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 53 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 54 | | | | | |
| 55 | 575 | 595 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 56 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 57 | 575 | 595 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 58 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| 59 | | | | | |
| 60 | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |
| | 742 | 762 UAAUCUGCAL |:: | GUUGCUUCA(Cleavage | pacid=371658 |

| | | | | |
|----|------|--------------------------------|------------------------|--------------|
| 1 | | | | |
| 2 | 1681 | 1701 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 3 | 1868 | 1888 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 4 | 1214 | 1234 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 5 | | | | |
| 6 | 1684 | 1704 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 7 | 1681 | 1701 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 8 | 1868 | 1888 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 9 | | | | |
| 10 | 1214 | 1234 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 11 | 1684 | 1704 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 12 | 1681 | 1701 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 13 | | | | |
| 14 | 1868 | 1888 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 15 | 1214 | 1234 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 16 | 1684 | 1704 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 17 | | | | |
| 18 | 1681 | 1701 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 19 | 1868 | 1888 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 20 | 1214 | 1234 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 21 | | | | |
| 22 | 1684 | 1704 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 23 | 1681 | 1701 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 24 | 1868 | 1888 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 25 | 1214 | 1234 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 26 | 1684 | 1704 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 27 | | | | |
| 28 | 1681 | 1701 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 29 | 1868 | 1888 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 30 | 1214 | 1234 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 31 | 1684 | 1704 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 32 | 1681 | 1701 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 33 | | | | |
| 34 | 1868 | 1888 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 35 | 1214 | 1234 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 36 | 1684 | 1704 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 37 | | | | |
| 38 | 1681 | 1701 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 39 | 1868 | 1888 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 40 | 1214 | 1234 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 41 | 1684 | 1704 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 42 | 1681 | 1701 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 43 | | | | |
| 44 | 1868 | 1888 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 45 | 1214 | 1234 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 46 | 1684 | 1704 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 47 | | | | |
| 48 | 1681 | 1701 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 49 | 1868 | 1888 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 50 | 1214 | 1234 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 51 | 1684 | 1704 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 52 | 1681 | 1701 UAAUCUGCAL :..... : | UGGGCUUGG Cleavage | pacid=371651 |
| 53 | 259 | 279 UAAUCUGCAL :..... : | GAAACUUCAC Translation | pacid=371594 |
| 54 | 259 | 279 UAAUCUGCAL :..... : | GAAACUUCAC Translation | pacid=371594 |
| 55 | 259 | 279 UAAUCUGCAL :..... : | GAAACUUCAC Translation | pacid=371594 |
| 56 | 259 | 279 UAAUCUGCAL :..... : | GAAACUUCAC Translation | pacid=371594 |
| 57 | 259 | 279 UAAUCUGCAL :..... : | GAAACUUCAC Translation | pacid=371594 |
| 58 | 259 | 279 UAAUCUGCAL :..... : | GAAACUUCAC Translation | pacid=371594 |
| 59 | 259 | 279 UAAUCUGCAL :..... : | GAAACUUCAC Translation | pacid=371594 |
| 60 | 259 | 279 UAAUCUGCAL :..... : | GAAACUUCAC Translation | pacid=371594 |
| | 259 | 279 UAAUCUGCAL :..... : | GAAACUUCAC Translation | pacid=371594 |

| | | | | |
|----|------|---|--|--------------|
| 1 | | | | |
| 2 | 970 | 990 UAAUCUGCAL :::: :.....: UAAAUUUUG(Cleavage | | pacid=371744 |
| 3 | 970 | 990 UAAUCUGCAL :::: :.....: UAAAUUUUG(Cleavage | | pacid=371744 |
| 4 | 970 | 990 UAAUCUGCAL :::: :.....: UAAAUUUUG(Cleavage | | pacid=371744 |
| 5 | | | | |
| 6 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 7 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 8 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 9 | | | | |
| 10 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 11 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 12 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 13 | | | | |
| 14 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 15 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 16 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 17 | | | | |
| 18 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 19 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 20 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 21 | | | | |
| 22 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 23 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 24 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 25 | | | | |
| 26 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 27 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 28 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 29 | | | | |
| 30 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 31 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 32 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 33 | | | | |
| 34 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 35 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 36 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 37 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 38 | | | | |
| 39 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 40 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 41 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 42 | | | | |
| 43 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 44 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 45 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 46 | | | | |
| 47 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 48 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 49 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 50 | | | | |
| 51 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 52 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 53 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 54 | | | | |
| 55 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 56 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 57 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 58 | | | | |
| 59 | 2673 | 2697 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| 60 | 2728 | 2752 UAAUCUGCAL:..... :.....: UAAGCUUUG, Cleavage | | pacid=371756 |
| | 377 | 397 UAAUCUGCAL :::: :.....: UAAACCAGAC Cleavage | | pacid=371772 |

| | | | | |
|----|-----|----------------|------------------------------|-----------------------|
| 1 | | | | |
| 2 | 861 | 881 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 3 | 754 | 774 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 4 | 798 | 818 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 5 | 861 | 881 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 6 | 754 | 774 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 7 | 798 | 818 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 8 | 861 | 881 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 9 | 754 | 774 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 10 | 798 | 818 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 11 | 861 | 881 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 12 | 754 | 774 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 13 | 798 | 818 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 14 | 861 | 881 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 15 | 754 | 774 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 16 | 798 | 818 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 17 | 861 | 881 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 18 | 754 | 774 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 19 | 798 | 818 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 20 | 861 | 881 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 21 | 754 | 774 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 22 | 798 | 818 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 23 | 861 | 881 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 24 | 754 | 774 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 25 | 798 | 818 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 26 | 861 | 881 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 27 | 754 | 774 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 28 | 798 | 818 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 29 | 861 | 881 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 30 | 754 | 774 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 31 | 798 | 818 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 32 | 861 | 881 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 33 | 754 | 774 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 34 | 798 | 818 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 35 | 861 | 881 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 36 | 754 | 774 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 37 | 798 | 818 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 38 | 861 | 881 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 39 | 754 | 774 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 40 | 798 | 818 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 41 | 861 | 881 UAAUCUGCAL | :::::::::: :... : AAAACCUUAC | Cleavage pacid=371574 |
| 42 | | | | |
| 43 | | | | |
| 44 | | | | |
| 45 | | | | |
| 46 | | | | |
| 47 | | | | |
| 48 | | | | |
| 49 | | | | |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

| | | | | |
|----|----------------------|------------------|--------------------------------------|-------------|
| 1 | | | | |
| 2 | 1 Phvul.L002946.3 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 3 | 1 Phvul.L002946.1 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 4 | 1 Phvul.L002946.2 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 5 | | | | |
| 6 | 1 Phvul.L002946.3 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 7 | 1 Phvul.L002946.1 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 8 | 1 Phvul.L002946.2 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 9 | | | | |
| 10 | 1 Phvul.L002946.3 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 11 | 1 Phvul.L002946.1 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 12 | 1 Phvul.L002946.2 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 13 | | | | |
| 14 | 1 Phvul.L002946.3 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 15 | 1 Phvul.L002946.1 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 16 | 1 Phvul.L002946.2 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 17 | | | | |
| 18 | 1 Phvul.L002946.3 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 19 | 1 Phvul.L002946.1 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 20 | 1 Phvul.L002946.2 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 21 | | | | |
| 22 | 1 Phvul.L002946.3 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 23 | 1 Phvul.L002946.1 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 24 | 1 Phvul.L002946.2 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 25 | | | | |
| 26 | 1 Phvul.L002946.3 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 27 | 1 Phvul.L002946.1 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 28 | 1 Phvul.L002946.2 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 29 | | | | |
| 30 | 1 Phvul.L002946.3 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 31 | 1 Phvul.L002946.1 | Phvul.L002946 | Phvul.L00294(PF01833,PF13PTHR23335,P | |
| 32 | 1 Phvul.002G141800.1 | Phvul.002G141800 | Phvul.002G14 PF05678 | PTHR33783,P |
| 33 | 1 Phvul.002G141800.1 | Phvul.002G141800 | Phvul.002G14 PF05678 | PTHR33783,P |
| 34 | | | | |
| 35 | 1 Phvul.002G141800.1 | Phvul.002G141800 | Phvul.002G14 PF05678 | PTHR33783,P |
| 36 | 1 Phvul.002G141800.1 | Phvul.002G141800 | Phvul.002G14 PF05678 | PTHR33783,P |
| 37 | | | | |
| 38 | 1 Phvul.002G141800.1 | Phvul.002G141800 | Phvul.002G14 PF05678 | PTHR33783,P |
| 39 | 1 Phvul.002G141800.1 | Phvul.002G141800 | Phvul.002G14 PF05678 | PTHR33783,P |
| 40 | | | | |
| 41 | 1 Phvul.002G141800.1 | Phvul.002G141800 | Phvul.002G14 PF05678 | PTHR33783,P |
| 42 | 1 Phvul.002G141800.1 | Phvul.002G141800 | Phvul.002G14 PF05678 | PTHR33783,P |
| 43 | | | | |
| 44 | 1 Phvul.002G141800.1 | Phvul.002G141800 | Phvul.002G14 PF05678 | PTHR33783,P |
| 45 | 1 Phvul.002G141800.1 | Phvul.002G141800 | Phvul.002G14 PF05678 | PTHR33783,P |
| 46 | | | | |
| 47 | 1 Phvul.002G141800.1 | Phvul.002G141800 | Phvul.002G14 PF05678 | PTHR33783,P |
| 48 | 1 Phvul.002G141800.1 | Phvul.002G141800 | Phvul.002G14 PF05678 | PTHR33783,P |
| 49 | | | | |
| 50 | 1 Phvul.002G141800.1 | Phvul.002G141800 | Phvul.002G14 PF05678 | PTHR33783,P |
| 51 | 1 Phvul.002G141800.1 | Phvul.002G141800 | Phvul.002G14 PF05678 | PTHR33783,P |
| 52 | | | | |
| 53 | 1 Phvul.002G141800.1 | Phvul.002G141800 | Phvul.002G14 PF05678 | PTHR33783,P |
| 54 | 1 Phvul.002G141800.1 | Phvul.002G141800 | Phvul.002G14 PF05678 | PTHR33783,P |
| 55 | | | | |
| 56 | 1 Phvul.002G141800.1 | Phvul.002G141800 | Phvul.002G14 PF05678 | PTHR33783,P |
| 57 | 1 Phvul.002G141800.1 | Phvul.002G141800 | Phvul.002G14 PF05678 | PTHR33783,P |
| 58 | | | | |
| 59 | 1 Phvul.002G141800.1 | Phvul.002G141800 | Phvul.002G14 PF05678 | PTHR33783,P |
| 60 | 1 Phvul.001G062700.2 | Phvul.001G062700 | Phvul.001G06 PF00566 | PTHR22957,P |
| | 1 Phvul.001G062700.2 | Phvul.001G062700 | Phvul.001G06 PF00566 | PTHR22957,P |

| | | | | |
|----|-------------------|---------------|-----------------------|-------------|
| 1 | | | | |
| 2 | 1 Phvul.L002060.1 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 3 | 1 Phvul.L002060.3 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 4 | 1 Phvul.L002060.2 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 5 | | | | |
| 6 | 1 Phvul.L002060.1 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 7 | 1 Phvul.L002060.3 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 8 | 1 Phvul.L002060.2 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 9 | | | | |
| 10 | 1 Phvul.L002060.1 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 11 | 1 Phvul.L002060.3 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 12 | 1 Phvul.L002060.2 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 13 | | | | |
| 14 | 1 Phvul.L002060.1 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 15 | 1 Phvul.L002060.3 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 16 | 1 Phvul.L002060.2 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 17 | | | | |
| 18 | 1 Phvul.L002060.1 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 19 | 1 Phvul.L002060.3 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 20 | 1 Phvul.L002060.2 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 21 | | | | |
| 22 | 1 Phvul.L002060.1 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 23 | 1 Phvul.L002060.3 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 24 | 1 Phvul.L002060.2 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 25 | | | | |
| 26 | 1 Phvul.L002060.1 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 27 | 1 Phvul.L002060.3 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 28 | 1 Phvul.L002060.2 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 29 | | | | |
| 30 | 1 Phvul.L002060.1 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 31 | 1 Phvul.L002060.3 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 32 | 1 Phvul.L002060.2 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 33 | | | | |
| 34 | 1 Phvul.L002060.1 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 35 | 1 Phvul.L002060.3 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 36 | 1 Phvul.L002060.2 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 37 | | | | |
| 38 | 1 Phvul.L002060.1 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 39 | 1 Phvul.L002060.3 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 40 | 1 Phvul.L002060.2 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 41 | | | | |
| 42 | 1 Phvul.L002060.1 | Phvul.L002060 | Phvul.L002060(PF00155 | PTHR10289,P |
| 43 | | | | |
| 44 | | | | |
| 45 | | | | |
| 46 | | | | |
| 47 | | | | |
| 48 | | | | |
| 49 | | | | |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

| 1 | KOG | KEGG | KOG | GO | Best-hit-arabi-arabi-symbol | |
|----|---------|------------|----------|-------------------------|-----------------------------|---|
| 2 | | | | | | |
| 3 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 4 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 5 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 6 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 7 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 8 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 9 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 10 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 11 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 12 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 13 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 14 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 15 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 16 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 17 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 18 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 19 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 20 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 21 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 22 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 23 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 24 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 25 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 26 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 27 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 28 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 29 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 30 | | 0 | 0 | 0 GO:0005515 | AT3G27150.1 | 0 |
| 31 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 32 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 33 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 34 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 35 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 36 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 37 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 38 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 39 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 40 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 41 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 42 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 43 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 44 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 45 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 46 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 47 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 48 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 49 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 50 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 51 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 52 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 53 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 54 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 55 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 56 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 57 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G10970.1 | ATZIP4,ZIP4 | |
| 58 | | | | | | |
| 59 | | 0 2.7.11.1 | | 0 GO:0005515 | AT3G28890.1 AtRLP43,RLP43 | |
| 60 | | 0 2.7.11.1 | | 0 GO:0005515 | AT3G28890.1 AtRLP43,RLP43 | |
| | | 0 2.7.11.1 | | 0 GO:0005515 | AT3G28890.1 AtRLP43,RLP43 | |

| | | | | | |
|----|---------|----------|---|--------------|---------------------------|
| 1 | | | | | |
| 2 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 3 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 4 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 5 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 6 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 7 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 8 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 9 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 10 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 11 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 12 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 13 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 14 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 15 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 16 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 17 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 18 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 19 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 20 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 21 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 22 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 23 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 24 | 0 | 2.7.11.1 | 0 | GO:0005515 | AT3G28890.1 AtRLP43,RLP43 |
| 25 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 26 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 27 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 28 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 29 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 30 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 31 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 32 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 33 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 34 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 35 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 36 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 37 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 38 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 39 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 40 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 41 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 42 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 43 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 44 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 45 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 46 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 47 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 48 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 49 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 50 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 51 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 52 | 0 | | 0 | GO:0005515 | AT5G12300.1 |
| 53 | KOG0907 | 3.5.1.52 | 0 | GO:0045454,(| AT1G08570.1 ACHT4 |
| 54 | KOG0907 | 3.5.1.52 | 0 | GO:0045454,(| AT1G08570.1 ACHT4 |
| 55 | KOG0907 | 3.5.1.52 | 0 | GO:0045454,(| AT1G08570.1 ACHT4 |
| 56 | KOG0907 | 3.5.1.52 | 0 | GO:0045454,(| AT1G08570.1 ACHT4 |
| 57 | KOG0907 | 3.5.1.52 | 0 | GO:0045454,(| AT1G08570.1 ACHT4 |
| 58 | KOG0907 | 3.5.1.52 | 0 | GO:0045454,(| AT1G08570.1 ACHT4 |
| 59 | KOG0907 | 3.5.1.52 | 0 | GO:0045454,(| AT1G08570.1 ACHT4 |
| 60 | KOG0907 | 3.5.1.52 | 0 | GO:0045454,(| AT1G08570.1 ACHT4 |
| | KOG0907 | 3.5.1.52 | 0 | GO:0045454,(| AT1G08570.1 ACHT4 |

| | | | | |
|----|---------|------------|---------------------------------|---|
| 1 | | | | |
| 2 | KOG0907 | 3.5.1.52 | 0 GO:0045454,(AT1G08570.1 ACHT4 | |
| 3 | KOG0907 | 3.5.1.52 | 0 GO:0045454,(AT1G08570.1 ACHT4 | |
| 4 | KOG0907 | 3.5.1.52 | 0 GO:0045454,(AT1G08570.1 ACHT4 | |
| 5 | KOG0907 | 3.5.1.52 | 0 GO:0045454,(AT1G08570.1 ACHT4 | |
| 6 | KOG0907 | 3.5.1.52 | 0 GO:0045454,(AT1G08570.1 ACHT4 | |
| 7 | KOG0907 | 3.5.1.52 | 0 GO:0045454,(AT1G08570.1 ACHT4 | |
| 8 | KOG0907 | 3.5.1.52 | 0 GO:0045454,(AT1G08570.1 ACHT4 | |
| 9 | KOG0907 | 3.5.1.52 | 0 GO:0045454,(AT1G08570.1 ACHT4 | |
| 10 | KOG0907 | 3.5.1.52 | 0 GO:0045454,(AT1G08570.1 ACHT4 | |
| 11 | KOG0907 | 3.5.1.52 | 0 GO:0045454,(AT1G08570.1 ACHT4 | |
| 12 | KOG0907 | 3.5.1.52 | 0 GO:0045454,(AT1G08570.1 ACHT4 | |
| 13 | KOG0907 | 3.5.1.52 | 0 GO:0045454,(AT1G08570.1 ACHT4 | |
| 14 | KOG0907 | 3.5.1.52 | 0 GO:0045454,(AT1G08570.1 ACHT4 | |
| 15 | KOG0907 | 3.5.1.52 | 0 GO:0045454,(AT1G08570.1 ACHT4 | |
| 16 | KOG0907 | 3.5.1.52 | 0 GO:0045454,(AT1G08570.1 ACHT4 | |
| 17 | KOG0907 | 3.5.1.52 | 0 GO:0045454,(AT1G08570.1 ACHT4 | |
| 18 | KOG0907 | 3.5.1.52 | 0 GO:0045454,(AT1G08570.1 ACHT4 | |
| 19 | KOG0907 | 3.5.1.52 | 0 GO:0045454,(AT1G08570.1 ACHT4 | |
| 20 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 21 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 22 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 23 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 24 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 25 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 26 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 27 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 28 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 29 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 30 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 31 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 32 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 33 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 34 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 35 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 36 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 37 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 38 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 39 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 40 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 41 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 42 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 43 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 44 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 45 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 46 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 47 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 48 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 49 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 50 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 51 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 52 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 53 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 54 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 55 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 56 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 57 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 58 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 59 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 60 | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| | | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |

| | | | |
|----|------------|---------------------------|---|
| 1 | | | |
| 2 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 3 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 4 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 5 | | | |
| 6 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 7 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 8 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 9 | | | |
| 10 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 11 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 12 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 13 | | | |
| 14 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 15 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 16 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 17 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 18 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 19 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 20 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 21 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 22 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 23 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 24 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 25 | | | |
| 26 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 27 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 28 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 29 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 30 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 31 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 32 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 33 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 34 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 35 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 36 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 37 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 38 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 39 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 40 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 41 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 42 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 43 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 44 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 45 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 46 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 47 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 48 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 49 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 50 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 51 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 52 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 53 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 54 | | | |
| 55 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 56 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 57 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 58 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 59 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| 60 | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |
| | 0 3.2.1.39 | 0 GO:0005975,(AT4G31140.1 | 0 |

| | | | | |
|----|------------|---|---------------------------------|---|
| 1 | | | | |
| 2 | 0 3.2.1.39 | | 0 GO:0005975,(AT4G31140.1 | 0 |
| 3 | 0 3.2.1.39 | | 0 GO:0005975,(AT4G31140.1 | 0 |
| 4 | 0 3.2.1.39 | | 0 GO:0005975,(AT4G31140.1 | 0 |
| 5 | 0 3.2.1.39 | | 0 GO:0005975,(AT4G31140.1 | 0 |
| 6 | 0 3.2.1.39 | | 0 GO:0005975,(AT4G31140.1 | 0 |
| 7 | 0 3.2.1.39 | | 0 GO:0005975,(AT4G31140.1 | 0 |
| 8 | 0 3.2.1.39 | | 0 GO:0005975,(AT4G31140.1 | 0 |
| 9 | 0 | | 0 GO:0003676,(AT3G53500.2 RSZ32 | 0 |
| 10 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 11 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 12 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 13 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 14 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 15 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 16 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 17 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 18 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 19 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 20 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 21 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 22 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 23 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 24 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 25 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 26 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 27 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 28 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 29 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 30 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 31 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 32 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 33 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 34 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 35 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 36 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 37 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 38 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 39 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 40 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 41 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 42 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 43 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 44 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 45 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 46 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 47 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 48 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 49 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 50 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 51 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 52 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 53 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 54 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 55 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 56 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 57 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 58 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 59 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| 60 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |
| | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 | |

| | | | |
|----|---------|---------|---------------------------------|
| 1 | | | |
| 2 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 3 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 4 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 5 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 6 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 7 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 8 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 9 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 10 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 11 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 12 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 13 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 14 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 15 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 16 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 17 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 18 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 19 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 20 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 21 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 22 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 23 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 24 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 25 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 26 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 27 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 28 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 29 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 30 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 31 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 32 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 33 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 34 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 35 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 36 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 37 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 38 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 39 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 40 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 41 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 42 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 43 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 44 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 45 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 46 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 47 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 48 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 49 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 50 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 51 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 52 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 53 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 54 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 55 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 56 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 57 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 58 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 59 | 0 | 0 | 0 GO:0003676,(AT3G53500.2 RSZ32 |
| 60 | KOG1448 | 2.7.6.1 | 0 GO:0009116 AT1G10700.1 PRS3 |
| | KOG1448 | 2.7.6.1 | 0 GO:0009116 AT1G10700.1 PRS3 |

| | | | | | | |
|----|-------------|---------|--------|-------------------------|---------------|---|
| 1 | | | | | | |
| 2 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 3 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 4 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 5 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 6 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 7 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 8 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 9 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 10 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 11 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 12 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 13 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 14 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 15 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 16 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 17 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 18 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 19 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 20 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 21 | KOG2095 | 2.7.7.7 | K03509 | GO:0006281,(AT5G44740.2 | POLH | |
| 22 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 23 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 24 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 25 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 26 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 27 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 28 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 29 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 30 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 31 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 32 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 33 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 34 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 35 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 36 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 37 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 38 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 39 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 40 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 41 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 42 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 43 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 44 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 45 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 46 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 47 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 48 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 49 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 50 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 51 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 52 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 53 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 54 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 55 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 56 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 57 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 58 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 59 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| 60 | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |
| | KOG1853,KOC | | 0 | 0 | 0 AT4G03000.1 | 0 |

| | | | | | |
|----|-------------|---|---|---------------------------|---|
| 1 | | | | | |
| 2 | KOG1853,KOC | 0 | 0 | 0 AT4G03000.1 | 0 |
| 3 | KOG1853,KOC | 0 | 0 | 0 AT4G03000.1 | 0 |
| 4 | KOG1853,KOC | 0 | 0 | 0 AT4G03000.1 | 0 |
| 5 | KOG1853,KOC | 0 | 0 | 0 AT4G03000.1 | 0 |
| 6 | KOG1853,KOC | 0 | 0 | 0 AT4G03000.1 | 0 |
| 7 | KOG1853,KOC | 0 | 0 | 0 AT4G03000.1 | 0 |
| 8 | KOG1853,KOC | 0 | 0 | 0 AT4G03000.1 | 0 |
| 9 | KOG1853,KOC | 0 | 0 | 0 AT4G03000.1 | 0 |
| 10 | KOG1853,KOC | 0 | 0 | 0 AT4G03000.1 | 0 |
| 11 | KOG1853,KOC | 0 | 0 | 0 AT4G03000.1 | 0 |
| 12 | KOG1853,KOC | 0 | 0 | 0 AT4G03000.1 | 0 |
| 13 | KOG1853,KOC | 0 | 0 | 0 AT4G03000.1 | 0 |
| 14 | KOG1853,KOC | 0 | 0 | 0 AT4G03000.1 | 0 |
| 15 | KOG1853,KOC | 0 | 0 | 0 AT4G03000.1 | 0 |
| 16 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 17 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 18 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 19 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 20 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 21 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 22 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 23 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 24 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 25 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 26 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 27 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 28 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 29 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 30 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 31 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 32 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 33 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 34 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 35 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 36 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 37 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 38 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 39 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 40 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 41 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 42 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 43 | 0 | 0 | 0 | 0 AT4G16695.1 | 0 |
| 44 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.2 | 0 |
| 45 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.2 | 0 |
| 46 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.2 | 0 |
| 47 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.2 | 0 |
| 48 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.2 | 0 |
| 49 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.2 | 0 |
| 50 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.2 | 0 |
| 51 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.2 | 0 |
| 52 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.2 | 0 |
| 53 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.2 | 0 |
| 54 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.2 | 0 |
| 55 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.2 | 0 |
| 56 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.2 | 0 |
| 57 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.2 | 0 |
| 58 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.2 | 0 |
| 59 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.2 | 0 |
| 60 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.2 | 0 |
| | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.2 | 0 |

| | | | | | |
|----|---|---|---|-------------------------|---|
| 1 | | | | | |
| 2 | 0 | 0 | 0 | GO:0019901,(AT5G48630.2 | 0 |
| 3 | 0 | 0 | 0 | GO:0019901,(AT5G48630.2 | 0 |
| 4 | 0 | 0 | 0 | GO:0019901,(AT5G48630.2 | 0 |
| 5 | 0 | 0 | 0 | GO:0019901,(AT5G48630.2 | 0 |
| 6 | 0 | 0 | 0 | GO:0019901,(AT5G48630.2 | 0 |
| 7 | 0 | 0 | 0 | GO:0019901,(AT5G48630.2 | 0 |
| 8 | 0 | 0 | 0 | GO:0019901,(AT5G48630.2 | 0 |
| 9 | 0 | 0 | 0 | GO:0019901,(AT5G48630.2 | 0 |
| 10 | 0 | 0 | 0 | GO:0019901,(AT5G48630.2 | 0 |
| 11 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 12 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 13 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 14 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 15 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 16 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 17 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 18 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 19 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 20 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 21 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 22 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 23 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 24 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 25 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 26 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 27 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 28 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 29 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 30 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 31 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 32 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 33 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 34 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 35 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 36 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 37 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 38 | 0 | 0 | 0 | AT5G45480.1 | 0 |
| 39 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 40 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 41 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 42 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 43 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 44 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 45 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 46 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 47 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 48 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 49 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 50 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 51 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 52 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 53 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 54 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 55 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 56 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 57 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 58 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 59 | 0 | 0 | 0 | AT3G10420.2 | 0 |
| 60 | 0 | 0 | 0 | AT3G10420.2 | 0 |

| | | | | | |
|----|---|---|---|---------------------------|---|
| 1 | | | | | |
| 2 | 0 | 0 | 0 | 0 AT3G10420.2 | 0 |
| 3 | 0 | 0 | 0 | 0 AT3G10420.2 | 0 |
| 4 | 0 | 0 | 0 | 0 AT3G10420.2 | 0 |
| 5 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 6 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 7 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 8 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 9 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 10 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 11 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 12 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 13 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 14 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 15 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 16 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 17 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 18 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 19 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 20 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 21 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 22 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 23 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 24 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 25 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 26 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 27 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 28 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 29 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 30 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 31 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 32 | 0 | 0 | 0 | 0 AT1G25550.1 | 0 |
| 33 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 34 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 35 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 36 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 37 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 38 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 39 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 40 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 41 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 42 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 43 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 44 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 45 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 46 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 47 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 48 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 49 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 50 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 51 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 52 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 53 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 54 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 55 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 56 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 57 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 58 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 59 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 60 | 0 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |

| | | | | |
|----|---|---|---------------------------|---|
| 1 | | | | |
| 2 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 3 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 4 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 5 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 6 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 7 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 8 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 9 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 10 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 11 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 12 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 13 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 14 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 15 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 16 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 17 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 18 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 19 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 20 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 21 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 22 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 23 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 24 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 25 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 26 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 27 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 28 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 29 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 30 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 31 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 32 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 33 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 34 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 35 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 36 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 37 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 38 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 39 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 40 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 41 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 42 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 43 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 44 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 45 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 46 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 47 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 48 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 49 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 50 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 51 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 52 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 53 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 54 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 55 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 56 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 57 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 58 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 59 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 60 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |

| | | | | |
|----|---|---|---------------------------|---|
| 1 | | | | |
| 2 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 3 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 4 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 5 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 6 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 7 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 8 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 9 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 10 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 11 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 12 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 13 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 14 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 15 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 16 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 17 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 18 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 19 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 20 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 21 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 22 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 23 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 24 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 25 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 26 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 27 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 28 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 29 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 30 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 31 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 32 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 33 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 34 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 35 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 36 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 37 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 38 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 39 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 40 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 41 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 42 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 43 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 44 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 45 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 46 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 47 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 48 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 49 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 50 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 51 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 52 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 53 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 54 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 55 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 56 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 57 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 58 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 59 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 60 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |

| | | | | |
|----|---------|-----------|--------------------------------|---|
| 1 | | | | |
| 2 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 3 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 4 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 5 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 6 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 7 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 8 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 9 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 10 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 11 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 12 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 13 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 14 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 15 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 16 | 0 | 0 | 0 GO:0019901,(AT5G48630.1 | 0 |
| 17 | | | | |
| 18 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 19 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 20 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 21 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 22 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 23 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 24 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 25 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 26 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 27 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 28 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 29 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 30 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 31 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 32 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 33 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 34 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 35 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 36 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 37 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 38 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 39 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 40 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 41 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 42 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 43 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 44 | KOG1893 | 0 | 0 GO:0016021,(AT2G48060.1 | 0 |
| 45 | KOG1502 | 1.1.1.348 | 0 GO:0050662,(AT2G45400.1 BEN1 | |
| 46 | KOG1502 | 1.1.1.348 | 0 GO:0050662,(AT2G45400.1 BEN1 | |
| 47 | KOG1502 | 1.1.1.348 | 0 GO:0050662,(AT2G45400.1 BEN1 | |
| 48 | KOG1502 | 1.1.1.348 | 0 GO:0050662,(AT2G45400.1 BEN1 | |
| 49 | KOG1502 | 1.1.1.348 | 0 GO:0050662,(AT2G45400.1 BEN1 | |
| 50 | KOG1502 | 1.1.1.348 | 0 GO:0050662,(AT2G45400.1 BEN1 | |
| 51 | KOG1502 | 1.1.1.348 | 0 GO:0050662,(AT2G45400.1 BEN1 | |
| 52 | KOG1502 | 1.1.1.348 | 0 GO:0050662,(AT2G45400.1 BEN1 | |
| 53 | KOG1502 | 1.1.1.348 | 0 GO:0050662,(AT2G45400.1 BEN1 | |
| 54 | KOG1502 | 1.1.1.348 | 0 GO:0050662,(AT2G45400.1 BEN1 | |
| 55 | KOG1502 | 1.1.1.348 | 0 GO:0050662,(AT2G45400.1 BEN1 | |
| 56 | KOG1502 | 1.1.1.348 | 0 GO:0050662,(AT2G45400.1 BEN1 | |
| 57 | KOG1502 | 1.1.1.348 | 0 GO:0050662,(AT2G45400.1 BEN1 | |
| 58 | KOG1502 | 1.1.1.348 | 0 GO:0050662,(AT2G45400.1 BEN1 | |
| 59 | KOG1502 | 1.1.1.348 | 0 GO:0050662,(AT2G45400.1 BEN1 | |
| 60 | KOG1502 | 1.1.1.348 | 0 GO:0050662,(AT2G45400.1 BEN1 | |
| | KOG1502 | 1.1.1.348 | 0 GO:0050662,(AT2G45400.1 BEN1 | |

| | | | | | |
|----|---------|-----------|---|--------------------------------|---|
| 1 | | | | | |
| 2 | KOG1502 | 1.1.1.348 | 0 | GO:0050662,(AT2G45400.1 BEN1 | |
| 3 | KOG1502 | 1.1.1.348 | 0 | GO:0050662,(AT2G45400.1 BEN1 | |
| 4 | KOG1502 | 1.1.1.348 | 0 | GO:0050662,(AT2G45400.1 BEN1 | |
| 5 | KOG1502 | 1.1.1.348 | 0 | GO:0050662,(AT2G45400.1 BEN1 | |
| 6 | KOG1502 | 1.1.1.348 | 0 | GO:0050662,(AT2G45400.1 BEN1 | |
| 7 | KOG1502 | 1.1.1.348 | 0 | GO:0050662,(AT2G45400.1 BEN1 | |
| 8 | KOG1502 | 1.1.1.348 | 0 | GO:0050662,(AT2G45400.1 BEN1 | |
| 9 | KOG1502 | 1.1.1.348 | 0 | GO:0050662,(AT2G45400.1 BEN1 | |
| 10 | KOG1502 | 1.1.1.348 | 0 | GO:0050662,(AT2G45400.1 BEN1 | |
| 11 | KOG1502 | 1.1.1.348 | 0 | GO:0050662,(AT2G45400.1 BEN1 | |
| 12 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 13 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 14 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 15 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 16 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 17 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 18 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 19 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 20 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 21 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 22 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 23 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 24 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 25 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 26 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 27 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 28 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 29 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 30 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 31 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 32 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 33 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 34 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 35 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 36 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 37 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 38 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 39 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 40 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 41 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 42 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 43 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 44 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 45 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 46 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 47 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 48 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 49 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 50 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 51 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 52 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 53 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 54 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 55 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 56 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 57 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 58 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 59 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| 60 | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |
| | KOG0794 | | 0 | K15161 GO:0019901,(AT5G48630.1 | 0 |

| | | | | | | |
|----|---------|----------|-------------------------|---|---|---|
| 1 | | | | | | |
| 2 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 3 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 4 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 5 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 6 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 7 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 8 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 9 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 10 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 11 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 12 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 13 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 14 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 15 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 16 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 17 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 18 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 19 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 20 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 21 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 22 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 23 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 24 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 25 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 26 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 27 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 28 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 29 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 30 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 31 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 32 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 33 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 34 | KOG0794 | 0 K15161 | GO:0019901,(AT5G48630.1 | | | 0 |
| 35 | 0 | 0 | 0 | 0 | 0 | 0 |
| 36 | 0 | 0 | 0 | 0 | 0 | 0 |
| 37 | 0 | 0 | 0 | 0 | 0 | 0 |
| 38 | 0 | 0 | 0 | 0 | 0 | 0 |
| 39 | 0 | 0 | 0 | 0 | 0 | 0 |
| 40 | 0 | 0 | 0 | 0 | 0 | 0 |
| 41 | 0 | 0 | 0 | 0 | 0 | 0 |
| 42 | 0 | 0 | 0 | 0 | 0 | 0 |
| 43 | 0 | 0 | 0 | 0 | 0 | 0 |
| 44 | 0 | 0 | 0 | 0 | 0 | 0 |
| 45 | 0 | 0 | 0 | 0 | 0 | 0 |
| 46 | 0 | 0 | 0 | 0 | 0 | 0 |
| 47 | 0 | 0 | 0 | 0 | 0 | 0 |
| 48 | 0 | 0 | 0 | 0 | 0 | 0 |
| 49 | 0 | 0 | 0 | 0 | 0 | 0 |
| 50 | 0 | 0 | 0 | 0 | 0 | 0 |
| 51 | 0 | 0 | 0 | 0 | 0 | 0 |
| 52 | 0 | 0 | 0 | 0 | 0 | 0 |
| 53 | 0 | 0 | 0 | 0 | 0 | 0 |
| 54 | 0 | 0 | 0 | 0 | 0 | 0 |
| 55 | 0 | 0 | 0 | 0 | 0 | 0 |
| 56 | 0 | 0 | 0 | 0 | 0 | 0 |
| 57 | 0 | 0 | 0 | 0 | 0 | 0 |
| 58 | 0 | 0 | 0 | 0 | 0 | 0 |
| 59 | 0 | 0 | 0 | 0 | 0 | 0 |
| 60 | 0 | 0 | 0 | 0 | 0 | 0 |
| | 0 | 0 | 0 | 0 | 0 | 0 |

| | | | | | |
|----|---------|----------|---|-------------------------|---|
| 1 | | | | | |
| 2 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 3 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 4 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 5 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 6 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 7 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 8 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 9 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 10 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 11 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 12 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 13 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 14 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 15 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 16 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 17 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 18 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 19 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 20 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 21 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 22 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 23 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 24 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 25 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 26 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 27 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 28 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 29 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 30 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 31 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 32 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 33 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 34 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 35 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 36 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 37 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 38 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 39 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 40 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 41 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 42 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 43 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 44 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 45 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 46 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 47 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 48 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 49 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 50 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 51 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 52 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 53 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 54 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 55 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 56 | KOG3109 | 3.1.3.74 | 0 | 0 AT5G02230.2 | 0 |
| 57 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 58 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 59 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 60 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |

| | | | | | |
|----|---------|----------|---|-------------------------|---|
| 1 | | | | | |
| 2 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 3 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 4 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 5 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 6 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 7 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 8 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 9 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 10 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 11 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 12 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 13 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 14 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 15 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 16 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 17 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 18 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 19 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 20 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 21 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 22 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 23 | KOG1187 | 2.7.11.1 | 0 | GO:0005515,(AT3G56370.1 | 0 |
| 24 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 25 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 26 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 27 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 28 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 29 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 30 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 31 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 32 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 33 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 34 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 35 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 36 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 37 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 38 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 39 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 40 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 41 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 42 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 43 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 44 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 45 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 46 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 47 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 48 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 49 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 50 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 51 | | 0 | 0 | 0 AT4G37460.1 SRFR1 | |
| 52 | KOG2521 | | 0 | 0 AT2G18245.1 | 0 |
| 53 | KOG2521 | | 0 | 0 AT2G18245.1 | 0 |
| 54 | KOG2521 | | 0 | 0 AT2G18245.1 | 0 |
| 55 | KOG2521 | | 0 | 0 AT2G18245.1 | 0 |
| 56 | KOG2521 | | 0 | 0 AT2G18245.1 | 0 |
| 57 | KOG2521 | | 0 | 0 AT2G18245.1 | 0 |
| 58 | KOG2521 | | 0 | 0 AT2G18245.1 | 0 |
| 59 | KOG2521 | | 0 | 0 AT2G18245.1 | 0 |
| 60 | KOG2521 | | 0 | 0 AT2G18245.1 | 0 |
| | KOG2521 | | 0 | 0 AT2G18245.1 | 0 |

| | | | | | |
|----|---------|---|---|---------------------------|---|
| 1 | | | | | |
| 2 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 3 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 4 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 5 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 6 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 7 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 8 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 9 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 10 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 11 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 12 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 13 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 14 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 15 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 16 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 17 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 18 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 19 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 20 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 21 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 22 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 23 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 24 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 25 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 26 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 27 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 28 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 29 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 30 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 31 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 32 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 33 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 34 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 35 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 36 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 37 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 38 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 39 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 40 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 41 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 42 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 43 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 44 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 45 | KOG2521 | 0 | 0 | 0 AT2G18245.1 | 0 |
| 46 | | | | | |
| 47 | 0 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 48 | 0 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 49 | 0 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 50 | 0 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 51 | 0 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 52 | 0 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 53 | 0 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 54 | 0 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 55 | 0 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 56 | 0 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 57 | 0 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 58 | 0 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 59 | 0 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 60 | 0 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| | 0 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |

| | | | | |
|----|---|---|---------------------------|---|
| 1 | | | | |
| 2 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 3 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 4 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 5 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 6 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 7 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 8 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 9 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 10 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 11 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 12 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 13 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 14 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 15 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 16 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 17 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 18 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 19 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 20 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 21 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 22 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 23 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 24 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 25 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 26 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 27 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 28 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 29 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 30 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 31 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 32 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 33 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 34 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 35 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 36 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 37 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 38 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 39 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 40 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 41 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 42 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 43 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 44 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 45 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 46 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 47 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 48 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 49 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 50 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 51 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 52 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 53 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 54 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 55 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 56 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 57 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 58 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 59 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 60 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |

| | | | | |
|----|---|---|---------------------------|---|
| 1 | | | | |
| 2 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 3 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 4 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 5 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 6 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 7 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 8 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 9 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 10 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 11 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 12 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 13 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 14 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 15 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 16 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 17 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 18 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 19 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 20 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 21 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 22 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 23 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 24 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 25 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 26 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 27 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 28 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 29 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 30 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 31 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 32 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 33 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 34 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 35 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 36 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 37 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 38 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 39 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 40 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 41 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 42 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 43 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 44 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 45 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 46 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 47 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 48 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 49 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 50 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 51 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 52 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 53 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 54 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 55 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 56 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 57 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 58 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 59 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| 60 | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |
| | 0 | 0 | 0 GO:0019901,(AT5G45190.1 | 0 |

| | | | | | | |
|----|---------|----------|--------|------------|-------------------------------------|---|
| 1 | | | | | | |
| 2 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 3 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 4 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 5 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 6 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 7 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 8 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 9 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 10 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 11 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 12 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 13 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 14 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 15 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 16 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 17 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 18 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 19 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 20 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 21 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 22 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 23 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 24 | KOG0406 | 2.5.1.18 | K00799 | GO:0005515 | AT1G10360.1 ATGSTU18,GST29,GSTL | |
| 25 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 26 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 27 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 28 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 29 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 30 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 31 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 32 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 33 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 34 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 35 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 36 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 37 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 38 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 39 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 40 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 41 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 42 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 43 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 44 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 45 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 46 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 47 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 48 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 49 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 50 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 51 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 52 | KOG1650 | | 0 | 0 | GO:0006813,(AT4G04850.2 ATKEA3,KEA3 | |
| 53 | | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 54 | | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 55 | | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 56 | | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 57 | | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 58 | | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 59 | | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 60 | | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| | | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |

| | | | | | |
|----|-----------|--------|------------------------------|---------------|---|
| 1 | | | | | |
| 2 | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 3 | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 4 | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 5 | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 6 | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 7 | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 8 | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 9 | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 10 | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 11 | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 12 | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 13 | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 14 | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 15 | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 16 | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 17 | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 18 | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 19 | 0 | 0 | 0 | 0 AT5G42655.1 | 0 |
| 20 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 21 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 22 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 23 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 24 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 25 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 26 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 27 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 28 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 29 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 30 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 31 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 32 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 33 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 34 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 35 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 36 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 37 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 38 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 39 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 40 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 41 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 42 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 43 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 44 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 45 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 46 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 47 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 48 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 49 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 50 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 51 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 52 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 53 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 54 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 55 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 56 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 57 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 58 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 59 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |
| 60 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | | |

| | | | | | |
|----|---------|-----------|--------|-----------------------------------|---|
| 1 | | | | | |
| 2 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | |
| 3 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | |
| 4 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | |
| 5 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | |
| 6 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | |
| 7 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | |
| 8 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | |
| 9 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | |
| 10 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | |
| 11 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | |
| 12 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | |
| 13 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | |
| 14 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.2 FRA1 | |
| 15 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 16 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 17 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 18 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 19 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 20 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 21 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 22 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 23 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 24 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 25 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 26 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 27 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 28 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 29 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 30 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 31 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 32 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 33 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 34 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 35 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 36 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 37 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 38 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 39 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 40 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 41 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 42 | KOG4529 | 0 | 0 | 0 AT1G73380.1 | 0 |
| 43 | | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA | |
| 44 | | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA | |
| 45 | | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA | |
| 46 | | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA | |
| 47 | | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA | |
| 48 | | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA | |
| 49 | | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA | |
| 50 | | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA | |
| 51 | | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA | |
| 52 | | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA | |
| 53 | | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA | |
| 54 | | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA | |
| 55 | | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA | |
| 56 | | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA | |
| 57 | | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA | |
| 58 | | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA | |
| 59 | | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA | |
| 60 | | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA | |
| | | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA | |

| | | | | | |
|----|---------|------------------|---|-----------------------------------|-----------------------------------|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA |
| 3 | | 0 | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA |
| 4 | | 0 | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA |
| 5 | | 0 | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA |
| 6 | | 0 | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA |
| 7 | | 0 | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA |
| 8 | | 0 | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA |
| 9 | | 0 | 0 | 0 | 0 AT1G65680.1 ATEXPB2,ATHEXP BETA |
| 10 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 11 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 12 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 13 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 14 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 15 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 16 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 17 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 18 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 19 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 20 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 21 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 22 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 23 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 24 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 25 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 26 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 27 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 28 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 29 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 30 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 31 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 32 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 33 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 34 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 35 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 36 | KOG4495 | | 0 | 0 GO:0005515 | AT5G57860.3 0 |
| 37 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 38 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 39 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 40 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 41 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 42 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 43 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 44 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 45 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 46 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 47 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 48 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 49 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 50 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 51 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 52 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 53 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 54 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 55 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 56 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 57 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 58 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 59 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |
| 60 | | 0 2.7.11.22,2.7. | | 0 GO:0006468,(AT5G39420.1 cdc2cAt | |

| | | | | | |
|----|------------|--------|---|---|---|
| 1 | | | | | |
| 2 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 3 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 4 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 5 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 6 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 7 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 8 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 9 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 10 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 11 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 12 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 13 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 14 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 15 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 16 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 17 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 18 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 19 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 20 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 21 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 22 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 23 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 24 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 25 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 26 | KOG4696 | 0 | 0 | 0 AT5G24680.1 | 0 |
| 27 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 28 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 29 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 30 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 31 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 32 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 33 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 34 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 35 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 36 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 37 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 38 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 39 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 40 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 41 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 42 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 43 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 44 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 45 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 46 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 47 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 48 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 49 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 50 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 51 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 52 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 53 | 0 | 0 | 0 | 0 AT2G40820.1 | 0 |
| 54 | | | | | |
| 55 | 0 3.6.3.44 | K05658 | | GO:0016887,(AT2G36910.1 ABCB1,ATPGP1,PGP1 | |
| 56 | 0 3.6.3.44 | K05658 | | GO:0016887,(AT2G36910.1 ABCB1,ATPGP1,PGP1 | |
| 57 | 0 3.6.3.44 | K05658 | | GO:0016887,(AT2G36910.1 ABCB1,ATPGP1,PGP1 | |
| 58 | 0 3.6.3.44 | K05658 | | GO:0016887,(AT2G36910.1 ABCB1,ATPGP1,PGP1 | |
| 59 | 0 3.6.3.44 | K05658 | | GO:0016887,(AT2G36910.1 ABCB1,ATPGP1,PGP1 | |
| 60 | 0 3.6.3.44 | K05658 | | GO:0016887,(AT2G36910.1 ABCB1,ATPGP1,PGP1 | |
| | 0 3.6.3.44 | K05658 | | GO:0016887,(AT2G36910.1 ABCB1,ATPGP1,PGP1 | |

| | | | | | |
|----|---|----------|-----------------------------|---------------------|---|
| 1 | | | | | |
| 2 | 0 | 0 K15164 | GO:0016592,(AT1G55325.2 GCT | | |
| 3 | 0 | 0 K15164 | GO:0016592,(AT1G55325.2 GCT | | |
| 4 | 0 | 0 K15164 | GO:0016592,(AT1G55325.2 GCT | | |
| 5 | 0 | 0 K15164 | GO:0016592,(AT1G55325.2 GCT | | |
| 6 | 0 | 0 K15164 | GO:0016592,(AT1G55325.2 GCT | | |
| 7 | 0 | 0 K15164 | GO:0016592,(AT1G55325.2 GCT | | |
| 8 | 0 | 0 K15164 | GO:0016592,(AT1G55325.2 GCT | | |
| 9 | 0 | 0 K15164 | GO:0016592,(AT1G55325.2 GCT | | |
| 10 | 0 | 0 K15164 | GO:0016592,(AT1G55325.2 GCT | | |
| 11 | 0 | 0 K15164 | GO:0016592,(AT1G55325.2 GCT | | |
| 12 | 0 | 0 K15164 | GO:0016592,(AT1G55325.2 GCT | | |
| 13 | 0 | 0 K15164 | GO:0016592,(AT1G55325.2 GCT | | |
| 14 | 0 | 0 K15164 | GO:0016592,(AT1G55325.2 GCT | | |
| 15 | 0 | 0 K15164 | GO:0016592,(AT1G55325.2 GCT | | |
| 16 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 17 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 18 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 19 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 20 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 21 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 22 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 23 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 24 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 25 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 26 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 27 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 28 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 29 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 30 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 31 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 32 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 33 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 34 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 35 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 36 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 37 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 38 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 39 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 40 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 41 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 42 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 43 | 0 | 0 | 0 | 0 AT2G22560.1 | 0 |
| 44 | 0 | 0 | 0 | 0 AT1G34370.2 STOP1 | |
| 45 | 0 | 0 | 0 | 0 AT1G34370.2 STOP1 | |
| 46 | 0 | 0 | 0 | 0 AT1G34370.2 STOP1 | |
| 47 | 0 | 0 | 0 | 0 AT1G34370.2 STOP1 | |
| 48 | 0 | 0 | 0 | 0 AT1G34370.2 STOP1 | |
| 49 | 0 | 0 | 0 | 0 AT1G34370.2 STOP1 | |
| 50 | 0 | 0 | 0 | 0 AT1G34370.2 STOP1 | |
| 51 | 0 | 0 | 0 | 0 AT1G34370.2 STOP1 | |
| 52 | 0 | 0 | 0 | 0 AT1G34370.2 STOP1 | |
| 53 | 0 | 0 | 0 | 0 AT1G34370.2 STOP1 | |
| 54 | 0 | 0 | 0 | 0 AT1G34370.2 STOP1 | |
| 55 | 0 | 0 | 0 | 0 AT1G34370.2 STOP1 | |
| 56 | 0 | 0 | 0 | 0 AT1G34370.2 STOP1 | |
| 57 | 0 | 0 | 0 | 0 AT1G34370.2 STOP1 | |
| 58 | 0 | 0 | 0 | 0 AT1G34370.2 STOP1 | |
| 59 | 0 | 0 | 0 | 0 AT1G34370.2 STOP1 | |
| 60 | 0 | 0 | 0 | 0 AT1G34370.2 STOP1 | |

| | | | | | | |
|----|------------|---|---|---|-----------------------------------|---|
| 1 | | | | | | |
| 2 | 0 | 0 | 0 | 0 | AT1G34370.2 STOP1 | |
| 3 | 0 | 0 | 0 | 0 | AT1G34370.2 STOP1 | |
| 4 | 0 | 0 | 0 | 0 | AT1G34370.2 STOP1 | |
| 5 | 0 | 0 | 0 | 0 | AT1G34370.2 STOP1 | |
| 6 | 0 | 0 | 0 | 0 | AT1G34370.2 STOP1 | |
| 7 | 0 | 0 | 0 | 0 | AT1G34370.2 STOP1 | |
| 8 | 0 | 0 | 0 | 0 | AT1G34370.2 STOP1 | |
| 9 | 0 | 0 | 0 | 0 | AT1G34370.2 STOP1 | |
| 10 | 0 | 0 | 0 | 0 | AT1G34370.2 STOP1 | |
| 11 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 12 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 13 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 14 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 15 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 16 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 17 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 18 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 19 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 20 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 21 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 22 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 23 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 24 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 25 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 26 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 27 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 28 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 29 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 30 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 31 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 32 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 33 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 34 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 35 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 36 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 37 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 38 | 0 2.3.1.12 | | | 0 | GO:0016746,(AT3G25860.1 LTA2,PLE2 | |
| 39 | 0 | 0 | 0 | 0 | 0 | 0 |
| 40 | 0 | 0 | 0 | 0 | 0 | 0 |
| 41 | 0 | 0 | 0 | 0 | 0 | 0 |
| 42 | 0 | 0 | 0 | 0 | 0 | 0 |
| 43 | 0 | 0 | 0 | 0 | 0 | 0 |
| 44 | 0 | 0 | 0 | 0 | 0 | 0 |
| 45 | 0 | 0 | 0 | 0 | 0 | 0 |
| 46 | 0 | 0 | 0 | 0 | 0 | 0 |
| 47 | 0 | 0 | 0 | 0 | 0 | 0 |
| 48 | 0 | 0 | 0 | 0 | 0 | 0 |
| 49 | 0 | 0 | 0 | 0 | 0 | 0 |
| 50 | 0 | 0 | 0 | 0 | 0 | 0 |
| 51 | 0 | 0 | 0 | 0 | 0 | 0 |
| 52 | 0 | 0 | 0 | 0 | 0 | 0 |
| 53 | 0 | 0 | 0 | 0 | 0 | 0 |
| 54 | 0 | 0 | 0 | 0 | 0 | 0 |
| 55 | 0 | 0 | 0 | 0 | 0 | 0 |
| 56 | 0 | 0 | 0 | 0 | 0 | 0 |
| 57 | 0 | 0 | 0 | 0 | 0 | 0 |
| 58 | 0 | 0 | 0 | 0 | 0 | 0 |
| 59 | 0 | 0 | 0 | 0 | 0 | 0 |
| 60 | 0 | 0 | 0 | 0 | 0 | 0 |

| | | | | | | |
|----|-----------|----------|---|-------------------------|-------------|---|
| 1 | | | | | | |
| 2 | 0 | 0 | 0 | 0 | 0 | 0 |
| 3 | 0 | 0 | 0 | 0 | 0 | 0 |
| 4 | 0 | 0 | 0 | 0 | 0 | 0 |
| 5 | | | | | | |
| 6 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 7 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 8 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 9 | | | | | | |
| 10 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 11 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 12 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 13 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 14 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 15 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 16 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 17 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 18 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 19 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 20 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 21 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 22 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 23 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 24 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 25 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 26 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 27 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 28 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 29 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 30 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 31 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 32 | 0 1.2.1.3 | | 0 | GO:0055114,(AT3G66658.2 | ALDH22A1 | |
| 33 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 34 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 35 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 36 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 37 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 38 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 39 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 40 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 41 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 42 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 43 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 44 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 45 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 46 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 47 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 48 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 49 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 50 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 51 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 52 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 53 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 54 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 55 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 56 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 57 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 58 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 59 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| 60 | 0 | 0 K13462 | 0 | GO:0032012,(AT3G43300.1 | ATMIN7,BEN1 | |
| | 0 | 0 K17086 | 0 | GO:0016021 | AT5G35160.2 | 0 |

| | | | | | |
|----|---|----------|---|--|---|
| 1 | | | | | |
| 2 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 3 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 4 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 5 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 6 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 7 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 8 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 9 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 10 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 11 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 12 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 13 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 14 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 15 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 16 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 17 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 18 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 19 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 20 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 21 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 22 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 23 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 24 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 25 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 26 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 27 | 0 | 0 K17086 | GO:0016021 AT5G35160.2 | | 0 |
| 28 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 29 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 30 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 31 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 32 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 33 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 34 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 35 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 36 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 37 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 38 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 39 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 40 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 41 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 42 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 43 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 44 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 45 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 46 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 47 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 48 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 49 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 50 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 51 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 52 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 53 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 54 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 55 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 56 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 57 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 58 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 59 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |
| 60 | 0 | 0 | 0 GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | | |

| | | | | | |
|----|---------|----------|------------|---|---|
| 1 | | | | | |
| 2 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 3 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 4 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 5 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 6 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 7 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 8 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 9 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 10 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 11 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 12 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 13 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 14 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 15 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 16 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 17 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 18 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 19 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 20 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 21 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 22 | 0 | 0 | 0 | GO:0043565,(AT3G01470.1 ATHB-1,ATHB1,HAT5,H | |
| 23 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 24 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 25 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 26 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 27 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 28 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 29 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 30 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 31 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 32 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 33 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 34 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 35 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 36 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 37 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 38 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 39 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 40 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 41 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 42 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 43 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 44 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 45 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 46 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 47 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 48 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 49 | KOG4208 | 0 K14838 | GO:0003676 | AT5G04600.1 | 0 |
| 50 | | | | | |
| 51 | 0 | 0 | 0 | AT5G54970.1 | 0 |
| 52 | 0 | 0 | 0 | AT5G54970.1 | 0 |
| 53 | 0 | 0 | 0 | AT5G54970.1 | 0 |
| 54 | 0 | 0 | 0 | AT5G54970.1 | 0 |
| 55 | 0 | 0 | 0 | AT5G54970.1 | 0 |
| 56 | 0 | 0 | 0 | AT5G54970.1 | 0 |
| 57 | 0 | 0 | 0 | AT5G54970.1 | 0 |
| 58 | 0 | 0 | 0 | AT5G54970.1 | 0 |
| 59 | 0 | 0 | 0 | AT5G54970.1 | 0 |
| 60 | 0 | 0 | 0 | AT5G54970.1 | 0 |
| | 0 | 0 | 0 | AT5G54970.1 | 0 |

| | | | | | |
|----|---|---|---|-------------------------------|---|
| 1 | | | | | |
| 2 | 0 | 0 | 0 | 0 AT5G54970.1 | 0 |
| 3 | 0 | 0 | 0 | 0 AT5G54970.1 | 0 |
| 4 | 0 | 0 | 0 | 0 AT5G54970.1 | 0 |
| 5 | 0 | 0 | 0 | 0 AT5G54970.1 | 0 |
| 6 | 0 | 0 | 0 | 0 AT5G54970.1 | 0 |
| 7 | 0 | 0 | 0 | 0 AT5G54970.1 | 0 |
| 8 | 0 | 0 | 0 | 0 AT5G54970.1 | 0 |
| 9 | 0 | 0 | 0 | 0 AT5G54970.1 | 0 |
| 10 | 0 | 0 | 0 | 0 AT5G54970.1 | 0 |
| 11 | 0 | 0 | 0 | 0 AT5G54970.1 | 0 |
| 12 | 0 | 0 | 0 | 0 AT5G54970.1 | 0 |
| 13 | 0 | 0 | 0 | 0 AT5G54970.1 | 0 |
| 14 | 0 | 0 | 0 | 0 AT5G54970.1 | 0 |
| 15 | 0 | 0 | 0 | 0 AT5G54970.1 | 0 |
| 16 | 0 | 0 | 0 | 0 AT5G54970.1 | 0 |
| 17 | 0 | 0 | 0 | 0 AT5G54970.1 | 0 |
| 18 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 19 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 20 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 21 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 22 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 23 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 24 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 25 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 26 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 27 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 28 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 29 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 30 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 31 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 32 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 33 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 34 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 35 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 36 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 37 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 38 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 39 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 40 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 41 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 42 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 43 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 44 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 45 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 46 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 47 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 48 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 49 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 50 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 51 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 52 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 53 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 54 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 55 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 56 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 57 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 58 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 59 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |
| 60 | 0 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 | 0 |

| | | | |
|----|---|---|-------------------------------|
| 1 | | | |
| 2 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 3 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 4 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 5 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 6 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 7 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 8 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 9 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 10 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 11 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 12 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 13 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 14 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 15 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 16 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 17 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 18 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 19 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 20 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 21 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 22 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 23 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 24 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 25 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 26 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 27 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 28 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 29 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 30 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 31 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 32 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 33 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 34 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 35 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 36 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 37 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 38 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 39 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 40 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 41 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 42 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 43 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 44 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 45 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 46 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 47 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 48 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 49 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 50 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 51 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 52 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 53 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 54 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 55 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 56 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 57 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 58 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 59 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| 60 | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |
| | 0 | 0 | 0 GO:0005515 AT2G26180.1 IQD6 |

| | | | | | |
|----|---------|----------|---|-----------------------------|---|
| 1 | | | | | |
| 2 | 0 | 0 | 0 | GO:0005515 AT2G26180.1 IQD6 | |
| 3 | 0 | 0 | 0 | GO:0005515 AT2G26180.1 IQD6 | |
| 4 | 0 | 0 | 0 | GO:0005515 AT2G26180.1 IQD6 | |
| 5 | 0 | 0 | 0 | GO:0005515 AT2G26180.1 IQD6 | |
| 6 | 0 | 0 | 0 | GO:0005515 AT2G26180.1 IQD6 | |
| 7 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 8 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 9 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 10 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 11 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 12 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 13 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 14 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 15 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 16 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 17 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 18 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 19 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 20 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 21 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 22 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 23 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 24 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 25 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 26 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 27 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 28 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 29 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 30 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 31 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 32 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 33 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 34 | 0 | 0 | 0 | AT3G15390.1 SDE5 | |
| 35 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 36 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 37 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 38 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 39 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 40 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 41 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 42 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 43 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 44 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 45 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 46 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 47 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 48 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 49 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 50 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 51 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 52 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 53 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 54 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 55 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 56 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 57 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 58 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 59 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| 60 | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |
| | KOG0995 | 0 K11547 | 0 | AT3G54630.1 | 0 |

| | | | | | |
|----|---------|---|--------------|-------------|---|
| 1 | | | | | |
| 2 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 3 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 4 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 5 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 6 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 7 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 8 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 9 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 10 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 11 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 12 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 13 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 14 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 15 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 16 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 17 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 18 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 19 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 20 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 21 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 22 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 23 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 24 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 25 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 26 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 27 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 28 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 29 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 30 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 31 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 32 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 33 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 34 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 35 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 36 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 37 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 38 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 39 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 40 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 41 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 42 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 43 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 44 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 45 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 46 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 47 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 48 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 49 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 50 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 51 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 52 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 53 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 54 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 55 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 56 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 57 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 58 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 59 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| 60 | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |
| | KOG3427 | 0 | 0 GO:0005515 | AT2G41020.1 | 0 |

| | | | | | |
|----|---------|---|---|------------------------|---|
| 1 | | | | | |
| 2 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 3 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 4 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 5 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 6 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 7 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 8 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 9 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 10 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 11 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 12 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 13 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 14 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 15 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 16 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 17 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 18 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 19 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 20 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 21 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 22 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 23 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 24 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 25 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 26 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 27 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 28 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 29 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 30 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 31 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 32 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 33 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 34 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 35 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 36 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 37 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 38 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 39 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 40 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 41 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 42 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 43 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 44 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 45 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 46 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 47 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 48 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 49 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 50 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 51 | KOG3427 | 0 | 0 | GO:0005515 AT2G41020.1 | 0 |
| 52 | KOG2674 | 0 | 0 | AT2G44140.1 | 0 |
| 53 | KOG2674 | 0 | 0 | AT2G44140.1 | 0 |
| 54 | KOG2674 | 0 | 0 | AT2G44140.1 | 0 |
| 55 | KOG2674 | 0 | 0 | AT2G44140.1 | 0 |
| 56 | KOG2674 | 0 | 0 | AT2G44140.1 | 0 |
| 57 | KOG2674 | 0 | 0 | AT2G44140.1 | 0 |
| 58 | KOG2674 | 0 | 0 | AT2G44140.1 | 0 |
| 59 | KOG2674 | 0 | 0 | AT2G44140.1 | 0 |
| 60 | KOG2674 | 0 | 0 | AT2G44140.1 | 0 |
| | KOG2674 | 0 | 0 | AT2G44140.1 | 0 |

| | | | | | |
|----|----------------------|---|---|-------------------------------|---|
| 1 | | | | | |
| 2 | KOG2674 | 0 | 0 | 0 AT2G44140.1 | 0 |
| 3 | KOG2674 | 0 | 0 | 0 AT2G44140.1 | 0 |
| 4 | KOG2674 | 0 | 0 | 0 AT2G44140.1 | 0 |
| 5 | KOG2674 | 0 | 0 | 0 AT2G44140.1 | 0 |
| 6 | KOG2674 | 0 | 0 | 0 AT2G44140.1 | 0 |
| 7 | KOG2674 | 0 | 0 | 0 AT2G44140.1 | 0 |
| 8 | KOG2674 | 0 | 0 | 0 AT2G44140.1 | 0 |
| 9 | KOG2674 | 0 | 0 | 0 AT2G44140.1 | 0 |
| 10 | KOG2674 | 0 | 0 | 0 AT2G44140.1 | 0 |
| 11 | KOG2674 | 0 | 0 | 0 AT2G44140.1 | 0 |
| 12 | KOG2674 | 0 | 0 | 0 AT2G44140.1 | 0 |
| 13 | KOG2674 | 0 | 0 | 0 AT2G44140.1 | 0 |
| 14 | KOG2674 | 0 | 0 | 0 AT2G44140.1 | 0 |
| 15 | KOG2674 | 0 | 0 | 0 AT2G44140.1 | 0 |
| 16 | KOG2674 | 0 | 0 | 0 AT2G44140.1 | 0 |
| 17 | KOG2674 | 0 | 0 | 0 AT2G44140.1 | 0 |
| 18 | KOG2674 | 0 | 0 | 0 AT2G44140.1 | 0 |
| 19 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 20 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 21 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 22 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 23 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 24 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 25 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 26 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 27 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 28 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 29 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 30 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 31 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 32 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 33 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 34 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 35 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 36 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 37 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 38 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 39 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 40 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 41 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 42 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 43 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 44 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 45 | 0 | 0 | 0 | 0 AT2G37660.1 | 0 |
| 46 | | | | | |
| 47 | 0 PROLINE-MUL K12657 | | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 48 | 0 PROLINE-MUL K12657 | | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 49 | 0 PROLINE-MUL K12657 | | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 50 | 0 PROLINE-MUL K12657 | | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 51 | 0 PROLINE-MUL K12657 | | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 52 | 0 PROLINE-MUL K12657 | | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 53 | 0 PROLINE-MUL K12657 | | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 54 | 0 PROLINE-MUL K12657 | | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 55 | 0 PROLINE-MUL K12657 | | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 56 | 0 PROLINE-MUL K12657 | | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 57 | 0 PROLINE-MUL K12657 | | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 58 | 0 PROLINE-MUL K12657 | | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 59 | 0 PROLINE-MUL K12657 | | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 60 | 0 PROLINE-MUL K12657 | | | GO:0055114,(AT3G55610.1 P5CS2 | |
| | 0 PROLINE-MUL K12657 | | | GO:0055114,(AT3G55610.1 P5CS2 | |

| | | | | | |
|----|---------|----------------------|---|----------------------------------|---|
| 1 | | | | | |
| 2 | | 0 PROLINE-MUL K12657 | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 3 | | 0 PROLINE-MUL K12657 | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 4 | | 0 PROLINE-MUL K12657 | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 5 | | 0 PROLINE-MUL K12657 | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 6 | | 0 PROLINE-MUL K12657 | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 7 | | 0 PROLINE-MUL K12657 | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 8 | | 0 PROLINE-MUL K12657 | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 9 | | 0 PROLINE-MUL K12657 | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 10 | | 0 PROLINE-MUL K12657 | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 11 | | 0 PROLINE-MUL K12657 | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 12 | | 0 PROLINE-MUL K12657 | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 13 | | 0 PROLINE-MUL K12657 | | GO:0055114,(AT3G55610.1 P5CS2 | |
| 14 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 15 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 16 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 17 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 18 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 19 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 20 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 21 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 22 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 23 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 24 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 25 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 26 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 27 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 28 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 29 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 30 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 31 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 32 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 33 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 34 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 35 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 36 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 37 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 38 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 39 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 40 | KOG3470 | 0 K17292 | | GO:0051082,(AT2G30410.2 KIS,TFCA | |
| 41 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| 42 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| 43 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| 44 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| 45 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| 46 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| 47 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| 48 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| 49 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| 50 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| 51 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| 52 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| 53 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| 54 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| 55 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| 56 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| 57 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| 58 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| 59 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| 60 | | 0 | 0 | 0 AT5G48310.1 | 0 |
| | | 0 | 0 | 0 AT5G48310.1 | 0 |

| | | | | | |
|----|---|---|---|---------------|---|
| 1 | | | | | |
| 2 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 3 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 4 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 5 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 6 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 7 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 8 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 9 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 10 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 11 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 12 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 13 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 14 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 15 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 16 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 17 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 18 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 19 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 20 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 21 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 22 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 23 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 24 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 25 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 26 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 27 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 28 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 29 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 30 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 31 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 32 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 33 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 34 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 35 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 36 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 37 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 38 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 39 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 40 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 41 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 42 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 43 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 44 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 45 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 46 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 47 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 48 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 49 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 50 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 51 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 52 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 53 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 54 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 55 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 56 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 57 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 58 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 59 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 60 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |

| | | | | | |
|----|------------|--------|---|---------------|---|
| 1 | | | | | |
| 2 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 3 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 4 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 5 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 6 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 7 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 8 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 9 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 10 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 11 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 12 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 13 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 14 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 15 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 16 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 17 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 18 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 19 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 20 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 21 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 22 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 23 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 24 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 25 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 26 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 27 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 28 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 29 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 30 | 0 | 0 | 0 | 0 AT5G48310.1 | 0 |
| 31 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 32 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 33 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 34 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 35 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 36 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 37 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 38 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 39 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 40 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 41 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 42 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 43 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 44 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 45 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 46 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 47 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 48 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 49 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 50 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 51 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 52 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 53 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 54 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 55 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 56 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 57 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 58 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 59 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| 60 | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |
| | 0 3.2.1.22 | K07407 | | 0 AT3G56310.1 | 0 |

| | | | | | | |
|----|---|----------|--------|------------|--------------------|---|
| 1 | | | | | | |
| 2 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 3 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 4 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 5 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 6 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 7 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 8 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 9 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 10 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 11 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 12 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 13 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 14 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 15 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 16 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 17 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 18 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 19 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 20 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 21 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 22 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 23 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 24 | 0 | 3.2.1.22 | K07407 | 0 | AT3G56310.1 | 0 |
| 25 | 0 | | | | | |
| 26 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 27 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 28 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 29 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 30 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 31 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 32 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 33 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 34 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 35 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 36 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 37 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 38 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 39 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 40 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 41 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 42 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 43 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 44 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 45 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 46 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 47 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 48 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 49 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 50 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 51 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 52 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 53 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 54 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 55 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 56 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 57 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 58 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 59 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| 60 | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |
| | 0 | 0 | K06195 | GO:0005515 | AT1G06110.1 SKIP16 | |

| | | | | | |
|----|---------|----------|---------------------------|-------------------------------|---|
| 1 | | | | | |
| 2 | | 0 | 0 K06195 | GO:0005515 AT1G06110.1 SKIP16 | |
| 3 | | 0 | 0 K06195 | GO:0005515 AT1G06110.1 SKIP16 | |
| 4 | | 0 | 0 K06195 | GO:0005515 AT1G06110.1 SKIP16 | |
| 5 | | 0 | 0 K06195 | GO:0005515 AT1G06110.1 SKIP16 | |
| 6 | | 0 | 0 K06195 | GO:0005515 AT1G06110.1 SKIP16 | |
| 7 | | 0 | 0 K06195 | GO:0005515 AT1G06110.1 SKIP16 | |
| 8 | | 0 | 0 K06195 | GO:0005515 AT1G06110.1 SKIP16 | |
| 9 | | 0 | 0 K06195 | GO:0005515 AT1G06110.1 SKIP16 | |
| 10 | | 0 | 0 K06195 | GO:0005515 AT1G06110.1 SKIP16 | |
| 11 | | 0 | 0 K06195 | GO:0005515 AT1G06110.1 SKIP16 | |
| 12 | | 0 | 0 K06195 | GO:0005515 AT1G06110.1 SKIP16 | |
| 13 | | 0 | 0 K06195 | GO:0005515 AT1G06110.1 SKIP16 | |
| 14 | | 0 | 0 K06195 | GO:0005515 AT1G06110.1 SKIP16 | |
| 15 | | 0 | 0 K06195 | GO:0005515 AT1G06110.1 SKIP16 | |
| 16 | | 0 | 0 K06195 | GO:0005515 AT1G06110.1 SKIP16 | |
| 17 | | 0 | 0 K06195 | GO:0005515 AT1G06110.1 SKIP16 | |
| 18 | | 0 | 0 K06195 | GO:0005515 AT1G06110.1 SKIP16 | |
| 19 | | 0 | 0 K06195 | GO:0005515 AT1G06110.1 SKIP16 | |
| 20 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 21 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 22 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 23 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 24 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 25 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 26 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 27 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 28 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 29 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 30 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 31 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 32 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 33 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 34 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 35 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 36 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 37 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 38 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 39 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 40 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 41 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 42 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 43 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 44 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 45 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 46 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 47 | KOG1187 | 2.7.11.1 | 0 GO:0006468,(AT1G56720.3 | | 0 |
| 48 | | 0 | 0 | 0 AT4G10810.1 | 0 |
| 49 | | 0 | 0 | 0 AT4G10810.1 | 0 |
| 50 | | 0 | 0 | 0 AT4G10810.1 | 0 |
| 51 | | 0 | 0 | 0 AT4G10810.1 | 0 |
| 52 | | 0 | 0 | 0 AT4G10810.1 | 0 |
| 53 | | 0 | 0 | 0 AT4G10810.1 | 0 |
| 54 | | 0 | 0 | 0 AT4G10810.1 | 0 |
| 55 | | 0 | 0 | 0 AT4G10810.1 | 0 |
| 56 | | 0 | 0 | 0 AT4G10810.1 | 0 |
| 57 | | 0 | 0 | 0 AT4G10810.1 | 0 |
| 58 | | 0 | 0 | 0 AT4G10810.1 | 0 |
| 59 | | 0 | 0 | 0 AT4G10810.1 | 0 |
| 60 | | 0 | 0 | 0 AT4G10810.1 | 0 |
| | | 0 | 0 | 0 AT4G10810.1 | 0 |

| | | | | | |
|----|---------|----------|---|---|-------------------------|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 | 0 AT4G10810.1 |
| 3 | | 0 | 0 | 0 | 0 AT4G10810.1 |
| 4 | | 0 | 0 | 0 | 0 AT4G10810.1 |
| 5 | | 0 | 0 | 0 | 0 AT4G10810.1 |
| 6 | | 0 | 0 | 0 | 0 AT4G10810.1 |
| 7 | | 0 | 0 | 0 | 0 AT4G10810.1 |
| 8 | | 0 | 0 | 0 | 0 AT4G10810.1 |
| 9 | | 0 | 0 | 0 | 0 AT4G10810.1 |
| 10 | | 0 | 0 | 0 | 0 AT4G10810.1 |
| 11 | | 0 | 0 | 0 | 0 AT4G10810.1 |
| 12 | | 0 | 0 | 0 | 0 AT4G10810.1 |
| 13 | | 0 | 0 | 0 | 0 AT4G10810.1 |
| 14 | | 0 | 0 | 0 | 0 AT4G10810.1 |
| 15 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 16 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 17 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 18 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 19 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 20 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 21 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 22 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 23 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 24 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 25 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 26 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 27 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 28 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 29 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 30 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 31 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 32 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 33 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 34 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 35 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 36 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 37 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 38 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 39 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 40 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 41 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 42 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT1G51940.1 |
| 43 | | 0 | 0 | 0 | GO:0046983 AT2G42280.1 |
| 44 | | 0 | 0 | 0 | GO:0046983 AT2G42280.1 |
| 45 | | 0 | 0 | 0 | GO:0046983 AT2G42280.1 |
| 46 | | 0 | 0 | 0 | GO:0046983 AT2G42280.1 |
| 47 | | 0 | 0 | 0 | GO:0046983 AT2G42280.1 |
| 48 | | 0 | 0 | 0 | GO:0046983 AT2G42280.1 |
| 49 | | 0 | 0 | 0 | GO:0046983 AT2G42280.1 |
| 50 | | 0 | 0 | 0 | GO:0046983 AT2G42280.1 |
| 51 | | 0 | 0 | 0 | GO:0046983 AT2G42280.1 |
| 52 | | 0 | 0 | 0 | GO:0046983 AT2G42280.1 |
| 53 | | 0 | 0 | 0 | GO:0046983 AT2G42280.1 |
| 54 | | 0 | 0 | 0 | GO:0046983 AT2G42280.1 |
| 55 | | 0 | 0 | 0 | GO:0046983 AT2G42280.1 |
| 56 | | 0 | 0 | 0 | GO:0046983 AT2G42280.1 |
| 57 | | 0 | 0 | 0 | GO:0046983 AT2G42280.1 |
| 58 | | 0 | 0 | 0 | GO:0046983 AT2G42280.1 |
| 59 | | 0 | 0 | 0 | GO:0046983 AT2G42280.1 |
| 60 | | 0 | 0 | 0 | GO:0046983 AT2G42280.1 |
| | | 0 | 0 | 0 | GO:0046983 AT2G42280.1 |

| | | | | | |
|----|---|---|---------------------------|-------------|---|
| 1 | | | | | |
| 2 | 0 | 0 | 0 GO:0046983 | AT2G42280.1 | 0 |
| 3 | 0 | 0 | 0 GO:0046983 | AT2G42280.1 | 0 |
| 4 | 0 | 0 | 0 GO:0046983 | AT2G42280.1 | 0 |
| 5 | 0 | 0 | 0 GO:0046983 | AT2G42280.1 | 0 |
| 6 | 0 | 0 | 0 GO:0046983 | AT2G42280.1 | 0 |
| 7 | 0 | 0 | 0 GO:0046983 | AT2G42280.1 | 0 |
| 8 | 0 | 0 | 0 GO:0046983 | AT2G42280.1 | 0 |
| 9 | 0 | 0 | 0 GO:0046983 | AT2G42280.1 | 0 |
| 10 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 11 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 12 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 13 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 14 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 15 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 16 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 17 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 18 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 19 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 20 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 21 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 22 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 23 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 24 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 25 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 26 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 27 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 28 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 29 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 30 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 31 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 32 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 33 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 34 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 35 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 36 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 37 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 38 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 39 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 40 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 41 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 42 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 43 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 44 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 45 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 46 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 47 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 48 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 49 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 50 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 51 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 52 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 53 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 54 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 55 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 56 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 57 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 58 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 59 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 60 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |

| | | | | | |
|----|---------|---|---------------------------|--------------------|---|
| 1 | | | | | |
| 2 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 3 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 4 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 5 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 6 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 7 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 8 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 9 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 10 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 11 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 12 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 13 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 14 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 15 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 16 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 17 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 18 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 19 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 20 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 21 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 22 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 23 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 24 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 25 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 26 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 27 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 28 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 29 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 30 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 31 | 0 | 0 | 0 GO:0005515,(AT1G67310.1 | | 0 |
| 32 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 33 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 34 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 35 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 36 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 37 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 38 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 39 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 40 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 41 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 42 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 43 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 44 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 45 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 46 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 47 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 48 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 49 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 50 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 51 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 52 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 53 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 54 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 55 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 56 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 57 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 58 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 59 | 0 | 0 | 0 | 0 AT2G35230.1 IKU1 | |
| 60 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |

| | | | | | |
|----|---------|---|---|---------------|---|
| 1 | | | | | |
| 2 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 3 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 4 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 5 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 6 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 7 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 8 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 9 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 10 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 11 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 12 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 13 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 14 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 15 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 16 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 17 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 18 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 19 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 20 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 21 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 22 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 23 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 24 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 25 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 26 | KOG2197 | 0 | 0 | 0 AT3G49350.1 | 0 |
| 27 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 28 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 29 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 30 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 31 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 32 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 33 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 34 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 35 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 36 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 37 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 38 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 39 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 40 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 41 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 42 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 43 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 44 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 45 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 46 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 47 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 48 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 49 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 50 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 51 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 52 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 53 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 54 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 55 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 56 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 57 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 58 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 59 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 60 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |

| | | | | | |
|----|---------|-------------|---|----------------------------------|---|
| 1 | | | | | |
| 2 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 3 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 4 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 5 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 6 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 7 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 8 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 9 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 10 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 11 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 12 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 13 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 14 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 15 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 16 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 17 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 18 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 19 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 20 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 21 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 22 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 23 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 24 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 25 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 26 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 27 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 28 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 29 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 30 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 31 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 32 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 33 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 34 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 35 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 36 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 37 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 38 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 39 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 40 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 41 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 42 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 43 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 44 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 45 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 46 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 47 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 48 | KOG4172 | 0 | 0 | 0 AT2G35330.1 | 0 |
| 49 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | |
| 50 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | |
| 51 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | |
| 52 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | |
| 53 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | |
| 54 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | |
| 55 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | |
| 56 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | |
| 57 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | |
| 58 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | |
| 59 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | |
| 60 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | |
| | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | |

| | | | | | | |
|----|---------|-------------|---|----------------------------------|-------------|---|
| 1 | | | | | | |
| 2 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | | |
| 3 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | | |
| 4 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | | |
| 5 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | | |
| 6 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | | |
| 7 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | | |
| 8 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | | |
| 9 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | | |
| 10 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | | |
| 11 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | | |
| 12 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | | |
| 13 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | | |
| 14 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | | |
| 15 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26330.1 CYP71B37 | | |
| 16 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 17 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 18 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 19 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 20 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 21 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 22 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 23 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 24 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 25 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 26 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 27 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 28 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 29 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 30 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 31 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 32 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 33 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 34 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 35 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 36 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 37 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 38 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 39 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 40 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 41 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 42 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 43 | KOG0156 | 1.14.13.121 | 0 | GO:0055114,(AT3G26300.1 CYP71B34 | | |
| 44 | | 0 | 0 | 0 | AT5G47380.1 | 0 |
| 45 | | 0 | 0 | 0 | AT5G47380.1 | 0 |
| 46 | | 0 | 0 | 0 | AT5G47380.1 | 0 |
| 47 | | 0 | 0 | 0 | AT5G47380.1 | 0 |
| 48 | | 0 | 0 | 0 | AT5G47380.1 | 0 |
| 49 | | 0 | 0 | 0 | AT5G47380.1 | 0 |
| 50 | | 0 | 0 | 0 | AT5G47380.1 | 0 |
| 51 | | 0 | 0 | 0 | AT5G47380.1 | 0 |
| 52 | | 0 | 0 | 0 | AT5G47380.1 | 0 |
| 53 | | 0 | 0 | 0 | AT5G47380.1 | 0 |
| 54 | | 0 | 0 | 0 | AT5G47380.1 | 0 |
| 55 | | 0 | 0 | 0 | AT5G47380.1 | 0 |
| 56 | | 0 | 0 | 0 | AT5G47380.1 | 0 |
| 57 | | 0 | 0 | 0 | AT5G47380.1 | 0 |
| 58 | | 0 | 0 | 0 | AT5G47380.1 | 0 |
| 59 | | 0 | 0 | 0 | AT5G47380.1 | 0 |
| 60 | | 0 | 0 | 0 | AT5G47380.1 | 0 |
| | | 0 | 0 | 0 | AT5G47380.1 | 0 |

| | | | | | |
|----|---------|---|---|---|---------------------------|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 | 0 AT5G47380.1 |
| 3 | | 0 | 0 | 0 | 0 AT5G47380.1 |
| 4 | | 0 | 0 | 0 | 0 AT5G47380.1 |
| 5 | | 0 | 0 | 0 | 0 AT5G47380.1 |
| 6 | | 0 | 0 | 0 | 0 AT5G47380.1 |
| 7 | | 0 | 0 | 0 | 0 AT5G47380.1 |
| 8 | | 0 | 0 | 0 | 0 AT5G47380.1 |
| 9 | | 0 | 0 | 0 | 0 AT5G47380.1 |
| 10 | | 0 | 0 | 0 | 0 AT5G47380.1 |
| 11 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 12 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 13 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 14 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 15 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 16 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 17 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 18 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 19 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 20 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 21 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 22 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 23 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 24 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 25 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 26 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 27 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 28 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 29 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 30 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 31 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 32 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 33 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 34 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 35 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 36 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 37 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 38 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 39 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 40 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 41 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 42 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 43 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 44 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 45 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 46 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 47 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 48 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 49 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 50 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 51 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 52 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 53 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 54 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 55 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 56 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 57 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 58 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 59 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| 60 | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |
| | KOG2647 | | 0 | 0 | 0 GO:0006506,(AT1G11880.1 |

| | | | | | |
|----|---------|---|--------|-----------------------------|---|
| 1 | | | | | |
| 2 | KOG2647 | 0 | 0 | GO:0006506,(AT1G11880.1 | 0 |
| 3 | KOG2647 | 0 | 0 | GO:0006506,(AT1G11880.1 | 0 |
| 4 | KOG2647 | 0 | 0 | GO:0006506,(AT1G11880.1 | 0 |
| 5 | | | | | |
| 6 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 7 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 8 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 9 | | | | | |
| 10 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 11 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 12 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 13 | | | | | |
| 14 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 15 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 16 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 17 | | | | | |
| 18 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 19 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 20 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 21 | | | | | |
| 22 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 23 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 24 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 25 | | | | | |
| 26 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 27 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 28 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 29 | | | | | |
| 30 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 31 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 32 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 33 | | | | | |
| 34 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 35 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 36 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 37 | | | | | |
| 38 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 39 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 40 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 41 | | | | | |
| 42 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 43 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 44 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 45 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 46 | | | | | |
| 47 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 48 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 49 | | | | | |
| 50 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 51 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 52 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 53 | | | | | |
| 54 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 55 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 56 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 57 | | | | | |
| 58 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 59 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| 60 | KOG0265 | 0 | K16240 | GO:0005515 AT4G11110.1 SPA2 | |
| | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |

| | | | | | |
|----|---------|----------|---|---------------------|---|
| 1 | | | | | |
| 2 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 3 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 4 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 5 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 6 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 7 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 8 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 9 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 10 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 11 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 12 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 13 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 14 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 15 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 16 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 17 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 18 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 19 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 20 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 21 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 22 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 23 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 24 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 25 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 26 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 27 | 0 | 0 | 0 | 0 AT4G21720.1 | 0 |
| 28 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 29 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 30 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 31 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 32 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 33 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 34 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 35 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 36 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 37 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 38 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 39 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 40 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 41 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 42 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 43 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 44 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 45 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 46 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 47 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 48 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 49 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 50 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 51 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 52 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 53 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 54 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 55 | KOG0001 | 0 K08770 | | 0 AT4G05320.2 UBQ10 | |
| 56 | 0 | 0 K14794 | | 0 AT2G34357.1 | 0 |
| 57 | 0 | 0 K14794 | | 0 AT2G34357.1 | 0 |
| 58 | 0 | 0 K14794 | | 0 AT2G34357.1 | 0 |
| 59 | 0 | 0 K14794 | | 0 AT2G34357.1 | 0 |
| 60 | 0 | 0 K14794 | | 0 AT2G34357.1 | 0 |
| | 0 | 0 K14794 | | 0 AT2G34357.1 | 0 |

| | | | | |
|----|---|----------|--|---|
| 1 | | | | |
| 2 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 3 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 4 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 5 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 6 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 7 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 8 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 9 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 10 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 11 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 12 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 13 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 14 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 15 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 16 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 17 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 18 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 19 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 20 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 21 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 22 | 0 | 0 K14794 | 0 AT2G34357.1 | 0 |
| 23 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 24 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 25 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 26 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 27 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 28 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 29 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 30 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 31 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 32 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 33 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 34 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 35 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 36 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 37 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 38 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 39 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 40 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 41 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 42 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 43 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 44 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 45 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 46 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 47 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 48 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 49 | 0 | 0 | 0 GO:0046983 AT5G56960.1 | 0 |
| 50 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE | 0 |
| 51 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE | 0 |
| 52 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE | 0 |
| 53 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE | 0 |
| 54 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE | 0 |
| 55 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE | 0 |
| 56 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE | 0 |
| 57 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE | 0 |
| 58 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE | 0 |
| 59 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE | 0 |
| 60 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE | 0 |

| | | | |
|----|------------|---|--|
| 1 | | | |
| 2 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 3 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 4 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 5 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 6 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 7 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 8 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 9 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 10 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 11 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 12 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 13 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 14 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 15 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 16 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 17 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 18 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 19 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 20 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 21 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 22 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 23 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 24 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 25 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 26 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 27 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 28 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 29 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 30 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 31 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 32 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 33 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 34 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 35 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 36 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 37 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 38 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 39 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 40 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 41 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 42 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 43 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 44 | 0 | 0 | 0 GO:0055114,(AT5G57800.1 CER3,FLP1,WAX2,YRE |
| 45 | 0 1.10.3.3 | | 0 GO:0055114,(AT4G12420.2 SKU5 |
| 46 | 0 1.10.3.3 | | 0 GO:0055114,(AT4G12420.2 SKU5 |
| 47 | 0 1.10.3.3 | | 0 GO:0055114,(AT4G12420.2 SKU5 |
| 48 | 0 1.10.3.3 | | 0 GO:0055114,(AT4G12420.2 SKU5 |
| 49 | 0 1.10.3.3 | | 0 GO:0055114,(AT4G12420.2 SKU5 |
| 50 | 0 1.10.3.3 | | 0 GO:0055114,(AT4G12420.2 SKU5 |
| 51 | 0 1.10.3.3 | | 0 GO:0055114,(AT4G12420.2 SKU5 |
| 52 | 0 1.10.3.3 | | 0 GO:0055114,(AT4G12420.2 SKU5 |
| 53 | 0 1.10.3.3 | | 0 GO:0055114,(AT4G12420.2 SKU5 |
| 54 | 0 1.10.3.3 | | 0 GO:0055114,(AT4G12420.2 SKU5 |
| 55 | 0 1.10.3.3 | | 0 GO:0055114,(AT4G12420.2 SKU5 |
| 56 | 0 1.10.3.3 | | 0 GO:0055114,(AT4G12420.2 SKU5 |
| 57 | 0 1.10.3.3 | | 0 GO:0055114,(AT4G12420.2 SKU5 |
| 58 | 0 1.10.3.3 | | 0 GO:0055114,(AT4G12420.2 SKU5 |
| 59 | 0 1.10.3.3 | | 0 GO:0055114,(AT4G12420.2 SKU5 |
| 60 | 0 1.10.3.3 | | 0 GO:0055114,(AT4G12420.2 SKU5 |
| | 0 1.10.3.3 | | 0 GO:0055114,(AT4G12420.2 SKU5 |

| | | | | |
|----|--------------|----------|--|---|
| 1 | | | | |
| 2 | 0 3.1.3.48 | | 0 GO:0004725 AT2G35320.1 ATEYA,EYA | |
| 3 | 0 3.1.3.48 | | 0 GO:0004725 AT2G35320.1 ATEYA,EYA | |
| 4 | 0 3.1.3.48 | | 0 GO:0004725 AT2G35320.1 ATEYA,EYA | |
| 5 | 0 3.1.3.48 | | 0 GO:0004725 AT2G35320.1 ATEYA,EYA | |
| 6 | 0 3.1.3.48 | | 0 GO:0004725 AT2G35320.1 ATEYA,EYA | |
| 7 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 8 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 9 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 10 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 11 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 12 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 13 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 14 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 15 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 16 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 17 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 18 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 19 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 20 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 21 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 22 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 23 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 24 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 25 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 26 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 27 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 28 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 29 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 30 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 31 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 32 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 33 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 34 | 0 1.14.11.27 | | 0 AT5G46910.1 | 0 |
| 35 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 36 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 37 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 38 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 39 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 40 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 41 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 42 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 43 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 44 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 45 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 46 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 47 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 48 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 49 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 50 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 51 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 52 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 53 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 54 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 55 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 56 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 57 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 58 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 59 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| 60 | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |
| | KOG0498 | 0 K05391 | GO:0055085,(AT3G17700.1 ATCNGC20,CNBT1,CNG | |

| | | | | | | | |
|----|---------|-----------|--------|---|------------------------------|---|---|
| 1 | | | | | | | |
| 2 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 3 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 4 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 5 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 6 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 7 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 8 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 9 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 10 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 11 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 12 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 13 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 14 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 15 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 16 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 17 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 18 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 19 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 20 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 21 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 22 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 23 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 24 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 25 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 26 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 27 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 28 | KOG0541 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 | | |
| 29 | | | | | | | |
| 30 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 31 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 32 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 33 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 34 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 35 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 36 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 37 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 38 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 39 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 40 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 41 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 42 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 43 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 44 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 45 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 46 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 47 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 48 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 49 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 50 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 51 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 52 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 53 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 54 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 55 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 56 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 57 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1 | | | |
| 58 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1 | | | |
| 59 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1 | | | |
| 60 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 ATNLP1,CPA,NLP1 | | | |

| | | | | | | |
|----|---------|-----------|--------|-------------------------|-----------------|---|
| 1 | | | | | | |
| 2 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 3 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 4 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 5 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 6 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 7 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 8 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 9 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 10 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 11 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 12 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 13 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 14 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 15 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 16 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 17 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 18 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 19 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 20 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 21 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 22 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 23 | KOG0806 | 3.5.1.53 | K12251 | GO:0016810,(AT2G27450.1 | ATNLP1,CPA,NLP1 | |
| 24 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 25 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 26 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 27 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 28 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 29 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 30 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 31 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 32 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 33 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 34 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 35 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 36 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 37 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 38 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 39 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 40 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 41 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 42 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 43 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 44 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 45 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 46 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 47 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 48 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 49 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 50 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 51 | | 0 | 0 | 0 | 0 AT5G45480.1 | 0 |
| 52 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | | 0 |
| 53 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | | 0 |
| 54 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | | 0 |
| 55 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | | 0 |
| 56 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | | 0 |
| 57 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | | 0 |
| 58 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | | 0 |
| 59 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | | 0 |
| 60 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | | 0 |
| | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | | 0 |

| | | | | | |
|----|---------|-----------|--------|------------------------------|---|
| 1 | | | | | |
| 2 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | 0 |
| 3 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | 0 |
| 4 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | 0 |
| 5 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | 0 |
| 6 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | 0 |
| 7 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | 0 |
| 8 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | 0 |
| 9 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | 0 |
| 10 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | 0 |
| 11 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | 0 |
| 12 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | 0 |
| 13 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | 0 |
| 14 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | 0 |
| 15 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | 0 |
| 16 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | 0 |
| 17 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | 0 |
| 18 | KOG2915 | 2.1.1.220 | K07442 | GO:0031515,(AT5G14600.1 | 0 |
| 19 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 20 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 21 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 22 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 23 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 24 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 25 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 26 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 27 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 28 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 29 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 30 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 31 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 32 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 33 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 34 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 35 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 36 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 37 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 38 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 39 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 40 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 41 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 42 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 43 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 44 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 45 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 46 | | 0 1.8.1.9 | K00384 | GO:0045454,(AT2G41680.1 NTRC | |
| 47 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 48 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 49 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 50 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 51 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 52 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 53 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 54 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 55 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 56 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 57 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 58 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 59 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 60 | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| | | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |

| | | | | |
|----|-----------|--------|---------------------------|---|
| 1 | | | | |
| 2 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 3 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 4 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 5 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 6 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 7 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 8 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 9 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 10 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 11 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 12 | 0 3.6.4.4 | K10395 | GO:0008017,(AT5G60930.1 | 0 |
| 13 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 14 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 15 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 16 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 17 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 18 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 19 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 20 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 21 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 22 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 23 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 24 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 25 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 26 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 27 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 28 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 29 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 30 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 31 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 32 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 33 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 34 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 35 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 36 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 37 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 38 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 39 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 40 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 41 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 42 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 43 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 44 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 45 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 46 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 47 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 48 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 49 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 50 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 51 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 52 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 53 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 54 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 55 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 56 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 57 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 58 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 59 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 60 | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |

| | | | | | |
|----|---------|---|---|---------------------------|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 3 | | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 4 | | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 5 | | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 6 | | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 7 | | 0 | 0 | 0 GO:0010468,(AT5G64710.1 | 0 |
| 8 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 9 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 10 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 11 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 12 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 13 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 14 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 15 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 16 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 17 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 18 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 19 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 20 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 21 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 22 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 23 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 24 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 25 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 26 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 27 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 28 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 29 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 30 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 31 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 32 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 33 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 34 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 35 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 36 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 37 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 38 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 39 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 40 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 41 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 42 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 43 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 44 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 45 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 46 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 47 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 48 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 49 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 50 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 51 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 52 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 53 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 54 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 55 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 56 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 57 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 58 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 59 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| 60 | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |
| | KOG2131 | | 0 | 0 AT5G63080.1 | 0 |

| | | | | | | |
|----|---------|----------|---|-----------------------------|--|---|
| 1 | | | | | | |
| 2 | KOG2131 | 0 | 0 | 0 AT5G63080.1 | | 0 |
| 3 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 4 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 5 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 6 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 7 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 8 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 9 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 10 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 11 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 12 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 13 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 14 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 15 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 16 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 17 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 18 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 19 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 20 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 21 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 22 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 23 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 24 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 25 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 26 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 27 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 28 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 29 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 30 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 31 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 32 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 33 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 34 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 35 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 36 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 37 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 38 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 39 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 40 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 41 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 42 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 43 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 44 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 45 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 46 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 47 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 48 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 49 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 50 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 51 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 52 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 53 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 54 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 55 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 56 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 57 | KOG3882 | 0 | 0 | GO:0016021 AT4G28050.1 TET7 | | |
| 58 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | | 0 |
| 59 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | | 0 |
| 60 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | | 0 |

| | | | | | |
|----|---------|----------|----------|--|---|
| 1 | | | | | |
| 2 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 3 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 4 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 5 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 6 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 7 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 8 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 9 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 10 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 11 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 12 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 13 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 14 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 15 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 16 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 17 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 18 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 19 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 20 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 21 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 22 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 23 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 24 | KOG1187 | 2.7.11.1 | 0 | GO:0006468,(AT1G56720.3 | 0 |
| 25 | | | | | |
| 26 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 27 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 28 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 29 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 30 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 31 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 32 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 33 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 34 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 35 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 36 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 37 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 38 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 39 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 40 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 41 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 42 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 43 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 44 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 45 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 46 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 47 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 48 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 49 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 50 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 51 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 52 | | 0 | 0 K14832 | 0 AT1G72440.1 EDA25,SWA2 | |
| 53 | | 0 | 0 | 0 GO:0006355,(AT4G25470.1 ATCBF2,CBF2,DREB1C,F | |
| 54 | | 0 | 0 | 0 GO:0006355,(AT4G25470.1 ATCBF2,CBF2,DREB1C,F | |
| 55 | | 0 | 0 | 0 GO:0006355,(AT4G25470.1 ATCBF2,CBF2,DREB1C,F | |
| 56 | | 0 | 0 | 0 GO:0006355,(AT4G25470.1 ATCBF2,CBF2,DREB1C,F | |
| 57 | | 0 | 0 | 0 GO:0006355,(AT4G25470.1 ATCBF2,CBF2,DREB1C,F | |
| 58 | | 0 | 0 | 0 GO:0006355,(AT4G25470.1 ATCBF2,CBF2,DREB1C,F | |
| 59 | | 0 | 0 | 0 GO:0006355,(AT4G25470.1 ATCBF2,CBF2,DREB1C,F | |
| 60 | | 0 | 0 | 0 GO:0006355,(AT4G25470.1 ATCBF2,CBF2,DREB1C,F | |

| | | | |
|----|---------|-----------------|--------------------------------|
| 1 | | | |
| 2 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 3 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 4 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 5 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 6 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 7 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 8 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 9 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 10 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 11 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 12 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 13 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 14 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 15 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 16 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 17 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 18 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 19 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 20 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 21 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 22 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 23 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 24 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 25 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 26 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 27 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 28 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 29 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 30 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 31 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 32 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 33 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 34 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 35 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 36 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 37 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 38 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 39 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 40 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 41 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 42 | KOG1368 | 4.1.2.5,4.1.2.4 | 0 GO:0030170,(AT1G08630.4 THA1 |
| 43 | | | |
| 44 | | | |
| 45 | | | |
| 46 | | | |
| 47 | | | |
| 48 | | | |
| 49 | | | |
| 50 | | | |
| 51 | | | |
| 52 | | | |
| 53 | | | |
| 54 | | | |
| 55 | | | |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

1 Cyclin family protein Phvul.002G04PTHR10026//IPhvu.002G04Cell cycle orga cyclin (CYCT) (
2
3 Glutathione S-transferase fanPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
4
5 Glutathione S-transferase fanPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
6
7 Glutathione S-transferase fanPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
8
9 Glutathione S-transferase fanPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
10
11 Glutathione S-transferase fanPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
12
13 Glutathione S-transferase fanPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
14
15 Glutathione S-transferase fanPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
16
17 Glutathione S-transferase fanPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
18
19 Glutathione S-transferase fanPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
20
21 Glutathione S-transferase fanPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
22
23 Glutathione S-transferase fanPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
24
25 Glutathione S-transferase fanPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
26
27 Glutathione S-transferase fanPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
28
29 Glutathione S-transferase fanPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
30
31 glutathione S-transferase TALPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
32
33 glutathione S-transferase TALPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
34
35 glutathione S-transferase TALPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
36
37 glutathione S-transferase TALPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
38
39 glutathione S-transferase TALPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
40
41 glutathione S-transferase TALPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
42
43 glutathione S-transferase TALPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
44
45 glutathione S-transferase TALPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
46
47 glutathione S-transferase TALPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
48
49 glutathione S-transferase TALPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
50
51 glutathione S-transferase TALPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
52
53 glutathione S-transferase TALPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
54
55 glutathione S-transferase TALPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
56
57 glutathione S-transferase TALPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
58
59 glutathione S-transferase TALPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta
60
61 glutathione S-transferase TALPhvul.002G08PTHR11260:SIPhvu.002G08Protein modif class tau gluta

| | | | |
|----|-----------------------------|---------------------------|---|
| 1 | | | |
| 2 | | 0 | 0 |
| 3 | | 0 | 0 |
| 4 | | 0 | 0 |
| 5 | | 0 | 0 |
| 6 | | 0 | 0 |
| 7 | | 0 | 0 |
| 8 | | 0 | 0 |
| 9 | | 0 | 0 |
| 10 | | 0 | 0 |
| 11 | | 0 | 0 |
| 12 | | 0 | 0 |
| 13 | | 0 | 0 |
| 14 | | 0 | 0 |
| 15 | | 0 | 0 |
| 16 | | 0 | 0 |
| 17 | | 0 | 0 |
| 18 | | 0 | 0 |
| 19 | | 0 | 0 |
| 20 | | 0 | 0 |
| 21 | | 0 | 0 |
| 22 | | 0 | 0 |
| 23 | | 0 | 0 |
| 24 | | 0 | 0 |
| 25 | | 0 | 0 |
| 26 | | 0 | 0 |
| 27 | | 0 | 0 |
| 28 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 29 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 30 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 31 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 32 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 33 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 34 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 35 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 36 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 37 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 38 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 39 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 40 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 41 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 42 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 43 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 44 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 45 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 46 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 47 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 48 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 49 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 50 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 51 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 52 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 53 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 54 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 55 | polyubiquitin 10 | Phvul.003G12K08770 - ubiq | Phvul.003G12Protein home ubiquitin-fold |
| 56 | ARM repeat superfamily prot | Phvul.003G12PTHR21576:SI | Phvul.003G12not assigned.r no hits & (ori |
| 57 | ARM repeat superfamily prot | Phvul.003G12PTHR21576:SI | Phvul.003G12not assigned.r no hits & (ori |
| 58 | ARM repeat superfamily prot | Phvul.003G12PTHR21576:SI | Phvul.003G12not assigned.r no hits & (ori |
| 59 | ARM repeat superfamily prot | Phvul.003G12PTHR21576:SI | Phvul.003G12not assigned.r no hits & (ori |
| 60 | ARM repeat superfamily prot | Phvul.003G12PTHR21576:SI | Phvul.003G12not assigned.r no hits & (ori |

| | | |
|----|----------------------|------------------------------|
| 1 | | |
| 2 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 3 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 4 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 5 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 6 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 7 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 8 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 9 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 10 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 11 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 12 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 13 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 14 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 15 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 16 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 17 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 18 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 19 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 20 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 21 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 22 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 23 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 24 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 25 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 26 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 27 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 28 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 29 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 30 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 31 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 32 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 33 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 34 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 35 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 36 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 37 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 38 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 39 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 40 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 41 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 42 | threonine aldolase 1 | Phvul.L00206(4.1.2.5 - L-thr |
| 43 | | |
| 44 | | |
| 45 | | |
| 46 | | |
| 47 | | |
| 48 | | |
| 49 | | |
| 50 | | |
| 51 | | |
| 52 | | |
| 53 | | |
| 54 | | |
| 55 | | |
| 56 | | |
| 57 | | |
| 58 | | |
| 59 | | |
| 60 | | |

1
2 vul.004G099600.1.v2.1 annot-version=v2.1)
3 vul.004G099600.1.v2.1 annot-version=v2.1)
4 vul.004G099600.1.v2.1 annot-version=v2.1)
5 vul.004G099600.1.v2.1 annot-version=v2.1)
6 vul.004G099600.1.v2.1 annot-version=v2.1)
7 vul.004G099600.1.v2.1 annot-version=v2.1)
8 vul.004G099600.1.v2.1 annot-version=v2.1)
9 vul.004G099600.1.v2.1 annot-version=v2.1)
10 vul.004G099600.1.v2.1 annot-version=v2.1)
11 vul.004G099600.1.v2.1 annot-version=v2.1)
12 vul.004G099600.1.v2.1 annot-version=v2.1)
13 vul.004G099600.1.v2.1 annot-version=v2.1)
14 vul.004G099600.1.v2.1 annot-version=v2.1)
15 vul.004G099600.1.v2.1 annot-version=v2.1)
16 vul.004G099600.1.v2.1 annot-version=v2.1)
17 vul.004G099600.1.v2.1 annot-version=v2.1)
18 vul.004G099600.1.v2.1 annot-version=v2.1)
19 vul.004G099600.1.v2.1 annot-version=v2.1)
20 vul.004G099600.1.v2.1 annot-version=v2.1)
21 vul.004G099600.1.v2.1 annot-version=v2.1)
22 vul.004G099600.1.v2.1 annot-version=v2.1)
23 vul.004G099600.1.v2.1 annot-version=v2.1)
24 vul.004G099600.1.v2.1 annot-version=v2.1)
25 vul.006G030900.1.v2.1 annot-version=v2.1)
26 vul.006G030900.1.v2.1 annot-version=v2.1)
27 vul.006G030900.1.v2.1 annot-version=v2.1)
28 vul.006G030900.1.v2.1 annot-version=v2.1)
29 vul.006G030900.1.v2.1 annot-version=v2.1)
30 vul.006G030900.1.v2.1 annot-version=v2.1)
31 vul.006G030900.1.v2.1 annot-version=v2.1)
32 vul.006G030900.1.v2.1 annot-version=v2.1)
33 vul.006G030900.1.v2.1 annot-version=v2.1)
34 vul.006G030900.1.v2.1 annot-version=v2.1)
35 vul.006G030900.1.v2.1 annot-version=v2.1)
36 vul.006G030900.1.v2.1 annot-version=v2.1)
37 vul.006G030900.1.v2.1 annot-version=v2.1)
38 vul.006G030900.1.v2.1 annot-version=v2.1)
39 vul.006G030900.1.v2.1 annot-version=v2.1)
40 vul.006G030900.1.v2.1 annot-version=v2.1)
41 vul.006G030900.1.v2.1 annot-version=v2.1)
42 vul.006G030900.1.v2.1 annot-version=v2.1)
43 vul.006G030900.1.v2.1 annot-version=v2.1)
44 vul.006G030900.1.v2.1 annot-version=v2.1)
45 vul.006G030900.1.v2.1 annot-version=v2.1)
46 vul.006G030900.1.v2.1 annot-version=v2.1)
47 vul.006G030900.1.v2.1 annot-version=v2.1)
48 vul.006G030900.1.v2.1 annot-version=v2.1)
49 vul.006G030900.1.v2.1 annot-version=v2.1)
50 vul.006G030900.1.v2.1 annot-version=v2.1)
51 vul.006G030900.1.v2.1 annot-version=v2.1)
52 vul.006G030900.1.v2.1 annot-version=v2.1)
53 09G186300 ID=Phvul.009G186300.1.v2.1 annot-version=v2.1) &
54 09G186300 ID=Phvul.009G186300.1.v2.1 annot-version=v2.1) &
55 09G186300 ID=Phvul.009G186300.1.v2.1 annot-version=v2.1) &
56 09G186300 ID=Phvul.009G186300.1.v2.1 annot-version=v2.1) &
57 09G186300 ID=Phvul.009G186300.1.v2.1 annot-version=v2.1) &
58 09G186300 ID=Phvul.009G186300.1.v2.1 annot-version=v2.1) &
59 09G186300 ID=Phvul.009G186300.1.v2.1 annot-version=v2.1) &
60 09G186300 ID=Phvul.009G186300.1.v2.1 annot-version=v2.1) &

1 vul.010G014800.2.v2.1 annot-version=v2.1)
2 vul.010G014800.2.v2.1 annot-version=v2.1)
3 vul.010G014800.2.v2.1 annot-version=v2.1)
4 vul.010G014800.2.v2.1 annot-version=v2.1)
5 vul.010G014800.2.v2.1 annot-version=v2.1)
6 vul.010G014800.2.v2.1 annot-version=v2.1)
7 vul.010G014800.2.v2.1 annot-version=v2.1)
8 vul.010G014800.2.v2.1 annot-version=v2.1)
9 vul.010G014800.2.v2.1 annot-version=v2.1)
10 vul.010G014800.2.v2.1 annot-version=v2.1)
11 vul.010G014800.2.v2.1 annot-version=v2.1)
12 vul.010G014800.2.v2.1 annot-version=v2.1)
13 vul.010G014800.2.v2.1 annot-version=v2.1)
14 vul.010G014800.2.v2.1 annot-version=v2.1)
15 vul.010G014800.2.v2.1 annot-version=v2.1)
16 vul.010G014800.2.v2.1 annot-version=v2.1)
17 vul.010G014800.2.v2.1 annot-version=v2.1)
18 vul.010G014800.2.v2.1 annot-version=v2.1)
19 vul.010G014800.2.v2.1 annot-version=v2.1)
20 vul.010G014800.2.v2.1 annot-version=v2.1)
21 vul.010G014800.2.v2.1 annot-version=v2.1)
22 vul.010G014800.2.v2.1 annot-version=v2.1)
23 vul.010G014800.2.v2.1 annot-version=v2.1)
24 vul.010G014800.2.v2.1 annot-version=v2.1)
25 vul.010G014800.2.v2.1 annot-version=v2.1)
26 vul.010G014800.2.v2.1 annot-version=v2.1)
27 vul.010G014800.2.v2.1 annot-version=v2.1)
28 vul.010G014800.2.v2.1 annot-version=v2.1)
29 vul.010G014800.2.v2.1 annot-version=v2.1)
30 vul.010G014800.2.v2.1 annot-version=v2.1)
31 vul.010G014800.2.v2.1 annot-version=v2.1)
32 vul.010G014800.2.v2.1 annot-version=v2.1)
33 vul.010G014800.2.v2.1 annot-version=v2.1)
34 vul.010G014800.2.v2.1 annot-version=v2.1)
35 vul.010G014800.2.v2.1 annot-version=v2.1)
36 vul.010G014800.2.v2.1 annot-version=v2.1)
37 vul.010G014800.2.v2.1 annot-version=v2.1)
38 vul.010G014800.2.v2.1 annot-version=v2.1)
39 vul.010G014800.2.v2.1 annot-version=v2.1)
40 vul.010G014800.2.v2.1 annot-version=v2.1)
41 vul.010G014800.2.v2.1 annot-version=v2.1)
42 vul.010G014800.2.v2.1 annot-version=v2.1)
43 vul.010G014800.2.v2.1 annot-version=v2.1)
44 vul.010G014800.2.v2.1 annot-version=v2.1)
45 vul.010G014800.2.v2.1 annot-version=v2.1)
46 vul.010G014800.2.v2.1 annot-version=v2.1)
47 vul.010G014800.2.v2.1 annot-version=v2.1)
48 vul.010G014800.2.v2.1 annot-version=v2.1)
49 vul.010G014800.2.v2.1 annot-version=v2.1)
50 vul.010G014800.2.v2.1 annot-version=v2.1)
51 vul.010G014800.2.v2.1 annot-version=v2.1)
52 vul.010G014800.2.v2.1 annot-version=v2.1)
53 vul.010G014800.2.v2.1 annot-version=v2.1)
54 vul.010G014800.2.v2.1 annot-version=v2.1)
55 vul.010G014800.2.v2.1 annot-version=v2.1)
56 vul.010G014800.2.v2.1 annot-version=v2.1)
57 070400 ID=Phvul.010G070400.1.v2.1 annot-version=v2.1) &
58 070400 ID=Phvul.010G070400.1.v2.1 annot-version=v2.1) &
59 070400 ID=Phvul.010G070400.1.v2.1 annot-version=v2.1) &
60 070400 ID=Phvul.010G070400.1.v2.1 annot-version=v2.1) &

1
2 rsul.L002060.3.v2.1 annot-version=v2.1) &
3 rsul.L002060.3.v2.1 annot-version=v2.1) &
4 rsul.L002060.3.v2.1 annot-version=v2.1) &
5 rsul.L002060.3.v2.1 annot-version=v2.1) &
6 rsul.L002060.3.v2.1 annot-version=v2.1) &
7 rsul.L002060.3.v2.1 annot-version=v2.1) &
8 rsul.L002060.3.v2.1 annot-version=v2.1) &
9 rsul.L002060.3.v2.1 annot-version=v2.1) &
10 rsul.L002060.3.v2.1 annot-version=v2.1) &
11 rsul.L002060.3.v2.1 annot-version=v2.1) &
12 rsul.L002060.3.v2.1 annot-version=v2.1) &
13 rsul.L002060.3.v2.1 annot-version=v2.1) &
14 rsul.L002060.3.v2.1 annot-version=v2.1) &
15 rsul.L002060.3.v2.1 annot-version=v2.1) &
16 rsul.L002060.3.v2.1 annot-version=v2.1) &
17 rsul.L002060.3.v2.1 annot-version=v2.1) &
18 rsul.L002060.3.v2.1 annot-version=v2.1) &
19 rsul.L002060.3.v2.1 annot-version=v2.1) &
20 rsul.L002060.3.v2.1 annot-version=v2.1) &
21 rsul.L002060.3.v2.1 annot-version=v2.1) &
22 rsul.L002060.3.v2.1 annot-version=v2.1) &
23 rsul.L002060.3.v2.1 annot-version=v2.1) &
24 rsul.L002060.3.v2.1 annot-version=v2.1) &
25 rsul.L002060.3.v2.1 annot-version=v2.1) &
26 rsul.L002060.3.v2.1 annot-version=v2.1) &
27 rsul.L002060.3.v2.1 annot-version=v2.1) &
28 rsul.L002060.3.v2.1 annot-version=v2.1) &
29 rsul.L002060.3.v2.1 annot-version=v2.1) &
30 rsul.L002060.3.v2.1 annot-version=v2.1) &
31 rsul.L002060.3.v2.1 annot-version=v2.1) &
32 rsul.L002060.3.v2.1 annot-version=v2.1) &
33 rsul.L002060.3.v2.1 annot-version=v2.1) &
34 rsul.L002060.3.v2.1 annot-version=v2.1) &
35 rsul.L002060.3.v2.1 annot-version=v2.1) &
36 rsul.L002060.3.v2.1 annot-version=v2.1) &
37 rsul.L002060.3.v2.1 annot-version=v2.1) &
38 rsul.L002060.3.v2.1 annot-version=v2.1) &
39 rsul.L002060.3.v2.1 annot-version=v2.1) &
40 rsul.L002060.3.v2.1 annot-version=v2.1) &
41 rsul.L002060.3.v2.1 annot-version=v2.1) &
42 rsul.L002060.3.v2.1 annot-version=v2.1) &
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3 1a (sp|q9li89|fbk70_arath : 372.0)
4 1a (sp|q9li89|fbk70_arath : 372.0)
5 1a (sp|q9li89|fbk70_arath : 372.0)
6 1a (sp|q9li89|fbk70_arath : 372.0)
7 1a (sp|q9li89|fbk70_arath : 372.0)
8 1a (sp|q9li89|fbk70_arath : 372.0)
9
10 1a (sp|q9li89|fbk70_arath : 372.0)
11 1a (sp|q9li89|fbk70_arath : 372.0)
12 1a (sp|q9li89|fbk70_arath : 372.0)
13
14 1a (sp|q9li89|fbk70_arath : 372.0)
15 1a (sp|q9li89|fbk70_arath : 372.0)
16 1a (sp|q9li89|fbk70_arath : 372.0)
17
18 1a (sp|q9li89|fbk70_arath : 372.0)
19 1a (sp|q9li89|fbk70_arath : 372.0)
20 1a (sp|q9li89|fbk70_arath : 372.0)
21
22 1a (sp|q9li89|fbk70_arath : 372.0)
23 1a (sp|q9li89|fbk70_arath : 372.0)
24 1a (sp|q9li89|fbk70_arath : 372.0)
25
26 1a (sp|q9li89|fbk70_arath : 372.0)
27 1a (sp|q9li89|fbk70_arath : 372.0)
28 1a (sp|q9li89|fbk70_arath : 372.0)
29 1a (sp|q9li89|fbk70_arath : 372.0)
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1 nscript=Phvul.001G057100.4 locus=Phvul.001G057100 ID=Phvul.001G057100.4.v2.1 annot-version
2 nscript=Phvul.001G057100.4 locus=Phvul.001G057100 ID=Phvul.001G057100.4.v2.1 annot-version
3 nscript=Phvul.001G057100.4 locus=Phvul.001G057100 ID=Phvul.001G057100.4.v2.1 annot-version
4 nscript=Phvul.001G057100.4 locus=Phvul.001G057100 ID=Phvul.001G057100.4.v2.1 annot-version
5 nscript=Phvul.001G057100.4 locus=Phvul.001G057100 ID=Phvul.001G057100.4.v2.1 annot-version
6 nscript=Phvul.001G057100.4 locus=Phvul.001G057100 ID=Phvul.001G057100.4.v2.1 annot-version
7 nscript=Phvul.001G057100.4 locus=Phvul.001G057100 ID=Phvul.001G057100.4.v2.1 annot-version
8 nscript=Phvul.001G057100.4 locus=Phvul.001G057100 ID=Phvul.001G057100.4.v2.1 annot-version
9

10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2 ina (sp|q9zvt8|rf4_arath : 323.0)
3 ina (sp|q9zvt8|rf4_arath : 323.0)
4 ina (sp|q9zvt8|rf4_arath : 323.0)
5 ina (sp|q9zvt8|rf4_arath : 323.0)
6 ina (sp|q9zvt8|rf4_arath : 323.0)
7 ina (sp|q9zvt8|rf4_arath : 323.0)
8 ina (sp|q9zvt8|rf4_arath : 323.0)
9 ina (sp|q9zvt8|rf4_arath : 323.0)
10 ina (sp|q9zvt8|rf4_arath : 323.0)
11 ina (sp|q9zvt8|rf4_arath : 323.0)
12 ina (sp|q9zvt8|rf4_arath : 323.0)
13 ina (sp|q9zvt8|rf4_arath : 323.0)
14 ina (sp|q9zvt8|rf4_arath : 323.0)
15 ina (sp|q9zvt8|rf4_arath : 323.0)
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43

44 innot-version=v2.1) &
45 innot-version=v2.1) &
46 innot-version=v2.1) &
47 innot-version=v2.1) &
48 innot-version=v2.1) &
49 innot-version=v2.1) &
50 innot-version=v2.1) &
51 innot-version=v2.1) &
52 innot-version=v2.1) &
53 innot-version=v2.1) &
54 innot-version=v2.1) &
55 innot-version=v2.1) &
56 innot-version=v2.1) &
57 innot-version=v2.1) &
58 innot-version=v2.1) &
59 innot-version=v2.1) &
60 innot-version=v2.1) &
innot-version=v2.1) &

Do not distribute

1
2 innot-version=v2.1) &
3 innot-version=v2.1) &
4 innot-version=v2.1) &
5 innot-version=v2.1) &
6 innot-version=v2.1) &
7 innot-version=v2.1) &
8 innot-version=v2.1) &
9 innot-version=v2.1) &
10 innot-version=v2.1) &

Do not distribute

11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2 innot-version=v2.1) &
3 innot-version=v2.1) &
4 innot-version=v2.1) &
5 innot-version=v2.1) &
6 innot-version=v2.1) &
7 innot-version=v2.1) &
8 innot-version=v2.1) &
9 innot-version=v2.1) &
10 innot-version=v2.1) &
11 innot-version=v2.1) &
12 innot-version=v2.1) &
13 innot-version=v2.1) &
14 innot-version=v2.1) &
15 innot-version=v2.1) &
16 innot-version=v2.1) &
17 innot-version=v2.1) &
18 innot-version=v2.1) &
19 innot-version=v2.1) &
20 innot-version=v2.1) &
21 innot-version=v2.1) &
22 innot-version=v2.1) &
23 innot-version=v2.1) &
24 innot-version=v2.1) &
25 innot-version=v2.1) &
26 innot-version=v2.1) &
27 innot-version=v2.1) &
28 innot-version=v2.1) &
29 innot-version=v2.1) &
30 innot-version=v2.1) &
31 innot-version=v2.1) &
32 innot-version=v2.1) &
33 innot-version=v2.1) &
34 innot-version=v2.1) &
35 innot-version=v2.1) &
36 innot-version=v2.1) &
37 innot-version=v2.1) &
38 innot-version=v2.1) &
39 innot-version=v2.1) &
40 innot-version=v2.1) &
41 innot-version=v2.1) &
42 innot-version=v2.1) &
43 innot-version=v2.1) &
44 innot-version=v2.1) &
45 innot-version=v2.1) &
46 innot-version=v2.1) &
47 innot-version=v2.1) &
48 innot-version=v2.1) &
49 innot-version=v2.1) &
50 innot-version=v2.1) &
51 innot-version=v2.1) &
52 innot-version=v2.1) &
53 innot-version=v2.1) &
54 innot-version=v2.1) &
55 innot-version=v2.1) &
56 innot-version=v2.1) &
57 innot-version=v2.1) &
58 innot-version=v2.1) &
59 innot-version=v2.1) &
60 innot-version=v2.1) &
innot-version=v2.1) &

Do not distribute

1
2 innot-version=v2.1) &
3 innot-version=v2.1) &
4 innot-version=v2.1) &
5 innot-version=v2.1) &
6 innot-version=v2.1) &
7 innot-version=v2.1) &
8 innot-version=v2.1) &
9 innot-version=v2.1) &
10 innot-version=v2.1) &
11 innot-version=v2.1) &
12 innot-version=v2.1) &
13 innot-version=v2.1) &
14 innot-version=v2.1) &
15 innot-version=v2.1) &
16 innot-version=v2.1) &
17 innot-version=v2.1) &
18 innot-version=v2.1) &
19 innot-version=v2.1) &
20 innot-version=v2.1) &
21 innot-version=v2.1) &
22 innot-version=v2.1) &
23 innot-version=v2.1) &
24 innot-version=v2.1) &
25 innot-version=v2.1) &
26 innot-version=v2.1) &
27 innot-version=v2.1) &
28 innot-version=v2.1) &
29 innot-version=v2.1) &
30 innot-version=v2.1) &
31 innot-version=v2.1) &
32 innot-version=v2.1) &
33 innot-version=v2.1) &
34 innot-version=v2.1) &
35 innot-version=v2.1) &
36 innot-version=v2.1) &
37 innot-version=v2.1) &
38 innot-version=v2.1) &
39 innot-version=v2.1) &
40 innot-version=v2.1) &
41 innot-version=v2.1) &
42 innot-version=v2.1) &
43 innot-version=v2.1) &
44 innot-version=v2.1) &
45 innot-version=v2.1) &
46 innot-version=v2.1) &
47 innot-version=v2.1) &
48 innot-version=v2.1) &
49 innot-version=v2.1) &
50 innot-version=v2.1) &
51 innot-version=v2.1) &
52 innot-version=v2.1) &
53 innot-version=v2.1) &
54 innot-version=v2.1) &
55 innot-version=v2.1) &
56 innot-version=v2.1) &
57 innot-version=v2.1) &
58 innot-version=v2.1) &
59 innot-version=v2.1) &
60 innot-version=v2.1) &

Do not distribute

1
2 innot-version=v2.1) &
3 innot-version=v2.1) &
4 innot-version=v2.1) &
5 innot-version=v2.1) &
6 innot-version=v2.1) &
7 innot-version=v2.1) &
8 innot-version=v2.1) &
9 innot-version=v2.1) &
10 innot-version=v2.1) &
11 innot-version=v2.1) &
12 innot-version=v2.1) &
13 innot-version=v2.1) &
14 innot-version=v2.1) &
15 innot-version=v2.1) &
16 innot-version=v2.1) &
17 innot-version=v2.1) &
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44

45 rdsa : 399.0)
46 rdsa : 399.0)
47 rdsa : 399.0)
48 rdsa : 399.0)
49 rdsa : 399.0)
50 rdsa : 399.0)
51 rdsa : 399.0)
52 rdsa : 399.0)
53 rdsa : 399.0)
54 rdsa : 399.0)
55 rdsa : 399.0)
56 rdsa : 399.0)
57 rdsa : 399.0)
58 rdsa : 399.0)
59 rdsa : 399.0)
60 rdsa : 399.0)
rdsa : 399.0)

Do not distribute

1
2 rdsa : 399.0)
3 rdsa : 399.0)
4 rdsa : 399.0)
5 rdsa : 399.0)
6 rdsa : 399.0)
7 rdsa : 399.0)
8 rdsa : 399.0)
9 rdsa : 399.0)
10 rdsa : 399.0)
11 rdsa : 399.0)
12 innot-version=v2.1) &
13 innot-version=v2.1) &
14 innot-version=v2.1) &
15 innot-version=v2.1) &
16 innot-version=v2.1) &
17 innot-version=v2.1) &
18 innot-version=v2.1) &
19 innot-version=v2.1) &
20 innot-version=v2.1) &
21 innot-version=v2.1) &
22 innot-version=v2.1) &
23 innot-version=v2.1) &
24 innot-version=v2.1) &
25 innot-version=v2.1) &
26 innot-version=v2.1) &
27 innot-version=v2.1) &
28 innot-version=v2.1) &
29 innot-version=v2.1) &
30 innot-version=v2.1) &
31 innot-version=v2.1) &
32 innot-version=v2.1) &
33 innot-version=v2.1) &
34 innot-version=v2.1) &
35 innot-version=v2.1) &
36 innot-version=v2.1) &
37 innot-version=v2.1) &
38 innot-version=v2.1) &
39 innot-version=v2.1) &
40 innot-version=v2.1) &
41 innot-version=v2.1) &
42 innot-version=v2.1) &
43 innot-version=v2.1) &
44 innot-version=v2.1) &
45 innot-version=v2.1) &
46 innot-version=v2.1) &
47 innot-version=v2.1) &
48 innot-version=v2.1) &
49 innot-version=v2.1) &
50 innot-version=v2.1) &
51 innot-version=v2.1) &
52 innot-version=v2.1) &
53 innot-version=v2.1) &
54 innot-version=v2.1) &
55 innot-version=v2.1) &
56 innot-version=v2.1) &
57 innot-version=v2.1) &
58 innot-version=v2.1) &
59 innot-version=v2.1) &
60 innot-version=v2.1) &
innot-version=v2.1) &

Do not distribute

1
2 innot-version=v2.1) &
3 innot-version=v2.1) &
4 innot-version=v2.1) &
5 innot-version=v2.1) &
6 innot-version=v2.1) &
7 innot-version=v2.1) &
8 innot-version=v2.1) &
9 innot-version=v2.1) &
10 innot-version=v2.1) &
11 innot-version=v2.1) &
12 innot-version=v2.1) &
13 innot-version=v2.1) &
14 innot-version=v2.1) &
15 innot-version=v2.1) &
16 innot-version=v2.1) &
17 innot-version=v2.1) &
18 innot-version=v2.1) &
19 innot-version=v2.1) &
20 innot-version=v2.1) &
21 innot-version=v2.1) &
22 innot-version=v2.1) &
23 innot-version=v2.1) &
24 innot-version=v2.1) &
25 innot-version=v2.1) &
26 innot-version=v2.1) &
27 innot-version=v2.1) &
28 innot-version=v2.1) &
29 innot-version=v2.1) &
30 innot-version=v2.1) &
31 innot-version=v2.1) &
32 innot-version=v2.1) &
33 innot-version=v2.1) &
34 innot-version=v2.1) &
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2 5h677|exb14_orysj : 290.0)
3 5h677|exb14_orysj : 290.0)
4 5h677|exb14_orysj : 290.0)
5 5h677|exb14_orysj : 290.0)
6 5h677|exb14_orysj : 290.0)
7 5h677|exb14_orysj : 290.0)
8 5h677|exb14_orysj : 290.0)
9

10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2 1 annot-version=v2.1) &
3 1 annot-version=v2.1) &
4 1 annot-version=v2.1) &
5 1 annot-version=v2.1) &
6 1 annot-version=v2.1) &
7 1 annot-version=v2.1) &
8 1 annot-version=v2.1) &
9 1 annot-version=v2.1) &
10 1 annot-version=v2.1) &
11 1 annot-version=v2.1) &
12 1 annot-version=v2.1) &
13 1 annot-version=v2.1) &
14 1 annot-version=v2.1) &
15 1 annot-version=v2.1) &
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
7 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
8 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
9 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
10 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
11 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
12 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
13 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
14 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
15 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
16 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
17 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
18 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
19 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
20 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
21 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
22 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
23 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
24 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
25 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
26 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
27 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
28 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
29 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
30 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
31 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
32 34.6) (original description: pacid=37147731 transcript=Phvul.003G113500.1 locus=Phvul.003G1135
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

aliana (sp|q9fyq8|tmn11_arath : 1113.0)

1
2 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
3 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
4 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
5 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
6 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
7 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
8 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
9 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
10 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
11 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
12 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
13 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
14 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
15 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
16 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
17 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
18 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
19 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
20 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
21 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
22 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
23 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
24 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
25 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
26 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
27 aliana (sp|q9fyq8|tmn11_arath : 1113.0)
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7 ana (sp|q9luq3|sde5_arath : 224.0)
8 ana (sp|q9luq3|sde5_arath : 224.0)
9 ana (sp|q9luq3|sde5_arath : 224.0)
10 ana (sp|q9luq3|sde5_arath : 224.0)
11 ana (sp|q9luq3|sde5_arath : 224.0)
12 ana (sp|q9luq3|sde5_arath : 224.0)
13 ana (sp|q9luq3|sde5_arath : 224.0)
14 ana (sp|q9luq3|sde5_arath : 224.0)
15 ana (sp|q9luq3|sde5_arath : 224.0)
16 ana (sp|q9luq3|sde5_arath : 224.0)
17 ana (sp|q9luq3|sde5_arath : 224.0)
18 ana (sp|q9luq3|sde5_arath : 224.0)
19 ana (sp|q9luq3|sde5_arath : 224.0)
20 ana (sp|q9luq3|sde5_arath : 224.0)
21 ana (sp|q9luq3|sde5_arath : 224.0)
22 ana (sp|q9luq3|sde5_arath : 224.0)
23 ana (sp|q9luq3|sde5_arath : 224.0)
24 ana (sp|q9luq3|sde5_arath : 224.0)
25 ana (sp|q9luq3|sde5_arath : 224.0)
26 ana (sp|q9luq3|sde5_arath : 224.0)
27 ana (sp|q9luq3|sde5_arath : 224.0)
28 ana (sp|q9luq3|sde5_arath : 224.0)
29 ana (sp|q9luq3|sde5_arath : 224.0)
30 ana (sp|q9luq3|sde5_arath : 224.0)
31 ana (sp|q9luq3|sde5_arath : 224.0)
32 ana (sp|q9luq3|sde5_arath : 224.0)
33 ana (sp|q9luq3|sde5_arath : 224.0)
34 ana (sp|q9luq3|sde5_arath : 224.0)

35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
2)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
3)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
4)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
5)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
6)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
7)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
8)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
9)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
10)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
11)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
12)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
13)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
14)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
15)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
16)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
17)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
18)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
19)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
20)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
21)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
22)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
23)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
24)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
25)09G142100.1 locus=Phvul.009G142100 ID=Phvul.009G142100.1.v2.1 annot-version=v2.1) &
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2 :22|mip1_arath : 389.0)
3 :22|mip1_arath : 389.0)
4 :22|mip1_arath : 389.0)
5 :22|mip1_arath : 389.0)
6 :22|mip1_arath : 389.0)
7 :22|mip1_arath : 389.0)
8 :22|mip1_arath : 389.0)
9 :22|mip1_arath : 389.0)
10 :22|mip1_arath : 389.0)
11 :22|mip1_arath : 389.0)
12 :22|mip1_arath : 389.0)
13 :22|mip1_arath : 389.0)
14 :22|mip1_arath : 389.0)
15 :22|mip1_arath : 389.0)
16 :22|mip1_arath : 389.0)
17 :22|mip1_arath : 389.0)
18 :22|mip1_arath : 389.0)
19 :22|mip1_arath : 389.0)
20 :22|mip1_arath : 389.0)
21 :22|mip1_arath : 389.0)
22 :22|mip1_arath : 389.0)
23 :22|mip1_arath : 389.0)
24 :22|mip1_arath : 389.0)
25 :22|mip1_arath : 389.0)
26 :22|mip1_arath : 389.0)
27 :22|mip1_arath : 389.0)
28 :22|mip1_arath : 389.0)
29 :22|mip1_arath : 389.0)
30 :22|mip1_arath : 389.0)
31 :22|mip1_arath : 389.0)
32 :22|mip1_arath : 389.0)
33 :22|mip1_arath : 389.0)
34 :22|mip1_arath : 389.0)
35 :22|mip1_arath : 389.0)
36 :22|mip1_arath : 389.0)
37 :22|mip1_arath : 389.0)
38 :22|mip1_arath : 389.0)
39 :22|mip1_arath : 389.0)
40 :22|mip1_arath : 389.0)
41 :22|mip1_arath : 389.0)
42 :22|mip1_arath : 389.0)
43 :22|mip1_arath : 389.0)
44 :22|mip1_arath : 389.0)
45 :22|mip1_arath : 389.0)
46 :22|mip1_arath : 389.0)
47 :22|mip1_arath : 389.0)
48 :22|mip1_arath : 389.0)
49 ular oxygen(50.1.13 : 362.9) (original description: pacid=37177715 transcript=Phvul.002G025200.1
50 ular oxygen(50.1.13 : 362.9) (original description: pacid=37177715 transcript=Phvul.002G025200.1
51 ular oxygen(50.1.13 : 362.9) (original description: pacid=37177715 transcript=Phvul.002G025200.1
52 ular oxygen(50.1.13 : 362.9) (original description: pacid=37177715 transcript=Phvul.002G025200.1
53 ular oxygen(50.1.13 : 362.9) (original description: pacid=37177715 transcript=Phvul.002G025200.1
54 ular oxygen(50.1.13 : 362.9) (original description: pacid=37177715 transcript=Phvul.002G025200.1
55 ular oxygen(50.1.13 : 362.9) (original description: pacid=37177715 transcript=Phvul.002G025200.1
56 ular oxygen(50.1.13 : 362.9) (original description: pacid=37177715 transcript=Phvul.002G025200.1
57 ular oxygen(50.1.13 : 362.9) (original description: pacid=37177715 transcript=Phvul.002G025200.1
58 ular oxygen(50.1.13 : 362.9) (original description: pacid=37177715 transcript=Phvul.002G025200.1
59 ular oxygen(50.1.13 : 362.9) (original description: pacid=37177715 transcript=Phvul.002G025200.1
60 ular oxygen(50.1.13 : 362.9) (original description: pacid=37177715 transcript=Phvul.002G025200.1
ular oxygen(50.1.13 : 362.9) (original description: pacid=37177715 transcript=Phvul.002G025200.1

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6 2.v2.1 annot-version=v2.1) &
7 2.v2.1 annot-version=v2.1) &
8 2.v2.1 annot-version=v2.1) &
9 2.v2.1 annot-version=v2.1) &
10 2.v2.1 annot-version=v2.1) &
11 2.v2.1 annot-version=v2.1) &
12 2.v2.1 annot-version=v2.1) &
13 2.v2.1 annot-version=v2.1) &
14 2.v2.1 annot-version=v2.1) &
15 2.v2.1 annot-version=v2.1) &
16 2.v2.1 annot-version=v2.1) &
17 2.v2.1 annot-version=v2.1) &
18 2.v2.1 annot-version=v2.1) &
19 2.v2.1 annot-version=v2.1) &
20 2.v2.1 annot-version=v2.1) &
21 2.v2.1 annot-version=v2.1) &
22 2.v2.1 annot-version=v2.1) &
23 2.v2.1 annot-version=v2.1) &
24 2.v2.1 annot-version=v2.1) &
25 2.v2.1 annot-version=v2.1) &
26 2.v2.1 annot-version=v2.1) &
27 2.v2.1 annot-version=v2.1) &
28 2.v2.1 annot-version=v2.1) &
29 2.v2.1 annot-version=v2.1) &
30 2.v2.1 annot-version=v2.1) &
31 2.v2.1 annot-version=v2.1) &
32 2.v2.1 annot-version=v2.1) &
33 2.v2.1 annot-version=v2.1) &
34 2.v2.1 annot-version=v2.1) &
35 2.v2.1 annot-version=v2.1) &
36 2.v2.1 annot-version=v2.1) &
37 2.v2.1 annot-version=v2.1) &
38 2.v2.1 annot-version=v2.1) &
39 2.v2.1 annot-version=v2.1) &
40 2.v2.1 annot-version=v2.1) &
41 2.v2.1 annot-version=v2.1) &
42 2.v2.1 annot-version=v2.1) &
43 2.v2.1 annot-version=v2.1) &
44 2.v2.1 annot-version=v2.1) &
45 2.v2.1 annot-version=v2.1) &
46 2.v2.1 annot-version=v2.1) &
47 2.v2.1 annot-version=v2.1) &
48 2.v2.1 annot-version=v2.1) &
49 2.v2.1 annot-version=v2.1) &
50 2.v2.1 annot-version=v2.1) &
51 2.v2.1 annot-version=v2.1) &
52 2.v2.1 annot-version=v2.1) &
53 2.v2.1 annot-version=v2.1) &
54 2.v2.1 annot-version=v2.1) &
55 2.v2.1 annot-version=v2.1) &
56 2.v2.1 annot-version=v2.1) &
57 2.v2.1 annot-version=v2.1) &
58 2.v2.1 annot-version=v2.1) &
59 2.v2.1 annot-version=v2.1) &
60 2.v2.1 annot-version=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

/ersion=v2.1) &
/ersion=v2.1) &
/ersion=v2.1) &
/ersion=v2.1) &
/ersion=v2.1) &
/ersion=v2.1) &
/ersion=v2.1) &
/ersion=v2.1) &
/ersion=v2.1) &
/ersion=v2.1) &

Do not distribute

1 /ersion=v2.1) &
2 /ersion=v2.1) &
3 /ersion=v2.1) &
4 /ersion=v2.1) &
5 /ersion=v2.1) &
6 /ersion=v2.1) &
7 /ersion=v2.1) &
8 /ersion=v2.1) &
9 /ersion=v2.1) &
10 /ersion=v2.1) &
11 /ersion=v2.1) &
12 /ersion=v2.1) &
13 /ersion=v2.1) &
14 /ersion=v2.1) &
15 /ersion=v2.1) &
16 /ersion=v2.1) &
17 /ersion=v2.1) &
18 /ersion=v2.1) &
19 /ersion=v2.1) &
20 /ersion=v2.1) &
21 /ersion=v2.1) &
22 /ersion=v2.1) &
23 /ersion=v2.1) &
24 /ersion=v2.1) &
25 /ersion=v2.1) &
26 /ersion=v2.1) &
27 /ersion=v2.1) &
28 /ersion=v2.1) &
29 /ersion=v2.1) &
30 /ersion=v2.1) &
31 /ersion=v2.1) &
32 /ersion=v2.1) &
33 /ersion=v2.1) &
34 /ersion=v2.1) &
35 /ersion=v2.1) &
36 /ersion=v2.1) &
37 /ersion=v2.1) &
38 /ersion=v2.1) &
39 /ersion=v2.1) &
40 /ersion=v2.1) &
41 /ersion=v2.1) &
42 /ersion=v2.1) &
43 /ersion=v2.1) &
44 /ersion=v2.1) &
45 donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
46 donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
47 donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
48 donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
49 donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
50 donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
51 donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
52 donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
53 donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
54 donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
55 donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
56 donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
57 donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
58 donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
59 donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
60 donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=
donor(50.1.10 : 145.5) (original description: pacid=37144860 transcript=Phvul.003G217800.1 locus=

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51

ot-version=v2.1) &
ot-version=v2.1) &
ot-version=v2.1) &
ot-version=v2.1) &
ot-version=v2.1) &
ot-version=v2.1) &
ot-version=v2.1) &
ot-version=v2.1) &

Do not distribute

1
2 ot-version=v2.1) &
3 ot-version=v2.1) &
4 ot-version=v2.1) &
5 ot-version=v2.1) &
6 ot-version=v2.1) &
7 ot-version=v2.1) &
8 ot-version=v2.1) &
9 ot-version=v2.1) &
10 ot-version=v2.1) &
11 ot-version=v2.1) &
12 ot-version=v2.1) &
13 ot-version=v2.1) &
14 ot-version=v2.1) &
15 ot-version=v2.1) &
16 ot-version=v2.1) &
17 ot-version=v2.1) &
18 ot-version=v2.1) &
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3 h : 247.0)
4 h : 247.0)
5 h : 247.0)
6 h : 247.0)
7 h : 247.0)
8 h : 247.0)
9 h : 247.0)
10 h : 247.0)
11 h : 247.0)
12 h : 247.0)
13 h : 247.0)
14 h : 247.0)
15 h : 247.0)
16 h : 247.0)
17 h : 247.0)
18 h : 247.0)
19 h : 247.0)
20 h : 247.0)
21 h : 247.0)
22 h : 247.0)
23 h : 247.0)
24 h : 247.0)
25 h : 247.0)
26 h : 247.0)
27 h : 247.0)
28 h : 247.0)
29 h : 247.0)
30 h : 247.0)
31 h : 247.0)
32 h : 247.0)
33 h : 247.0)
34 h : 247.0)
35 h : 247.0)
36 h : 247.0)
37 h : 247.0)
38 h : 247.0)
39 h : 247.0)
40 h : 247.0)
41 h : 247.0)
42 h : 247.0)
43 h : 247.0)
44 h : 247.0)
45 h : 247.0)
46 h : 247.0)
47 h : 247.0)
48 h : 247.0)
49 h : 247.0)
50 h : 247.0)
51 h : 247.0)
52 h : 247.0)
53 h : 247.0)
54 h : 247.0)
55 h : 247.0)
56 h : 247.0)
57 h : 247.0)
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2 |=v2.1) &
3 |=v2.1) &
4 |=v2.1) &
5 |=v2.1) &
6 |=v2.1) &
7 |=v2.1) &
8 |=v2.1) &
9 |=v2.1) &
10 |=v2.1) &
11 |=v2.1) &
12 |=v2.1) &
13 |=v2.1) &
14 |=v2.1) &
15 |=v2.1) &
16 |=v2.1) &
17 |=v2.1) &
18 |=v2.1) &
19 |=v2.1) &
20 |=v2.1) &
21 |=v2.1) &
22 |=v2.1) &
23 |=v2.1) &
24 |=v2.1) &
25 |=v2.1) &
26 |=v2.1) &
27 |=v2.1) &
28 |=v2.1) &
29 |=v2.1) &
30 |=v2.1) &
31 |=v2.1) &
32 |=v2.1) &
33 |=v2.1) &
34 |=v2.1) &
35 |=v2.1) &
36 |=v2.1) &
37 |=v2.1) &
38 |=v2.1) &
39 |=v2.1) &
40 |=v2.1) &
41 |=v2.1) &
42 |=v2.1) &
43 |=v2.1) &
44 |=v2.1) &
45 |=v2.1) &
46 |=v2.1) &
47 |=v2.1) &
48 |=v2.1) &
49 |=v2.1) &
50 |=v2.1) &
51 |=v2.1) &
52 |=v2.1) &
53 |=v2.1) &
54 |=v2.1) &
55 |=v2.1) &
56 |=v2.1) &
57 |=v2.1) &
58 |=v2.1) &
59 |=v2.1) &
60 |=v2.1) &
 |=v2.1) &

Do not distribute

1
2 I=V2.1) &
3 I=V2.1) &
4 I=V2.1) &
5 I=V2.1) &
6 I=V2.1) &
7 I=V2.1) &
8 I=V2.1) &
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11 : 161.0)
- 12 : 161.0)
- 13 : 161.0)
- 14 : 161.0)
- 15 : 161.0)
- 16 : 161.0)
- 17 : 161.0)
- 18 : 161.0)
- 19 : 161.0)
- 20 : 161.0)
- 21 : 161.0)
- 22 : 161.0)
- 23 : 161.0)
- 24 : 161.0)
- 25 : 161.0)
- 26 : 161.0)
- 27 : 161.0)
- 28 : 161.0)
- 29 : 161.0)
- 30 : 161.0)
- 31 : 161.0)
- 32 : 161.0)
- 33 : 161.0)
- 34 : 161.0)
- 35 : 161.0)
- 36 : 161.0)
- 37 : 161.0)
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &
;00 ID=Phvul.003G113500.1.v2.1 annot-version=v2.1) &

bioRxiv preprint doi: <https://doi.org/10.1101/199558>; this version posted August 1, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1 =Phvul.003G217800 ID=Phvul.003G217800.1.v2.1 annot-version=v2.1) &
2 =Phvul.003G217800 ID=Phvul.003G217800.1.v2.1 annot-version=v2.1) &
3 =Phvul.003G217800 ID=Phvul.003G217800.1.v2.1 annot-version=v2.1) &
4 =Phvul.003G217800 ID=Phvul.003G217800.1.v2.1 annot-version=v2.1) &
5 =Phvul.003G217800 ID=Phvul.003G217800.1.v2.1 annot-version=v2.1) &
6 =Phvul.003G217800 ID=Phvul.003G217800.1.v2.1 annot-version=v2.1) &
7 =Phvul.003G217800 ID=Phvul.003G217800.1.v2.1 annot-version=v2.1) &
8 =Phvul.003G217800 ID=Phvul.003G217800.1.v2.1 annot-version=v2.1) &
9 =Phvul.003G217800 ID=Phvul.003G217800.1.v2.1 annot-version=v2.1) &
10 =Phvul.003G217800 ID=Phvul.003G217800.1.v2.1 annot-version=v2.1) &
11 =Phvul.003G217800 ID=Phvul.003G217800.1.v2.1 annot-version=v2.1) &
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

| | miRNA_Acc. | Target_Acc. | Expectation | UPE\$ | miRNA_start | miRNA_end |
|----|------------|--------------------|-------------|-------|-------------|-----------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ggaau | Phvul.008G004800.1 | 2.5 | -1 | 1 | 22 |
| 4 | ggaau | Phvul.009G006000.1 | 2.5 | -1 | 1 | 22 |
| 5 | ggaau | Phvul.009G006000.2 | 2.5 | -1 | 1 | 22 |
| 6 | ggaau | Phvul.002G315000.1 | 3 | -1 | 1 | 22 |
| 7 | ggaau | Phvul.002G315000.2 | 3 | -1 | 1 | 22 |
| 8 | ggaau | Phvul.004G164800.1 | 3 | -1 | 1 | 22 |
| 9 | ggaau | Phvul.005G049000.1 | 3 | -1 | 1 | 22 |
| 10 | ggaau | Phvul.010G108200.1 | 3 | -1 | 1 | 22 |
| 11 | ggaau | Phvul.L008143.1 | 3 | -1 | 1 | 22 |
| 12 | ggaau | Phvul.002G189700.1 | 3.5 | -1 | 1 | 22 |
| 13 | ggaau | Phvul.002G189700.2 | 3.5 | -1 | 1 | 22 |
| 14 | ggaau | Phvul.002G189700.3 | 3.5 | -1 | 1 | 22 |
| 15 | ggaau | Phvul.002G189700.4 | 3.5 | -1 | 1 | 22 |
| 16 | ggaau | Phvul.002G258800.1 | 3.5 | -1 | 1 | 22 |
| 17 | ggaau | Phvul.003G202100.1 | 3.5 | -1 | 1 | 22 |
| 18 | ggaau | Phvul.003G282800.1 | 3.5 | -1 | 1 | 22 |
| 19 | ggaau | Phvul.004G083900.1 | 3.5 | -1 | 1 | 22 |
| 20 | ggaau | Phvul.006G110000.1 | 3.5 | -1 | 1 | 22 |
| 21 | ggaau | Phvul.007G031800.1 | 3.5 | -1 | 1 | 22 |
| 22 | ggaau | Phvul.007G031800.2 | 3.5 | -1 | 1 | 22 |
| 23 | ggaau | Phvul.007G094100.1 | 3.5 | -1 | 1 | 22 |
| 24 | ggaau | Phvul.008G081700.2 | 3.5 | -1 | 1 | 22 |
| 25 | ggaau | Phvul.009G201900.1 | 3.5 | -1 | 1 | 22 |
| 26 | ggaau | Phvul.009G233100.2 | 3.5 | -1 | 1 | 22 |
| 27 | ggaau | Phvul.009G246200.2 | 3.5 | -1 | 1 | 22 |
| 28 | ggaau | Phvul.010G125200.1 | 3.5 | -1 | 1 | 22 |
| 29 | ggaau | Phvul.011G073400.1 | 3.5 | -1 | 1 | 22 |
| 30 | ggaau | Phvul.001G001700.1 | 4 | -1 | 1 | 22 |
| 31 | ggaau | Phvul.001G160000.1 | 4 | -1 | 1 | 22 |
| 32 | ggaau | Phvul.002G011900.1 | 4 | -1 | 1 | 22 |
| 33 | ggaau | Phvul.002G028700.1 | 4 | -1 | 1 | 22 |
| 34 | ggaau | Phvul.002G185800.1 | 4 | -1 | 1 | 22 |
| 35 | ggaau | Phvul.002G206900.1 | 4 | -1 | 1 | 22 |
| 36 | ggaau | Phvul.002G206900.2 | 4 | -1 | 1 | 22 |
| 37 | ggaau | Phvul.003G078900.1 | 4 | -1 | 1 | 22 |
| 38 | ggaau | Phvul.003G210500.1 | 4 | -1 | 1 | 22 |
| 39 | ggaau | Phvul.003G262300.3 | 4 | -1 | 1 | 22 |
| 40 | ggaau | Phvul.003G262300.1 | 4 | -1 | 1 | 22 |
| 41 | ggaau | Phvul.003G262300.2 | 4 | -1 | 1 | 22 |
| 42 | ggaau | Phvul.003G262300.4 | 4 | -1 | 1 | 22 |
| 43 | ggaau | Phvul.004G093900.4 | 4 | -1 | 1 | 22 |
| 44 | ggaau | Phvul.004G093900.6 | 4 | -1 | 1 | 22 |
| 45 | ggaau | Phvul.004G093900.5 | 4 | -1 | 1 | 22 |
| 46 | ggaau | Phvul.004G093900.3 | 4 | -1 | 1 | 22 |
| 47 | ggaau | Phvul.004G093900.1 | 4 | -1 | 1 | 22 |
| 48 | ggaau | Phvul.004G093900.1 | 4 | -1 | 1 | 22 |
| 49 | ggaau | Phvul.004G093900.1 | 4 | -1 | 1 | 22 |
| 50 | ggaau | Phvul.004G093900.1 | 4 | -1 | 1 | 22 |
| 51 | ggaau | Phvul.004G093900.1 | 4 | -1 | 1 | 22 |
| 52 | ggaau | Phvul.004G093900.1 | 4 | -1 | 1 | 22 |
| 53 | ggaau | Phvul.004G093900.1 | 4 | -1 | 1 | 22 |
| 54 | ggaau | Phvul.004G093900.1 | 4 | -1 | 1 | 22 |
| 55 | ggaau | Phvul.004G093900.1 | 4 | -1 | 1 | 22 |
| 56 | ggaau | Phvul.004G093900.1 | 4 | -1 | 1 | 22 |
| 57 | ggaau | Phvul.004G093900.1 | 4 | -1 | 1 | 22 |
| 58 | ggaau | Phvul.004G093900.1 | 4 | -1 | 1 | 22 |
| 59 | ggaau | Phvul.004G093900.1 | 4 | -1 | 1 | 22 |
| 60 | ggaau | Phvul.004G093900.1 | 4 | -1 | 1 | 22 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | ggaaugggcuga Phvul.004G093900.2 | 4 | -1 | 1 | 22 |
| 3 | ggaaugggcuga Phvul.004G093900.7 | 4 | -1 | 1 | 22 |
| 4 | ggaaugggcuga Phvul.004G105600.1 | 4 | -1 | 1 | 22 |
| 5 | ggaaugggcuga Phvul.004G135400.1 | 4 | -1 | 1 | 22 |
| 6 | ggaaugggcuga Phvul.004G159500.1 | 4 | -1 | 1 | 22 |
| 7 | ggaaugggcuga Phvul.004G159500.1 | 4 | -1 | 1 | 22 |
| 8 | ggaaugggcuga Phvul.004G170000.1 | 4 | -1 | 1 | 22 |
| 9 | ggaaugggcuga Phvul.005G001000.1 | 4 | -1 | 1 | 22 |
| 10 | ggaaugggcuga Phvul.005G022800.1 | 4 | -1 | 1 | 22 |
| 11 | ggaaugggcuga Phvul.005G022800.1 | 4 | -1 | 1 | 22 |
| 12 | ggaaugggcuga Phvul.005G072300.1 | 4 | -1 | 1 | 22 |
| 13 | ggaaugggcuga Phvul.007G034000.1 | 4 | -1 | 1 | 22 |
| 14 | ggaaugggcuga Phvul.007G034000.2 | 4 | -1 | 1 | 22 |
| 15 | ggaaugggcuga Phvul.007G244033.1 | 4 | -1 | 1 | 22 |
| 16 | ggaaugggcuga Phvul.007G244033.1 | 4 | -1 | 1 | 22 |
| 17 | ggaaugggcuga Phvul.007G244033.1 | 4 | -1 | 1 | 22 |
| 18 | ggaaugggcuga Phvul.007G244066.1 | 4 | -1 | 1 | 22 |
| 19 | ggaaugggcuga Phvul.008G079000.1 | 4 | -1 | 1 | 22 |
| 20 | ggaaugggcuga Phvul.008G267400.5 | 4 | -1 | 1 | 22 |
| 21 | ggaaugggcuga Phvul.008G267400.2 | 4 | -1 | 1 | 22 |
| 22 | ggaaugggcuga Phvul.008G267400.3 | 4 | -1 | 1 | 22 |
| 23 | ggaaugggcuga Phvul.008G267400.4 | 4 | -1 | 1 | 22 |
| 24 | ggaaugggcuga Phvul.009G053900.2 | 4 | -1 | 1 | 22 |
| 25 | ggaaugggcuga Phvul.009G081900.1 | 4 | -1 | 1 | 22 |
| 26 | ggaaugggcuga Phvul.009G213000.1 | 4 | -1 | 1 | 22 |
| 27 | ggaaugggcuga Phvul.011G065200.2 | 4 | -1 | 1 | 22 |
| 28 | ggaaugggcuga Phvul.001G079400.1 | 4.5 | -1 | 1 | 22 |
| 29 | ggaaugggcuga Phvul.001G087700.1 | 4.5 | -1 | 1 | 22 |
| 30 | ggaaugggcuga Phvul.001G117500.1 | 4.5 | -1 | 1 | 22 |
| 31 | ggaaugggcuga Phvul.002G007100.1 | 4.5 | -1 | 1 | 22 |
| 32 | ggaaugggcuga Phvul.002G115800.1 | 4.5 | -1 | 1 | 22 |
| 33 | ggaaugggcuga Phvul.002G115800.3 | 4.5 | -1 | 1 | 22 |
| 34 | ggaaugggcuga Phvul.002G163600.1 | 4.5 | -1 | 1 | 22 |
| 35 | ggaaugggcuga Phvul.002G168500.1 | 4.5 | -1 | 1 | 22 |
| 36 | ggaaugggcuga Phvul.002G168500.2 | 4.5 | -1 | 1 | 22 |
| 37 | ggaaugggcuga Phvul.002G177500.1 | 4.5 | -1 | 1 | 22 |
| 38 | ggaaugggcuga Phvul.002G315000.1 | 4.5 | -1 | 1 | 22 |
| 39 | ggaaugggcuga Phvul.002G315000.2 | 4.5 | -1 | 1 | 22 |
| 40 | ggaaugggcuga Phvul.003G185300.1 | 4.5 | -1 | 1 | 22 |
| 41 | ggaaugggcuga Phvul.003G212800.2 | 4.5 | -1 | 1 | 22 |
| 42 | ggaaugggcuga Phvul.004G121900.1 | 4.5 | -1 | 1 | 22 |
| 43 | ggaaugggcuga Phvul.006G033600.1 | 4.5 | -1 | 1 | 22 |
| 44 | ggaaugggcuga Phvul.006G033600.2 | 4.5 | -1 | 1 | 22 |
| 45 | ggaaugggcuga Phvul.006G219000.1 | 4.5 | -1 | 1 | 22 |
| 46 | ggaaugggcuga Phvul.007G008100.2 | 4.5 | -1 | 1 | 22 |
| 47 | ggaaugggcuga Phvul.007G086600.1 | 4.5 | -1 | 1 | 22 |
| 48 | ggaaugggcuga Phvul.007G168600.1 | 4.5 | -1 | 1 | 22 |
| 49 | ggaaugggcuga Phvul.008G002700.1 | 4.5 | -1 | 1 | 22 |
| 50 | ggaaugggcuga Phvul.009G062500.1 | 4.5 | -1 | 1 | 22 |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaugggcuga Phvul.001G186500.1 | 5 | -1 | 1 | 22 |
| 3 | ggaaugggcuga Phvul.002G028700.1 | 5 | -1 | 1 | 22 |
| 4 | ggaaugggcuga Phvul.003G202300.1 | 5 | -1 | 1 | 22 |
| 5 | ggaaugggcuga Phvul.003G202300.2 | 5 | -1 | 1 | 22 |
| 6 | ggaaugggcuga Phvul.003G248400.1 | 5 | -1 | 1 | 22 |
| 7 | ggaaugggcuga Phvul.003G248400.2 | 5 | -1 | 1 | 22 |
| 8 | ggaaugggcuga Phvul.003G248400.3 | 5 | -1 | 1 | 22 |
| 9 | ggaaugggcuga Phvul.004G024400.1 | 5 | -1 | 1 | 22 |
| 10 | ggaaugggcuga Phvul.004G071800.1 | 5 | -1 | 1 | 22 |
| 11 | ggaaugggcuga Phvul.004G178500.1 | 5 | -1 | 1 | 22 |
| 12 | ggaaugggcuga Phvul.004G178500.1 | 5 | -1 | 1 | 22 |
| 13 | ggaaugggcuga Phvul.005G175600.1 | 5 | -1 | 1 | 22 |
| 14 | ggaaugggcuga Phvul.005G175600.2 | 5 | -1 | 1 | 22 |
| 15 | ggaaugggcuga Phvul.006G053300.1 | 5 | -1 | 1 | 22 |
| 16 | ggaaugggcuga Phvul.006G053300.2 | 5 | -1 | 1 | 22 |
| 17 | ggaaugggcuga Phvul.006G110000.1 | 5 | -1 | 1 | 22 |
| 18 | ggaaugggcuga Phvul.007G204100.1 | 5 | -1 | 1 | 22 |
| 19 | ggaaugggcuga Phvul.008G006800.1 | 5 | -1 | 1 | 22 |
| 20 | ggaaugggcuga Phvul.008G034200.2 | 5 | -1 | 1 | 22 |
| 21 | ggaaugggcuga Phvul.009G184400.1 | 5 | -1 | 1 | 22 |
| 22 | ggaaugggcuga Phvul.009G184400.2 | 5 | -1 | 1 | 22 |
| 23 | | | | | |
| 24 | | | | | |
| 25 | | | | | |
| 26 | | | | | |
| 27 | | | | | |
| 28 | | | | | |
| 29 | | | | | |
| 30 | | | | | |
| 31 | | | | | |
| 32 | | | | | |
| 33 | | | | | |
| 34 | | | | | |
| 35 | | | | | |
| 36 | | | | | |
| 37 | | | | | |
| 38 | | | | | |
| 39 | | | | | |
| 40 | | | | | |
| 41 | | | | | |
| 42 | | | | | |
| 43 | | | | | |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | |
|----|------|-----------------|-----------------|--------------------------|
| 1 | | | | |
| 2 | 96 | 117 GGAAUGGGCI |CAUUUCUCA/ | Cleavage pacid=371628 |
| 3 | 69 | 90 GGAAUGGGCI |CAUUUCUCA/ | Cleavage pacid=371628 |
| 4 | 212 | 233 GGAAUGGGCI |GCCUUUCCG/ | Cleavage pacid=371629 |
| 5 | 357 | 378 GGAAUGGGCI |AACUCCCAA | Cleavage pacid=371629 |
| 6 | 1475 | 1496 GGAAUGGGCI |UCUUUCUCA/ | Cleavage pacid=371632 |
| 7 | | | | |
| 8 | 273 | 294 GGAAUGGGCI |GCCUUCUCG/ | Translation pacid=371616 |
| 9 | | | | |
| 10 | 2164 | 2185 GGAAUGGGCI |UGCUUCUCA/ | Cleavage pacid=371530 |
| 11 | 1223 | 1244 GGAAUGGGCI |AUCUUCUCA/ | Cleavage pacid=371540 |
| 12 | 885 | 906 GGAAUGGGCI |AUUUUCUCA/ | Translation pacid=371543 |
| 13 | | | | |
| 14 | 1650 | 1671 GGAAUGGGCI |UGAUUCGUA/ | Cleavage pacid=371676 |
| 15 | 1160 | 1181 GGAAUGGGCI |UGAUUCGUA/ | Cleavage pacid=371676 |
| 16 | 311 | 332 GGAAUGGGCI |CUCUCCCAA | Translation pacid=371653 |
| 17 | 497 | 518 GGAAUGGGCI |CUCUCCCAA | Translation pacid=371653 |
| 18 | | | | |
| 19 | 497 | 518 GGAAUGGGCI |CUCUCCCAA | Translation pacid=371643 |
| 20 | 1570 | 1591 GGAAUGGGCI |AUCUUUCCA/ | Cleavage pacid=371607 |
| 21 | 1521 | 1542 GGAAUGGGCI |UGCUUCACA/ | Cleavage pacid=371602 |
| 22 | 1517 | 1538 GGAAUGGGCI |UGCUUCACA/ | Cleavage pacid=371602 |
| 23 | 1636 | 1657 GGAAUGGGCI |UGCUUCACA/ | Cleavage pacid=371602 |
| 24 | 1630 | 1651 GGAAUGGGCI |UGCUUCACA/ | Cleavage pacid=371602 |
| 25 | | | | |
| 26 | 5313 | 5334 GGAAUGGGCI |GAAAACCAA | Cleavage pacid=371507 |
| 27 | 3042 | 3063 GGAAUGGGCI |UUUUUCUA/ | Cleavage pacid=371520 |
| 28 | | | | |
| 29 | 21 | 42 GGAAUGGGCI |CCUCCUAG | Cleavage pacid=371495 |
| 30 | 114 | 135 GGAAUGGGCI |GGCUACGCAC | Cleavage pacid=371555 |
| 31 | 154 | 175 GGAAUGGGCI |GACUCCAC | Cleavage pacid=371688 |
| 32 | 537 | 558 GGAAUGGGCI |CGCUCCCAA | Cleavage pacid=371681 |
| 33 | | | | |
| 34 | 179 | 200 GGAAUGGGCI |UUCUUCUCA/ | Translation pacid=371685 |
| 35 | 9 | 30 GGAAUGGGCI |AGCUGCUUA/ | Cleavage pacid=371751 |
| 36 | 39 | 60 GGAAUGGGCI |GGUUUUUCA | Cleavage pacid=371771 |
| 37 | | | | |
| 38 | 39 | 60 GGAAUGGGCI |GGUUUUUCA | Cleavage pacid=371771 |
| 39 | 340 | 361 GGAAUGGGCI |AGUUUCCG/ | Cleavage pacid=371780 |
| 40 | 745 | 766 GGAAUGGGCI |ACCUUCCAA | Cleavage pacid=371779 |
| 41 | 745 | 766 GGAAUGGGCI |ACCUUCCAA | Cleavage pacid=371779 |
| 42 | 190 | 211 GGAAUGGGCI |UUCUCCAA | Translation pacid=371764 |
| 43 | 296 | 317 GGAAUGGGCI |CCUCUUUCA/ | Cleavage pacid=371747 |
| 44 | 296 | 317 GGAAUGGGCI |CCUCUUUCA/ | Cleavage pacid=371747 |
| 45 | 775 | 796 GGAAUGGGCI |AGUUUCUUA/ | Cleavage pacid=371444 |
| 46 | | | | |
| 47 | 3 | 24 GGAAUGGGCI |CGUUUCUCA/ | Cleavage pacid=371453 |
| 48 | 938 | 959 GGAAUGGGCI |CUCUUCUCA/ | Translation pacid=371625 |
| 49 | 2003 | 2024 GGAAUGGGCI |UGCUUCUA/ | Cleavage pacid=371727 |
| 50 | 1944 | 1965 GGAAUGGGCI |UGCUUCUA/ | Cleavage pacid=371727 |
| 51 | 2213 | 2234 GGAAUGGGCI |UCCUUCUCAC | Cleavage pacid=371737 |
| 52 | 610 | 630 GGAAUGGGCI |UGCU-CCUUA | Cleavage pacid=371646 |
| 53 | 72 | 93 GGAAUGGGCI |CCCUUCUCAA | Cleavage pacid=371652 |
| 54 | 428 | 449 GGAAUGGGCI |AUCUUCCA/ | Cleavage pacid=371667 |
| 55 | 2027 | 2048 GGAAUGGGCI |UGUUUCUUA | Cleavage pacid=371597 |
| 56 | 431 | 452 GGAAUGGGCI |CUCUUCUCA/ | Cleavage pacid=371494 |

| | Multiplicity | Target_Acc. | ID | locusName | Pfam |
|----|--------------|--------------------|------------------|------------------|--------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | 1 | Phvul.008G004800.1 | Phvul.008G004800 | Phvul.008G004800 | PF00175,PF00 |
| 4 | 1 | Phvul.009G006000.1 | Phvul.009G006000 | Phvul.009G006000 | PF00650 |
| 5 | 1 | Phvul.009G006000.2 | Phvul.009G006000 | Phvul.009G006000 | PF00650 |
| 6 | 1 | Phvul.009G006000.2 | Phvul.009G006000 | Phvul.009G006000 | PF00650 |
| 7 | 2 | Phvul.002G315000.1 | Phvul.002G315000 | Phvul.002G315000 | 0 |
| 8 | 2 | Phvul.002G315000.2 | Phvul.002G315000 | Phvul.002G315000 | 0 |
| 9 | | | | | |
| 10 | 1 | Phvul.004G164800.1 | Phvul.004G164800 | Phvul.004G164800 | PF16113,PF00 |
| 11 | 1 | Phvul.005G049000.1 | Phvul.005G049000 | Phvul.005G049000 | PF10184 |
| 12 | 1 | Phvul.010G108200.1 | Phvul.010G108200 | Phvul.010G108200 | PF07707,PF00 |
| 13 | 1 | Phvul.L008143.1 | Phvul.L008143 | Phvul.L008143 | 0 |
| 14 | | | | | |
| 15 | 1 | Phvul.002G189700.1 | Phvul.002G189700 | Phvul.002G189700 | PF00627,PF14 |
| 16 | 1 | Phvul.002G189700.2 | Phvul.002G189700 | Phvul.002G189700 | PF00627,PF14 |
| 17 | 1 | Phvul.002G189700.3 | Phvul.002G189700 | Phvul.002G189700 | PF00627,PF14 |
| 18 | 1 | Phvul.002G189700.4 | Phvul.002G189700 | Phvul.002G189700 | PF00627,PF14 |
| 19 | | | | | |
| 20 | 1 | Phvul.002G258800.1 | Phvul.002G258800 | Phvul.002G258800 | 0 |
| 21 | | | | | |
| 22 | 1 | Phvul.003G202100.1 | Phvul.003G202100 | Phvul.003G202100 | PF08263,PF00 |
| 23 | 1 | Phvul.003G282800.1 | Phvul.003G282800 | Phvul.003G282800 | PF05965 |
| 24 | 1 | Phvul.004G083900.1 | Phvul.004G083900 | Phvul.004G083900 | PF00155 |
| 25 | | | | | |
| 26 | 2 | Phvul.006G110000.1 | Phvul.006G110000 | Phvul.006G110000 | 0 |
| 27 | 1 | Phvul.007G031800.1 | Phvul.007G031800 | Phvul.007G031800 | PF02358,PF00 |
| 28 | 1 | Phvul.007G031800.2 | Phvul.007G031800 | Phvul.007G031800 | PF02358,PF00 |
| 29 | | | | | |
| 30 | 1 | Phvul.007G094100.1 | Phvul.007G094100 | Phvul.007G094100 | PF04715,PF00 |
| 31 | 1 | Phvul.008G081700.2 | Phvul.008G081700 | Phvul.008G081700 | PF00122,PF12 |
| 32 | 1 | Phvul.009G201900.1 | Phvul.009G201900 | Phvul.009G201900 | 0 |
| 33 | | | | | |
| 34 | 1 | Phvul.009G233100.2 | Phvul.009G233100 | Phvul.009G233100 | 0 |
| 35 | 1 | Phvul.009G246200.2 | Phvul.009G246200 | Phvul.009G246200 | PF03171,PF14 |
| 36 | 1 | Phvul.010G125200.1 | Phvul.010G125200 | Phvul.010G125200 | PF03914 |
| 37 | | | | | |
| 38 | 1 | Phvul.011G073400.1 | Phvul.011G073400 | Phvul.011G073400 | PF09786 |
| 39 | 1 | Phvul.001G001700.1 | Phvul.001G001700 | Phvul.001G001700 | PF00326,PF02 |
| 40 | 1 | Phvul.001G160000.1 | Phvul.001G160000 | Phvul.001G160000 | PF13639 |
| 41 | 1 | Phvul.002G011900.1 | Phvul.002G011900 | Phvul.002G011900 | PF00332,PF07 |
| 42 | | | | | |
| 43 | 2 | Phvul.002G028700.1 | Phvul.002G028700 | Phvul.002G028700 | PF04788 |
| 44 | 1 | Phvul.002G185800.1 | Phvul.002G185800 | Phvul.002G185800 | PF00282 |
| 45 | 1 | Phvul.002G206900.1 | Phvul.002G206900 | Phvul.002G206900 | PF08263,PF00 |
| 46 | | | | | |
| 47 | 1 | Phvul.002G206900.2 | Phvul.002G206900 | Phvul.002G206900 | PF08263,PF00 |
| 48 | 1 | Phvul.003G078900.1 | Phvul.003G078900 | Phvul.003G078900 | 0 |
| 49 | 1 | Phvul.003G210500.1 | Phvul.003G210500 | Phvul.003G210500 | PF02201 |
| 50 | | | | | |
| 51 | 1 | Phvul.003G262300.3 | Phvul.003G262300 | Phvul.003G262300 | PF00641 |
| 52 | 1 | Phvul.003G262300.1 | Phvul.003G262300 | Phvul.003G262300 | PF00641 |
| 53 | 1 | Phvul.003G262300.2 | Phvul.003G262300 | Phvul.003G262300 | PF00641 |
| 54 | | | | | |
| 55 | 1 | Phvul.003G262300.4 | Phvul.003G262300 | Phvul.003G262300 | PF00641 |
| 56 | 1 | Phvul.004G093900.4 | Phvul.004G093900 | Phvul.004G093900 | PF00201,PF03 |
| 57 | 1 | Phvul.004G093900.6 | Phvul.004G093900 | Phvul.004G093900 | PF00201,PF03 |
| 58 | | | | | |
| 59 | 1 | Phvul.004G093900.5 | Phvul.004G093900 | Phvul.004G093900 | PF00201,PF03 |
| 60 | 1 | Phvul.004G093900.3 | Phvul.004G093900 | Phvul.004G093900 | PF00201,PF03 |
| | 1 | Phvul.004G093900.1 | Phvul.004G093900 | Phvul.004G093900 | PF00201,PF03 |

| | | | | | |
|----|---|--------------------|------------------|------------------|--------------|
| 1 | | | | | |
| 2 | 1 | Phvul.004G093900.2 | Phvul.004G093900 | Phvul.004G093900 | PF00201,PF03 |
| 3 | 1 | Phvul.004G093900.7 | Phvul.004G093900 | Phvul.004G093900 | PF00201,PF03 |
| 4 | 1 | Phvul.004G105600.1 | Phvul.004G105600 | Phvul.004G105600 | PF00560 |
| 5 | 1 | Phvul.004G135400.1 | Phvul.004G135400 | Phvul.004G135400 | PF00005,PF01 |
| 6 | 1 | Phvul.004G159500.1 | Phvul.004G159500 | Phvul.004G159500 | PF00067 |
| 7 | 1 | Phvul.004G170000.1 | Phvul.004G170000 | Phvul.004G170000 | PF02516 |
| 8 | 1 | Phvul.005G001000.1 | Phvul.005G001000 | Phvul.005G001000 | PF03552 |
| 9 | 1 | Phvul.005G022800.1 | Phvul.005G022800 | Phvul.005G022800 | PF00022 |
| 10 | 1 | Phvul.005G072300.1 | Phvul.005G072300 | Phvul.005G072300 | PF00179 |
| 11 | 1 | Phvul.007G034000.1 | Phvul.007G034000 | Phvul.007G034000 | PF03034 |
| 12 | 1 | Phvul.007G034000.2 | Phvul.007G034000 | Phvul.007G034000 | PF03034 |
| 13 | 2 | Phvul.007G244033.1 | Phvul.007G244033 | Phvul.007G244033 | 0 |
| 14 | 2 | Phvul.007G244033.1 | Phvul.007G244033 | Phvul.007G244033 | 0 |
| 15 | 1 | Phvul.007G244066.1 | Phvul.007G244066 | Phvul.007G244066 | 0 |
| 16 | 1 | Phvul.008G079000.1 | Phvul.008G079000 | Phvul.008G079000 | PF06697 |
| 17 | 1 | Phvul.008G267400.5 | Phvul.008G267400 | Phvul.008G267400 | PF00012 |
| 18 | 1 | Phvul.008G267400.2 | Phvul.008G267400 | Phvul.008G267400 | PF00012 |
| 19 | 1 | Phvul.008G267400.3 | Phvul.008G267400 | Phvul.008G267400 | PF00012 |
| 20 | 1 | Phvul.008G267400.4 | Phvul.008G267400 | Phvul.008G267400 | PF00012 |
| 21 | 1 | Phvul.009G053900.2 | Phvul.009G053900 | Phvul.009G053900 | PF14691,PF07 |
| 22 | 1 | Phvul.009G081900.1 | Phvul.009G081900 | Phvul.009G081900 | PF12937 |
| 23 | 1 | Phvul.009G213000.1 | Phvul.009G213000 | Phvul.009G213000 | PF14531,PF03 |
| 24 | 1 | Phvul.011G065200.2 | Phvul.011G065200 | Phvul.011G065200 | 0 |
| 25 | 1 | Phvul.001G079400.1 | Phvul.001G079400 | Phvul.001G079400 | PF11145 |
| 26 | 1 | Phvul.001G087700.1 | Phvul.001G087700 | Phvul.001G087700 | PF03982,PF00 |
| 27 | 1 | Phvul.001G117500.1 | Phvul.001G117500 | Phvul.001G117500 | PF02446,PF00 |
| 28 | 1 | Phvul.002G007100.1 | Phvul.002G007100 | Phvul.002G007100 | PF13912 |
| 29 | 1 | Phvul.002G115800.1 | Phvul.002G115800 | Phvul.002G115800 | PF07714 |
| 30 | 1 | Phvul.002G115800.3 | Phvul.002G115800 | Phvul.002G115800 | PF07714 |
| 31 | 1 | Phvul.002G163600.1 | Phvul.002G163600 | Phvul.002G163600 | 0 |
| 32 | 1 | Phvul.002G168500.1 | Phvul.002G168500 | Phvul.002G168500 | PF13912 |
| 33 | 1 | Phvul.002G168500.2 | Phvul.002G168500 | Phvul.002G168500 | PF13912 |
| 34 | 1 | Phvul.002G177500.1 | Phvul.002G177500 | Phvul.002G177500 | PF01762,PF00 |
| 35 | 2 | Phvul.002G315000.1 | Phvul.002G315000 | Phvul.002G315000 | 0 |
| 36 | 2 | Phvul.002G315000.2 | Phvul.002G315000 | Phvul.002G315000 | 0 |
| 37 | 1 | Phvul.003G185300.1 | Phvul.003G185300 | Phvul.003G185300 | PF07983 |
| 38 | 1 | Phvul.003G212800.2 | Phvul.003G212800 | Phvul.003G212800 | PF00847 |
| 39 | 1 | Phvul.004G121900.1 | Phvul.004G121900 | Phvul.004G121900 | PF01554 |
| 40 | 1 | Phvul.006G033600.1 | Phvul.006G033600 | Phvul.006G033600 | PF00069 |
| 41 | 1 | Phvul.006G033600.2 | Phvul.006G033600 | Phvul.006G033600 | PF00069 |
| 42 | 1 | Phvul.006G219000.1 | Phvul.006G219000 | Phvul.006G219000 | PF00439 |
| 43 | 1 | Phvul.007G008100.2 | Phvul.007G008100 | Phvul.007G008100 | PF10075 |
| 44 | 1 | Phvul.007G086600.1 | Phvul.007G086600 | Phvul.007G086600 | PF00847 |
| 45 | 1 | Phvul.007G168600.1 | Phvul.007G168600 | Phvul.007G168600 | PF07883 |
| 46 | 1 | Phvul.008G002700.1 | Phvul.008G002700 | Phvul.008G002700 | PF03141 |
| 47 | 1 | Phvul.009G062500.1 | Phvul.009G062500 | Phvul.009G062500 | PF04130 |

| | | | | | |
|----|---|--------------------|------------------|------------------|--------------|
| 1 | | | | | |
| 2 | 1 | Phvul.001G186500.1 | Phvul.001G186500 | Phvul.001G186500 | PF15629,PF15 |
| 3 | 2 | Phvul.002G028700.1 | Phvul.002G028700 | Phvul.002G028700 | PF04788 |
| 4 | 1 | Phvul.003G202300.1 | Phvul.003G202300 | Phvul.003G202300 | 0 |
| 5 | | | | | 0 |
| 6 | 1 | Phvul.003G202300.2 | Phvul.003G202300 | Phvul.003G202300 | 0 |
| 7 | 1 | Phvul.003G248400.1 | Phvul.003G248400 | Phvul.003G248400 | PF14694,PF14 |
| 8 | 1 | Phvul.003G248400.2 | Phvul.003G248400 | Phvul.003G248400 | PF14694,PF14 |
| 9 | | | | | |
| 10 | 1 | Phvul.003G248400.3 | Phvul.003G248400 | Phvul.003G248400 | PF14694,PF14 |
| 11 | 1 | Phvul.004G024400.1 | Phvul.004G024400 | Phvul.004G024400 | 0 |
| 12 | 1 | Phvul.004G071800.1 | Phvul.004G071800 | Phvul.004G071800 | PF03094 |
| 13 | | | | | |
| 14 | 2 | Phvul.004G178500.1 | Phvul.004G178500 | Phvul.004G178500 | PF00432 |
| 15 | 2 | Phvul.004G178500.1 | Phvul.004G178500 | Phvul.004G178500 | PF00432 |
| 16 | 1 | Phvul.005G175600.1 | Phvul.005G175600 | Phvul.005G175600 | PF00005,PF00 |
| 17 | 1 | Phvul.005G175600.2 | Phvul.005G175600 | Phvul.005G175600 | PF00005,PF00 |
| 18 | 1 | Phvul.006G053300.1 | Phvul.006G053300 | Phvul.006G053300 | PF03106 |
| 19 | 1 | Phvul.006G053300.2 | Phvul.006G053300 | Phvul.006G053300 | PF03106 |
| 20 | | | | | |
| 21 | 2 | Phvul.006G110000.1 | Phvul.006G110000 | Phvul.006G110000 | 0 |
| 22 | 1 | Phvul.007G204100.1 | Phvul.007G204100 | Phvul.007G204100 | PF04810,PF08 |
| 23 | 1 | Phvul.008G006800.1 | Phvul.008G006800 | Phvul.008G006800 | PF00400,PF12 |
| 24 | | | | | |
| 25 | 1 | Phvul.008G034200.2 | Phvul.008G034200 | Phvul.008G034200 | PF00201 |
| 26 | 1 | Phvul.009G184400.1 | Phvul.009G184400 | Phvul.009G184400 | PF05904 |
| 27 | 1 | Phvul.009G184400.2 | Phvul.009G184400 | Phvul.009G184400 | PF05904 |
| 28 | | | | | |
| 29 | | | | | |
| 30 | | | | | |
| 31 | | | | | |
| 32 | | | | | |
| 33 | | | | | |
| 34 | | | | | |
| 35 | | | | | |
| 36 | | | | | |
| 37 | | | | | |
| 38 | | | | | |
| 39 | | | | | |
| 40 | | | | | |
| 41 | | | | | |
| 42 | | | | | |
| 43 | | | | | |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | Panther | KOG | KEGG | KOG | GO | Best-hit-arabi |
|----|--------------------------|---------|-------------------|----------|----------------|----------------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | PTHR19384,P ⁻ | | 0 1.5.1.30 | | 0 GO:0055114,(| AT3G02280.1 |
| 4 | PTHR23324,P ⁻ | | 0 | 0 | 0 | 0 AT4G39170.1 |
| 5 | PTHR23324,P ⁻ | | 0 | 0 | 0 | 0 AT4G39170.1 |
| 6 | PTHR23324,P ⁻ | | 0 | 0 | 0 | 0 AT4G39170.1 |
| 7 | PTHR11005,P ⁻ | KOG2624 | 3.1.1.3 | | 0 | 0 AT1G73920.1 |
| 8 | PTHR11005,P ⁻ | KOG2624 | 3.1.1.3 | | 0 | 0 AT1G73920.1 |
| 9 | PTHR23309,P ⁻ | KOG1683 | 5.1.2.3,1.1.1.3 | K10527 | GO:0055114,(| AT4G29010.1 |
| 10 | PTHR22750,P ⁻ | KOG4457 | | 0 | 0 | 0 AT1G79510.1 |
| 11 | PTHR24412,P ⁻ | | 0 | 0 | 0 GO:0005515 | AT3G61600.1 |
| 12 | PTHR24412,P ⁻ | | 0 | 0 | 0 | 0 |
| 13 | PTHR33912,P ⁻ | | 0 | 0 | 0 | 0 |
| 14 | PTHR33912,P ⁻ | | 0 | 0 | 0 | 0 |
| 15 | PTHR11254,P ⁻ | | 0 6.3.2.19 | K10592 | GO:0004842 | AT1G55860.2 |
| 16 | PTHR11254,P ⁻ | | 0 6.3.2.19 | K10592 | GO:0004842 | AT1G55860.2 |
| 17 | PTHR11254,P ⁻ | | 0 6.3.2.19 | K10592 | GO:0004842 | AT1G55860.2 |
| 18 | PTHR11254,P ⁻ | | 0 6.3.2.19 | K10592 | GO:0004842 | AT1G55860.2 |
| 19 | PTHR11254,P ⁻ | | 0 6.3.2.19 | K10592 | GO:0004842 | AT1G55860.2 |
| 20 | PTHR31852,P ⁻ | | 0 | 0 | 0 | 0 AT3G26350.1 |
| 21 | PTHR27000,P ⁻ | KOG0472 | 2.7.11.1 | | 0 GO:0005515 | AT4G20140.1 |
| 22 | PTHR22715,P ⁻ | | 0 2.1.1.43 | | 0 GO:0005634 | AT1G26330.1 |
| 23 | PTHR22715,P ⁻ | | 0 2.1.1.43 | | 0 GO:0005634 | AT1G26330.1 |
| 24 | PTHR11751,P ⁻ | KOG0633 | 2.6.1.9 | K00817 | GO:0030170,(| AT1G71920.2 |
| 25 | PTHR11751,P ⁻ | KOG0633 | 2.6.1.9 | K00817 | GO:0030170,(| AT1G71920.2 |
| 26 | PTHR31234,P ⁻ | | 0 | 0 | 0 | 0 AT4G01110.1 |
| 27 | PTHR10788,P ⁻ | | 0 2.4.1.15,3.1.3 | K16055 | GO:0005992,(| AT4G17770.1 |
| 28 | PTHR10788,P ⁻ | | 0 2.4.1.15,3.1.3 | K16055 | GO:0005992,(| AT4G17770.1 |
| 29 | PTHR10788,P ⁻ | | 0 2.4.1.15,3.1.3 | K16055 | GO:0005992,(| AT4G17770.1 |
| 30 | PTHR11236,P ⁻ | | 0 2.6.1.85 | K13950 | GO:0016833,(| AT2G28880.1 |
| 31 | PTHR11236,P ⁻ | | 0 2.6.1.85 | K13950 | GO:0016833,(| AT2G28880.1 |
| 32 | PTHR24092,P ⁻ | | 0 3.6.3.1 | K14802 | GO:0046872,(| AT5G04930.1 |
| 33 | PTHR24092,P ⁻ | | 0 3.6.3.1 | K14802 | GO:0046872,(| AT5G04930.1 |
| 34 | PTHR33673,P ⁻ | | 0 | 0 | 0 | 0 AT1G74220.1 |
| 35 | PTHR33673,P ⁻ | | 0 | 0 | 0 | 0 AT1G74220.1 |
| 36 | PTHR33977,P ⁻ | | 0 | 0 | 0 | 0 AT4G13970.1 |
| 37 | PTHR33977,P ⁻ | | 0 | 0 | 0 | 0 AT4G13970.1 |
| 38 | PTHR10209,P ⁻ | KOG0143 | 1.14.11.32 | | 0 GO:0055114,(| AT3G21420.1 |
| 39 | PTHR10209,P ⁻ | KOG0143 | 1.14.11.32 | | 0 GO:0055114,(| AT3G21420.1 |
| 40 | PTHR12048 | | 0 | 0 K14832 | GO:0008236,(| AT1G72440.1 |
| 41 | PTHR12048 | | 0 | 0 K14832 | GO:0008236,(| AT1G72440.1 |
| 42 | PTHR21780,P ⁻ | KOG4670 | | 0 | 0 | 0 AT1G07970.1 |
| 43 | PTHR21780,P ⁻ | KOG4670 | | 0 | 0 | 0 AT1G07970.1 |
| 44 | PTHR11757,P ⁻ | | 0 3.4.21.26 | K01322 | GO:0008236,(| AT1G76140.1 |
| 45 | PTHR11757,P ⁻ | | 0 3.4.21.26 | K01322 | GO:0008236,(| AT1G76140.1 |
| 46 | PTHR14155,P ⁻ | | 0 | 0 | 0 GO:0008270,(| AT5G43420.1 |
| 47 | PTHR14155,P ⁻ | | 0 | 0 | 0 GO:0008270,(| AT5G43420.1 |
| 48 | PTHR32227,P ⁻ | | 0 3.2.1.39 | | 0 GO:0005975,(| AT5G67460.1 |
| 49 | PTHR32227,P ⁻ | | 0 3.2.1.39 | | 0 GO:0005975,(| AT5G67460.1 |
| 50 | PTHR31300,P ⁻ | | 0 | 0 | 0 | 0 AT5G66740.1 |
| 51 | PTHR31300,P ⁻ | | 0 | 0 | 0 | 0 AT5G66740.1 |
| 52 | PTHR11999,P ⁻ | | 0 4.1.1.15 | K01580 | GO:0030170,(| AT5G17330.1 |
| 53 | PTHR11999,P ⁻ | | 0 4.1.1.15 | K01580 | GO:0030170,(| AT5G17330.1 |
| 54 | PTHR27001,P ⁻ | KOG1187 | 2.7.11.1,2.7.11.1 | | 0 GO:0006468,(| AT4G33430.1 |
| 55 | PTHR27001,P ⁻ | KOG1187 | 2.7.11.1,2.7.11.1 | | 0 GO:0006468,(| AT4G33430.1 |
| 56 | PTHR27001,P ⁻ | KOG1187 | 2.7.11.1,2.7.11.1 | | 0 GO:0006468,(| AT4G33430.1 |
| 57 | PTHR27001,P ⁻ | KOG1187 | 2.7.11.1,2.7.11.1 | | 0 GO:0006468,(| AT4G33430.1 |
| 58 | PTHR34775,P ⁻ | | 0 | 0 | 0 | 0 AT2G16270.1 |
| 59 | PTHR34775,P ⁻ | | 0 | 0 | 0 | 0 AT2G16270.1 |
| 60 | PTHR13844,P ⁻ | KOG2570 | | 0 K11650 | GO:0005515 | AT5G14170.1 |
| 61 | PTHR13844,P ⁻ | KOG2570 | | 0 K11650 | GO:0005515 | AT5G14170.1 |
| 62 | PTHR23111,P ⁻ | | 0 | 0 | 0 GO:0008270 | AT2G17975.1 |
| 63 | PTHR23111,P ⁻ | | 0 | 0 | 0 GO:0008270 | AT2G17975.1 |
| 64 | PTHR23111,P ⁻ | | 0 | 0 | 0 GO:0008270 | AT2G17975.1 |
| 65 | PTHR23111,P ⁻ | | 0 | 0 | 0 GO:0008270 | AT2G17975.1 |
| 66 | PTHR23111,P ⁻ | | 0 | 0 | 0 GO:0008270 | AT2G17975.1 |
| 67 | PTHR11926,P ⁻ | | 0 2.4.1.173 | | 0 GO:0016758,(| AT1G43620.3 |
| 68 | PTHR11926,P ⁻ | | 0 2.4.1.173 | | 0 GO:0016758,(| AT1G43620.3 |
| 69 | PTHR11926,P ⁻ | | 0 2.4.1.173 | | 0 GO:0016758,(| AT1G43620.3 |
| 70 | PTHR11926,P ⁻ | | 0 2.4.1.173 | | 0 GO:0016758,(| AT1G43620.3 |
| 71 | PTHR11926,P ⁻ | | 0 2.4.1.173 | | 0 GO:0016758,(| AT1G43620.3 |

| | | | | | | |
|----|----------------------------------|-------------------|----------|----------------|---------------|---|
| 1 | | | | | | |
| 2 | PTHR11926,P ⁻ | 0 2.4.1.173 | | 0 GO:0016758,(| AT1G43620.3 | |
| 3 | PTHR11926,P ⁻ | 0 2.4.1.173 | | 0 GO:0016758,(| AT1G43620.3 | |
| 4 | PTHR27004,P ⁻ KOG0472 | 2.7.11.1 | | 0 GO:0005515 | AT2G34930.1 | |
| 5 | | | | | | |
| 6 | PTHR19241,P ⁻ | 0 3.6.3.25 | | 0 GO:0016887,(| AT1G17840.1 | |
| 7 | PTHR24298,P ⁻ | 0 1.14.13.123,1. | | 0 GO:0055114,(| AT3G26300.1 | |
| 8 | PTHR13872,P ⁻ | 0 2.4.99.18 | K07151 | GO:0016020,(| AT5G19690.1 | |
| 9 | | | | | | |
| 10 | PTHR13301,P ⁻ | 0 2.4.1.12 | | 0 GO:0030244,(| AT4G24010.1 | |
| 11 | PTHR11937,P ⁻ KOG0676 | | 0 K16615 | | 0 AT3G60830.1 | |
| 12 | PTHR24067,P ⁻ KOG0417 | 6.3.2.19 | K10581 | | 0 AT3G15355.1 | |
| 13 | | | | | | |
| 14 | PTHR15362,P ⁻ | 0 2.7.8.8 | K08730 | GO:0006659 | AT1G15110.1 | |
| 15 | PTHR15362,P ⁻ | 0 2.7.8.8 | K08730 | GO:0006659 | AT1G15110.1 | |
| 16 | 0 | 0 | 0 | 0 | 0 | 0 |
| 17 | 0 | 0 | 0 | 0 | 0 | 0 |
| 18 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | PTHR33512,P ⁻ | 0 | 0 | 0 | 0 AT3G08600.1 | |
| 21 | PTHR19375,P ⁻ | 0 | 0 K09489 | | 0 AT1G11660.1 | |
| 22 | PTHR19375,P ⁻ | 0 | 0 K09489 | | 0 AT1G11660.1 | |
| 23 | PTHR19375,P ⁻ | 0 | 0 K09489 | | 0 AT1G11660.1 | |
| 24 | PTHR19375,P ⁻ | 0 | 0 K09489 | | 0 AT1G11660.1 | |
| 25 | PTHR19375,P ⁻ | 0 | 0 K09489 | | 0 AT1G11660.1 | |
| 26 | PTHR19375,P ⁻ | 0 | 0 K09489 | | 0 AT1G11660.1 | |
| 27 | PTHR11938,P ⁻ | 0 1.4.1.14 | K00264 | GO:0055114,(| AT5G53460.1 | |
| 28 | PTHR24006,P ⁻ KOG4341 | | 0 | 0 GO:0005515 | AT4G33210.1 | |
| 29 | PTHR24343,P ⁻ KOG0583 | 2.7.11.1 | | 0 GO:0007165 | AT1G30270.1 | |
| 30 | | | | | | |
| 31 | 0 | 0 | 0 | 0 | 0 AT5G59305.1 | |
| 32 | PTHR33389,P ⁻ | 0 | 0 | 0 | 0 AT4G21700.1 | |
| 33 | PTHR22753,P ⁻ | 0 | 0 | 0 GO:0016747 | AT5G41130.1 | |
| 34 | | | | | | |
| 35 | PTHR32518,P ⁻ | 0 2.4.1.25 | K00705 | GO:0005975,(| AT2G40840.1 | |
| 36 | PTHR26374,P ⁻ | 0 | 0 | 0 | 0 AT4G17810.1 | |
| 37 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1,2.7.11.1 | | 0 GO:0006468,(| AT2G17220.1 | |
| 38 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1,2.7.11.1 | | 0 GO:0006468,(| AT2G17220.1 | |
| 39 | | | | | | |
| 40 | 0 | 0 | 0 | 0 | 0 | 0 |
| 41 | PTHR26374,P ⁻ | 0 | 0 | 0 | 0 AT1G26610.1 | |
| 42 | PTHR26374,P ⁻ | 0 | 0 | 0 | 0 AT1G26610.1 | |
| 43 | | | | | | |
| 44 | PTHR11214,P ⁻ KOG2287 | 2.4.1.134 | | 0 GO:0016020,(| AT4G21060.2 | |
| 45 | PTHR11005,P ⁻ KOG2624 | 3.1.1.3 | | 0 | 0 AT1G73920.1 | |
| 46 | PTHR11005,P ⁻ KOG2624 | 3.1.1.3 | | 0 | 0 AT1G73920.1 | |
| 47 | | | | | | |
| 48 | PTHR32227,P ⁻ | 0 | 0 | 0 | 0 AT1G18650.1 | |
| 49 | PTHR31839,P ⁻ | 0 | 0 | 0 GO:0006355,(| AT5G51990.1 | |
| 50 | | | | | | |
| 51 | PTHR11206,P ⁻ KOG1347 | | 0 K03327 | GO:0055085,(| AT4G23030.1 | |
| 52 | PTHR24055,P ⁻ KOG0660 | 2.7.11.24 | K04371 | GO:0006468,(| AT2G42880.1 | |
| 53 | PTHR24055,P ⁻ KOG0660 | 2.7.11.24 | K04371 | GO:0006468,(| AT2G42880.1 | |
| 54 | | | | | | |
| 55 | PTHR22880,P ⁻ | 0 | 0 | 0 GO:0005515 | AT1G58025.3 | |
| 56 | PTHR12436,P ⁻ KOG1861 | | 0 | 0 | 0 AT2G39340.1 | |
| 57 | PTHR31677,P ⁻ | 0 | 0 | 0 GO:0006355,(| AT1G12890.1 | |
| 58 | PTHR37236,P ⁻ | 0 | 0 | 0 | 0 AT4G02980.1 | |
| 59 | | | | | | |
| 60 | PTHR10108,P ⁻ | 0 2.1.1.41 | | 0 GO:0008168 | AT2G43200.1 | |
| | PTHR19302,P ⁻ | 0 | 0 K16572 | GO:0005815,(| AT1G80260.1 | |

| | | | | | |
|----|--------------------------|-------------|----------|--------------|-------------|
| 1 | | | | | |
| 2 | PTHR10359,P ⁻ | 0 4.2.99.18 | 0 | 0 | AT5G04560.2 |
| 3 | PTHR31300,P ⁻ | 0 | 0 | 0 | AT5G66740.1 |
| 4 | PTHR34805 | 0 | 0 | 0 | AT4G24680.1 |
| 5 | PTHR34805 | 0 | 0 | 0 | AT4G24680.1 |
| 6 | PTHR16057,P ⁻ | 0 | 0 | 0 | AT3G50430.1 |
| 7 | PTHR16057,P ⁻ | 0 | 0 | 0 | AT3G50430.1 |
| 8 | PTHR16057,P ⁻ | 0 | 0 | 0 | AT3G50430.1 |
| 9 | PTHR16057,P ⁻ | 0 | 0 | 0 | AT3G50430.1 |
| 10 | PTHR16057,P ⁻ | 0 | 0 | 0 | AT3G50430.1 |
| 11 | 0 | 0 | 0 | 0 | 0 0 |
| 12 | PTHR31942,P ⁻ | 0 | 0 K08472 | GO:0016021,C | AT2G39200.1 |
| 13 | PTHR11764,P ⁻ | 0 5.4.99.41 | 0 | GO:0003824 | AT2G07050.1 |
| 14 | PTHR11764,P ⁻ | 0 5.4.99.41 | 0 | GO:0003824 | AT2G07050.1 |
| 15 | PTHR24223,P ⁻ | 0 3.6.3.44 | K05674 | GO:0016887,C | AT2G07680.1 |
| 16 | PTHR24223,P ⁻ | 0 3.6.3.44 | K05674 | GO:0016887,C | AT2G07680.1 |
| 17 | PTHR24223,P ⁻ | 0 3.6.3.44 | K05674 | GO:0016887,C | AT2G07680.1 |
| 18 | PTHR31221,P ⁻ | 0 | 0 | GO:0043565,C | AT4G26640.2 |
| 19 | PTHR31221,P ⁻ | 0 | 0 | GO:0043565,C | AT4G26640.2 |
| 20 | PTHR31221,P ⁻ | 0 | 0 | GO:0043565,C | AT4G26640.2 |
| 21 | PTHR31234,P ⁻ | 0 | 0 | 0 | AT4G01110.1 |
| 22 | PTHR31234,P ⁻ | 0 | 0 | 0 | AT4G01110.1 |
| 23 | PTHR13803,P ⁻ | 0 | 0 K14007 | GO:0030127,C | AT3G07100.1 |
| 24 | PTHR22850 | 0 | 0 K14848 | GO:0005515 | AT2G19540.1 |
| 25 | PTHR11926,P ⁻ | 0 2.4.1.170 | 0 | GO:0016758,C | AT3G02100.1 |
| 26 | PTHR11926,P ⁻ | 0 2.4.1.170 | 0 | GO:0016758,C | AT3G02100.1 |
| 27 | PTHR33167,P ⁻ | 0 | 0 | 0 | AT1G13940.1 |
| 28 | PTHR33167,P ⁻ | 0 | 0 | 0 | AT1G13940.1 |
| 29 | | | | | |
| 30 | | | | | |
| 31 | | | | | |
| 32 | | | | | |
| 33 | | | | | |
| 34 | | | | | |
| 35 | | | | | |
| 36 | | | | | |
| 37 | | | | | |
| 38 | | | | | |
| 39 | | | | | |
| 40 | | | | | |
| 41 | | | | | |
| 42 | | | | | |
| 43 | | | | | |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| 1 | arabi-symbol | arabi-defline | ID | Annot_defline |
|----|---|--|------------------------------|---------------|
| 2 | | 0 Flavodoxin family protein | Phvul.008G001.5.1.30 - Flav | |
| 3 | | 0 Sec14p-like phosphatidylinositol transfer family | Phvul.009G00PTHR23324:SF | |
| 4 | | 0 Sec14p-like phosphatidylinositol transfer family | Phvul.009G00PTHR23324:SF | |
| 5 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.002G31PTHR11005:SF | |
| 6 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.002G31PTHR11005:SF | |
| 7 | AIM1 | Enoyl-CoA hydratase/isomerase family | Phvul.004G161.1.1.35//4.2. | |
| 8 | | 0 Uncharacterized conserved protein (DUF2358) | Phvul.005G04PTHR22750 - C | |
| 9 | ATPOB1,POB1 | POZ/BTB containin G-protein 1 | Phvul.010G10PF00651//PFC | |
| 10 | | 0 | 0 Phvul.L00814:PTHR33912:SF | |
| 11 | UPL1 | ubiquitin-protein ligase 1 | Phvul.002G18PTHR11254:SF | |
| 12 | UPL1 | ubiquitin-protein ligase 1 | Phvul.002G18PTHR11254:SF | |
| 13 | UPL1 | ubiquitin-protein ligase 1 | Phvul.002G18PTHR11254:SF | |
| 14 | UPL1 | ubiquitin-protein ligase 1 | Phvul.002G18PTHR11254:SF | |
| 15 | | 0 | 0 Phvul.002G25PTHR31852:SF | |
| 16 | GSO1 | Leucine-rich repeat transmembrane protein kin | Phvul.003G20PF00560//PFC | |
| 17 | | 0 DNA binding | Phvul.003G28PTHR22715 - | |
| 18 | HISN6B | HISTIDINE BIOSYNTHESIS 6B | Phvul.004G082.6.1.9 - Histic | |
| 19 | | 0 | 0 Phvul.006G11PTHR31234:SF | |
| 20 | ATPS5,TPS5 | trehalose phosphatase/synthase 5 | Phvul.007G03PTHR10788:SF | |
| 21 | ATPS5,TPS5 | trehalose phosphatase/synthase 5 | Phvul.007G03PTHR10788:SF | |
| 22 | ADCS,emb1997 | para-aminobenzoate (PABA) synthase family pr | Phvul.007G092.6.1.85 - Ami | |
| 23 | ALA1 | aminophospholipid ATPase 1 | Phvul.008G08K14802 - phos | |
| 24 | | 0 | 0 0 0 | |
| 25 | | 0 zinc ion binding | Phvul.009G23PTHR33977:SF | |
| 26 | | 0 2-oxoglutarate (2OG) and Fe(II)-dependent oxy | Phvul.009G24PTHR10209//I | |
| 27 | EDA25,SWA2 | CCAAT-binding factor | Phvul.010G12K14832 - ribos | |
| 28 | | 0 | 0 Phvul.011G07PTHR21780:SF | |
| 29 | | 0 Prolyl oligopeptidase family protein | Phvul.001G003.4.21.26 - Pro | |
| 30 | | 0 RING/U-box superfamily protein | Phvul.001G16PTHR14155//I | |
| 31 | | 0 O-Glycosyl hydrolases family 17 protein | Phvul.002G01PTHR32227:SF | |
| 32 | | 0 Protein of unknown function (DUF620) | Phvul.002G02PF04788 - Pro | |
| 33 | GAD,GAD1 | glutamate decarboxylase | Phvul.002G18PTHR11999//I | |
| 34 | ATBAK1,ATSERK3,BAK: BRI1-associated receptor kinase | | Phvul.002G20K13416 - bras: | |
| 35 | ATBAK1,ATSERK3,BAK: BRI1-associated receptor kinase | | Phvul.002G20K13416 - bras: | |
| 36 | | 0 | 0 0 0 | |
| 37 | CHC1 | SWIB/MDM2 domain superfamily protein | Phvul.003G21K11650 - SWI/ | |
| 38 | | 0 zinc finger (Ran-binding) family protein | Phvul.003G26PTHR23111//I | |
| 39 | | 0 zinc finger (Ran-binding) family protein | Phvul.003G26PTHR23111//I | |
| 40 | | 0 zinc finger (Ran-binding) family protein | Phvul.003G26PTHR23111//I | |
| 41 | | 0 zinc finger (Ran-binding) family protein | Phvul.003G26PTHR23111//I | |
| 42 | TT15,UGT80B1 | UDP-Glycosyltransferase superfamily protein | Phvul.004G09PTHR11926:SF | |
| 43 | TT15,UGT80B1 | UDP-Glycosyltransferase superfamily protein | Phvul.004G09PTHR11926:SF | |
| 44 | TT15,UGT80B1 | UDP-Glycosyltransferase superfamily protein | Phvul.004G09PTHR11926:SF | |
| 45 | TT15,UGT80B1 | UDP-Glycosyltransferase superfamily protein | Phvul.004G09PTHR11926:SF | |
| 46 | TT15,UGT80B1 | UDP-Glycosyltransferase superfamily protein | Phvul.004G09PTHR11926:SF | |

| | | | | | |
|----|----------------------|--|-----------------------------------|----------|----------|
| 1 | | | | | |
| 2 | TT15,UGT80B1 | UDP-Glycosyltransferase superfamily protein | Phvul.004G09PTHR11926:SI | | |
| 3 | TT15,UGT80B1 | UDP-Glycosyltransferase superfamily protein | Phvul.004G09PTHR11926:SI | | |
| 4 | | 0 disease resistance family protein / LRR family protein | Phvul.004G10KOG0472 - Leu | | |
| 5 | | | | | |
| 6 | ABCG11,ATWBC11,CO | white-brown complex homolog protein 11 | Phvul.004G13PTHR19241://I | | |
| 7 | CYP71B34 | cytochrome P450, family 71, subfamily B, polyp | Phvul.004G15PF00067 - Cyt | | |
| 8 | STT3A | staurosporin and temperature sensitive 3-like | A Phvul.004G17PTHR13872:SI | | |
| 9 | | | | | |
| 10 | ATCSLG1,CSLG1 | cellulose synthase like G1 | Phvul.005G00PTHR13301://I | | |
| 11 | ARP7,ATARP7 | actin-related protein 7 | Phvul.005G02K16615 - actin | | |
| 12 | PFU1,UBC25 | ubiquitin-conjugating enzyme 25 | Phvul.005G07PTHR24067:SI | | |
| 13 | | | | | |
| 14 | | 0 phosphatidyl serine synthase family protein | Phvul.007G032.7.8.8 - CDP- | | |
| 15 | | 0 phosphatidyl serine synthase family protein | Phvul.007G032.7.8.8 - CDP- | | |
| 16 | | 0 | 0 | 0 | 0 |
| 17 | | 0 | 0 | 0 | 0 |
| 18 | | 0 | 0 | 0 | 0 |
| 19 | | 0 | 0 | 0 | 0 |
| 20 | | 0 Protein of unknown function (DUF1191) | Phvul.008G07PF06697 - Pro | | |
| 21 | | 0 heat shock protein 70 (Hsp 70) family protein | Phvul.008G26PTHR19375://I | | |
| 22 | | 0 heat shock protein 70 (Hsp 70) family protein | Phvul.008G26PTHR19375://I | | |
| 23 | | 0 heat shock protein 70 (Hsp 70) family protein | Phvul.008G26PTHR19375://I | | |
| 24 | | 0 heat shock protein 70 (Hsp 70) family protein | Phvul.008G26PTHR19375://I | | |
| 25 | | 0 heat shock protein 70 (Hsp 70) family protein | Phvul.008G26PTHR19375://I | | |
| 26 | | | | | |
| 27 | GLT1 | NADH-dependent glutamate synthase 1 | Phvul.009G051.4.1.14 - Glut | | |
| 28 | SLOMO | F-box family protein | Phvul.009G08PTHR24006:SI | | |
| 29 | ATCIPK23,CIPK23,LKS1 | CBL-interacting protein kinase 23 | Phvul.009G21PTHR24343:SI | | |
| 30 | | | | | |
| 31 | | 0 | 0 | 0 | 0 |
| 32 | | 0 Protein of unknown function (DUF2921) | Phvul.001G07PF11145 - Pro | | |
| 33 | | 0 Esterase/lipase/thioesterase family protein | Phvul.001G08PTHR22753:SI | | |
| 34 | | | | | |
| 35 | DPE2 | disproportionating enzyme 2 | Phvul.001G112.4.1.25 - 4-al | | |
| 36 | | 0 C2H2 and C2HC zinc fingers superfamily protein | Phvul.002G00PF13912 - C2f | | |
| 37 | | 0 Protein kinase superfamily protein | Phvul.002G11PTHR27001:SI | | |
| 38 | | 0 Protein kinase superfamily protein | Phvul.002G11PTHR27001:SI | | |
| 39 | | 0 | 0 | 0 | 0 |
| 40 | | 0 C2H2-like zinc finger protein | Phvul.002G16PTHR26374:SI | | |
| 41 | | 0 C2H2-like zinc finger protein | Phvul.002G16PTHR26374:SI | | |
| 42 | | 0 Galactosyltransferase family protein | Phvul.002G17PTHR11214:SI | | |
| 43 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.002G31PTHR11005:SI | | |
| 44 | | 0 alpha/beta-Hydrolases superfamily protein | Phvul.002G31PTHR11005:SI | | |
| 45 | | | | | |
| 46 | PDCB3 | plasmodesmata callose-binding protein 3 | Phvul.003G18PTHR32227:SI | | |
| 47 | | | | | |
| 48 | CBF4,DREB1D | C-repeat-binding factor 4 | Phvul.003G21PTHR31839:SI | | |
| 49 | | | | | |
| 50 | | 0 MATE efflux family protein | Phvul.004G12PTHR11206:SI | | |
| 51 | | | | | |
| 52 | ATMPK20,MPK20 | MAP kinase 20 | Phvul.006G03PTHR24055:SI | | |
| 53 | ATMPK20,MPK20 | MAP kinase 20 | Phvul.006G03PTHR24055:SI | | |
| 54 | | | | | |
| 55 | | 0 DNA-binding bromodomain-containing protein | Phvul.006G21PTHR22880:SI | | |
| 56 | | 0 SAC3/GANP/Nin1/mts3/eIF-3 p25 family | Phvul.007G00PTHR12436:SI | | |
| 57 | | 0 Integrase-type DNA-binding superfamily protein | Phvul.007G08PF00847 - APz | | |
| 58 | | | | | |
| 59 | ABP,ABP1 | endoplasmic reticulum auxin binding protein 1 | Phvul.007G16PTHR37236:SI | | |
| 60 | | 0 S-adenosyl-L-methionine-dependent methyltra | Phvul.008G00PTHR10108://I | | |
| | emb1427 | Spc97 / Spc98 family of spindle pole body (SBP) | Phvul.009G06K16572 - gam | | |

| | | | |
|----|-----------------|--|-----------------------------|
| 1 | | | |
| 2 | DME | HhH-GPD base excision DNA repair family prote | Phvul.001G18PTHR10359:SI |
| 3 | | 0 Protein of unknown function (DUF620) | Phvul.002G02PF04788 - Pro |
| 4 | MOS1 | modifier of snc1 | Phvul.003G20PF07001 - BA1 |
| 5 | MOS1 | modifier of snc1 | Phvul.003G20PF07001 - BA1 |
| 6 | | 0 | 0 Phvul.003G24PTHR16057 - \ |
| 7 | | 0 | 0 Phvul.003G24PTHR16057 - \ |
| 8 | | 0 | 0 Phvul.003G24PTHR16057 - \ |
| 9 | | 0 | 0 Phvul.003G24PTHR16057 - \ |
| 10 | | 0 | 0 Phvul.003G24PTHR16057 - \ |
| 11 | | 0 | 0 0 0 |
| 12 | ATMLO12,MLO12 | Seven transmembrane MLO family protein | Phvul.004G07PTHR31942:SI |
| 13 | CAS1 | cycloartenol synthase 1 | Phvul.004G17PTHR11764//I |
| 14 | CAS1 | cycloartenol synthase 1 | Phvul.004G17PTHR11764//I |
| 15 | ATMRP11,MRP11 | multidrug resistance-associated protein 11 | Phvul.005G17K05674 - ATP- |
| 16 | ATMRP11,MRP11 | multidrug resistance-associated protein 11 | Phvul.005G17K05674 - ATP- |
| 17 | AtWRKY20,WRKY20 | WRKY family transcription factor family protein | Phvul.006G05PTHR31221:SI |
| 18 | AtWRKY20,WRKY20 | WRKY family transcription factor family protein | Phvul.006G05PTHR31221:SI |
| 19 | | 0 | 0 Phvul.006G11PTHR31234:SI |
| 20 | ERMO2,SEC24A | Sec23/Sec24 protein transport family protein | Phvul.007G20K14007 - prot |
| 21 | | 0 Transducin family protein / WD-40 repeat famil | Phvul.008G00K14848 - ribos |
| 22 | | 0 UDP-Glycosyltransferase superfamily protein | Phvul.008G03PTHR11926//I |
| 23 | | 0 Plant protein of unknown function (DUF863) | Phvul.009G18PTHR33167:SI |
| 24 | | 0 Plant protein of unknown function (DUF863) | Phvul.009G18PTHR33167:SI |
| 25 | | | |
| 26 | | | |
| 27 | | | |
| 28 | | | |
| 29 | | | |
| 30 | | | |
| 31 | | | |
| 32 | | | |
| 33 | | | |
| 34 | | | |
| 35 | | | |
| 36 | | | |
| 37 | | | |
| 38 | | | |
| 39 | | | |
| 40 | | | |
| 41 | | | |
| 42 | | | |
| 43 | | | |
| 44 | | | |
| 45 | | | |
| 46 | | | |
| 47 | | | |
| 48 | | | |
| 49 | | | |
| 50 | | | |
| 51 | | | |
| 52 | | | |
| 53 | | | |
| 54 | | | |
| 55 | | | |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

| IDENTIFIER | NAME | DESCRIPTION |
|--------------|--|-------------|
| Phvul.008G00 | Coenzyme me component TAH18 of cytosolic CIA system assembly phase (original de | |
| Phvul.009G00 | not assigned.ε (original description: pacid=37150821 transcript=Phvul.009G006000.3 | |
| Phvul.009G00 | not assigned.ε (original description: pacid=37150821 transcript=Phvul.009G006000.3 | |
| Phvul.002G31 | not assigned.r no hits & (original description: pacid=37174769 transcript=Phvul.002G | |
| Phvul.002G31 | not assigned.r no hits & (original description: pacid=37174769 transcript=Phvul.002G | |
| Phvul.004G16 | Lipid metaboli multifunctional enzyme (MFP) (original description: pacid=37162576 tr | |
| Phvul.005G04 | not assigned.r no hits & (original description: pacid=37153695 transcript=Phvul.005G | |
| Phvul.010G10 | Protein home component LRB of CUL3-BTB E3 ubiquitin ligase complex (original desc | |
| Phvul.L00814 | :not assigned.r no hits & (original description: pacid=37178968 transcript=Phvul.L008 | |
| Phvul.002G18 | Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=3717 | |
| Phvul.002G18 | Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=3717 | |
| Phvul.002G18 | Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=3717 | |
| Phvul.002G18 | Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=3717 | |
| Phvul.002G25 | not assigned.r no hits & (original description: pacid=37175064 transcript=Phvul.002G | |
| Phvul.003G20 | Phytohormon CIF-peptide receptor (GSO) (original description: pacid=37147649 tran: | |
| Phvul.003G28 | not assigned.r no hits & (original description: pacid=37147414 transcript=Phvul.003G | |
| Phvul.004G08 | Amino acid m histidinol-phosphate aminotransferase (original description: pacid=371 | |
| Phvul.006G11 | not assigned.r no hits & (original description: pacid=37173968 transcript=Phvul.006G | |
| Phvul.007G03 | Enzyme classii Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 5 OS=Arabic | |
| Phvul.007G03 | Enzyme classii Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 5 OS=Arabic | |
| Phvul.007G09 | Coenzyme me aminodeoxychorismate synthase (original description: pacid=3716718(| |
| Phvul.008G08 | Solute transpc P4-type ATPase component ALA of phospholipid flippase complex (orig | |
| Phvul.009G20 | not assigned.r no hits & (original description: pacid=37150792 transcript=Phvul.009G | |
| Phvul.009G23 | not assigned.r no hits & (original description: pacid=37149731 transcript=Phvul.009G | |
| Phvul.009G24 | Phytohormon oxidoreductase (LBO) (original description: pacid=37151443 transcript: | |
| Phvul.010G12 | Protein biosyr component NOC1 of ribosomal subunit nuclear export complex (origin | |
| Phvul.011G07 | not assigned.r no hits & (original description: pacid=37154989 transcript=Phvul.011G | |
| Phvul.001G00 | Enzyme classii Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting on pepi | |
| Phvul.001G16 | Protein home RING-H2-class E3 ligase (original description: pacid=37168057 transcrip | |
| Phvul.002G01 | Enzyme classii Glucan endo-1,3-beta-glucosidase 13 OS=Arabidopsis thaliana (sp q9fj | |
| Phvul.002G02 | Multi-process GTPase effector (BDR) (original description: pacid=37174686 transcript | |
| Phvul.002G18 | Amino acid m glutamate decarboxylase (original description: pacid=37174418 transcr | |
| Phvul.002G20 | Protein modif protein kinase (LRR-II) (original description: pacid=37176803 transcript | |
| Phvul.002G20 | Protein modif protein kinase (LRR-II) (original description: pacid=37176803 transcript | |
| Phvul.003G07 | not assigned.r no hits & (original description: pacid=37147041 transcript=Phvul.003G | |
| Phvul.003G21 | Chromatin orç component BAF60 of chromatin remodeling complex (original descript | |
| Phvul.003G26 | not assigned.r no hits & (original description: pacid=37145402 transcript=Phvul.003G | |
| Phvul.003G26 | not assigned.r no hits & (original description: pacid=37145402 transcript=Phvul.003G | |
| Phvul.003G26 | not assigned.r no hits & (original description: pacid=37145402 transcript=Phvul.003G | |
| Phvul.003G26 | not assigned.r no hits & (original description: pacid=37145402 transcript=Phvul.003G | |
| Phvul.004G09 | Lipid metaboli UDP-glucose:sterol glucosyltransferase (original description: pacid=371 | |
| Phvul.004G09 | Lipid metaboli UDP-glucose:sterol glucosyltransferase (original description: pacid=371 | |
| Phvul.004G09 | Lipid metaboli UDP-glucose:sterol glucosyltransferase (original description: pacid=371 | |
| Phvul.004G09 | Lipid metaboli UDP-glucose:sterol glucosyltransferase (original description: pacid=371 | |
| Phvul.004G09 | Lipid metaboli UDP-glucose:sterol glucosyltransferase (original description: pacid=371 | |

1 Phvul.004G09Lipid metabolite UDP-glucose:sterol glucosyltransferase (original description: pacid=371
2 Phvul.004G09Lipid metabolite UDP-glucose:sterol glucosyltransferase (original description: pacid=371
3 Phvul.004G10not assigned.ε (original description: pacid=37162970 transcript=Phvul.004G105600.1
4 Phvul.004G13Solute transport subfamily ABCG transporter (original description: pacid=37162910 tra
5 Phvul.004G15Enzyme class II Cytochrome P450 CYP736A12 OS=Panax ginseng (sp|h2dh18|c7a12_p
6 **Phvul.004G17Protein modification component STT3 of oligosaccharyl transferase (OST) complex (original**
7 **Phvul.005G00not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1**
8 Phvul.005G02Chromatin organization component ARP7 of chromatin remodeling complex (original descriptio
9 Phvul.005G07not assigned.ε (original description: pacid=37154333 transcript=Phvul.005G072300.1
10 Phvul.007G03Lipid metabolite base-exchange-type phosphatidylserine synthase (original description:
11 Phvul.007G03Lipid metabolite base-exchange-type phosphatidylserine synthase (original description:
12 Phvul.007G24not assigned.r no hits & (original description: pacid=37165375 transcript=Phvul.007G
13 Phvul.007G24not assigned.r no hits & (original description: pacid=37165375 transcript=Phvul.007G
14 **Phvul.007G24not assigned.r no hits & (original description: pacid=37164381 transcript=Phvul.007G**
15 Phvul.008G07not assigned.r no hits & (original description: pacid=37160757 transcript=Phvul.008G
16 Phvul.008G26Protein homeodomain chaperone (Hsp110) (original description: pacid=37160259 transcript=
17 Phvul.008G26Protein homeodomain chaperone (Hsp110) (original description: pacid=37160259 transcript=
18 Phvul.008G26Protein homeodomain chaperone (Hsp110) (original description: pacid=37160259 transcript=
19 Phvul.008G26Protein homeodomain chaperone (Hsp110) (original description: pacid=37160259 transcript=
20 Phvul.009G05Nutrient uptake NADH-dependent glutamate synthase (original description: pacid=371
21 Phvul.009G08not assigned.ε (original description: pacid=37152092 transcript=Phvul.009G081900.1
22 Phvul.009G21Protein modification SNF1-related protein kinase (SnRK3) (original description: pacid=37149
23 Phvul.011G06Phytohormone CLE precursor polypeptide (original description: pacid=37155545 trans
24 Phvul.001G07not assigned.r no hits & (original description: pacid=37168871 transcript=Phvul.001G
25 Phvul.001G08not assigned.ε (original description: pacid=37168110 transcript=Phvul.001G087700.1
26 Phvul.001G11not assigned.ε (original description: pacid=37168578 transcript=Phvul.001G117500.1
27 Phvul.002G00RNA biosynthesis C2H2 zinc finger transcription factor (original description: pacid=37175
28 Phvul.002G11Protein modification receptor-like protein kinase (RLCK-VIIa) (original description: pacid=37
29 Phvul.002G11Protein modification receptor-like protein kinase (RLCK-VIIa) (original description: pacid=37
30 Phvul.002G16not assigned.r no hits & (original description: pacid=37178055 transcript=Phvul.002G
31 Phvul.002G16RNA biosynthesis C2H2 zinc finger transcription factor (original description: pacid=37177
32 Phvul.002G16RNA biosynthesis C2H2 zinc finger transcription factor (original description: pacid=37177
33 Phvul.002G17Cell wall organization AGP hydroxyproline O-galactosyltransferase (original description: pacid
34 Phvul.002G31not assigned.r no hits & (original description: pacid=37174769 transcript=Phvul.002G
35 Phvul.002G31not assigned.r no hits & (original description: pacid=37174769 transcript=Phvul.002G
36 Phvul.003G18not assigned.ε (original description: pacid=37144453 transcript=Phvul.003G185300.1
37 Phvul.003G21RNA biosynthesis transcription factor (DREB) (original description: pacid=37145319 trans
38 Phvul.004G12Solute transport metabolite transporter (DTX) (original description: pacid=37162548 tra
39 Phvul.006G03Protein modification protein kinase (MAPK) (original description: pacid=37172750 transcrip
40 Phvul.006G03Protein modification protein kinase (MAPK) (original description: pacid=37172750 transcrip
41 Phvul.006G21not assigned.r no hits & (original description: pacid=37173703 transcript=Phvul.006G
42 Phvul.007G00RNA processing scaffold component GANP/SAC3 of TREX-2 mRNP trafficking complex (o
43 Phvul.007G08RNA biosynthesis transcription factor (ERF) (original description: pacid=37165267 transcri
44 Phvul.007G16not assigned.ε (original description: pacid=37166775 transcript=Phvul.007G168600.1
45 Phvul.008G00not assigned.ε (original description: pacid=37159786 transcript=Phvul.008G002700.1
46 Phvul.009G06Cytoskeleton organization component GCP5 of gamma-Tubulin ring complex (gamma-TuRC) (orig

1 Phvul.001G18DNA damage bifunctional DNA glycosylase/lyase (ROS1) (original description: pacid=
2 Phvul.002G02Multi-process GTPase effector (BDR) (original description: pacid=37174686 transcript=
3 Phvul.003G20not assigned.ε (original description: pacid=37147665 transcript=Phvul.003G202300.2
4 Phvul.003G20not assigned.ε (original description: pacid=37147665 transcript=Phvul.003G202300.2
5 Phvul.003G24not assigned.r no hits & (original description: pacid=37147737 transcript=Phvul.003C
6 Phvul.003G24not assigned.r no hits & (original description: pacid=37147737 transcript=Phvul.003C
7 Phvul.003G24not assigned.r no hits & (original description: pacid=37147737 transcript=Phvul.003C
8 Phvul.003G24not assigned.r no hits & (original description: pacid=37147737 transcript=Phvul.003C
9 Phvul.003G24not assigned.r no hits & (original description: pacid=37147737 transcript=Phvul.003C
10 Phvul.004G02not assigned.r no hits & (original description: pacid=37162719 transcript=Phvul.004C
11 Phvul.004G02not assigned.r no hits & (original description: pacid=37162719 transcript=Phvul.004C
12 Phvul.004G07not assigned.ε (original description: pacid=37163131 transcript=Phvul.004G071800.1
13 Phvul.004G17Secondary me triterpenoid synthase (original description: pacid=37162519 transcript:
14 Phvul.004G17Secondary me triterpenoid synthase (original description: pacid=37162519 transcript:
15 Phvul.005G17Solute transpεsubfamily ABCC transporter (original description: pacid=37153148 tran
16 Phvul.005G17Solute transpεsubfamily ABCC transporter (original description: pacid=37153148 tran
17 Phvul.005G17Solute transpεsubfamily ABCC transporter (original description: pacid=37153148 tran
18 Phvul.006G05RNA biosynthεtranscription factor (WRKY) (original description: pacid=37171441 tran
19 Phvul.006G05RNA biosynthεtranscription factor (WRKY) (original description: pacid=37171441 tran
20 Phvul.006G05RNA biosynthεtranscription factor (WRKY) (original description: pacid=37171441 tran
21 Phvul.006G11not assigned.r no hits & (original description: pacid=37173968 transcript=Phvul.006C
22 Phvul.007G20Vesicle traffice component Sec24 of Sec23/24 cargo adaptor subcomplex (original des
23 Phvul.008G00not assigned.ε (original description: pacid=37158292 transcript=Phvul.008G006800.1
24 Phvul.008G03Enzyme classii UDP-glycosyltransferase 83A1 OS=Arabidopsis thaliana (sp|q9sga8|u8
25 Phvul.009G18not assigned.r no hits & (original description: pacid=37149447 transcript=Phvul.009C
26 Phvul.009G18not assigned.r no hits & (original description: pacid=37149447 transcript=Phvul.009C
27 Phvul.009G18not assigned.r no hits & (original description: pacid=37149447 transcript=Phvul.009C
28 Phvul.009G18not assigned.r no hits & (original description: pacid=37149447 transcript=Phvul.009C
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3 description: pacid=37161177 transcript=Phvul.008G004800.1 locus=Phvul.008G004800 ID=Phvul.008G004800.1.v2.1 annot-version=v2.1) & Phosphatidylinositol
4 } locus=Phvul.009G006000 ID=Phvul.009G006000.3.v2.1 annot-version=v2.1) & Phosphatidylinositol
5 } locus=Phvul.009G006000 ID=Phvul.009G006000.3.v2.1 annot-version=v2.1) & Phosphatidylinositol
6 } 315000.2 locus=Phvul.002G315000 ID=Phvul.002G315000.2.v2.1 annot-version=v2.1)
7 } 315000.2 locus=Phvul.002G315000 ID=Phvul.002G315000.2.v2.1 annot-version=v2.1)
8
9 transcript=Phvul.004G164800.1 locus=Phvul.004G164800 ID=Phvul.004G164800.1.v2.1 annot-version=v2.1)
10 } 049000.1 locus=Phvul.005G049000 ID=Phvul.005G049000.1.v2.1 annot-version=v2.1)
11
12 description: pacid=37142307 transcript=Phvul.010G108200.1 locus=Phvul.010G108200 ID=Phvul.010G108200.1.v2.1 annot-version=v2.1)
13 } 143.1 locus=Phvul.L008143 ID=Phvul.L008143.1.v2.1 annot-version=v2.1)
14
15 **76691 transcript=Phvul.002G189700.4 locus=Phvul.002G189700 ID=Phvul.002G189700.4.v2.1 annot-version=v2.1)**
16 **76691 transcript=Phvul.002G189700.4 locus=Phvul.002G189700 ID=Phvul.002G189700.4.v2.1 annot-version=v2.1)**
17 **76691 transcript=Phvul.002G189700.4 locus=Phvul.002G189700 ID=Phvul.002G189700.4.v2.1 annot-version=v2.1)**
18 **76691 transcript=Phvul.002G189700.4 locus=Phvul.002G189700 ID=Phvul.002G189700.4.v2.1 annot-version=v2.1)**
19
20 } 258800.1 locus=Phvul.002G258800 ID=Phvul.002G258800.1.v2.1 annot-version=v2.1)
21
22 transcript=Phvul.003G202100.1 locus=Phvul.003G202100 ID=Phvul.003G202100.1.v2.1 annot-version=v2.1)
23 } 282800.1 locus=Phvul.003G282800 ID=Phvul.003G282800.1.v2.1 annot-version=v2.1)
24
25 161692 transcript=Phvul.004G083900.1 locus=Phvul.004G083900 ID=Phvul.004G083900.1.v2.1 annot-version=v2.1)
26 } 110000.1 locus=Phvul.006G110000 ID=Phvul.006G110000.1.v2.1 annot-version=v2.1)
27
28 } *At1g01010* (original description: pacid=37169558 transcript=Phvul.001G016000.1 locus=Phvul.001G016000.1.v2.1 annot-version=v2.1) & Enzyme classification.EC_2 transferases.EC_2.4 phosphatidylinositol 3-kinase (phosphatidylinositol 3-kinase)
29 } *At1g01010* (original description: pacid=37169558 transcript=Phvul.001G016000.1 locus=Phvul.001G016000.1.v2.1 annot-version=v2.1) & Enzyme classification.EC_2 transferases.EC_2.4 phosphatidylinositol 3-kinase (phosphatidylinositol 3-kinase)
30 } 0 transcript=Phvul.007G094100.1 locus=Phvul.007G094100 ID=Phvul.007G094100.1.v2.1 annot-version=v2.1)
31
32 original description: pacid=37159191 transcript=Phvul.008G081700.2 locus=Phvul.008G081700 ID=Phvul.008G081700.2.v2.1 annot-version=v2.1)
33 } 201900.1 locus=Phvul.009G201900 ID=Phvul.009G201900.1.v2.1 annot-version=v2.1)
34 } 233100.3 locus=Phvul.009G233100 ID=Phvul.009G233100.3.v2.1 annot-version=v2.1)
35 } 246200.2 locus=Phvul.009G246200 ID=Phvul.009G246200.2.v2.1 annot-version=v2.1) & Enzyme classification.EC_3 hydrolases.EC_3.2 glycosylase (glycosylase)
36
37 **original description: pacid=37144247 transcript=Phvul.010G125200.1 locus=Phvul.010G125200 ID=Phvul.010G125200.1.v2.1 annot-version=v2.1)**
38 } 073400.1 locus=Phvul.011G073400 ID=Phvul.011G073400.1.v2.1 annot-version=v2.1)
39
40 } tide bond (peptidase)(50.3.4 : 947.8) (original description: pacid=37169558 transcript=Phvul.001G016000.1 locus=Phvul.001G016000.1.v2.1 annot-version=v2.1) & Enzyme classification.EC_3 hydrolases.EC_3.2 glycosylase (glycosylase)
41 } pt=Phvul.001G160000.1 locus=Phvul.001G160000 ID=Phvul.001G160000.1.v2.1 annot-version=v2.1)
42 } ju9|e1313_arath : 127.0) & Enzyme classification.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2 : 56.6)
43 } t=Phvul.002G028700.1 locus=Phvul.002G028700 ID=Phvul.002G028700.1.v2.1 annot-version=v2.1)
44 } ript=Phvul.002G185800.1 locus=Phvul.002G185800 ID=Phvul.002G185800.1.v2.1 annot-version=v2.1)
45 } t=Phvul.002G206900.3 locus=Phvul.002G206900 ID=Phvul.002G206900.3.v2.1 annot-version=v2.1)
46 } t=Phvul.002G206900.3 locus=Phvul.002G206900 ID=Phvul.002G206900.3.v2.1 annot-version=v2.1)
47 } 078900.1 locus=Phvul.003G078900 ID=Phvul.003G078900.1.v2.1 annot-version=v2.1)
48
49 } ion: pacid=37144401 transcript=Phvul.003G210500.1 locus=Phvul.003G210500 ID=Phvul.003G210500.1.v2.1 annot-version=v2.1)
50 } 262300.4 locus=Phvul.003G262300 ID=Phvul.003G262300.4.v2.1 annot-version=v2.1)
51 } 262300.4 locus=Phvul.003G262300 ID=Phvul.003G262300.4.v2.1 annot-version=v2.1)
52 } 262300.4 locus=Phvul.003G262300 ID=Phvul.003G262300.4.v2.1 annot-version=v2.1)
53 } 262300.4 locus=Phvul.003G262300 ID=Phvul.003G262300.4.v2.1 annot-version=v2.1)
54 } 262300.4 locus=Phvul.003G262300 ID=Phvul.003G262300.4.v2.1 annot-version=v2.1)
55 } 162803 transcript=Phvul.004G093900.7 locus=Phvul.004G093900 ID=Phvul.004G093900.7.v2.1 annot-version=v2.1)
56 } 162803 transcript=Phvul.004G093900.7 locus=Phvul.004G093900 ID=Phvul.004G093900.7.v2.1 annot-version=v2.1)
57 } 162803 transcript=Phvul.004G093900.7 locus=Phvul.004G093900 ID=Phvul.004G093900.7.v2.1 annot-version=v2.1)
58 } 162803 transcript=Phvul.004G093900.7 locus=Phvul.004G093900 ID=Phvul.004G093900.7.v2.1 annot-version=v2.1)
59 } 162803 transcript=Phvul.004G093900.7 locus=Phvul.004G093900 ID=Phvul.004G093900.7.v2.1 annot-version=v2.1)
60 } 162803 transcript=Phvul.004G093900.7 locus=Phvul.004G093900 ID=Phvul.004G093900.7.v2.1 annot-version=v2.1)

1
2 162803 transcript=Phvul.004G093900.7 locus=Phvul.004G093900 ID=Phvul.004G093900.7.v2.1 ann
3 162803 transcript=Phvul.004G093900.7 locus=Phvul.004G093900 ID=Phvul.004G093900.7.v2.1 ann
4 l locus=Phvul.004G105600 ID=Phvul.004G105600.1.v2.1 annot-version=v2.1) & Receptor-like protei
5 nscript=Phvul.004G135400.1 locus=Phvul.004G135400 ID=Phvul.004G135400.1.v2.1 annot-version=
6 ang : 559.0) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paire
7 **description: pacid=37161693 transcript=Phvul.004G170000.1 locus=Phvul.004G170000 ID=Phvul.004G170000.1.v2.1**
8 **l locus=Phvul.005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-l**
9 **on: pacid=37154025 transcript=Phvul.005G022800.1 locus=Phvul.005G022800 ID=Phvul.005G022800.1.v2.1**
10 **l locus=Phvul.005G072300 ID=Phvul.005G072300.1.v2.1 annot-version=v2.1) & Probable ubiquitin-**
11 **: pacid=37167617 transcript=Phvul.007G034000.2 locus=Phvul.007G034000 ID=Phvul.007G034000.**
12 **: pacid=37167617 transcript=Phvul.007G034000.2 locus=Phvul.007G034000 ID=Phvul.007G034000.**
13 **5244033.1 locus=Phvul.007G244033 ID=Phvul.007G244033.1.v2.1 annot-version=v2.1)**
14 **5244033.1 locus=Phvul.007G244033 ID=Phvul.007G244033.1.v2.1 annot-version=v2.1)**
15 **5244066.1 locus=Phvul.007G244066 ID=Phvul.007G244066.1.v2.1 annot-version=v2.1)**
16 **5079000.1 locus=Phvul.008G079000 ID=Phvul.008G079000.1.v2.1 annot-version=v2.1)**
17 Phvul.008G267400.5 locus=Phvul.008G267400 ID=Phvul.008G267400.5.v2.1 annot-version=v2.1) &
18 Phvul.008G267400.5 locus=Phvul.008G267400 ID=Phvul.008G267400.5.v2.1 annot-version=v2.1) &
19 Phvul.008G267400.5 locus=Phvul.008G267400 ID=Phvul.008G267400.5.v2.1 annot-version=v2.1) &
20 Phvul.008G267400.5 locus=Phvul.008G267400 ID=Phvul.008G267400.5.v2.1 annot-version=v2.1) &
21 50765 transcript=Phvul.009G053900.2 locus=Phvul.009G053900 ID=Phvul.009G053900.2.v2.1 ann
22 l locus=Phvul.009G081900 ID=Phvul.009G081900.1.v2.1 annot-version=v2.1) & F-box/LRR-repeat p
23 50546 transcript=Phvul.009G213000.1 locus=Phvul.009G213000 ID=Phvul.009G213000.1.v2.1 annot-
24 script=Phvul.011G065200.2 locus=Phvul.011G065200 ID=Phvul.011G065200.2.v2.1 annot-version=v
25 5079400.1 locus=Phvul.001G079400 ID=Phvul.001G079400.1.v2.1 annot-version=v2.1)
26 l locus=Phvul.001G087700 ID=Phvul.001G087700.1.v2.1 annot-version=v2.1) & Acyltransferase-like
27 l locus=Phvul.001G117500 ID=Phvul.001G117500.1.v2.1 annot-version=v2.1) & 4-alpha-glucanotrar
28 5159 transcript=Phvul.002G007100.1 locus=Phvul.002G007100 ID=Phvul.002G007100.1.v2.1 annot-
29 177142 transcript=Phvul.002G115800.3 locus=Phvul.002G115800 ID=Phvul.002G115800.3.v2.1 an
30 177142 transcript=Phvul.002G115800.3 locus=Phvul.002G115800 ID=Phvul.002G115800.3.v2.1 an
31 5163600.1 locus=Phvul.002G163600 ID=Phvul.002G163600.1.v2.1 annot-version=v2.1)
32 7986 transcript=Phvul.002G168500.2 locus=Phvul.002G168500 ID=Phvul.002G168500.2.v2.1 annot-
33 7986 transcript=Phvul.002G168500.2 locus=Phvul.002G168500 ID=Phvul.002G168500.2.v2.1 annot-
34 d=37176445 transcript=Phvul.002G177500.1 locus=Phvul.002G177500 ID=Phvul.002G177500.1.v2.1
35 5315000.2 locus=Phvul.002G315000 ID=Phvul.002G315000.2.v2.1 annot-version=v2.1)
36 5315000.2 locus=Phvul.002G315000 ID=Phvul.002G315000.2.v2.1 annot-version=v2.1)
37 l locus=Phvul.003G185300 ID=Phvul.003G185300.1.v2.1 annot-version=v2.1) & PLASMODESMATA (
38 script=Phvul.003G212800.2 locus=Phvul.003G212800 ID=Phvul.003G212800.2.v2.1 annot-version=v
39 50546 transcript=Phvul.004G121900.1 locus=Phvul.004G121900 ID=Phvul.004G121900.1.v2.1 annot-versior
40 t=Phvul.006G033600.2 locus=Phvul.006G033600 ID=Phvul.006G033600.2.v2.1 annot-version=v2.1)
41 t=Phvul.006G033600.2 locus=Phvul.006G033600 ID=Phvul.006G033600.2.v2.1 annot-version=v2.1)
42 5219000.1 locus=Phvul.006G219000 ID=Phvul.006G219000.1.v2.1 annot-version=v2.1)
43 original description: pacid=37164656 transcript=Phvul.007G008100.2 locus=Phvul.007G008100 ID=
44 ript=Phvul.007G086600.1 locus=Phvul.007G086600 ID=Phvul.007G086600.1.v2.1 annot-version=v2
45 l locus=Phvul.007G168600 ID=Phvul.007G168600.1.v2.1 annot-version=v2.1) & Auxin-binding prote
46 l locus=Phvul.008G002700 ID=Phvul.008G002700.1.v2.1 annot-version=v2.1) & Probable methyltra
47 jinal description: pacid=37149462 transcript=Phvul.009G062500.1 locus=Phvul.009G062500 ID=Phv

1 =37168174 transcript=Phvul.001G186500.1 locus=Phvul.001G186500 ID=Phvul.001G186500.1.v2.1 ;
2 t=Phvul.002G028700.1 locus=Phvul.002G028700 ID=Phvul.002G028700.1.v2.1 annot-version=v2.1)
3 ? locus=Phvul.003G202300 ID=Phvul.003G202300.2.v2.1 annot-version=v2.1) & Protein MODIFIER C
4 ? locus=Phvul.003G202300 ID=Phvul.003G202300.2.v2.1 annot-version=v2.1) & Protein MODIFIER C
5 5248400.3 locus=Phvul.003G248400 ID=Phvul.003G248400.3.v2.1 annot-version=v2.1)
6 5248400.3 locus=Phvul.003G248400 ID=Phvul.003G248400.3.v2.1 annot-version=v2.1)
7 5248400.3 locus=Phvul.003G248400 ID=Phvul.003G248400.3.v2.1 annot-version=v2.1)
8 5024400.1 locus=Phvul.004G024400 ID=Phvul.004G024400.1.v2.1 annot-version=v2.1)
9 l locus=Phvul.004G071800 ID=Phvul.004G071800.1.v2.1 annot-version=v2.1) & MLO-like protein 12
10 =Phvul.004G178500.1 locus=Phvul.004G178500 ID=Phvul.004G178500.1.v2.1 annot-version=v2.1) ;
11 =Phvul.004G178500.1 locus=Phvul.004G178500 ID=Phvul.004G178500.1.v2.1 annot-version=v2.1) ;
12 rscript=Phvul.005G175600.2 locus=Phvul.005G175600 ID=Phvul.005G175600.2.v2.1 annot-version=
13 rscript=Phvul.005G175600.2 locus=Phvul.005G175600 ID=Phvul.005G175600.2.v2.1 annot-version=
14 rscript=Phvul.006G053300.2 locus=Phvul.006G053300 ID=Phvul.006G053300.2.v2.1 annot-version=
15 rscript=Phvul.006G053300.2 locus=Phvul.006G053300 ID=Phvul.006G053300.2.v2.1 annot-version=
16 5110000.1 locus=Phvul.006G110000 ID=Phvul.006G110000.1.v2.1 annot-version=v2.1)
17 ;cription: pacid=37167521 transcript=Phvul.007G204100.1 locus=Phvul.007G204100 ID=Phvul.007G
18 l locus=Phvul.008G006800 ID=Phvul.008G006800.1.v2.1 annot-version=v2.1) & Histone-binding pro
19 3a1_arath : 307.0) & Enzyme classification.EC_2 transferases.EC_2.4 glycosyltransferase(50.2.4 : 19
20 5184400.2 locus=Phvul.009G184400 ID=Phvul.009G184400.2.v2.1 annot-version=v2.1)
21 5184400.2 locus=Phvul.009G184400 ID=Phvul.009G184400.2.v2.1 annot-version=v2.1)
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3 G004800.1.v2.1 annot-version=v2.1) &

4 |/phosphatidylcholine transfer protein SFH8 OS=Arabidopsis thaliana (sp|f4ihj0|sfh8_arath : 681.0

5 |/phosphatidylcholine transfer protein SFH8 OS=Arabidopsis thaliana (sp|f4ihj0|sfh8_arath : 681.0

6
7
8
9
10 n=v2.1) &

11
12 108200.1.v2.1 annot-version=v2.1) &

13
14
15 t-version=v2.1) &

16 t-version=v2.1) &

17 t-version=v2.1) &

18 t-version=v2.1) &

19
20
21 v2.1) &

22
23
24 ot-version=v2.1) &

25
26
27 glycosyltransferase(50.2.4 : 545.4) (original description: pacid=37165866 transcript=Phvul.007G031

28 glycosyltransferase(50.2.4 : 545.4) (original description: pacid=37165866 transcript=Phvul.007G031

29 rsion=v2.1) &

30
31 vul.008G081700.2.v2.1 annot-version=v2.1) &

32
33
34
35 &

36 l.010G125200.1.v2.1 annot-version=v2.1) &

37
38
39 01700.1 locus=Phvul.001G001700 ID=Phvul.001G001700.1.v2.1 annot-version=v2.1) &

40 l) &

41 (original description: pacid=37175571 transcript=Phvul.002G011900.1 locus=Phvul.002G011900 ID

42 &

43
44 l.1) &

45 &

46 &

47
48
49 500.1.v2.1 annot-version=v2.1) &

50
51
52
53
54
55
56 ot-version=v2.1) &

57 ot-version=v2.1) &

58 ot-version=v2.1) &

59 ot-version=v2.1) &

60 ot-version=v2.1) &

1
 2 not-version=v2.1) &
 3 not-version=v2.1) &
 4 in EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2_sollc : 345.0)
 5 =v2.1) &
 6 ed donor with incorporation or reduction of molecular oxygen(50.1.13 : 407.0) (original description:
 7 **04G170000.1.v2.1 annot-version=v2.1) &**
 8 like protein G1 OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
 9 00.1.v2.1 annot-version=v2.1) &
 10 conjugating enzyme E2 26 OS=Arabidopsis thaliana (sp|q8gy87|ubc26_arath : 359.0)
 11 .2.v2.1 annot-version=v2.1) &
 12 .2.v2.1 annot-version=v2.1) &
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27 ot-version=v2.1) &
 28 rotein 15 OS=Arabidopsis thaliana (sp|q9smy8|fbl15_arath : 1013.0)
 29 -version=v2.1) &
 30 /2.1) &
 31
 32
 33 e protein At3g26840, chloroplastic OS=Arabidopsis thaliana (sp|q9lw26|y3684_arath : 661.0)
 34 nsferase DPE2 OS=Oryza sativa subsp. japonica (sp|q69q02|dpe2_orysj : 394.0)
 35 -version=v2.1) &
 36 not-version=v2.1) &
 37 not-version=v2.1) &
 38
 39
 40
 41 -version=v2.1) &
 42 -version=v2.1) &
 43 1 annot-version=v2.1) &
 44
 45
 46
 47
 48 CALLOSE-BINDING PROTEIN 3 OS=Arabidopsis thaliana (sp|q9fz86|pdcb3_arath : 138.0)
 49 v2.1) &
 50 r=v2.1) &
 51) &
 52) &
 53
 54
 55
 56 =Phvul.007G008100.2.v2.1 annot-version=v2.1) &
 57 !.1) &
 58 e in T85 OS=Nicotiana tabacum (sp|p33490|abp1_tobac : 271.0)
 59 nsferase PMT19 OS=Arabidopsis thaliana (sp|q9zw75|pmtj_arath : 639.0)
 60 /ul.009G062500.1.v2.1 annot-version=v2.1) &

1
2 annot-version=v2.1) &

3 &

4 JF SNC1 1 OS=Arabidopsis thaliana (sp|q9sb63|mos1_arath : 429.0)

5 JF SNC1 1 OS=Arabidopsis thaliana (sp|q9sb63|mos1_arath : 429.0)

6
7
8
9
10
11
12 2 OS=Arabidopsis thaliana (sp|o80961|mlo12_arath : 669.0)

13 &

14 &

15 =v2.1) &

16 =v2.1) &

17 =v2.1) &

18 =v2.1) &

19 =v2.1) &

20
21
22
23 i204100.1.v2.1 annot-version=v2.1) &

24 rotein MSI1 homolog OS=Oryza sativa subsp. japonica (sp|q10g81|msi1_orysj : 130.0)

25
26 5.8) (original description: pacid=37160064 transcript=Phvul.008G034200.2 locus=Phvul.008G034200.2)

27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

)
)

.800.2 locus=Phvul.007G031800 ID=Phvul.007G031800.2.v2.1 annot-version=v2.1) &
.800.2 locus=Phvul.007G031800 ID=Phvul.007G031800.2.v2.1 annot-version=v2.1) &

)=Phvul.002G011900.1.v2.1 annot-version=v2.1) &

Do not distribute

1
2
3
4
5
6
7 : pacid=37163295 transcript=Phvul.004G159500.1 locus=Phvul.004G159500 ID=Phvul.004G159500.
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

00 ID=Phvul.008G034200.2.v2.1 annot-version=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

.1.v2.1 annot-version=v2.1) &

Do not distribute

| | miRNA_Acc. | Target_Acc. | Expectation | UPE\$ | miRNA_start | miRNA_end |
|----|--------------|--------------------|-------------|-------|-------------|-----------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ucgauaaaccuc | Phvul.002G040800.1 | 2.5 | -1 | 1 | 21 |
| 4 | uggaggcagcgg | Phvul.002G112900.2 | 2.5 | -1 | 1 | 22 |
| 5 | uggaggcagcgg | Phvul.002G112900.1 | 2.5 | -1 | 1 | 22 |
| 6 | uggaggcagcgg | Phvul.002G112900.2 | 2.5 | -1 | 1 | 22 |
| 7 | uggaggcagcgg | Phvul.002G112900.1 | 2.5 | -1 | 1 | 22 |
| 8 | uggaggcagcgg | Phvul.002G112900.1 | 2.5 | -1 | 1 | 22 |
| 9 | uggaggcagcgg | Phvul.001G016450.1 | 3 | -1 | 1 | 22 |
| 10 | uggaggcagcgg | Phvul.001G016450.1 | 3 | -1 | 1 | 22 |
| 11 | uggaggcagcgg | Phvul.002G255100.1 | 3 | -1 | 1 | 22 |
| 12 | uggaggcagcgg | Phvul.002G255100.1 | 3 | -1 | 1 | 22 |
| 13 | uggaggcagcgg | Phvul.002G332500.1 | 3 | -1 | 1 | 21 |
| 14 | uggaggcagcgg | Phvul.005G022900.2 | 3 | -1 | 1 | 22 |
| 15 | uggaggcagcgg | Phvul.005G022900.2 | 3 | -1 | 1 | 22 |
| 16 | uggaggcagcgg | Phvul.005G165300.1 | 3 | -1 | 1 | 22 |
| 17 | uggaggcagcgg | Phvul.005G165300.1 | 3 | -1 | 1 | 22 |
| 18 | uggaggcagcgg | Phvul.005G165300.1 | 3 | -1 | 1 | 22 |
| 19 | uggaggcagcgg | Phvul.005G165300.1 | 3 | -1 | 1 | 22 |
| 20 | uggaggcagcgg | Phvul.005G165300.1 | 3 | -1 | 1 | 22 |
| 21 | uggaggcagcgg | Phvul.005G165300.1 | 3 | -1 | 1 | 22 |
| 22 | ucgauaaaccuc | Phvul.006G176000.1 | 3 | -1 | 1 | 21 |
| 23 | ucgauaaaccuc | Phvul.007G172400.1 | 3 | -1 | 1 | 21 |
| 24 | uggaggcagcgg | Phvul.009G109200.2 | 3 | -1 | 1 | 22 |
| 25 | uggaggcagcgg | Phvul.009G109200.3 | 3 | -1 | 1 | 22 |
| 26 | uggaggcagcgg | Phvul.009G109200.1 | 3 | -1 | 1 | 22 |
| 27 | uggaggcagcgg | Phvul.009G109200.2 | 3 | -1 | 1 | 22 |
| 28 | uggaggcagcgg | Phvul.009G109200.3 | 3 | -1 | 1 | 22 |
| 29 | uggaggcagcgg | Phvul.009G109200.1 | 3 | -1 | 1 | 22 |
| 30 | uggaggcagcgg | Phvul.009G109200.1 | 3 | -1 | 1 | 22 |
| 31 | uggaggcagcgg | Phvul.009G109200.1 | 3 | -1 | 1 | 22 |
| 32 | ucgauaaaccuc | Phvul.009G260000.1 | 3 | -1 | 1 | 21 |
| 33 | uggaggcagcgg | Phvul.003G050000.1 | 3.5 | -1 | 1 | 22 |
| 34 | uggaggcagcgg | Phvul.003G050000.1 | 3.5 | -1 | 1 | 22 |
| 35 | uggaggcagcgg | Phvul.004G050550.1 | 3.5 | -1 | 1 | 22 |
| 36 | uggaggcagcgg | Phvul.004G050550.1 | 3.5 | -1 | 1 | 22 |
| 37 | uggaggcagcgg | Phvul.004G050550.1 | 3.5 | -1 | 1 | 22 |
| 38 | uggaggcagcgg | Phvul.005G136500.1 | 3.5 | -1 | 1 | 21 |
| 39 | uggaggcagcgg | Phvul.006G105000.1 | 3.5 | -1 | 1 | 22 |
| 40 | uggaggcagcgg | Phvul.006G105000.1 | 3.5 | -1 | 1 | 22 |
| 41 | uggaggcagcgg | Phvul.007G006700.1 | 3.5 | -1 | 1 | 22 |
| 42 | uggaggcagcgg | Phvul.007G006700.1 | 3.5 | -1 | 1 | 22 |
| 43 | uggaggcagcgg | Phvul.007G216500.4 | 3.5 | -1 | 1 | 22 |
| 44 | uggaggcagcgg | Phvul.007G216500.3 | 3.5 | -1 | 1 | 22 |
| 45 | uggaggcagcgg | Phvul.007G216500.1 | 3.5 | -1 | 1 | 22 |
| 46 | uggaggcagcgg | Phvul.007G216500.4 | 3.5 | -1 | 1 | 22 |
| 47 | uggaggcagcgg | Phvul.007G216500.3 | 3.5 | -1 | 1 | 22 |
| 48 | uggaggcagcgg | Phvul.007G216500.1 | 3.5 | -1 | 1 | 22 |
| 49 | uggaggcagcgg | Phvul.007G216500.4 | 3.5 | -1 | 1 | 22 |
| 50 | uggaggcagcgg | Phvul.007G216500.3 | 3.5 | -1 | 1 | 22 |
| 51 | uggaggcagcgg | Phvul.007G216500.1 | 3.5 | -1 | 1 | 22 |
| 52 | uggaggcagcgg | Phvul.007G216500.1 | 3.5 | -1 | 1 | 22 |
| 53 | ucgauaaaccuc | Phvul.008G055300.1 | 3.5 | -1 | 1 | 21 |
| 54 | uggaggcagcgg | Phvul.008G173900.2 | 3.5 | -1 | 1 | 22 |
| 55 | uggaggcagcgg | Phvul.008G173900.1 | 3.5 | -1 | 1 | 22 |
| 56 | uggaggcagcgg | Phvul.008G173900.2 | 3.5 | -1 | 1 | 22 |
| 57 | uggaggcagcgg | Phvul.008G173900.2 | 3.5 | -1 | 1 | 22 |
| 58 | uggaggcagcgg | Phvul.008G173900.1 | 3.5 | -1 | 1 | 22 |
| 59 | uggaggcagcgg | Phvul.011G132801.1 | 3.5 | -1 | 1 | 22 |
| 60 | uggaggcagcgg | Phvul.011G132801.1 | 3.5 | -1 | 1 | 22 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggaggcagcgg Phvul.011G157600.3 | 3.5 | -1 | 1 | 22 |
| 3 | uggaggcagcgg Phvul.011G157600.4 | 3.5 | -1 | 1 | 22 |
| 4 | uggaggcagcgg Phvul.011G157600.2 | 3.5 | -1 | 1 | 22 |
| 5 | | | | | |
| 6 | uggaggcagcgg Phvul.011G157600.3 | 3.5 | -1 | 1 | 22 |
| 7 | uggaggcagcgg Phvul.011G157600.4 | 3.5 | -1 | 1 | 22 |
| 8 | | | | | |
| 9 | uggaggcagcgg Phvul.011G157600.2 | 3.5 | -1 | 1 | 22 |
| 10 | uggaggcagcgg Phvul.001G026200.1 | 4 | -1 | 1 | 22 |
| 11 | uggaggcagcgg Phvul.001G026200.1 | 4 | -1 | 1 | 22 |
| 12 | uggaggcagcgg Phvul.001G141300.1 | 4 | -1 | 1 | 22 |
| 13 | | | | | |
| 14 | uggaggcagcgg Phvul.001G141300.1 | 4 | -1 | 1 | 22 |
| 15 | uggaggcagcgg Phvul.001G256400.1 | 4 | -1 | 1 | 22 |
| 16 | uggaggcagcgg Phvul.001G256400.1 | 4 | -1 | 1 | 22 |
| 17 | | | | | |
| 18 | uggaggcagcgg Phvul.001G256600.1 | 4 | -1 | 1 | 22 |
| 19 | uggaggcagcgg Phvul.001G256600.1 | 4 | -1 | 1 | 22 |
| 20 | uggaggcagcgg Phvul.002G003600.1 | 4 | -1 | 1 | 22 |
| 21 | | | | | |
| 22 | uggaggcagcgg Phvul.002G003600.1 | 4 | -1 | 1 | 22 |
| 23 | uggaggcagcgg Phvul.002G075900.1 | 4 | -1 | 1 | 22 |
| 24 | uggaggcagcgg Phvul.002G075900.1 | 4 | -1 | 1 | 22 |
| 25 | | | | | |
| 26 | uggaggcagcgg Phvul.002G102800.2 | 4 | -1 | 1 | 22 |
| 27 | uggaggcagcgg Phvul.002G102800.2 | 4 | -1 | 1 | 22 |
| 28 | uggaggcagcgg Phvul.002G146600.2 | 4 | -1 | 1 | 22 |
| 29 | | | | | |
| 30 | uggaggcagcgg Phvul.002G146600.1 | 4 | -1 | 1 | 22 |
| 31 | uggaggcagcgg Phvul.002G146600.2 | 4 | -1 | 1 | 22 |
| 32 | uggaggcagcgg Phvul.002G146600.1 | 4 | -1 | 1 | 22 |
| 33 | | | | | |
| 34 | uggaggcagcgg Phvul.002G158200.1 | 4 | -1 | 1 | 22 |
| 35 | uggaggcagcgg Phvul.002G158200.1 | 4 | -1 | 1 | 22 |
| 36 | ucgauaaaccuc Phvul.003G013200.2 | 4 | -1 | 1 | 21 |
| 37 | uggaggcagcgg Phvul.003G156333.1 | 4 | -1 | 1 | 22 |
| 38 | | | | | |
| 39 | uggaggcagcgg Phvul.003G156333.1 | 4 | -1 | 1 | 22 |
| 40 | ucgauaaaccuc Phvul.003G179800.1 | 4 | -1 | 1 | 21 |
| 41 | uggaggcagcgg Phvul.003G179800.1 | 4 | -1 | 1 | 22 |
| 42 | | | | | |
| 43 | uggaggcagcgg Phvul.003G179800.1 | 4 | -1 | 1 | 22 |
| 44 | uggaggcagcgg Phvul.003G261400.2 | 4 | -1 | 1 | 22 |
| 45 | uggaggcagcgg Phvul.003G261400.1 | 4 | -1 | 1 | 22 |
| 46 | | | | | |
| 47 | uggaggcagcgg Phvul.003G261400.2 | 4 | -1 | 1 | 22 |
| 48 | uggaggcagcgg Phvul.003G261400.1 | 4 | -1 | 1 | 22 |
| 49 | | | | | |
| 50 | uggaggcagcgg Phvul.003G291600.1 | 4 | -1 | 1 | 22 |
| 51 | uggaggcagcgg Phvul.003G291600.2 | 4 | -1 | 1 | 22 |
| 52 | uggaggcagcgg Phvul.003G291600.1 | 4 | -1 | 1 | 22 |
| 53 | uggaggcagcgg Phvul.003G291600.2 | 4 | -1 | 1 | 22 |
| 54 | | | | | |
| 55 | uggaggcagcgg Phvul.004G068900.2 | 4 | -1 | 1 | 22 |
| 56 | uggaggcagcgg Phvul.004G068900.2 | 4 | -1 | 1 | 22 |
| 57 | ucgauaaaccuc Phvul.005G069600.1 | 4 | -1 | 1 | 21 |
| 58 | ucgauaaaccuc Phvul.007G157700.1 | 4 | -1 | 1 | 21 |
| 59 | ucgauaaaccuc Phvul.007G249600.1 | 4 | -1 | 1 | 21 |
| 60 | uggaggcagcgg Phvul.008G111200.1 | 4 | -1 | 1 | 22 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggaggcagcgg Phvul.008G111200.1 | 4 | -1 | 1 | 22 |
| 3 | ucgauaaaccuc Phvul.008G230800.1 | 4 | -1 | 1 | 21 |
| 4 | uggaggcagcgg Phvul.009G080800.1 | 4 | -1 | 1 | 22 |
| 5 | uggaggcagcgg Phvul.009G080800.1 | 4 | -1 | 1 | 22 |
| 6 | uggaggcagcgg Phvul.009G119700.1 | 4 | -1 | 1 | 22 |
| 7 | uggaggcagcgg Phvul.009G119700.1 | 4 | -1 | 1 | 22 |
| 8 | uggaggcagcgg Phvul.009G119700.1 | 4 | -1 | 1 | 22 |
| 9 | uggaggcagcgg Phvul.009G119700.1 | 4 | -1 | 1 | 22 |
| 10 | ucgauaaaccuc Phvul.010G119500.1 | 4 | -1 | 1 | 21 |
| 11 | uggaggcagcgg Phvul.011G008600.1 | 4 | -1 | 1 | 22 |
| 12 | uggaggcagcgg Phvul.011G008600.1 | 4 | -1 | 1 | 22 |
| 13 | uggaggcagcgg Phvul.011G140900.1 | 4 | -1 | 1 | 22 |
| 14 | uggaggcagcgg Phvul.011G140900.1 | 4 | -1 | 1 | 22 |
| 15 | uggaggcagcgg Phvul.011G140900.1 | 4 | -1 | 1 | 22 |
| 16 | ucgauaaaccuc Phvul.011G169222.1 | 4 | -1 | 1 | 21 |
| 17 | uggaggcagcgg Phvul.011G215900.1 | 4 | -1 | 1 | 22 |
| 18 | uggaggcagcgg Phvul.011G215900.1 | 4 | -1 | 1 | 22 |
| 19 | uggaggcagcgg Phvul.011G215900.1 | 4 | -1 | 1 | 22 |
| 20 | ucgauaaaccuc Phvul.001G096200.1 | 4.5 | -1 | 1 | 21 |
| 21 | uggaggcagcgg Phvul.001G104700.2 | 4.5 | -1 | 1 | 22 |
| 22 | uggaggcagcgg Phvul.001G104700.1 | 4.5 | -1 | 1 | 22 |
| 23 | uggaggcagcgg Phvul.001G104700.1 | 4.5 | -1 | 1 | 22 |
| 24 | uggaggcagcgg Phvul.001G104700.2 | 4.5 | -1 | 1 | 22 |
| 25 | uggaggcagcgg Phvul.001G104700.1 | 4.5 | -1 | 1 | 22 |
| 26 | uggaggcagcgg Phvul.001G211000.1 | 4.5 | -1 | 1 | 22 |
| 27 | uggaggcagcgg Phvul.001G211000.1 | 4.5 | -1 | 1 | 22 |
| 28 | uggaggcagcgg Phvul.001G211000.1 | 4.5 | -1 | 1 | 22 |
| 29 | uggaggcagcgg Phvul.002G147900.2 | 4.5 | -1 | 1 | 22 |
| 30 | uggaggcagcgg Phvul.002G147900.1 | 4.5 | -1 | 1 | 22 |
| 31 | uggaggcagcgg Phvul.002G147900.2 | 4.5 | -1 | 1 | 22 |
| 32 | uggaggcagcgg Phvul.002G147900.2 | 4.5 | -1 | 1 | 22 |
| 33 | uggaggcagcgg Phvul.002G147900.1 | 4.5 | -1 | 1 | 22 |
| 34 | ucgauaaaccuc Phvul.002G182700.2 | 4.5 | -1 | 1 | 21 |
| 35 | ucgauaaaccuc Phvul.002G182700.1 | 4.5 | -1 | 1 | 21 |
| 36 | ucgauaaaccuc Phvul.002G202300.1 | 4.5 | -1 | 1 | 21 |
| 37 | ucgauaaaccuc Phvul.002G202300.1 | 4.5 | -1 | 1 | 21 |
| 38 | ucgauaaaccuc Phvul.002G238000.1 | 4.5 | -1 | 1 | 21 |
| 39 | uggaggcagcgg Phvul.002G267100.1 | 4.5 | -1 | 1 | 22 |
| 40 | uggaggcagcgg Phvul.002G267100.1 | 4.5 | -1 | 1 | 22 |
| 41 | uggaggcagcgg Phvul.002G267100.1 | 4.5 | -1 | 1 | 22 |
| 42 | uggaggcagcgg Phvul.002G274400.2 | 4.5 | -1 | 1 | 22 |
| 43 | uggaggcagcgg Phvul.002G274400.1 | 4.5 | -1 | 1 | 22 |
| 44 | uggaggcagcgg Phvul.002G274400.2 | 4.5 | -1 | 1 | 22 |
| 45 | uggaggcagcgg Phvul.002G274400.1 | 4.5 | -1 | 1 | 22 |
| 46 | uggaggcagcgg Phvul.002G274400.2 | 4.5 | -1 | 1 | 22 |
| 47 | uggaggcagcgg Phvul.002G274400.1 | 4.5 | -1 | 1 | 22 |
| 48 | ucgauaaaccuc Phvul.002G304500.1 | 4.5 | -1 | 1 | 21 |
| 49 | uggaggcagcgg Phvul.002G327900.1 | 4.5 | -1 | 1 | 22 |
| 50 | uggaggcagcgg Phvul.002G327900.1 | 4.5 | -1 | 1 | 22 |
| 51 | uggaggcagcgg Phvul.002G327900.1 | 4.5 | -1 | 1 | 22 |
| 52 | ucgauaaaccuc Phvul.003G010700.1 | 4.5 | -1 | 1 | 21 |
| 53 | ucgauaaaccuc Phvul.003G023101.2 | 4.5 | -1 | 1 | 21 |
| 54 | ucgauaaaccuc Phvul.003G023101.1 | 4.5 | -1 | 1 | 21 |
| 55 | uggaggcagcgg Phvul.003G044200.1 | 4.5 | -1 | 1 | 22 |
| 56 | uggaggcagcgg Phvul.003G044200.1 | 4.5 | -1 | 1 | 22 |
| 57 | uggaggcagcgg Phvul.003G044200.1 | 4.5 | -1 | 1 | 22 |
| 58 | ucgauaaaccuc Phvul.003G080700.1 | 4.5 | -1 | 1 | 21 |
| 59 | uggaggcagcgg Phvul.003G090000.2 | 4.5 | -1 | 1 | 22 |
| 60 | uggaggcagcgg Phvul.003G090000.2 | 4.5 | -1 | 1 | 22 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | ucgauaaaccuc Phvul.003G096500.1 | 4.5 | -1 | 1 | 21 |
| 3 | uggaggcagcgg Phvul.003G113900.1 | 4.5 | -1 | 1 | 22 |
| 4 | uggaggcagcgg Phvul.003G113900.1 | 4.5 | -1 | 1 | 22 |
| 5 | uggaggcagcgg Phvul.003G154900.1 | 4.5 | -1 | 1 | 22 |
| 6 | uggaggcagcgg Phvul.003G154900.1 | 4.5 | -1 | 1 | 22 |
| 7 | uggaggcagcgg Phvul.003G154900.1 | 4.5 | -1 | 1 | 22 |
| 8 | uggaggcagcgg Phvul.003G209900.1 | 4.5 | -1 | 1 | 22 |
| 9 | uggaggcagcgg Phvul.003G209900.1 | 4.5 | -1 | 1 | 22 |
| 10 | uggaggcagcgg Phvul.003G209900.1 | 4.5 | -1 | 1 | 22 |
| 11 | uggaggcagcgg Phvul.003G254900.2 | 4.5 | -1 | 1 | 22 |
| 12 | uggaggcagcgg Phvul.003G254900.1 | 4.5 | -1 | 1 | 22 |
| 13 | uggaggcagcgg Phvul.003G254900.2 | 4.5 | -1 | 1 | 22 |
| 14 | uggaggcagcgg Phvul.003G254900.2 | 4.5 | -1 | 1 | 22 |
| 15 | uggaggcagcgg Phvul.003G254900.1 | 4.5 | -1 | 1 | 22 |
| 16 | ucgauaaaccuc Phvul.003G295700.2 | 4.5 | -1 | 1 | 21 |
| 17 | ucgauaaaccuc Phvul.003G295700.1 | 4.5 | -1 | 1 | 21 |
| 18 | uggaggcagcgg Phvul.005G088636.1 | 4.5 | -1 | 1 | 22 |
| 19 | uggaggcagcgg Phvul.005G088636.1 | 4.5 | -1 | 1 | 22 |
| 20 | uggaggcagcgg Phvul.005G088636.1 | 4.5 | -1 | 1 | 22 |
| 21 | uggaggcagcgg Phvul.005G088636.1 | 4.5 | -1 | 1 | 22 |
| 22 | ucgauaaaccuc Phvul.006G112000.1 | 4.5 | -1 | 1 | 21 |
| 23 | ucgauaaaccuc Phvul.006G112000.2 | 4.5 | -1 | 1 | 21 |
| 24 | ucgauaaaccuc Phvul.007G015000.1 | 4.5 | -1 | 1 | 21 |
| 25 | ucgauaaaccuc Phvul.007G028800.1 | 4.5 | -1 | 1 | 21 |
| 26 | ucgauaaaccuc Phvul.007G028800.1 | 4.5 | -1 | 1 | 21 |
| 27 | uggaggcagcgg Phvul.007G038000.1 | 4.5 | -1 | 1 | 22 |
| 28 | uggaggcagcgg Phvul.007G038000.1 | 4.5 | -1 | 1 | 22 |
| 29 | uggaggcagcgg Phvul.007G038000.1 | 4.5 | -1 | 1 | 22 |
| 30 | uggaggcagcgg Phvul.007G062900.1 | 4.5 | -1 | 1 | 22 |
| 31 | uggaggcagcgg Phvul.007G062900.1 | 4.5 | -1 | 1 | 22 |
| 32 | uggaggcagcgg Phvul.007G100700.1 | 4.5 | -1 | 1 | 22 |
| 33 | uggaggcagcgg Phvul.007G100700.1 | 4.5 | -1 | 1 | 22 |
| 34 | uggaggcagcgg Phvul.007G100700.1 | 4.5 | -1 | 1 | 22 |
| 35 | ucgauaaaccuc Phvul.007G149300.1 | 4.5 | -1 | 1 | 21 |
| 36 | ucgauaaaccuc Phvul.007G230450.1 | 4.5 | -1 | 1 | 21 |
| 37 | ucgauaaaccuc Phvul.007G230450.1 | 4.5 | -1 | 1 | 21 |
| 38 | ucgauaaaccuc Phvul.008G046100.1 | 4.5 | -1 | 1 | 21 |
| 39 | ucgauaaaccuc Phvul.008G177200.1 | 4.5 | -1 | 1 | 21 |
| 40 | ucgauaaaccuc Phvul.008G177200.2 | 4.5 | -1 | 1 | 21 |
| 41 | ucgauaaaccuc Phvul.008G181900.2 | 4.5 | -1 | 1 | 21 |
| 42 | ucgauaaaccuc Phvul.008G181900.1 | 4.5 | -1 | 1 | 21 |
| 43 | ucgauaaaccuc Phvul.008G181900.1 | 4.5 | -1 | 1 | 21 |
| 44 | uggaggcagcgg Phvul.008G260900.2 | 4.5 | -1 | 1 | 22 |
| 45 | uggaggcagcgg Phvul.008G260900.1 | 4.5 | -1 | 1 | 22 |
| 46 | uggaggcagcgg Phvul.008G260900.1 | 4.5 | -1 | 1 | 22 |
| 47 | uggaggcagcgg Phvul.008G260900.2 | 4.5 | -1 | 1 | 22 |
| 48 | uggaggcagcgg Phvul.008G260900.1 | 4.5 | -1 | 1 | 22 |
| 49 | uggaggcagcgg Phvul.008G260900.1 | 4.5 | -1 | 1 | 22 |
| 50 | uggaggcagcgg Phvul.009G041100.2 | 4.5 | -1 | 1 | 22 |
| 51 | uggaggcagcgg Phvul.009G041100.1 | 4.5 | -1 | 1 | 22 |
| 52 | uggaggcagcgg Phvul.009G041100.2 | 4.5 | -1 | 1 | 22 |
| 53 | uggaggcagcgg Phvul.009G041100.1 | 4.5 | -1 | 1 | 22 |
| 54 | uggaggcagcgg Phvul.009G041100.1 | 4.5 | -1 | 1 | 22 |
| 55 | ucgauaaaccuc Phvul.009G175100.3 | 4.5 | -1 | 1 | 21 |
| 56 | ucgauaaaccuc Phvul.009G175100.2 | 4.5 | -1 | 1 | 21 |
| 57 | ucgauaaaccuc Phvul.009G175100.1 | 4.5 | -1 | 1 | 21 |
| 58 | ucgauaaaccuc Phvul.009G175100.1 | 4.5 | -1 | 1 | 21 |
| 59 | uggaggcagcgg Phvul.009G200500.3 | 4.5 | -1 | 1 | 22 |
| 60 | uggaggcagcgg Phvul.009G200500.2 | 4.5 | -1 | 1 | 22 |
| | uggaggcagcgg Phvul.009G200500.3 | 4.5 | -1 | 1 | 22 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggaggcagcgg Phvul.009G200500.2 | 4.5 | -1 | 1 | 22 |
| 3 | uggaggcagcgg Phvul.011G080200.1 | 4.5 | -1 | 1 | 22 |
| 4 | uggaggcagcgg Phvul.011G080200.1 | 4.5 | -1 | 1 | 22 |
| 5 | | | | | |
| 6 | uggaggcagcgg Phvul.011G174000.1 | 4.5 | -1 | 1 | 22 |
| 7 | uggaggcagcgg Phvul.011G174000.1 | 4.5 | -1 | 1 | 22 |
| 8 | ucgauaaaccuc Phvul.001G110400.1 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggaggcagcgg Phvul.001G123400.1 | 5 | -1 | 1 | 22 |
| 11 | uggaggcagcgg Phvul.001G123400.1 | 5 | -1 | 1 | 22 |
| 12 | ucgauaaaccuc Phvul.001G154700.1 | 5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggaggcagcgg Phvul.001G179800.1 | 5 | -1 | 1 | 22 |
| 15 | uggaggcagcgg Phvul.001G179800.1 | 5 | -1 | 1 | 22 |
| 16 | ucgauaaaccuc Phvul.001G184000.1 | 5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggaggcagcgg Phvul.001G259000.1 | 5 | -1 | 1 | 22 |
| 19 | uggaggcagcgg Phvul.001G259000.1 | 5 | -1 | 1 | 22 |
| 20 | uggaggcagcgg Phvul.002G028100.1 | 5 | -1 | 1 | 22 |
| 21 | | | | | |
| 22 | uggaggcagcgg Phvul.002G028100.1 | 5 | -1 | 1 | 22 |
| 23 | ucgauaaaccuc Phvul.002G092900.2 | 5 | -1 | 1 | 21 |
| 24 | ucgauaaaccuc Phvul.002G092900.1 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | ucgauaaaccuc Phvul.002G137100.1 | 5 | -1 | 1 | 21 |
| 27 | uggaggcagcgg Phvul.002G137200.1 | 5 | -1 | 1 | 22 |
| 28 | uggaggcagcgg Phvul.002G137200.1 | 5 | -1 | 1 | 22 |
| 29 | | | | | |
| 30 | ucgauaaaccuc Phvul.002G139900.2 | 5 | -1 | 1 | 21 |
| 31 | ucgauaaaccuc Phvul.002G139900.1 | 5 | -1 | 1 | 21 |
| 32 | ucgauaaaccuc Phvul.002G156300.1 | 5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggaggcagcgg Phvul.003G032500.1 | 5 | -1 | 1 | 22 |
| 35 | uggaggcagcgg Phvul.003G032500.1 | 5 | -1 | 1 | 22 |
| 36 | uggaggcagcgg Phvul.003G252400.1 | 5 | -1 | 1 | 22 |
| 37 | | | | | |
| 38 | uggaggcagcgg Phvul.003G252400.1 | 5 | -1 | 1 | 22 |
| 39 | ucgauaaaccuc Phvul.003G265700.1 | 5 | -1 | 1 | 21 |
| 40 | uggaggcagcgg Phvul.003G291600.1 | 5 | -1 | 1 | 22 |
| 41 | uggaggcagcgg Phvul.003G291600.2 | 5 | -1 | 1 | 22 |
| 42 | | | | | |
| 43 | uggaggcagcgg Phvul.003G291600.1 | 5 | -1 | 1 | 22 |
| 44 | uggaggcagcgg Phvul.003G291600.2 | 5 | -1 | 1 | 22 |
| 45 | ucgauaaaccuc Phvul.004G176100.1 | 5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | ucgauaaaccuc Phvul.005G001500.2 | 5 | -1 | 1 | 21 |
| 48 | ucgauaaaccuc Phvul.005G001500.1 | 5 | -1 | 1 | 21 |
| 49 | uggaggcagcgg Phvul.005G043500.1 | 5 | -1 | 1 | 22 |
| 50 | | | | | |
| 51 | uggaggcagcgg Phvul.005G043500.1 | 5 | -1 | 1 | 22 |
| 52 | ucgauaaaccuc Phvul.005G093400.1 | 5 | -1 | 1 | 21 |
| 53 | ucgauaaaccuc Phvul.005G131700.1 | 5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | ucgauaaaccuc Phvul.005G183800.1 | 5 | -1 | 1 | 21 |
| 56 | ucgauaaaccuc Phvul.005G183800.2 | 5 | -1 | 1 | 21 |
| 57 | ucgauaaaccuc Phvul.006G098700.1 | 5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggaggcagcgg Phvul.006G131400.1 | 5 | -1 | 1 | 22 |
| 60 | uggaggcagcgg Phvul.006G131400.1 | 5 | -1 | 1 | 22 |
| | uggaggcagcgg Phvul.006G208400.1 | 5 | -1 | 1 | 22 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggaggcagcgg Phvul.006G208400.1 | 5 | -1 | 1 | 22 |
| 3 | uggaggcagcgg Phvul.007G043900.2 | 5 | -1 | 1 | 22 |
| 4 | uggaggcagcgg Phvul.007G043900.1 | 5 | -1 | 1 | 22 |
| 5 | uggaggcagcgg Phvul.007G043900.2 | 5 | -1 | 1 | 22 |
| 6 | uggaggcagcgg Phvul.007G043900.1 | 5 | -1 | 1 | 22 |
| 7 | uggaggcagcgg Phvul.007G043900.2 | 5 | -1 | 1 | 22 |
| 8 | uggaggcagcgg Phvul.007G043900.1 | 5 | -1 | 1 | 22 |
| 9 | ucgauaaaccuc Phvul.007G062100.1 | 5 | -1 | 1 | 21 |
| 10 | ucgauaaaccuc Phvul.007G067800.1 | 5 | -1 | 1 | 21 |
| 11 | uggaggcagcgg Phvul.007G080900.2 | 5 | -1 | 1 | 22 |
| 12 | uggaggcagcgg Phvul.007G080900.1 | 5 | -1 | 1 | 22 |
| 13 | uggaggcagcgg Phvul.007G080900.2 | 5 | -1 | 1 | 22 |
| 14 | uggaggcagcgg Phvul.007G080900.1 | 5 | -1 | 1 | 22 |
| 15 | uggaggcagcgg Phvul.007G139300.1 | 5 | -1 | 1 | 22 |
| 16 | uggaggcagcgg Phvul.007G139300.1 | 5 | -1 | 1 | 22 |
| 17 | uggaggcagcgg Phvul.007G139300.1 | 5 | -1 | 1 | 22 |
| 18 | ucgauaaaccuc Phvul.007G173400.1 | 5 | -1 | 1 | 21 |
| 19 | ucgauaaaccuc Phvul.007G246700.1 | 5 | -1 | 1 | 21 |
| 20 | uggaggcagcgg Phvul.007G274200.1 | 5 | -1 | 1 | 22 |
| 21 | uggaggcagcgg Phvul.007G274200.1 | 5 | -1 | 1 | 22 |
| 22 | uggaggcagcgg Phvul.007G274200.1 | 5 | -1 | 1 | 22 |
| 23 | ucgauaaaccuc Phvul.008G019000.1 | 5 | -1 | 1 | 21 |
| 24 | uggaggcagcgg Phvul.008G055500.1 | 5 | -1 | 1 | 22 |
| 25 | uggaggcagcgg Phvul.008G055500.1 | 5 | -1 | 1 | 22 |
| 26 | ucgauaaaccuc Phvul.008G077000.1 | 5 | -1 | 1 | 21 |
| 27 | uggaggcagcgg Phvul.008G114700.1 | 5 | -1 | 1 | 22 |
| 28 | uggaggcagcgg Phvul.008G114700.1 | 5 | -1 | 1 | 22 |
| 29 | ucgauaaaccuc Phvul.008G211500.4 | 5 | -1 | 1 | 21 |
| 30 | ucgauaaaccuc Phvul.008G211500.3 | 5 | -1 | 1 | 21 |
| 31 | ucgauaaaccuc Phvul.008G211500.1 | 5 | -1 | 1 | 21 |
| 32 | ucgauaaaccuc Phvul.008G211500.2 | 5 | -1 | 1 | 21 |
| 33 | uggaggcagcgg Phvul.008G250000.1 | 5 | -1 | 1 | 22 |
| 34 | uggaggcagcgg Phvul.008G250000.1 | 5 | -1 | 1 | 22 |
| 35 | uggaggcagcgg Phvul.009G086300.2 | 5 | -1 | 1 | 22 |
| 36 | uggaggcagcgg Phvul.009G086300.1 | 5 | -1 | 1 | 22 |
| 37 | uggaggcagcgg Phvul.009G086300.2 | 5 | -1 | 1 | 22 |
| 38 | uggaggcagcgg Phvul.009G086300.1 | 5 | -1 | 1 | 22 |
| 39 | ucgauaaaccuc Phvul.009G149800.1 | 5 | -1 | 1 | 21 |
| 40 | uggaggcagcgg Phvul.009G154300.6 | 5 | -1 | 1 | 22 |
| 41 | uggaggcagcgg Phvul.009G154300.5 | 5 | -1 | 1 | 22 |
| 42 | uggaggcagcgg Phvul.009G154300.3 | 5 | -1 | 1 | 22 |
| 43 | uggaggcagcgg Phvul.009G154300.4 | 5 | -1 | 1 | 22 |
| 44 | uggaggcagcgg Phvul.009G154300.1 | 5 | -1 | 1 | 22 |
| 45 | uggaggcagcgg Phvul.009G154300.6 | 5 | -1 | 1 | 22 |
| 46 | uggaggcagcgg Phvul.009G154300.5 | 5 | -1 | 1 | 22 |
| 47 | uggaggcagcgg Phvul.009G154300.3 | 5 | -1 | 1 | 22 |
| 48 | uggaggcagcgg Phvul.009G154300.4 | 5 | -1 | 1 | 22 |
| 49 | uggaggcagcgg Phvul.009G154300.1 | 5 | -1 | 1 | 22 |
| 50 | ucgauaaaccuc Phvul.009G240100.1 | 5 | -1 | 1 | 21 |
| 51 | uggaggcagcgg Phvul.011G017800.1 | 5 | -1 | 1 | 22 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggaggcagcgg Phvul.011G017800.1 | 5 | -1 | 1 | 22 |
| 3 | ucgauaaaccuc Phvul.011G100200.2 | 5 | -1 | 1 | 21 |
| 4 | ucgauaaaccuc Phvul.011G100200.1 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | ucgauaaaccuc Phvul.011G108300.1 | 5 | -1 | 1 | 21 |
| 7 | uggaggcagcgg Phvul.011G129700.1 | 5 | -1 | 1 | 22 |
| 8 | uggaggcagcgg Phvul.011G129700.1 | 5 | -1 | 1 | 22 |
| 9 | | | | | |
| 10 | ucgauaaaccuc Phvul.011G140050.2 | 5 | -1 | 1 | 21 |
| 11 | ucgauaaaccuc Phvul.011G140050.1 | 5 | -1 | 1 | 21 |
| 12 | | | | | |
| 13 | | | | | |
| 14 | | | | | |
| 15 | | | | | |
| 16 | | | | | |
| 17 | | | | | |
| 18 | | | | | |
| 19 | | | | | |
| 20 | | | | | |
| 21 | | | | | |
| 22 | | | | | |
| 23 | | | | | |
| 24 | | | | | |
| 25 | | | | | |
| 26 | | | | | |
| 27 | | | | | |
| 28 | | | | | |
| 29 | | | | | |
| 30 | | | | | |
| 31 | | | | | |
| 32 | | | | | |
| 33 | | | | | |
| 34 | | | | | |
| 35 | | | | | |
| 36 | | | | | |
| 37 | | | | | |
| 38 | | | | | |
| 39 | | | | | |
| 40 | | | | | |
| 41 | | | | | |
| 42 | | | | | |
| 43 | | | | | |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

Do not distribute

| | Target_start | Target_end | miRNA_alignment | Target_alignment | Inhibition | Target_Desc. |
|----|--------------|------------|-----------------|---------------------------|-------------|--------------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | 2888 | 2907 | UCGAUAAACC | ::: ::::: GGGGAUG-AC | Cleavage | pacid=371763 |
| 4 | 400 | 421 | UGGAGGCAG | : ::::: AACCGAUGG/ | Cleavage | pacid=371750 |
| 5 | 400 | 421 | UGGAGGCAG | : ::::: AACCGAUGG/ | Cleavage | pacid=371750 |
| 6 | 400 | 421 | UGGAGGCAG | : ::::: AACCGAUGG/ | Cleavage | pacid=371750 |
| 7 | 400 | 421 | UGGAGGCAG | : ::::: AACCGAUGG/ | Cleavage | pacid=371750 |
| 8 | 400 | 421 | UGGAGGCAG | : ::::: AACCGAUGG/ | Cleavage | pacid=371750 |
| 9 | 187 | 207 | UGGAGGCAG | : : ::::: CCACGA-GAA | Cleavage | pacid=371691 |
| 10 | 187 | 207 | UGGAGGCAG | : : ::::: CCACGA-GAA | Cleavage | pacid=371691 |
| 11 | 246 | 267 | UGGAGGCAG | : ::::: AGCAGAUGA | Cleavage | pacid=371771 |
| 12 | 246 | 267 | UGGAGGCAG | : ::::: AGCAGAUGA | Cleavage | pacid=371771 |
| 13 | 1000 | 1020 | UCGAUAAACC | ::: : ::::: AAGGGUGGA | Cleavage | pacid=371778 |
| 14 | 220 | 241 | UGGAGGCAG | : ::::: : ::::: GUUUGAUGG | Cleavage | pacid=371541 |
| 15 | 220 | 241 | UGGAGGCAG | : ::::: : ::::: GUUUGAUGG | Cleavage | pacid=371541 |
| 16 | 282 | 303 | UGGAGGCAG | : : ::::: CUAUGAGGA | Translation | pacid=371526 |
| 17 | 282 | 303 | UGGAGGCAG | : : ::::: CUAUGAGGA | Translation | pacid=371526 |
| 18 | 1116 | 1136 | UCGAUAAACC | : ::::: : : GAGGAUGCA | Translation | pacid=371738 |
| 19 | 473 | 493 | UCGAUAAACC | : ::::: : ::::: CAGGAUGGA | Cleavage | pacid=371646 |
| 20 | 315 | 336 | UGGAGGCAG | : : ::::: UGUUGACCA/ | Cleavage | pacid=371495 |
| 21 | 315 | 336 | UGGAGGCAG | : : ::::: UGUUGACCA/ | Cleavage | pacid=371495 |
| 22 | 315 | 336 | UGGAGGCAG | : : ::::: UGUUGACCA/ | Cleavage | pacid=371495 |
| 23 | 315 | 336 | UGGAGGCAG | : : ::::: UGUUGACCA/ | Cleavage | pacid=371495 |
| 24 | 315 | 336 | UGGAGGCAG | : : ::::: UGUUGACCA/ | Cleavage | pacid=371495 |
| 25 | 315 | 336 | UGGAGGCAG | : : ::::: UGUUGACCA/ | Cleavage | pacid=371495 |
| 26 | 315 | 336 | UGGAGGCAG | : : ::::: UGUUGACCA/ | Cleavage | pacid=371495 |
| 27 | 3637 | 3658 | UCGAUAA-AC | : ::::: : ::::: CUGGAUGCA | Cleavage | pacid=371490 |
| 28 | 1587 | 1608 | UGGAGGCAG | : ::::: : AAAAGGUGA/ | Cleavage | pacid=371459 |
| 29 | 1587 | 1608 | UGGAGGCAG | : ::::: : AAAAGGUGA/ | Cleavage | pacid=371459 |
| 30 | 3823 | 3844 | UGGAGGCAG | : : ::::: UGUUUUAUGG | Translation | pacid=371632 |
| 31 | 3823 | 3844 | UGGAGGCAG | : : ::::: UGUUUUAUGG | Translation | pacid=371632 |
| 32 | 427 | 447 | UCGAUAAACC | : : ::::: : UUGAAUGCG | Cleavage | pacid=371525 |
| 33 | 2271 | 2292 | UGGAGGCAG | : : ::::: : AACUGAUGA | Translation | pacid=371719 |
| 34 | 2271 | 2292 | UGGAGGCAG | : : ::::: : AACUGAUGA | Translation | pacid=371719 |
| 35 | 694 | 715 | UGGAGGCAG | : ::::: : UUGGGAUGG | Cleavage | pacid=371667 |
| 36 | 694 | 715 | UGGAGGCAG | : ::::: : UUGGGAUGG | Cleavage | pacid=371667 |
| 37 | 1058 | 1079 | UGGAGGCAG | : : ::::: : UGACUAUGG | Translation | pacid=371659 |
| 38 | 1056 | 1077 | UGGAGGCAG | : : ::::: : UGACUAUGG | Translation | pacid=371659 |
| 39 | 1058 | 1079 | UGGAGGCAG | : : ::::: : UGACUAUGG | Translation | pacid=371659 |
| 40 | 1058 | 1079 | UGGAGGCAG | : : ::::: : UGACUAUGG | Translation | pacid=371659 |
| 41 | 1056 | 1077 | UGGAGGCAG | : : ::::: : UGACUAUGG | Translation | pacid=371659 |
| 42 | 1058 | 1079 | UGGAGGCAG | : : ::::: : UGACUAUGG | Translation | pacid=371659 |
| 43 | 747 | 767 | UCGAUAAACC | : : ::::: : GAGGCAGCA | Cleavage | pacid=371602 |
| 44 | 1646 | 1667 | UGGAGGCAG | : : ::::: : GACCGAUGG/ | Cleavage | pacid=371611 |
| 45 | 1736 | 1757 | UGGAGGCAG | : : ::::: : GACCGAUGG/ | Cleavage | pacid=371611 |
| 46 | 1646 | 1667 | UGGAGGCAG | : : ::::: : GACCGAUGG/ | Cleavage | pacid=371611 |
| 47 | 1736 | 1757 | UGGAGGCAG | : : ::::: : GACCGAUGG/ | Cleavage | pacid=371611 |
| 48 | 2079 | 2101 | UGGAGGCAG | : : ::::: : GGACGACUG/ | Cleavage | pacid=371551 |
| 49 | 2079 | 2101 | UGGAGGCAG | : : ::::: : GGACGACUG/ | Cleavage | pacid=371551 |

| | | | | |
|----|------|-----------------|---------------------------|--------------------------|
| 1 | | | | |
| 2 | 240 | 261 UGGAGGCAG(| : : : : : GCGUGGUGG | Translation pacid=371603 |
| 3 | 759 | 779 UCGAUAAACC | : : : : : GUGGGUGGA | Cleavage pacid=371577 |
| 4 | 1095 | 1116 UGGAGGCAG(| : : : : : UCUUGAUGA | Cleavage pacid=371489 |
| 5 | 1095 | 1116 UGGAGGCAG(| : : : : : UCUUGAUGA | Cleavage pacid=371489 |
| 6 | 1778 | 1799 UGGAGGCAG(| : : : : : CGCAAUGA | Translation pacid=371487 |
| 7 | 1778 | 1799 UGGAGGCAG(| : : : : : CGCAAUGA | Translation pacid=371487 |
| 8 | | | | |
| 9 | | | | |
| 10 | 421 | 441 UCGAUAAACC | : : : : : CUAGCUGUG | Cleavage pacid=371439 |
| 11 | 78 | 99 UGGAGGCAG(| : : : : : UAACAAUGA | Translation pacid=371574 |
| 12 | 78 | 99 UGGAGGCAG(| : : : : : UAACAAUGA | Translation pacid=371574 |
| 13 | | | | |
| 14 | 719 | 740 UGGAGGCAG(| : : : : : GCUCGGUCA | Cleavage pacid=371549 |
| 15 | 719 | 740 UGGAGGCAG(| : : : : : GCUCGGUCA | Cleavage pacid=371549 |
| 16 | 844 | 864 UCGAUAAACC | : : : : : GAAGAUGCA | Translation pacid=371550 |
| 17 | | | | |
| 18 | 2952 | 2973 UGGAGGCAG(| : : : : : AAUCGAGCA | Cleavage pacid=371569 |
| 19 | 2952 | 2973 UGGAGGCAG(| : : : : : AAUCGAGCA | Cleavage pacid=371569 |
| 20 | 2488 | 2508 UCGAUAAACC | : : : : : UAGGAUGUA | Cleavage pacid=371678 |
| 21 | | | | |
| 22 | 1245 | 1266 UGGAGGCAG(| : : : : : AAGGGAUGG | Cleavage pacid=371677 |
| 23 | 1269 | 1290 UGGAGGCAG(| : : : : : AAGGGAUGG | Cleavage pacid=371677 |
| 24 | 1245 | 1266 UGGAGGCAG(| : : : : : AAGGGAUGG | Cleavage pacid=371677 |
| 25 | 1269 | 1290 UGGAGGCAG(| : : : : : AAGGGAUGG | Cleavage pacid=371677 |
| 26 | | | | |
| 27 | 902 | 923 UGGAGGCAG(| : : : : : UGAUGAUCA | Translation pacid=371686 |
| 28 | 902 | 923 UGGAGGCAG(| : : : : : UGAUGAUCA | Translation pacid=371686 |
| 29 | | | | |
| 30 | 252 | 273 UGGAGGCAG(| : : : : : GAGCGAUGC | Translation pacid=371759 |
| 31 | 252 | 273 UGGAGGCAG(| : : : : : GAGCGAUGC | Translation pacid=371759 |
| 32 | 252 | 273 UGGAGGCAG(| : : : : : GAGCGAUGC | Translation pacid=371759 |
| 33 | 252 | 273 UGGAGGCAG(| : : : : : GAGCGAUGC | Translation pacid=371759 |
| 34 | | | | |
| 35 | 405 | 425 UCGAUAAACC | : : : : : UUGGAUUCA | Translation pacid=371779 |
| 36 | 405 | 425 UCGAUAAACC | : : : : : UUGGAUUCA | Translation pacid=371779 |
| 37 | | | | |
| 38 | 1306 | 1326 UCGAUAAACC | : : : : : GUGGUGGCA | Cleavage pacid=371780 |
| 39 | 819 | 839 UCGAUAAACC | : : : : : UUGGAUGCA | Translation pacid=371752 |
| 40 | 521 | 542 UGGAGGCAG(| : : : : : GGAACAUGG | Cleavage pacid=371777 |
| 41 | 521 | 542 UGGAGGCAG(| : : : : : GGAACAUGG | Cleavage pacid=371777 |
| 42 | | | | |
| 43 | 1039 | 1060 UGGAGGCAG(| : : : : : GGACGAUGG | Translation pacid=371754 |
| 44 | 1132 | 1153 UGGAGGCAG(| : : : : : GGACGAUGG | Translation pacid=371754 |
| 45 | 1039 | 1060 UGGAGGCAG(| : : : : : GGACGAUGG | Translation pacid=371754 |
| 46 | 1132 | 1153 UGGAGGCAG(| : : : : : GGACGAUGG | Translation pacid=371754 |
| 47 | | | | |
| 48 | 2338 | 2358 UCGAUAAACC | : : : : : GUUGAUGAA | Cleavage pacid=371749 |
| 49 | 518 | 539 UGGAGGCAG(| : : : : : UGUUGAUGG | Translation pacid=371782 |
| 50 | 518 | 539 UGGAGGCAG(| : : : : : UGUUGAUGG | Translation pacid=371782 |
| 51 | | | | |
| 52 | 1259 | 1278 UCGAUAAACC | : : : : : GAGGAUGCG | Cleavage pacid=371466 |
| 53 | 1050 | 1069 UCGAUAAACC | : : : : : UUUGAUGCA | Cleavage pacid=371447 |
| 54 | 1169 | 1188 UCGAUAAACC | : : : : : UUUGAUGCA | Cleavage pacid=371447 |
| 55 | 1729 | 1750 UGGAGGCAG(| : : : : : UUGUUAUGA | Cleavage pacid=371481 |
| 56 | 1729 | 1750 UGGAGGCAG(| : : : : : UUGUUAUGA | Cleavage pacid=371481 |
| 57 | | | | |
| 58 | 940 | 960 UCGAUAAACC | : : : : : AUCGAUGAA | Cleavage pacid=371474 |
| 59 | 1008 | 1029 UGGAGGCAG(| : : : : : AUUAGAUGG | Translation pacid=371481 |
| 60 | 1008 | 1029 UGGAGGCAG(| : : : : : AUUAGAUGG | Translation pacid=371481 |

| | | | |
|----|------|---|--------------|
| 1 | | | |
| 2 | 1713 | 1733 UCGAUAAACC : : : : : : : : : : CGUGGUGCA(Translation | pacid=371465 |
| 3 | 1775 | 1796 UGGAGGCAG(: : : : : : : : : : GAUCGGUGA)Cleavage | pacid=371454 |
| 4 | 1775 | 1796 UGGAGGCAG(: : : : : : : : : : GAUCGGUGA)Cleavage | pacid=371454 |
| 5 | | | |
| 6 | 1063 | 1084 UGGAGGCAG(: : : : : : : : : : UCUUAAUGA)Translation | pacid=371483 |
| 7 | 1063 | 1084 UGGAGGCAG(: : : : : : : : : : UCUUAAUGA)Translation | pacid=371483 |
| 8 | 330 | 351 UGGAGGCAG(: : : : : : : : : : : : GAUCGAUGA)Cleavage | pacid=371453 |
| 9 | 330 | 351 UGGAGGCAG(: : : : : : : : : : : : GAUCGAUGA)Cleavage | pacid=371453 |
| 10 | 1029 | 1050 UGGAGGCAG(: : : : : : : : : : : : AUUUGAUGA)Translation | pacid=371443 |
| 11 | 1176 | 1197 UGGAGGCAG(: : : : : : : : : : : : AUUUGAUGA)Translation | pacid=371443 |
| 12 | | | |
| 13 | 1029 | 1050 UGGAGGCAG(: : : : ~ : : : : AUUUGAUGA)Translation | pacid=371443 |
| 14 | 1176 | 1197 UGGAGGCAG(: : : : ~ : : : : AUUUGAUGA)Translation | pacid=371443 |
| 15 | 2631 | 2651 UCGAUAAACC : : : : : : : : : : GACGAUGCAC)Cleavage | pacid=371476 |
| 16 | 2656 | 2676 UCGAUAAACC : : : : ~ : : : : GACGAUGCAC)Cleavage | pacid=371476 |
| 17 | 354 | 375 UGGAGGCAG(: : : : ~ : : : : GGCUGGUGA)Cleavage | pacid=371523 |
| 18 | 354 | 375 UGGAGGCAG(: : : : ~ : : : : GGCUGGUGA)Cleavage | pacid=371523 |
| 19 | 529 | 549 UCGAUAAACC : : : : ~ : : : : CUGGGUGGA)Cleavage | pacid=371726 |
| 20 | 607 | 627 UCGAUAAACC : : : : ~ : : : : CUGGGUGGA)Cleavage | pacid=371726 |
| 21 | 1546 | 1566 UCGAUAAACC : : : : ~ : : : : CCGGAUGAAC)Cleavage | pacid=371664 |
| 22 | 49 | 69 UCGAUAAACC : : : : ~ : : : : UGGGAUGUA)Cleavage | pacid=371660 |
| 23 | 1650 | 1671 UGGAGGCAG(: : : : ~ : : : : GUCUUGUGA)Cleavage | pacid=371649 |
| 24 | 1650 | 1671 UGGAGGCAG(: : : : ~ : : : : GUCUUGUGA)Cleavage | pacid=371649 |
| 25 | 735 | 756 UGGAGGCAG(: : : : ~ : : : : ACUUGGGGA)Translation | pacid=371669 |
| 26 | 735 | 756 UGGAGGCAG(: : : : ~ : : : : ACUUGGGGA)Translation | pacid=371669 |
| 27 | 756 | 777 UGGAGGCAG(: : : : ~ : : : : UGUUAUUGA)Cleavage | pacid=371674 |
| 28 | 756 | 777 UGGAGGCAG(: : : : ~ : : : : UGUUAUUGA)Cleavage | pacid=371674 |
| 29 | 290 | 310 UCGAUAAACC : : : : ~ : : : : UCCAAUACAC)Cleavage | pacid=371646 |
| 30 | 1604 | 1624 UCGAUAAACC : : : : ~ : : : : UUGGAUUCA)Cleavage | pacid=371645 |
| 31 | 812 | 832 UCGAUAAACC : : : : ~ : : : : CGGGAUGUG)Cleavage | pacid=371602 |
| 32 | 293 | 313 UCGAUAAACC : : : : ~ : : : : AGCGAUGAAC)Cleavage | pacid=371609 |
| 33 | 297 | 317 UCGAUAAACC : : : : ~ : : : : AGCGAUGAAC)Cleavage | pacid=371609 |
| 34 | 998 | 1018 UCGAUAAACC : : : : ~ : : : : CUGAAUUUA)Cleavage | pacid=371607 |
| 35 | 1005 | 1025 UCGAUAAACC : : : : ~ : : : : CUGAAUUUA)Cleavage | pacid=371607 |
| 36 | 1799 | 1820 UGGAGGCAG(: : : : ~ : : : : AAUCCAAGAC)Cleavage | pacid=371592 |
| 37 | 1887 | 1908 UGGAGGCAG(: : : : ~ : : : : AAUCCAAGAC)Cleavage | pacid=371592 |
| 38 | 1799 | 1820 UGGAGGCAG(: : : : ~ : : : : AAUCCAAGAC)Cleavage | pacid=371592 |
| 39 | 1887 | 1908 UGGAGGCAG(: : : : ~ : : : : AAUCCAAGAC)Cleavage | pacid=371592 |
| 40 | 280 | 301 UGGAGGCAG(: : : : ~ : : : : GGUCGAAGG)Cleavage | pacid=371513 |
| 41 | 352 | 373 UGGAGGCAG(: : : : ~ : : : : GGUCGAAGG)Cleavage | pacid=371513 |
| 42 | 280 | 301 UGGAGGCAG(: : : : ~ : : : : GGUCGAAGG)Cleavage | pacid=371513 |
| 43 | 352 | 373 UGGAGGCAG(: : : : ~ : : : : GGUCGAAGG)Cleavage | pacid=371513 |
| 44 | 678 | 698 UCGAUAAACC : : : : ~ : : : : GGGGAUGCA)Translation | pacid=371503 |
| 45 | 938 | 958 UCGAUAAACC : : : : ~ : : : : GGGGAUGCA)Translation | pacid=371503 |
| 46 | 1036 | 1056 UCGAUAAACC : : : : ~ : : : : GGGGAUGCA)Translation | pacid=371503 |
| 47 | 299 | 320 UGGAGGCAG(: : : : ~ : : : : CAACGAUGG)Cleavage | pacid=371518 |
| 48 | 299 | 320 UGGAGGCAG(: : : : ~ : : : : CAACGAUGG)Cleavage | pacid=371518 |
| 49 | 299 | 320 UGGAGGCAG(: : : : ~ : : : : CAACGAUGG)Cleavage | pacid=371518 |
| 50 | | | |
| 51 | | | |
| 52 | | | |
| 53 | | | |
| 54 | | | |
| 55 | | | |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

| | | | |
|----|-------------|---|---------------------|
| 1 | | | |
| 2 | 726 | 748 UGGAGGCAG(.....::ACUUGGUGA Cleavage | pacid=371730 |
| 3 | 502 | 523 UGGAGGCAG(.....:: AAUCGGUGG Cleavage | pacid=371657 |
| 4 | 502 | 523 UGGAGGCAG(.....:: AAUCGGUGG Cleavage | pacid=371657 |
| 5 | 502 | 523 UGGAGGCAG(.....:: AAUCGGUGG Cleavage | pacid=371657 |
| 6 | 502 | 523 UGGAGGCAG(.....:: AAUCGGUGG Cleavage | pacid=371657 |
| 7 | 502 | 523 UGGAGGCAG(.....:: AAUCGGUGG Cleavage | pacid=371657 |
| 8 | 226 | 246 UCGAUA AACC:: UUGGAUGUG Cleavage | pacid=371662 |
| 9 | | | |
| 10 | 38 | 58 UCGAUA AACC:: AUGAAUGUA Translation | pacid=371675 |
| 11 | 37 | 58 UGGAGGCAG(.....::GGUUGGAGA Translation | pacid=371673 |
| 12 | 37 | 58 UGGAGGCAG(.....::GGUUGGAGA Translation | pacid=371673 |
| 13 | 37 | 58 UGGAGGCAG(.....::GGUUGGAGA Translation | pacid=371673 |
| 14 | 37 | 58 UGGAGGCAG(.....::GGUUGGAGA Translation | pacid=371673 |
| 15 | 37 | 58 UGGAGGCAG(.....::GGUUGGAGA Translation | pacid=371673 |
| 16 | 483 | 505 UGGAGG-CAG::CUUCGUUGG Cleavage | pacid=371664 |
| 17 | 483 | 505 UGGAGG-CAG::CUUCGUUGG Cleavage | pacid=371664 |
| 18 | 483 | 505 UGGAGG-CAG::CUUCGUUGG Cleavage | pacid=371664 |
| 19 | 1346 | 1366 UCGAUA AACC:: GAGGAUGUA Cleavage | pacid=371674 |
| 20 | 1498 | 1518 UCGAUA AACC:: UUACAUGCA Cleavage | pacid=371644 |
| 21 | | | |
| 22 | 199 | 220 UGGAGGCAG(.....::GAUCGGAGG Cleavage | pacid=371654 |
| 23 | 199 | 220 UGGAGGCAG(.....::GAUCGGAGG Cleavage | pacid=371654 |
| 24 | 2208 | 2228 UCGAUA AACC:: CUGGAAGUG Cleavage | pacid=371593 |
| 25 | | | |
| 26 | 1369 | 1390 UGGAGGCAG(.....::CAUUGAUAG Cleavage | pacid=371605 |
| 27 | 1369 | 1390 UGGAGGCAG(.....::CAUUGAUAG Cleavage | pacid=371605 |
| 28 | 2716 | 2736 UCGAUA AACC:: AUUCUUGGG Cleavage | pacid=371580 |
| 29 | | | |
| 30 | 309 | 330 UGGAGGCAG(.....::GGUCGAUUG Cleavage | pacid=371606 |
| 31 | 309 | 330 UGGAGGCAG(.....::GGUCGAUUG Cleavage | pacid=371606 |
| 32 | 1568 | 1588 UCGAUA AACC:: UUGUAUGCA Cleavage | pacid=371577 |
| 33 | 1568 | 1588 UCGAUA AACC:: UUGUAUGCA Cleavage | pacid=371577 |
| 34 | 1568 | 1588 UCGAUA AACC:: UUGUAUGCA Cleavage | pacid=371577 |
| 35 | 1607 | 1627 UCGAUA AACC:: UUGUAUGCA Cleavage | pacid=371577 |
| 36 | 1610 | 1630 UCGAUA AACC:: UUGUAUGCA Cleavage | pacid=371577 |
| 37 | 702 | 724 UGGAGGCAG(.....::GGUUGAUAG Cleavage | pacid=371599 |
| 38 | 702 | 724 UGGAGGCAG(.....::GGUUGAUAG Cleavage | pacid=371599 |
| 39 | 702 | 724 UGGAGGCAG(.....::GGUUGAUAG Cleavage | pacid=371599 |
| 40 | 1138 | 1159 UGGAGGCAG(.....:: CCCUGAUGG Cleavage | pacid=371499 |
| 41 | 1251 | 1272 UGGAGGCAG(.....:: CCCUGAUGG Cleavage | pacid=371499 |
| 42 | 1251 | 1272 UGGAGGCAG(.....:: CCCUGAUGG Cleavage | pacid=371499 |
| 43 | 1138 | 1159 UGGAGGCAG(.....:: CCCUGAUGG Cleavage | pacid=371499 |
| 44 | 1251 | 1272 UGGAGGCAG(.....:: CCCUGAUGG Cleavage | pacid=371499 |
| 45 | 363 | 383 UCGAUA AACC:: AUUGAUGCA Cleavage | pacid=371495 |
| 46 | 99 | 120 UGGAGGCAG(.....::GGUUGAUGG Cleavage | pacid=371505 |
| 47 | 99 | 120 UGGAGGCAG(.....::GGUUGAUGG Cleavage | pacid=371505 |
| 48 | 99 | 120 UGGAGGCAG(.....::GGUUGAUGG Cleavage | pacid=371505 |
| 49 | 155 | 176 UGGAGGCAG(.....::GGUUGAUGG Cleavage | pacid=371505 |
| 50 | 99 | 120 UGGAGGCAG(.....::GGUUGAUGG Cleavage | pacid=371505 |
| 51 | 99 | 120 UGGAGGCAG(.....::GGUUGAUGG Cleavage | pacid=371505 |
| 52 | 155 | 176 UGGAGGCAG(.....::GGUUGAUGG Cleavage | pacid=371505 |
| 53 | 99 | 120 UGGAGGCAG(.....::GGUUGAUGG Cleavage | pacid=371505 |
| 54 | 99 | 120 UGGAGGCAG(.....::GGUUGAUGG Cleavage | pacid=371505 |
| 55 | 99 | 120 UGGAGGCAG(.....::GGUUGAUGG Cleavage | pacid=371505 |
| 56 | 155 | 176 UGGAGGCAG(.....::GGUUGAUGG Cleavage | pacid=371505 |
| 57 | 99 | 120 UGGAGGCAG(.....::GGUUGAUGG Cleavage | pacid=371505 |
| 58 | 155 | 176 UGGAGGCAG(.....::GGUUGAUGG Cleavage | pacid=371505 |
| 59 | 199 | 219 UCGAUA AACC:: GGGUAUGCA Cleavage | pacid=371521 |
| 60 | 372 | 393 UGGAGGCAG(.....::GGUUCUUGA Cleavage | pacid=371562 |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | |
|------|--|--------------|
| 372 | 393 UGGAGGCAG(:.: :.: :.: :GGUUCUUGA.Cleavage | pacid=371562 |
| 1076 | 1096 UCGAUAAACC.: :.: :.: :.: : UUUGAUCCG(Cleavage | pacid=371558 |
| 1076 | 1096 UCGAUAAACC.: :.: :.: :.: : UUUGAUCCG(Cleavage | pacid=371558 |
| 110 | 130 UCGAUAAACC :.: :.: :.: : : UGAGAUGCA(Cleavage | pacid=371546 |
| 1572 | 1593 UGGAGGCAG(:.: :.: :.: : : : :AGUUGGUGA Cleavage | pacid=371553 |
| 1572 | 1593 UGGAGGCAG(:.: :.: :.: : : : :AGUUGGUGA Cleavage | pacid=371553 |
| 2490 | 2510 UCGAUAAACC :.: :.: :.: : : : : GACGAUGCG(Cleavage | pacid=371551 |
| 2586 | 2606 UCGAUAAACC :.: :.: :.: : : : : GACGAUGCG(Cleavage | pacid=371551 |

Do not distribute

| Multiplicity | Target_Acc. | ID | locusName | Pfam | Panther |
|--------------|--------------------|------------------|--------------|--------------|---------------|
| 1 | Phvul.002G040800.1 | Phvul.002G040800 | Phvul.002G04 | PF00675,PF05 | PTHR11851,P |
| 1 | Phvul.002G112900.2 | Phvul.002G112900 | Phvul.002G11 | PF01529 | PTHR22883,P |
| 1 | Phvul.002G112900.1 | Phvul.002G112900 | Phvul.002G11 | PF01529 | PTHR22883,P |
| 1 | Phvul.002G112900.2 | Phvul.002G112900 | Phvul.002G11 | PF01529 | PTHR22883,P |
| 1 | Phvul.002G112900.1 | Phvul.002G112900 | Phvul.002G11 | PF01529 | PTHR22883,P |
| 1 | Phvul.001G016450.1 | Phvul.001G016450 | Phvul.001G01 | PF13656 | PTHR13946,P |
| 1 | Phvul.001G016450.1 | Phvul.001G016450 | Phvul.001G01 | PF13656 | PTHR13946,P |
| 1 | Phvul.002G255100.1 | Phvul.002G255100 | Phvul.002G25 | PF00083 | PTHR23505,P |
| 1 | Phvul.002G255100.1 | Phvul.002G255100 | Phvul.002G25 | PF00083 | PTHR23505,P |
| 1 | Phvul.002G332500.1 | Phvul.002G332500 | Phvul.002G33 | | 0 PTHR10593,P |
| 1 | Phvul.005G022900.2 | Phvul.005G022900 | Phvul.005G02 | PF02775,PF13 | PTHR18968,P |
| 1 | Phvul.005G022900.2 | Phvul.005G022900 | Phvul.005G02 | PF02775,PF13 | PTHR18968,P |
| 1 | Phvul.005G165300.1 | Phvul.005G165300 | Phvul.005G16 | PF00235 | PTHR11604,P |
| 1 | Phvul.005G165300.1 | Phvul.005G165300 | Phvul.005G16 | PF00235 | PTHR11604,P |
| 1 | Phvul.006G176000.1 | Phvul.006G176000 | Phvul.006G17 | PF13837 | PTHR31307,P |
| 1 | Phvul.007G172400.1 | Phvul.007G172400 | Phvul.007G17 | PF01765 | PTHR20982,P |
| 1 | Phvul.009G109200.2 | Phvul.009G109200 | Phvul.009G10 | PF03055 | PTHR10543,P |
| 1 | Phvul.009G109200.3 | Phvul.009G109200 | Phvul.009G10 | PF03055 | PTHR10543,P |
| 1 | Phvul.009G109200.1 | Phvul.009G109200 | Phvul.009G10 | PF03055 | PTHR10543,P |
| 1 | Phvul.009G109200.2 | Phvul.009G109200 | Phvul.009G10 | PF03055 | PTHR10543,P |
| 1 | Phvul.009G109200.3 | Phvul.009G109200 | Phvul.009G10 | PF03055 | PTHR10543,P |
| 1 | Phvul.009G109200.1 | Phvul.009G109200 | Phvul.009G10 | PF03055 | PTHR10543,P |
| 1 | Phvul.009G260000.1 | Phvul.009G260000 | Phvul.009G26 | PF04851,PF14 | PTHR14950,P |
| 1 | Phvul.003G050000.1 | Phvul.003G050000 | Phvul.003G05 | PF08241 | PTHR12176,P |
| 1 | Phvul.003G050000.1 | Phvul.003G050000 | Phvul.003G05 | PF08241 | PTHR12176,P |
| 1 | Phvul.004G050550.1 | Phvul.004G050550 | Phvul.004G05 | PF13650 | PTHR34482,P |
| 1 | Phvul.004G050550.1 | Phvul.004G050550 | Phvul.004G05 | PF13650 | PTHR34482,P |
| 1 | Phvul.005G136500.1 | Phvul.005G136500 | Phvul.005G13 | PF05739 | PTHR19957,P |
| 1 | Phvul.006G105000.1 | Phvul.006G105000 | Phvul.006G10 | PF13857,PF11 | PTHR12447,P |
| 1 | Phvul.006G105000.1 | Phvul.006G105000 | Phvul.006G10 | PF13857,PF11 | PTHR12447,P |
| 1 | Phvul.007G006700.1 | Phvul.007G006700 | Phvul.007G00 | PF01040 | PTHR11048,P |
| 1 | Phvul.007G006700.1 | Phvul.007G006700 | Phvul.007G00 | PF01040 | PTHR11048,P |
| 1 | Phvul.007G216500.4 | Phvul.007G216500 | Phvul.007G21 | PF07786 | PTHR31061,P |
| 1 | Phvul.007G216500.3 | Phvul.007G216500 | Phvul.007G21 | PF07786 | PTHR31061,P |
| 1 | Phvul.007G216500.1 | Phvul.007G216500 | Phvul.007G21 | PF07786 | PTHR31061,P |
| 1 | Phvul.007G216500.4 | Phvul.007G216500 | Phvul.007G21 | PF07786 | PTHR31061,P |
| 1 | Phvul.007G216500.3 | Phvul.007G216500 | Phvul.007G21 | PF07786 | PTHR31061,P |
| 1 | Phvul.007G216500.1 | Phvul.007G216500 | Phvul.007G21 | PF07786 | PTHR31061,P |
| 1 | Phvul.008G055300.1 | Phvul.008G055300 | Phvul.008G05 | PF00571 | PTHR13780,P |
| 1 | Phvul.008G173900.2 | Phvul.008G173900 | Phvul.008G17 | PF13855 | PTHR24365,P |
| 1 | Phvul.008G173900.1 | Phvul.008G173900 | Phvul.008G17 | PF13855 | PTHR24365,P |
| 1 | Phvul.008G173900.2 | Phvul.008G173900 | Phvul.008G17 | PF13855 | PTHR24365,P |
| 1 | Phvul.008G173900.1 | Phvul.008G173900 | Phvul.008G17 | PF13855 | PTHR24365,P |
| 1 | Phvul.011G132801.1 | Phvul.011G132801 | Phvul.011G13 | | 0 0 |
| 1 | Phvul.011G132801.1 | Phvul.011G132801 | Phvul.011G13 | | 0 0 |

| | | | | | |
|----|---|--------------------|------------------|---------------------------|---------------|
| 1 | | | | | |
| 2 | 1 | Phvul.011G157600.3 | Phvul.011G157600 | Phvul.011G15 | 0 PTHR24067,P |
| 3 | 1 | Phvul.011G157600.4 | Phvul.011G157600 | Phvul.011G15 | 0 PTHR24067,P |
| 4 | 1 | Phvul.011G157600.2 | Phvul.011G157600 | Phvul.011G15 | 0 PTHR24067,P |
| 5 | 1 | Phvul.011G157600.3 | Phvul.011G157600 | Phvul.011G15 | 0 PTHR24067,P |
| 6 | 1 | Phvul.011G157600.4 | Phvul.011G157600 | Phvul.011G15 | 0 PTHR24067,P |
| 7 | 1 | Phvul.011G157600.2 | Phvul.011G157600 | Phvul.011G15 | 0 PTHR24067,P |
| 8 | 1 | Phvul.001G026200.1 | Phvul.001G026200 | Phvul.001G02 PF00887 | PTHR23310,P |
| 9 | 1 | Phvul.001G026200.1 | Phvul.001G026200 | Phvul.001G02 PF00887 | PTHR23310,P |
| 10 | 1 | Phvul.001G141300.1 | Phvul.001G141300 | Phvul.001G14 PF00076 | PTHR24012,P |
| 11 | 1 | Phvul.001G141300.1 | Phvul.001G141300 | Phvul.001G14 PF00076 | PTHR24012,P |
| 12 | 1 | Phvul.001G256400.1 | Phvul.001G256400 | Phvul.001G25 | 0 PTHR10314,P |
| 13 | 1 | Phvul.001G256400.1 | Phvul.001G256400 | Phvul.001G25 | 0 PTHR10314,P |
| 14 | 1 | Phvul.001G256600.1 | Phvul.001G256600 | Phvul.001G25 PF15413,PF01 | PTHR10972,P |
| 15 | 1 | Phvul.001G256600.1 | Phvul.001G256600 | Phvul.001G25 PF15413,PF01 | PTHR10972,P |
| 16 | 1 | Phvul.002G003600.1 | Phvul.002G003600 | Phvul.002G00 PF02880,PF00 | PTHR22573,P |
| 17 | 1 | Phvul.002G003600.1 | Phvul.002G003600 | Phvul.002G00 PF02880,PF00 | PTHR22573,P |
| 18 | 1 | Phvul.002G075900.1 | Phvul.002G075900 | Phvul.002G07 | 0 0 |
| 19 | 1 | Phvul.002G075900.1 | Phvul.002G075900 | Phvul.002G07 | 0 0 |
| 20 | 1 | Phvul.002G102800.2 | Phvul.002G102800 | Phvul.002G10 PF00232 | PTHR10353,P |
| 21 | 1 | Phvul.002G102800.2 | Phvul.002G102800 | Phvul.002G10 PF00232 | PTHR10353,P |
| 22 | 1 | Phvul.002G146600.2 | Phvul.002G146600 | Phvul.002G14 PF04564 | PTHR27003 |
| 23 | 1 | Phvul.002G146600.1 | Phvul.002G146600 | Phvul.002G14 PF04564 | PTHR27003 |
| 24 | 1 | Phvul.002G146600.2 | Phvul.002G146600 | Phvul.002G14 PF04564 | PTHR27003 |
| 25 | 1 | Phvul.002G146600.1 | Phvul.002G146600 | Phvul.002G14 PF04564 | PTHR27003 |
| 26 | 1 | Phvul.002G158200.1 | Phvul.002G158200 | Phvul.002G15 | 0 PTHR31798,P |
| 27 | 1 | Phvul.002G158200.1 | Phvul.002G158200 | Phvul.002G15 | 0 PTHR31798,P |
| 28 | 1 | Phvul.003G013200.2 | Phvul.003G013200 | Phvul.003G01 PF03171 | PTHR10209,P |
| 29 | 1 | Phvul.003G156333.1 | Phvul.003G156333 | Phvul.003G15 PF01287 | PTHR11673,P |
| 30 | 1 | Phvul.003G156333.1 | Phvul.003G156333 | Phvul.003G15 PF01287 | PTHR11673,P |
| 31 | 1 | Phvul.003G179800.1 | Phvul.003G179800 | Phvul.003G17 | 0 0 |
| 32 | 1 | Phvul.003G179800.1 | Phvul.003G179800 | Phvul.003G17 | 0 0 |
| 33 | 1 | Phvul.003G179800.1 | Phvul.003G179800 | Phvul.003G17 | 0 0 |
| 34 | 1 | Phvul.003G261400.2 | Phvul.003G261400 | Phvul.003G26 PF10018 | PTHR13208,P |
| 35 | 1 | Phvul.003G261400.1 | Phvul.003G261400 | Phvul.003G26 PF10018 | PTHR13208,P |
| 36 | 1 | Phvul.003G261400.2 | Phvul.003G261400 | Phvul.003G26 PF10018 | PTHR13208,P |
| 37 | 1 | Phvul.003G261400.1 | Phvul.003G261400 | Phvul.003G26 PF10018 | PTHR13208,P |
| 38 | 2 | Phvul.003G291600.1 | Phvul.003G291600 | Phvul.003G29 PF01039 | PTHR22855,P |
| 39 | 2 | Phvul.003G291600.2 | Phvul.003G291600 | Phvul.003G29 PF01039 | PTHR22855,P |
| 40 | 2 | Phvul.003G291600.1 | Phvul.003G291600 | Phvul.003G29 PF01039 | PTHR22855,P |
| 41 | 2 | Phvul.003G291600.2 | Phvul.003G291600 | Phvul.003G29 PF01039 | PTHR22855,P |
| 42 | 1 | Phvul.004G068900.2 | Phvul.004G068900 | Phvul.004G06 PF00847 | PTHR31677,P |
| 43 | 1 | Phvul.004G068900.2 | Phvul.004G068900 | Phvul.004G06 PF00847 | PTHR31677,P |
| 44 | 1 | Phvul.005G069600.1 | Phvul.005G069600 | Phvul.005G06 PF13771,PF00 | PTHR23069,P |
| 45 | 1 | Phvul.007G157700.1 | Phvul.007G157700 | Phvul.007G15 PF13041 | PTHR24015,P |
| 46 | 1 | Phvul.007G249600.1 | Phvul.007G249600 | Phvul.007G24 PF08799,PF00 | PTHR19846 |
| 47 | 1 | Phvul.008G111200.1 | Phvul.008G111200 | Phvul.008G11 PF01612 | PTHR13620 |

| | | | | | |
|----|---|--------------------|------------------|---------------------------|---------------|
| 1 | | | | | |
| 2 | 1 | Phvul.008G111200.1 | Phvul.008G111200 | Phvul.008G11 PF01612 | PTHR13620 |
| 3 | 1 | Phvul.008G230800.1 | Phvul.008G230800 | Phvul.008G23 PF01535,PF13 | PTHR24015 |
| 4 | 1 | Phvul.009G080800.1 | Phvul.009G080800 | Phvul.009G08 PF02042 | PTHR32002 |
| 5 | 1 | Phvul.009G080800.1 | Phvul.009G080800 | Phvul.009G08 PF02042 | PTHR32002 |
| 6 | 1 | Phvul.009G119700.1 | Phvul.009G119700 | Phvul.009G11 PF00632 | PTHR11254,P |
| 7 | 1 | Phvul.009G119700.1 | Phvul.009G119700 | Phvul.009G11 PF00632 | PTHR11254,P |
| 8 | 1 | Phvul.010G119500.1 | Phvul.010G119500 | Phvul.010G11 PF00076 | PTHR24012 |
| 9 | 1 | Phvul.011G008600.1 | Phvul.011G008600 | Phvul.011G00 | 0 0 |
| 10 | 1 | Phvul.011G008600.1 | Phvul.011G008600 | Phvul.011G00 | 0 0 |
| 11 | 1 | Phvul.011G140900.1 | Phvul.011G140900 | Phvul.011G14 PF12490 | PTHR13268,P |
| 12 | 1 | Phvul.011G140900.1 | Phvul.011G140900 | Phvul.011G14 PF12490 | PTHR13268,P |
| 13 | 1 | Phvul.011G169222.1 | Phvul.011G169222 | Phvul.011G16 PF13639 | PTHR14155,P |
| 14 | 1 | Phvul.011G215900.1 | Phvul.011G215900 | Phvul.011G21 PF01926,PF00 | PTHR11566,P |
| 15 | 1 | Phvul.011G215900.1 | Phvul.011G215900 | Phvul.011G21 PF01926,PF00 | PTHR11566,P |
| 16 | 1 | Phvul.001G096200.1 | Phvul.001G096200 | Phvul.001G09 PF12796 | PTHR24158,P |
| 17 | 1 | Phvul.001G104700.2 | Phvul.001G104700 | Phvul.001G10 PF13906,PF13 | PTHR11785,P |
| 18 | 1 | Phvul.001G104700.1 | Phvul.001G104700 | Phvul.001G10 PF13906,PF13 | PTHR11785,P |
| 19 | 1 | Phvul.001G104700.2 | Phvul.001G104700 | Phvul.001G10 PF13906,PF13 | PTHR11785,P |
| 20 | 1 | Phvul.001G104700.1 | Phvul.001G104700 | Phvul.001G10 PF13906,PF13 | PTHR11785,P |
| 21 | 1 | Phvul.001G211000.1 | Phvul.001G211000 | Phvul.001G21 PF13632 | PTHR13301,P |
| 22 | 1 | Phvul.001G211000.1 | Phvul.001G211000 | Phvul.001G21 PF13632 | PTHR13301,P |
| 23 | 1 | Phvul.002G147900.2 | Phvul.002G147900 | Phvul.002G14 PF01663 | PTHR23072,P |
| 24 | 1 | Phvul.002G147900.1 | Phvul.002G147900 | Phvul.002G14 PF01663 | PTHR23072,P |
| 25 | 1 | Phvul.002G147900.2 | Phvul.002G147900 | Phvul.002G14 PF01663 | PTHR23072,P |
| 26 | 1 | Phvul.002G147900.1 | Phvul.002G147900 | Phvul.002G14 PF01663 | PTHR23072,P |
| 27 | 1 | Phvul.002G182700.2 | Phvul.002G182700 | Phvul.002G18 PF02746,PF13 | PTHR13794,P |
| 28 | 1 | Phvul.002G182700.1 | Phvul.002G182700 | Phvul.002G18 PF02746,PF13 | PTHR13794,P |
| 29 | 1 | Phvul.002G202300.1 | Phvul.002G202300 | Phvul.002G20 PF07800 | PTHR31197,P |
| 30 | 1 | Phvul.002G238000.1 | Phvul.002G238000 | Phvul.002G23 | 0 PTHR34669,P |
| 31 | 1 | Phvul.002G267100.1 | Phvul.002G267100 | Phvul.002G26 | 0 PTHR33828,P |
| 32 | 1 | Phvul.002G267100.1 | Phvul.002G267100 | Phvul.002G26 | 0 PTHR33828,P |
| 33 | 1 | Phvul.002G274400.2 | Phvul.002G274400 | Phvul.002G27 PF00646 | PTHR31370,P |
| 34 | 1 | Phvul.002G274400.1 | Phvul.002G274400 | Phvul.002G27 PF00646 | PTHR31370,P |
| 35 | 1 | Phvul.002G274400.2 | Phvul.002G274400 | Phvul.002G27 PF00646 | PTHR31370,P |
| 36 | 1 | Phvul.002G274400.1 | Phvul.002G274400 | Phvul.002G27 PF00646 | PTHR31370,P |
| 37 | 1 | Phvul.002G304500.1 | Phvul.002G304500 | Phvul.002G30 PF07714 | PTHR27001,P |
| 38 | 1 | Phvul.002G327900.1 | Phvul.002G327900 | Phvul.002G32 PF00462 | PTHR10168,P |
| 39 | 1 | Phvul.002G327900.1 | Phvul.002G327900 | Phvul.002G32 PF00462 | PTHR10168,P |
| 40 | 1 | Phvul.003G010700.1 | Phvul.003G010700 | Phvul.003G01 PF00067 | PTHR24286,P |
| 41 | 1 | Phvul.003G023101.2 | Phvul.003G023101 | Phvul.003G02 PF13906,PF13 | PTHR11785,P |
| 42 | 1 | Phvul.003G023101.1 | Phvul.003G023101 | Phvul.003G02 PF13906,PF13 | PTHR11785,P |
| 43 | 1 | Phvul.003G044200.1 | Phvul.003G044200 | Phvul.003G04 PF01536 | PTHR11570,P |
| 44 | 1 | Phvul.003G044200.1 | Phvul.003G044200 | Phvul.003G04 PF01536 | PTHR11570,P |
| 45 | 1 | Phvul.003G080700.1 | Phvul.003G080700 | Phvul.003G08 PF03595 | PTHR31269,P |
| 46 | 1 | Phvul.003G090000.2 | Phvul.003G090000 | Phvul.003G09 PF07714 | PTHR27003,P |
| 47 | 1 | Phvul.003G090000.2 | Phvul.003G090000 | Phvul.003G09 PF07714 | PTHR27003,P |

| | | | | |
|----|---|--------------------|------------------|--------------------------------------|
| 1 | | | | |
| 2 | 1 | Phvul.003G096500.1 | Phvul.003G096500 | Phvul.003G09PF161113,PF00PTHR23309,P |
| 3 | 1 | Phvul.003G113900.1 | Phvul.003G113900 | Phvul.003G11 0 PTHR36033,P |
| 4 | 1 | Phvul.003G113900.1 | Phvul.003G113900 | Phvul.003G11 0 PTHR36033,P |
| 5 | 1 | Phvul.003G154900.1 | Phvul.003G154900 | Phvul.003G15PF02847,PF02PTHR23253,P |
| 6 | 1 | Phvul.003G154900.1 | Phvul.003G154900 | Phvul.003G15PF02847,PF02PTHR23253,P |
| 7 | 1 | Phvul.003G209900.1 | Phvul.003G209900 | Phvul.003G20 PF08387 PTHR32212,P |
| 8 | 1 | Phvul.003G209900.1 | Phvul.003G209900 | Phvul.003G20 PF08387 PTHR32212,P |
| 9 | 1 | Phvul.003G254900.2 | Phvul.003G254900 | Phvul.003G25PF00646,PF01PTHR16517,P |
| 10 | 1 | Phvul.003G254900.1 | Phvul.003G254900 | Phvul.003G25PF00646,PF01PTHR16517,P |
| 11 | 1 | Phvul.003G254900.2 | Phvul.003G254900 | Phvul.003G25PF00646,PF01PTHR16517,P |
| 12 | 1 | Phvul.003G254900.1 | Phvul.003G254900 | Phvul.003G25PF00646,PF01PTHR16517,P |
| 13 | 1 | Phvul.003G254900.1 | Phvul.003G254900 | Phvul.003G25PF00646,PF01PTHR16517,P |
| 14 | 1 | Phvul.003G295700.2 | Phvul.003G295700 | Phvul.003G29PF01535,PF13PTHR24015,P |
| 15 | 1 | Phvul.003G295700.1 | Phvul.003G295700 | Phvul.003G29PF01535,PF13PTHR24015,P |
| 16 | 1 | Phvul.005G088636.1 | Phvul.005G088636 | Phvul.005G08 0 0 |
| 17 | 1 | Phvul.005G088636.1 | Phvul.005G088636 | Phvul.005G08 0 0 |
| 18 | 1 | Phvul.006G112000.1 | Phvul.006G112000 | Phvul.006G11 PF01764 PTHR21493,P |
| 19 | 1 | Phvul.006G112000.2 | Phvul.006G112000 | Phvul.006G11 PF01764 PTHR21493,P |
| 20 | 1 | Phvul.007G015000.1 | Phvul.007G015000 | Phvul.007G01 PF03634 PTHR31072,P |
| 21 | 1 | Phvul.007G028800.1 | Phvul.007G028800 | Phvul.007G02PF04557,PF03PTHR11451,P |
| 22 | 1 | Phvul.007G038000.1 | Phvul.007G038000 | Phvul.007G03 PF00403 PTHR22814,P |
| 23 | 1 | Phvul.007G038000.1 | Phvul.007G038000 | Phvul.007G03 PF00403 PTHR22814,P |
| 24 | 1 | Phvul.007G062900.1 | Phvul.007G062900 | Phvul.007G06PF14306,PF01PTHR11055,P |
| 25 | 1 | Phvul.007G062900.1 | Phvul.007G062900 | Phvul.007G06PF14306,PF01PTHR11055,P |
| 26 | 1 | Phvul.007G100700.1 | Phvul.007G100700 | Phvul.007G10 PF05512 PTHR33294,P |
| 27 | 1 | Phvul.007G100700.1 | Phvul.007G100700 | Phvul.007G10 PF05512 PTHR33294,P |
| 28 | 1 | Phvul.007G149300.1 | Phvul.007G149300 | Phvul.007G14 PF10270 PTHR21181 |
| 29 | 1 | Phvul.007G230450.1 | Phvul.007G230450 | Phvul.007G23 PF07766 PTHR14009,P |
| 30 | 1 | Phvul.008G046100.1 | Phvul.008G046100 | Phvul.008G04PF12854,PF13PTHR24015,P |
| 31 | 1 | Phvul.008G177200.1 | Phvul.008G177200 | Phvul.008G17 0 PTHR35689,P |
| 32 | 1 | Phvul.008G177200.2 | Phvul.008G177200 | Phvul.008G17 0 PTHR35689,P |
| 33 | 1 | Phvul.008G181900.2 | Phvul.008G181900 | Phvul.008G18 0 PTHR34464 |
| 34 | 1 | Phvul.008G181900.1 | Phvul.008G181900 | Phvul.008G18 0 PTHR34464 |
| 35 | 1 | Phvul.008G260900.2 | Phvul.008G260900 | Phvul.008G26PF00642,PF12PTHR14493,P |
| 36 | 1 | Phvul.008G260900.1 | Phvul.008G260900 | Phvul.008G26PF00642,PF12PTHR14493,P |
| 37 | 1 | Phvul.008G260900.2 | Phvul.008G260900 | Phvul.008G26PF00642,PF12PTHR14493,P |
| 38 | 1 | Phvul.008G260900.1 | Phvul.008G260900 | Phvul.008G26PF00642,PF12PTHR14493,P |
| 39 | 1 | Phvul.009G041100.2 | Phvul.009G041100 | Phvul.009G04 0 PTHR31789,P |
| 40 | 1 | Phvul.009G041100.1 | Phvul.009G041100 | Phvul.009G04 0 PTHR31789,P |
| 41 | 1 | Phvul.009G041100.2 | Phvul.009G041100 | Phvul.009G04 0 PTHR31789,P |
| 42 | 1 | Phvul.009G041100.1 | Phvul.009G041100 | Phvul.009G04 0 PTHR31789,P |
| 43 | 1 | Phvul.009G175100.3 | Phvul.009G175100 | Phvul.009G17PF01535,PF13PTHR24015,P |
| 44 | 1 | Phvul.009G175100.2 | Phvul.009G175100 | Phvul.009G17PF01535,PF13PTHR24015,P |
| 45 | 1 | Phvul.009G175100.1 | Phvul.009G175100 | Phvul.009G17PF01535,PF13PTHR24015,P |
| 46 | 1 | Phvul.009G200500.3 | Phvul.009G200500 | Phvul.009G20 PF08616 PTHR13677,P |
| 47 | 1 | Phvul.009G200500.2 | Phvul.009G200500 | Phvul.009G20 PF08616 PTHR13677,P |
| 48 | 1 | Phvul.009G200500.3 | Phvul.009G200500 | Phvul.009G20 PF08616 PTHR13677,P |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | |
|----------------------|------------------|-------------------------------------|---------------|
| 1 Phvul.009G200500.2 | Phvul.009G200500 | Phvul.009G20 PF08616 | PTHR13677,P |
| 1 Phvul.011G080200.1 | Phvul.011G080200 | Phvul.011G08 PF00320 | PTHR10071,P |
| 1 Phvul.011G080200.1 | Phvul.011G080200 | Phvul.011G08 PF00320 | PTHR10071,P |
| 1 Phvul.011G174000.1 | Phvul.011G174000 | Phvul.011G17PF13906,PF13PTHR11785,P | |
| 1 Phvul.011G174000.1 | Phvul.011G174000 | Phvul.011G17PF13906,PF13PTHR11785,P | |
| 1 Phvul.001G110400.1 | Phvul.001G110400 | Phvul.001G11 PF04410 | PTHR23237 |
| 1 Phvul.001G123400.1 | Phvul.001G123400 | Phvul.001G12 PF05678 | PTHR33624,P |
| 1 Phvul.001G123400.1 | Phvul.001G123400 | Phvul.001G12 PF05678 | PTHR33624,P |
| 1 Phvul.001G154700.1 | Phvul.001G154700 | Phvul.001G15 PF00447 | PTHR10015,P |
| 1 Phvul.001G179800.1 | Phvul.001G179800 | Phvul.001G17PF01535,PF13PTHR24015,P | |
| 1 Phvul.001G179800.1 | Phvul.001G179800 | Phvul.001G17PF01535,PF13PTHR24015,P | |
| 1 Phvul.001G184000.1 | Phvul.001G184000 | Phvul.001G18PF10312,PF09PTHR21737,P | |
| 1 Phvul.001G259000.1 | Phvul.001G259000 | Phvul.001G25PF00044,PF02PTHR10836,P | |
| 1 Phvul.001G259000.1 | Phvul.001G259000 | Phvul.001G25PF00044,PF02PTHR10836,P | |
| 1 Phvul.002G028100.1 | Phvul.002G028100 | Phvul.002G02 PF12171 | PTHR10593,P |
| 1 Phvul.002G028100.1 | Phvul.002G028100 | Phvul.002G02 PF12171 | PTHR10593,P |
| 1 Phvul.002G092900.2 | Phvul.002G092900 | Phvul.002G09PF00118,PF01PTHR11353,P | |
| 1 Phvul.002G092900.1 | Phvul.002G092900 | Phvul.002G09PF00118,PF01PTHR11353,P | |
| 1 Phvul.002G137100.1 | Phvul.002G137100 | Phvul.002G13PF02928,PF02PTHR10694,P | |
| 1 Phvul.002G137200.1 | Phvul.002G137200 | Phvul.002G13 PF00076 | PTHR24012,P |
| 1 Phvul.002G137200.1 | Phvul.002G137200 | Phvul.002G13 PF00076 | PTHR24012,P |
| 1 Phvul.002G139900.2 | Phvul.002G139900 | Phvul.002G13 PF00076 | PTHR24012,P |
| 1 Phvul.002G139900.1 | Phvul.002G139900 | Phvul.002G13 PF00076 | PTHR24012,P |
| 1 Phvul.002G156300.1 | Phvul.002G156300 | Phvul.002G15 PF14111 | PTHR24012,P |
| 1 Phvul.003G032500.1 | Phvul.003G032500 | Phvul.003G03 PF03547 | PTHR31752,P |
| 1 Phvul.003G032500.1 | Phvul.003G032500 | Phvul.003G03 PF03547 | PTHR31752,P |
| 1 Phvul.003G252400.1 | Phvul.003G252400 | Phvul.003G25 PF12171 | PTHR10593,P |
| 1 Phvul.003G252400.1 | Phvul.003G252400 | Phvul.003G25 PF12171 | PTHR10593,P |
| 1 Phvul.003G265700.1 | Phvul.003G265700 | Phvul.003G26 | 0 PTHR34049,P |
| 2 Phvul.003G291600.1 | Phvul.003G291600 | Phvul.003G29 PF01039 | PTHR22855,P |
| 2 Phvul.003G291600.2 | Phvul.003G291600 | Phvul.003G29 PF01039 | PTHR22855,P |
| 2 Phvul.003G291600.1 | Phvul.003G291600 | Phvul.003G29 PF01039 | PTHR22855,P |
| 2 Phvul.003G291600.2 | Phvul.003G291600 | Phvul.003G29 PF01039 | PTHR22855,P |
| 1 Phvul.004G176100.1 | Phvul.004G176100 | Phvul.004G17PF01426,PF00PTHR10629,P | |
| 1 Phvul.005G001500.2 | Phvul.005G001500 | Phvul.005G00 PF13417 | PTHR11260,P |
| 1 Phvul.005G001500.1 | Phvul.005G001500 | Phvul.005G00 PF13417 | PTHR11260,P |
| 1 Phvul.005G043500.1 | Phvul.005G043500 | Phvul.005G04PF08442,PF16PTHR23118,P | |
| 1 Phvul.005G043500.1 | Phvul.005G043500 | Phvul.005G04PF08442,PF16PTHR23118,P | |
| 1 Phvul.005G093400.1 | Phvul.005G093400 | Phvul.005G09 | 0 PTHR11017,P |
| 1 Phvul.005G131700.1 | Phvul.005G131700 | Phvul.005G13PF00076,PF14PTHR24012,P | |
| 1 Phvul.005G183800.1 | Phvul.005G183800 | Phvul.005G18 PF01167 | PTHR16517,P |
| 1 Phvul.005G183800.2 | Phvul.005G183800 | Phvul.005G18 PF01167 | PTHR16517,P |
| 1 Phvul.006G098700.1 | Phvul.006G098700 | Phvul.006G09 PF02458 | PTHR31642,P |
| 1 Phvul.006G131400.1 | Phvul.006G131400 | Phvul.006G13PF11900,PF00PTHR24413,P | |
| 1 Phvul.006G131400.1 | Phvul.006G131400 | Phvul.006G13PF11900,PF00PTHR24413,P | |
| 1 Phvul.006G208400.1 | Phvul.006G208400 | Phvul.006G20 PF00201 | PTHR11926,P |

| | | | | | |
|----|---|--------------------|------------------|---------------------------|---------------|
| 1 | | | | | |
| 2 | 1 | Phvul.006G208400.1 | Phvul.006G208400 | Phvul.006G20 PF00201 | PTHR11926,P |
| 3 | 1 | Phvul.007G043900.2 | Phvul.007G043900 | Phvul.007G04 PF04484 | PTHR31807,P |
| 4 | 1 | Phvul.007G043900.1 | Phvul.007G043900 | Phvul.007G04 PF04484 | PTHR31807,P |
| 5 | 1 | Phvul.007G043900.2 | Phvul.007G043900 | Phvul.007G04 PF04484 | PTHR31807,P |
| 6 | 1 | Phvul.007G043900.1 | Phvul.007G043900 | Phvul.007G04 PF04484 | PTHR31807,P |
| 7 | 1 | Phvul.007G062100.1 | Phvul.007G062100 | Phvul.007G06 PF00248 | PTHR11732,P |
| 8 | 1 | Phvul.007G062100.1 | Phvul.007G062100 | Phvul.007G06 PF00248 | PTHR11732,P |
| 9 | 1 | Phvul.007G062100.1 | Phvul.007G062100 | Phvul.007G06 PF00248 | PTHR11732,P |
| 10 | 1 | Phvul.007G067800.1 | Phvul.007G067800 | Phvul.007G06 PF00447 | PTHR10015,P |
| 11 | 1 | Phvul.007G080900.2 | Phvul.007G080900 | Phvul.007G08 PF05055 | PTHR31113,P |
| 12 | 1 | Phvul.007G080900.1 | Phvul.007G080900 | Phvul.007G08 PF05055 | PTHR31113,P |
| 13 | 1 | Phvul.007G080900.2 | Phvul.007G080900 | Phvul.007G08 PF05055 | PTHR31113,P |
| 14 | 1 | Phvul.007G080900.2 | Phvul.007G080900 | Phvul.007G08 PF05055 | PTHR31113,P |
| 15 | 1 | Phvul.007G080900.1 | Phvul.007G080900 | Phvul.007G08 PF05055 | PTHR31113,P |
| 16 | 1 | Phvul.007G139300.1 | Phvul.007G139300 | Phvul.007G13 PF00249,PF14 | PTHR31499,P |
| 17 | 1 | Phvul.007G139300.1 | Phvul.007G139300 | Phvul.007G13 PF00249,PF14 | PTHR31499,P |
| 18 | 1 | Phvul.007G139300.1 | Phvul.007G139300 | Phvul.007G13 PF00249,PF14 | PTHR31499,P |
| 19 | 1 | Phvul.007G173400.1 | Phvul.007G173400 | Phvul.007G17 PF04570 | PTHR33059,P |
| 20 | 1 | Phvul.007G246700.1 | Phvul.007G246700 | Phvul.007G24 PF04043,PF01 | PTHR31707,P |
| 21 | 1 | Phvul.007G246700.1 | Phvul.007G246700 | Phvul.007G24 PF04043,PF01 | PTHR31707,P |
| 22 | 1 | Phvul.007G274200.1 | Phvul.007G274200 | Phvul.007G27 PF01248 | PTHR23105,P |
| 23 | 1 | Phvul.007G274200.1 | Phvul.007G274200 | Phvul.007G27 PF01248 | PTHR23105,P |
| 24 | 1 | Phvul.008G019000.1 | Phvul.008G019000 | Phvul.008G01 PF00533,PF03 | PTHR23081,P |
| 25 | 1 | Phvul.008G019000.1 | Phvul.008G019000 | Phvul.008G01 PF00533,PF03 | PTHR23081,P |
| 26 | 1 | Phvul.008G055500.1 | Phvul.008G055500 | Phvul.008G05 PF00005 | PTHR24220,P |
| 27 | 1 | Phvul.008G055500.1 | Phvul.008G055500 | Phvul.008G05 PF00005 | PTHR24220,P |
| 28 | 1 | Phvul.008G077000.1 | Phvul.008G077000 | Phvul.008G07 PF03514 | PTHR31636,P |
| 29 | 1 | Phvul.008G114700.1 | Phvul.008G114700 | Phvul.008G11 PF03208 | PTHR12859 |
| 30 | 1 | Phvul.008G114700.1 | Phvul.008G114700 | Phvul.008G11 PF03208 | PTHR12859 |
| 31 | 1 | Phvul.008G114700.1 | Phvul.008G114700 | Phvul.008G11 PF03208 | PTHR12859 |
| 32 | 1 | Phvul.008G211500.4 | Phvul.008G211500 | Phvul.008G21 | 0 PTHR32098,P |
| 33 | 1 | Phvul.008G211500.3 | Phvul.008G211500 | Phvul.008G21 | 0 PTHR32098,P |
| 34 | 1 | Phvul.008G211500.1 | Phvul.008G211500 | Phvul.008G21 | 0 PTHR32098,P |
| 35 | 1 | Phvul.008G211500.1 | Phvul.008G211500 | Phvul.008G21 | 0 PTHR32098,P |
| 36 | 1 | Phvul.008G211500.2 | Phvul.008G211500 | Phvul.008G21 | 0 PTHR32098,P |
| 37 | 1 | Phvul.008G250000.1 | Phvul.008G250000 | Phvul.008G25 PF16940 | PTHR34935 |
| 38 | 1 | Phvul.008G250000.1 | Phvul.008G250000 | Phvul.008G25 PF16940 | PTHR34935 |
| 39 | 1 | Phvul.008G250000.1 | Phvul.008G250000 | Phvul.008G25 PF16940 | PTHR34935 |
| 40 | 1 | Phvul.009G086300.2 | Phvul.009G086300 | Phvul.009G08 PF12776 | PTHR31704,P |
| 41 | 1 | Phvul.009G086300.1 | Phvul.009G086300 | Phvul.009G08 PF12776 | PTHR31704,P |
| 42 | 1 | Phvul.009G086300.1 | Phvul.009G086300 | Phvul.009G08 PF12776 | PTHR31704,P |
| 43 | 1 | Phvul.009G086300.2 | Phvul.009G086300 | Phvul.009G08 PF12776 | PTHR31704,P |
| 44 | 1 | Phvul.009G086300.1 | Phvul.009G086300 | Phvul.009G08 PF12776 | PTHR31704,P |
| 45 | 1 | Phvul.009G149800.1 | Phvul.009G149800 | Phvul.009G14 PF00454 | PTHR10048,P |
| 46 | 1 | Phvul.009G154300.6 | Phvul.009G154300 | Phvul.009G15 PF02146 | PTHR11085,P |
| 47 | 1 | Phvul.009G154300.5 | Phvul.009G154300 | Phvul.009G15 PF02146 | PTHR11085,P |
| 48 | 1 | Phvul.009G154300.3 | Phvul.009G154300 | Phvul.009G15 PF02146 | PTHR11085,P |
| 49 | 1 | Phvul.009G154300.3 | Phvul.009G154300 | Phvul.009G15 PF02146 | PTHR11085,P |
| 50 | 1 | Phvul.009G154300.4 | Phvul.009G154300 | Phvul.009G15 PF02146 | PTHR11085,P |
| 51 | 1 | Phvul.009G154300.1 | Phvul.009G154300 | Phvul.009G15 PF02146 | PTHR11085,P |
| 52 | 1 | Phvul.009G154300.1 | Phvul.009G154300 | Phvul.009G15 PF02146 | PTHR11085,P |
| 53 | 1 | Phvul.009G154300.6 | Phvul.009G154300 | Phvul.009G15 PF02146 | PTHR11085,P |
| 54 | 1 | Phvul.009G154300.6 | Phvul.009G154300 | Phvul.009G15 PF02146 | PTHR11085,P |
| 55 | 1 | Phvul.009G154300.5 | Phvul.009G154300 | Phvul.009G15 PF02146 | PTHR11085,P |
| 56 | 1 | Phvul.009G154300.3 | Phvul.009G154300 | Phvul.009G15 PF02146 | PTHR11085,P |
| 57 | 1 | Phvul.009G154300.4 | Phvul.009G154300 | Phvul.009G15 PF02146 | PTHR11085,P |
| 58 | 1 | Phvul.009G154300.1 | Phvul.009G154300 | Phvul.009G15 PF02146 | PTHR11085,P |
| 59 | 1 | Phvul.009G154300.1 | Phvul.009G154300 | Phvul.009G15 PF02146 | PTHR11085,P |
| 60 | 1 | Phvul.009G240100.1 | Phvul.009G240100 | Phvul.009G24 PF07714 | PTHR27001,P |
| | 1 | Phvul.011G017800.1 | Phvul.011G017800 | Phvul.011G01 PF12537,PF12 | PTHR15948 |

| | | | | |
|----|----------------------|------------------|--------------------------|---------------|
| 1 | | | | |
| 2 | 1 Phvul.011G017800.1 | Phvul.011G017800 | Phvul.011G01PF12537,PF12 | PTHR15948 |
| 3 | 1 Phvul.011G100200.2 | Phvul.011G100200 | Phvul.011G10 | 0 PTHR34210,P |
| 4 | 1 Phvul.011G100200.1 | Phvul.011G100200 | Phvul.011G10 | 0 PTHR34210,P |
| 5 | | | | |
| 6 | 1 Phvul.011G108300.1 | Phvul.011G108300 | Phvul.011G10 PF14111 | 0 |
| 7 | 1 Phvul.011G129700.1 | Phvul.011G129700 | Phvul.011G12 | 0 PTHR24006,P |
| 8 | 1 Phvul.011G129700.1 | Phvul.011G129700 | Phvul.011G12 | 0 PTHR24006,P |
| 9 | | | | |
| 10 | 1 Phvul.011G140050.2 | Phvul.011G140050 | Phvul.011G14 PF13041 | PTHR24015,P |
| 11 | 1 Phvul.011G140050.1 | Phvul.011G140050 | Phvul.011G14 PF13041 | PTHR24015,P |
| 12 | | | | |
| 13 | | | | |
| 14 | | | | |
| 15 | | | | |
| 16 | | | | |
| 17 | | | | |
| 18 | | | | |
| 19 | | | | |
| 20 | | | | |
| 21 | | | | |
| 22 | | | | |
| 23 | | | | |
| 24 | | | | |
| 25 | | | | |
| 26 | | | | |
| 27 | | | | |
| 28 | | | | |
| 29 | | | | |
| 30 | | | | |
| 31 | | | | |
| 32 | | | | |
| 33 | | | | |
| 34 | | | | |
| 35 | | | | |
| 36 | | | | |
| 37 | | | | |
| 38 | | | | |
| 39 | | | | |
| 40 | | | | |
| 41 | | | | |
| 42 | | | | |
| 43 | | | | |
| 44 | | | | |
| 45 | | | | |
| 46 | | | | |
| 47 | | | | |
| 48 | | | | |
| 49 | | | | |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

Do not distribute

| 1 | KOG | KEGG | KOG | GO | Best-hit-arabi-arabi-symbol | |
|----|----------------|----------------|----------|-------------------------------------|-----------------------------|----------|
| 2 | KOG0959 | 3.4.21.102 | | 0 | 0 AT5G42390.1 | 0 |
| 3 | | 0 2.3.1.225 | K18932 | GO:0008270 | AT3G51390.1 | 0 |
| 4 | | 0 2.3.1.225 | K18932 | GO:0008270 | AT3G51390.1 | 0 |
| 5 | | 0 2.3.1.225 | K18932 | GO:0008270 | AT3G51390.1 | 0 |
| 6 | | 0 2.3.1.225 | K18932 | GO:0008270 | AT3G51390.1 | 0 |
| 7 | | 0 2.7.7.6 | | 0 | 0 AT2G29540.1 ATRPAC14,AT | |
| 8 | | 0 2.7.7.6 | | 0 | 0 AT2G29540.1 ATRPAC14,AT | |
| 9 | KOG1330 | | 0 | 0 GO:0055085,(AT5G10190.1 | | 0 |
| 10 | KOG1330 | | 0 | 0 GO:0055085,(AT5G10190.1 | | 0 |
| 11 | KOG2462 | | 0 | 0 AT2G01940.1 ATIDD15,SGR5 | | |
| 12 | KOG1223 | 2.2.1.9,4.2.99 | K14759 | GO:0030976,(AT1G68890.1 | | 0 |
| 13 | KOG1223 | 2.2.1.9,4.2.99 | K14759 | GO:0030976,(AT1G68890.1 | | 0 |
| 14 | KOG1755 | | 0 K05759 | 0 AT5G56600.1 PFN3,PRF3 | | |
| 15 | KOG1755 | | 0 K05759 | 0 AT5G56600.1 PFN3,PRF3 | | |
| 16 | KOG4282 | | 0 | 0 | 0 AT3G58630.1 | 0 |
| 17 | KOG4759 | | 0 K02838 | GO:0006412 AT3G63190.1 AtcpRRF,cpRR | | |
| 18 | KOG1285 | 1.13.11.51 | | 0 | 0 AT3G63520.1 ATCCD1,ATNC | |
| 19 | KOG1285 | 1.13.11.51 | | 0 | 0 AT3G63520.1 ATCCD1,ATNC | |
| 20 | KOG1285 | 1.13.11.51 | | 0 | 0 AT3G63520.1 ATCCD1,ATNC | |
| 21 | KOG1285 | 1.13.11.51 | | 0 | 0 AT3G63520.1 ATCCD1,ATNC | |
| 22 | KOG1285 | 1.13.11.51 | | 0 | 0 AT3G63520.1 ATCCD1,ATNC | |
| 23 | KOG1285 | 1.13.11.51 | | 0 | 0 AT3G63520.1 ATCCD1,ATNC | |
| 24 | | 0 3.1.26.3 | K11592 | GO:0016787,(AT1G01040.1 ASU1,ATDCL1 | | |
| 25 | KOG2352 | 3.4.24.71 | | 0 GO:0008168,(AT2G31740.1 | | 0 |
| 26 | KOG2352 | 3.4.24.71 | | 0 GO:0008168,(AT2G31740.1 | | 0 |
| 27 | | 0 | 0 | 0 | 0 AT3G29750.1 | 0 |
| 28 | | 0 | 0 | 0 | 0 AT3G29750.1 | 0 |
| 29 | | 0 | 0 K08506 | GO:0005515 AT3G09740.1 ATSYP71,SYP7 | | |
| 30 | | 0 | 0 | 0 | 0 AT3G04470.1 | 0 |
| 31 | | 0 | 0 | 0 | 0 AT3G04470.1 | 0 |
| 32 | KOG1380 | | 0 K02257 | GO:0016021,(AT2G44520.1 COX10 | | |
| 33 | KOG1380 | | 0 K02257 | GO:0016021,(AT2G44520.1 COX10 | | |
| 34 | KOG4683 | 2.3.1.78 | K10532 | 0 AT5G47900.1 | | 0 |
| 35 | KOG4683 | 2.3.1.78 | K10532 | 0 AT5G47900.1 | | 0 |
| 36 | KOG4683 | 2.3.1.78 | K10532 | 0 AT5G47900.1 | | 0 |
| 37 | KOG4683 | 2.3.1.78 | K10532 | 0 AT5G47900.1 | | 0 |
| 38 | KOG4683 | 2.3.1.78 | K10532 | 0 AT5G47900.1 | | 0 |
| 39 | KOG4683 | 2.3.1.78 | K10532 | 0 AT5G47900.1 | | 0 |
| 40 | KOG4683 | 2.3.1.78 | K10532 | 0 AT5G47900.1 | | 0 |
| 41 | KOG1764 | | 0 | 0 | 0 AT1G65320.1 | 0 |
| 42 | | 0 | 0 | 0 GO:0005515 AT1G78230.1 | | 0 |
| 43 | | 0 | 0 | 0 GO:0005515 AT1G78230.1 | | 0 |
| 44 | | 0 | 0 | 0 GO:0005515 AT1G78230.1 | | 0 |
| 45 | | 0 | 0 | 0 GO:0005515 AT1G78230.1 | | 0 |
| 46 | | 0 | 0 | 0 | 0 | 0 |
| 47 | | 0 | 0 | 0 | 0 | 0 |

| | | | | | |
|----|--------------------|----------|---|---------------------------------------|---|
| 1 | | | | | |
| 2 | 0 | 0 | 0 | 0 AT1G53025.1 | 0 |
| 3 | 0 | 0 | 0 | 0 AT1G53025.1 | 0 |
| 4 | 0 | 0 | 0 | 0 AT1G53025.1 | 0 |
| 5 | 0 | 0 | 0 | 0 AT1G53025.1 | 0 |
| 6 | 0 | 0 | 0 | 0 AT1G53025.1 | 0 |
| 7 | 0 | 0 | 0 | 0 AT1G53025.1 | 0 |
| 8 | 0 | 0 | 0 | 0 AT1G53025.1 | 0 |
| 9 | | | | | |
| 10 | KOG0817 | 0 | 0 | GO:0000062 AT4G24230.6 ACBP3 | |
| 11 | KOG0817 | 0 | 0 | GO:0000062 AT4G24230.6 ACBP3 | |
| 12 | KOG0148,KOC | 0 K12741 | | GO:0003676 AT3G15010.2 | 0 |
| 13 | KOG0148,KOC | 0 K12741 | | GO:0003676 AT3G15010.2 | 0 |
| 14 | | | | | |
| 15 | 0 4.4.1.15 | | 0 | 0 AT3G26115.1 | 0 |
| 16 | 0 4.4.1.15 | | 0 | 0 AT3G26115.1 | 0 |
| 17 | | | | | |
| 18 | 0 | 0 | 0 | 0 AT1G13170.1 ORP1D | |
| 19 | 0 | 0 | 0 | 0 AT1G13170.1 ORP1D | |
| 20 | 0 5.4.2.3 | K01836 | | GO:0016868,(AT5G18070.1 DRT101 | |
| 21 | 0 5.4.2.3 | K01836 | | GO:0016868,(AT5G18070.1 DRT101 | |
| 22 | | | | | |
| 23 | 0 | 0 | 0 | 0 AT5G06650.1 GIS2 | |
| 24 | 0 | 0 | 0 | 0 AT5G06650.1 GIS2 | |
| 25 | | | | | |
| 26 | 0 3.2.1.21 | K01188 | | GO:0005975,(AT1G26560.1 BGLU40 | |
| 27 | 0 3.2.1.21 | K01188 | | GO:0005975,(AT1G26560.1 BGLU40 | |
| 28 | 0 6.3.2.19 | | | 0 GO:0016567,(AT5G65500.1 | 0 |
| 29 | 0 6.3.2.19 | | | 0 GO:0016567,(AT5G65500.1 | 0 |
| 30 | 0 6.3.2.19 | | | 0 GO:0016567,(AT5G65500.1 | 0 |
| 31 | 0 6.3.2.19 | | | 0 GO:0016567,(AT5G65500.1 | 0 |
| 32 | 0 | | | 0 AT5G52430.1 | 0 |
| 33 | 0 | 0 | 0 | 0 AT5G52430.1 | 0 |
| 34 | | | | | |
| 35 | 0 | 0 | 0 | 0 AT5G52430.1 | 0 |
| 36 | KOG0143 1.14.11.31 | | | 0 GO:0055114,(AT4G25310.1 | 0 |
| 37 | KOG3271 | 0 K03263 | | GO:0045905,(AT1G13950.1 ATELF5A-1,EIF | |
| 38 | KOG3271 | 0 K03263 | | GO:0045905,(AT1G13950.1 ATELF5A-1,EIF | |
| 39 | | | | | |
| 40 | 0 | 0 | 0 | 0 0 | 0 |
| 41 | 0 | 0 | 0 | 0 0 | 0 |
| 42 | 0 | 0 | 0 | 0 0 | 0 |
| 43 | 0 | 0 | 0 | 0 0 | 0 |
| 44 | 0 | 0 | | 0 GO:0016592,(AT5G02850.1 | 0 |
| 45 | 0 | 0 | | 0 GO:0016592,(AT5G02850.1 | 0 |
| 46 | 0 | 0 | | 0 GO:0016592,(AT5G02850.1 | 0 |
| 47 | 0 | 0 | | 0 GO:0016592,(AT5G02850.1 | 0 |
| 48 | 0 | 0 | | 0 GO:0016592,(AT5G02850.1 | 0 |
| 49 | 0 6.4.1.4 | K01969 | | 0 AT4G34030.1 MCCB | |
| 50 | 0 6.4.1.4 | K01969 | | 0 AT4G34030.1 MCCB | |
| 51 | 0 6.4.1.4 | K01969 | | 0 AT4G34030.1 MCCB | |
| 52 | 0 6.4.1.4 | K01969 | | 0 AT4G34030.1 MCCB | |
| 53 | 0 | 0 K09286 | | GO:0006355,(AT5G13910.1 LEP | |
| 54 | 0 | 0 K09286 | | GO:0006355,(AT5G13910.1 LEP | |
| 55 | 0 | 0 | | 0 GO:0005524 AT3G15120.1 | 0 |
| 56 | 0 | 0 | | 0 AT3G53700.1 MEE40 | |
| 57 | 0 | 0 | | | |
| 58 | 0 | 0 K12662 | | GO:0005515 AT2G41500.1 EMB2776,LIS | |
| 59 | 0 3.6.4.12 | | | 0 GO:0008408,(AT4G13870.1 ATWEX,ATWR | |
| 60 | | | | | |

| | | | | | |
|----|-------------|----------|----------|--------------------------------------|------------------------------------|
| 1 | | | | | |
| 2 | 0 | 3.6.4.12 | | 0 | GO:0008408,(AT4G13870.1 ATWEX,ATWR |
| 3 | 0 | | 0 | 0 | 0 AT2G34400.1 |
| 4 | 0 | | 0 | 0 | 0 AT5G16100.1 |
| 5 | 0 | | 0 | 0 | 0 AT5G16100.1 |
| 6 | 0 | | 0 | 0 | 0 AT5G16100.1 |
| 7 | 0 | 6.3.2.19 | K10590 | GO:0004842 | AT4G38600.1 KAK,UPL3 |
| 8 | 0 | 6.3.2.19 | K10590 | GO:0004842 | AT4G38600.1 KAK,UPL3 |
| 9 | | | | | |
| 10 | KOG0131,KOC | | 0 K13126 | GO:0003676 | AT1G01080.1 |
| 11 | 0 | | 0 | 0 | 0 0 |
| 12 | 0 | | 0 | 0 | 0 0 |
| 13 | | | | | |
| 14 | KOG2109 | | 0 | 0 | 0 AT1G03380.1 ATATG18G,AT |
| 15 | KOG2109 | | 0 | 0 | 0 AT1G03380.1 ATATG18G,AT |
| 16 | 0 | | 0 | 0 | 0 GO:0008270,(AT3G05200.1 ATL6 |
| 17 | | | | | |
| 18 | KOG0446 | 3.6.5.5 | K01528 | GO:0005525,(AT1G59610.1 ADL3,CF1,DL3 | |
| 19 | KOG0446 | 3.6.5.5 | K01528 | GO:0005525,(AT1G59610.1 ADL3,CF1,DL3 | |
| 20 | KOG0508,KOC | | 0 | 0 | 0 AT5G14230.1 |
| 21 | | | | | |
| 22 | KOG1286 | | 0 K13863 | GO:0016020,(AT1G58030.1 CAT2 | |
| 23 | KOG1286 | | 0 K13863 | GO:0016020,(AT1G58030.1 CAT2 | |
| 24 | KOG1286 | | 0 K13863 | GO:0016020,(AT1G58030.1 CAT2 | |
| 25 | KOG1286 | | 0 K13863 | GO:0016020,(AT1G58030.1 CAT2 | |
| 26 | | | | | |
| 27 | 0 | 2.4.2.24 | K00770 | 0 | AT1G02730.1 ATCSLD5,CSLL |
| 28 | 0 | 2.4.2.24 | K00770 | 0 | AT1G02730.1 ATCSLD5,CSLL |
| 29 | | | | | |
| 30 | KOG2125 | | 0 | 0 | GO:0003824 AT2G22530.1 |
| 31 | KOG2125 | | 0 | 0 | GO:0003824 AT2G22530.1 |
| 32 | KOG2125 | | 0 | 0 | GO:0003824 AT2G22530.1 |
| 33 | KOG2125 | | 0 | 0 | GO:0003824 AT2G22530.1 |
| 34 | | | | | |
| 35 | 0 | | 0 | 0 | GO:0008152,(AT3G18270.1 CYP77A5P |
| 36 | 0 | | 0 | 0 | GO:0008152,(AT3G18270.1 CYP77A5P |
| 37 | 0 | | 0 | 0 | 0 AT1G68140.3 |
| 38 | 0 | | 0 | 0 | 0 AT4G28590.1 |
| 39 | 0 | | 0 | 0 | 0 AT5G11600.1 |
| 40 | 0 | | 0 | 0 | 0 AT5G11600.1 |
| 41 | 0 | | 0 | 0 | 0 AT5G11600.1 |
| 42 | 0 | | 0 | 0 | 0 GO:0005515 AT5G39450.1 |
| 43 | 0 | | 0 | 0 | 0 GO:0005515 AT5G39450.1 |
| 44 | 0 | | 0 | 0 | 0 GO:0005515 AT5G39450.1 |
| 45 | 0 | | 0 | 0 | 0 GO:0005515 AT5G39450.1 |
| 46 | 0 | | 0 | 0 | 0 GO:0005515 AT5G39450.1 |
| 47 | 0 | | 0 | 0 | 0 GO:0005515 AT5G39450.1 |
| 48 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT3G13690.1 |
| 49 | KOG2824 | | 0 K17479 | GO:0045454,(AT4G10630.1 | |
| 50 | KOG2824 | | 0 K17479 | GO:0045454,(AT4G10630.1 | |
| 51 | | | | | |
| 52 | 0 | | 0 K01723 | GO:0055114,(AT5G42650.1 AOS,CYP74A,[| |
| 53 | KOG1286 | | 0 | 0 | GO:0016020,(AT4G21120.1 AAT1,CAT1 |
| 54 | KOG1286 | | 0 | 0 | GO:0016020,(AT4G21120.1 AAT1,CAT1 |
| 55 | | | | | |
| 56 | KOG0788 | 4.1.1.50 | K01611 | GO:0008295,(AT3G25570.2 | 0 |
| 57 | KOG0788 | 4.1.1.50 | K01611 | GO:0008295,(AT3G25570.2 | 0 |
| 58 | | | | | |
| 59 | 0 | | 0 | 0 | GO:0055085,(AT1G62280.1 SLAH1 |
| 60 | KOG0472 | 2.7.11.1 | | 0 | GO:0006468,(AT5G49760.1 |
| | KOG0472 | 2.7.11.1 | | 0 | GO:0006468,(AT5G49760.1 |

| | | | | | | |
|----|---------|-----------------|----------|--------------|--------------|-------------|
| 1 | | | | | | |
| 2 | KOG1683 | 5.1.2.3,1.1.1.3 | K10527 | GO:0055114,(| AT3G06860.1 | ATMFP2,MFP: |
| 3 | | 0 | 0 | 0 | 0 | AT3G17030.1 |
| 4 | | 0 | 0 | 0 | 0 | AT3G17030.1 |
| 5 | | | | | | |
| 6 | KOG0401 | | 0 | K03260 | GO:0005515,(| AT5G57870.2 |
| 7 | KOG0401 | | 0 | K03260 | GO:0005515,(| AT5G57870.2 |
| 8 | | 0 | 0 | 0 | 0 | AT4G14096.1 |
| 9 | | 0 | 0 | 0 | 0 | AT4G14096.1 |
| 10 | | | | | | |
| 11 | KOG2502 | | 0 | 0 | GO:0005515 | AT2G18280.2 |
| 12 | KOG2502 | | 0 | 0 | GO:0005515 | AT2G18280.2 |
| 13 | KOG2502 | | 0 | 0 | GO:0005515 | AT2G18280.2 |
| 14 | KOG2502 | | 0 | 0 | GO:0005515 | AT2G18280.2 |
| 15 | KOG2502 | | 0 | 0 | GO:0005515 | AT2G18280.2 |
| 16 | | 0 | 0 | 0 | 0 | AT4G04790.1 |
| 17 | | 0 | 0 | 0 | 0 | AT4G04790.1 |
| 18 | | 0 | 0 | 0 | 0 | 0 |
| 19 | | 0 | 0 | 0 | 0 | 0 |
| 20 | | 0 | 0 | 0 | 0 | 0 |
| 21 | | 0 | 0 | 0 | 0 | 0 |
| 22 | | 0 | 0 | 0 | GO:0006629 | AT1G02660.1 |
| 23 | | 0 | 0 | 0 | GO:0006629 | AT1G02660.1 |
| 24 | | 0 | 0 | 0 | 0 | AT5G23280.1 |
| 25 | | 0 | 6.1.1.18 | K01886 | GO:0006425,(| AT1G25350.1 |
| 26 | | | | | | OVA9 |
| 27 | KOG1603 | | 0 | 0 | GO:0046872,(| AT1G23000.1 |
| 28 | KOG1603 | | 0 | 0 | GO:0046872,(| AT1G23000.1 |
| 29 | | 0 | 2.7.7.4 | K13811 | GO:0004781 | AT3G22890.1 |
| 30 | | 0 | 2.7.7.4 | K13811 | GO:0004781 | AT3G22890.1 |
| 31 | | 0 | | 0 | 0 | AT1G04560.1 |
| 32 | | 0 | | 0 | 0 | AT1G04560.1 |
| 33 | | 0 | | 0 | 0 | AT5G03345.1 |
| 34 | | 0 | | 0 | 0 | AT3G11560.4 |
| 35 | | 0 | | 0 | 0 | AT2G44880.1 |
| 36 | KOG1043 | | 0 | 0 | 0 | AT4G09060.1 |
| 37 | | 0 | | 0 | 0 | AT4G09060.1 |
| 38 | | 0 | | 0 | 0 | AT4G38060.2 |
| 39 | | 0 | | 0 | 0 | AT4G38060.2 |
| 40 | | 0 | | 0 | 0 | AT3G54190.1 |
| 41 | | 0 | | 0 | 0 | AT3G54190.1 |
| 42 | | 0 | | 0 | 0 | AT3G54190.1 |
| 43 | | 0 | | 0 | 0 | AT3G54190.1 |
| 44 | KOG1595 | | 0 | 0 | GO:0046872 | AT5G58620.1 |
| 45 | KOG1595 | | 0 | 0 | GO:0046872 | AT5G58620.1 |
| 46 | KOG1595 | | 0 | 0 | GO:0046872 | AT5G58620.1 |
| 47 | KOG1595 | | 0 | 0 | GO:0046872 | AT5G58620.1 |
| 48 | KOG1595 | | 0 | 0 | GO:0046872 | AT5G58620.1 |
| 49 | | 0 | | 0 | 0 | AT3G54190.1 |
| 50 | | 0 | | 0 | 0 | AT3G54190.1 |
| 51 | | 0 | | 0 | 0 | AT3G54190.1 |
| 52 | | 0 | | 0 | 0 | AT3G54190.1 |
| 53 | | 0 | | 0 | 0 | AT3G54190.1 |
| 54 | | 0 | | 0 | 0 | AT1G64310.1 |
| 55 | | 0 | | 0 | 0 | AT1G64310.1 |
| 56 | | 0 | | 0 | 0 | AT1G64310.1 |
| 57 | | 0 | | 0 | 0 | AT1G64310.1 |
| 58 | | 0 | | 0 | 0 | AT1G73930.2 |
| 59 | | 0 | | 0 | 0 | AT1G73930.2 |
| 60 | | 0 | | 0 | 0 | AT1G73930.2 |

| | | | | | |
|----|---------|--------------|----------|---|--------------------------------------|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 | 0 AT1G73930.2 |
| 3 | | 0 | 0 | 0 | 0 GO:0043565,(AT1G08000.2 GATA10 |
| 4 | | 0 | 0 | 0 | 0 GO:0043565,(AT1G08000.2 GATA10 |
| 5 | | 0 | 0 | 0 | 0 GO:0043565,(AT1G08000.2 GATA10 |
| 6 | KOG1286 | | 0 K03294 | | GO:0016020,(AT1G17120.1 CAT8 |
| 7 | KOG1286 | | 0 K03294 | | GO:0016020,(AT1G17120.1 CAT8 |
| 8 | | 0 | 0 K11128 | | GO:0042254,(AT3G03920.1 |
| 9 | | 0 | 0 | 0 | 0 AT2G41180.1 |
| 10 | | 0 | 0 | 0 | 0 AT2G41180.1 |
| 11 | | 0 | 0 | 0 | 0 AT2G41180.1 |
| 12 | KOG0627 | | 0 K09419 | | GO:0043565,(AT3G22830.1 AT-HSFA6B,HS |
| 13 | | 0 | 0 | 0 | 0 AT5G37570.1 |
| 14 | | 0 | 0 | 0 | 0 AT5G37570.1 |
| 15 | | 0 | 0 | 0 | 0 AT5G37570.1 |
| 16 | | 0 | 0 | 0 | 0 GO:0005515 AT1G03910.1 |
| 17 | | 0 | 0 | 0 | 0 AT5G66730.1 |
| 18 | KOG0657 | 1.2.1.12 | K00134 | | GO:0055114,(AT3G04120.1 GAPC,GAPC-1, |
| 19 | KOG0657 | 1.2.1.12 | K00134 | | GO:0055114,(AT3G04120.1 GAPC,GAPC-1, |
| 20 | | 0 | 0 | 0 | 0 AT5G66730.1 |
| 21 | | 0 | 0 | 0 | 0 AT5G66730.1 |
| 22 | | 0 | 0 | 0 | 0 AT5G66730.1 |
| 23 | | 0 2.7.1.150 | K00921 | | GO:0005524,(AT1G71010.1 FAB1C |
| 24 | | 0 2.7.1.150 | K00921 | | GO:0005524,(AT1G71010.1 FAB1C |
| 25 | | 0 1.14.11.27 | | 0 | 0 AT5G46910.1 |
| 26 | | 0 | 0 | 0 | 0 GO:0003676 |
| 27 | | 0 | 0 | 0 | 0 GO:0003676 |
| 28 | | 0 | 0 | 0 | 0 GO:0003676 |
| 29 | | 0 | 0 | 0 | 0 GO:0003676 AT5G46840.1 |
| 30 | | 0 | 0 | 0 | 0 GO:0003676 AT5G46840.1 |
| 31 | | 0 | 0 | 0 | 0 GO:0003676 AT5G46840.1 |
| 32 | | 0 | 0 | 0 | 0 |
| 33 | | 0 | 0 K13947 | | GO:0055085,(AT1G70940.1 ATPIN3,PIN3 |
| 34 | | 0 | 0 K13947 | | GO:0055085,(AT1G70940.1 ATPIN3,PIN3 |
| 35 | | 0 | 0 | 0 | 0 AT5G66730.1 |
| 36 | | 0 | 0 | 0 | 0 AT5G66730.1 |
| 37 | | 0 | 0 | 0 | 0 AT5G66730.1 |
| 38 | | 0 | 0 | 0 | 0 AT4G35930.1 |
| 39 | | 0 | 0 | 0 | 0 AT4G35930.1 |
| 40 | | 0 6.4.1.4 | K01969 | | 0 AT4G34030.1 MCCB |
| 41 | | 0 6.4.1.4 | K01969 | | 0 AT4G34030.1 MCCB |
| 42 | | 0 6.4.1.4 | K01969 | | 0 AT4G34030.1 MCCB |
| 43 | | 0 6.4.1.4 | K01969 | | 0 AT4G34030.1 MCCB |
| 44 | | 0 6.4.1.4 | K01969 | | 0 AT4G34030.1 MCCB |
| 45 | | 0 2.1.1.37 | K00558 | | GO:0003682 AT1G69770.1 CMT3 |
| 46 | | 0 | 0 | 0 | 0 GO:0005515 AT4G10000.1 |
| 47 | | 0 | 0 | 0 | 0 GO:0005515 AT4G10000.1 |
| 48 | | 0 | 0 | 0 | 0 GO:0005515 AT4G10000.1 |
| 49 | KOG1254 | 2.3.3.8 | K01648 | | 0 AT1G60810.1 ACLA-2 |
| 50 | KOG1254 | 2.3.3.8 | K01648 | | 0 AT1G60810.1 ACLA-2 |
| 51 | KOG4579 | | 0 | 0 | 0 AT1G69550.1 |
| 52 | | 0 | 0 | 0 | 0 GO:0003676 |
| 53 | | 0 | 0 | 0 | 0 GO:0003676 |
| 54 | KOG2502 | | 0 | 0 | 0 AT1G16070.1 AtTLP8,TLP8 |
| 55 | KOG2502 | | 0 | 0 | 0 AT1G16070.1 AtTLP8,TLP8 |
| 56 | | 0 2.3.1.196 | | 0 | 0 GO:0016747 AT5G17540.1 |
| 57 | | 0 | 0 K14508 | | GO:0005515 AT5G45110.1 ATNPR3,NPR3 |
| 58 | | 0 | 0 K14508 | | GO:0005515 AT5G45110.1 ATNPR3,NPR3 |
| 59 | | 0 | 0 K14508 | | GO:0005515 AT5G45110.1 ATNPR3,NPR3 |
| 60 | | 0 2.4.1.273 | | 0 | 0 GO:0016758,(AT2G22590.1 |

| | | | | | |
|----|---------|------------|----------|---------------------------------------|---|
| 1 | | | | | |
| 2 | 0 | 2.4.1.273 | | 0 GO:0016758,(AT2G22590.1 | 0 |
| 3 | 0 | | 0 | 0 AT1G49890.1 | 0 |
| 4 | 0 | | 0 | 0 AT1G49890.1 | 0 |
| 5 | 0 | | 0 | 0 AT1G49890.1 | 0 |
| 6 | 0 | | 0 | 0 AT1G49890.1 | 0 |
| 7 | 0 | | 0 | 0 AT1G49890.1 | 0 |
| 8 | KOG1575 | 1.1.1.317 | | 0 AT1G60710.1 ATB2 | |
| 9 | | | | | |
| 10 | 0 | | 0 K09419 | GO:0043565,(AT5G62020.1 AT-HSFB2A,H | |
| 11 | 0 | | 0 | 0 AT1G20180.1 | 0 |
| 12 | 0 | | 0 | 0 AT1G20180.1 | 0 |
| 13 | 0 | | 0 | 0 AT1G20180.1 | 0 |
| 14 | 0 | | 0 | 0 AT1G20180.1 | 0 |
| 15 | 0 | | 0 | 0 AT1G20180.1 | 0 |
| 16 | 0 | | 0 | 0 AT3G24120.1 | 0 |
| 17 | 0 | | 0 | 0 AT3G24120.1 | 0 |
| 18 | 0 | | 0 | 0 AT3G24120.1 | 0 |
| 19 | 0 | | 0 | 0 AT3G22550.1 | 0 |
| 20 | 0 | 3.1.1.11 | K01051 | GO:0004857,(AT4G02330.1 ATPMEPCRB | |
| 21 | | | | | |
| 22 | KOG3166 | | 0 K02936 | 0 AT3G62870.1 | 0 |
| 23 | KOG3166 | | 0 K02936 | 0 AT3G62870.1 | 0 |
| 24 | | 0 3.1.3.16 | K18999 | 0 AT2G33540.1 ATCPL3,CPL3 | |
| 25 | | | | | |
| 26 | | 0 3.6.3.25 | | 0 GO:0016887,(AT1G65410.1 ATNAP11,NAF | |
| 27 | | 0 3.6.3.25 | | 0 GO:0016887,(AT1G65410.1 ATNAP11,NAF | |
| 28 | | 0 | 0 | 0 AT3G54220.1 SCR,SGR1 | |
| 29 | | | | | |
| 30 | KOG4050 | | 0 | 0 AT5G02040.2 PRA1.A1 | |
| 31 | KOG4050 | | 0 | 0 AT5G02040.2 PRA1.A1 | |
| 32 | | 0 5.5.1.19 | | 0 AT2G32640.1 | 0 |
| 33 | | 0 5.5.1.19 | | 0 AT2G32640.1 | 0 |
| 34 | | 0 5.5.1.19 | | 0 AT2G32640.1 | 0 |
| 35 | | 0 5.5.1.19 | | 0 AT2G32640.1 | 0 |
| 36 | | 0 5.5.1.19 | | 0 AT2G32640.1 | 0 |
| 37 | | 0 | 0 | 0 AT1G06950.1 ATTIC110,TIC1 | |
| 38 | | 0 | 0 | 0 AT1G06950.1 ATTIC110,TIC1 | |
| 39 | | 0 | 0 | 0 AT1G06950.1 ATTIC110,TIC1 | |
| 40 | | 0 | 0 | 0 AT2G24960.2 | 0 |
| 41 | | 0 | 0 | 0 AT2G24960.2 | 0 |
| 42 | | 0 | 0 | 0 AT2G24960.2 | 0 |
| 43 | | 0 | 0 | 0 AT2G24960.2 | 0 |
| 44 | | 0 | 0 | 0 AT2G24960.2 | 0 |
| 45 | | 0 2.7.1.67 | K00888 | GO:0016773,(AT5G64070.1 PI-4KBETA1,PI | |
| 46 | | | | | |
| 47 | KOG2683 | 3.5.1.98 | K11414 | GO:0070403 AT5G09230.7 AtSRT2,SRT2 | |
| 48 | KOG2683 | 3.5.1.98 | K11414 | GO:0070403 AT5G09230.7 AtSRT2,SRT2 | |
| 49 | KOG2683 | 3.5.1.98 | K11414 | GO:0070403 AT5G09230.7 AtSRT2,SRT2 | |
| 50 | KOG2683 | 3.5.1.98 | K11414 | GO:0070403 AT5G09230.7 AtSRT2,SRT2 | |
| 51 | KOG2683 | 3.5.1.98 | K11414 | GO:0070403 AT5G09230.7 AtSRT2,SRT2 | |
| 52 | KOG2683 | 3.5.1.98 | K11414 | GO:0070403 AT5G09230.7 AtSRT2,SRT2 | |
| 53 | KOG2683 | 3.5.1.98 | K11414 | GO:0070403 AT5G09230.7 AtSRT2,SRT2 | |
| 54 | KOG2683 | 3.5.1.98 | K11414 | GO:0070403 AT5G09230.7 AtSRT2,SRT2 | |
| 55 | KOG2683 | 3.5.1.98 | K11414 | GO:0070403 AT5G09230.7 AtSRT2,SRT2 | |
| 56 | KOG2683 | 3.5.1.98 | K11414 | GO:0070403 AT5G09230.7 AtSRT2,SRT2 | |
| 57 | KOG2683 | 3.5.1.98 | K11414 | GO:0070403 AT5G09230.7 AtSRT2,SRT2 | |
| 58 | KOG2683 | 3.5.1.98 | K11414 | GO:0070403 AT5G09230.7 AtSRT2,SRT2 | |
| 59 | KOG2683 | 3.5.1.98 | K11414 | GO:0070403 AT5G09230.7 AtSRT2,SRT2 | |
| 60 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT2G18890.1 | 0 |
| | 0 | 0 | | 0 GO:0016020 AT4G27630.2 GTG2 | |

| | | | | | |
|----|---------|---|---|-------------------------------|---------------------------|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 GO:0016020 AT4G27630.2 GTG2 | |
| 3 | | 0 | 0 | 0 | 0 AT5G22040.2 |
| 4 | | 0 | 0 | 0 | 0 AT5G22040.2 |
| 5 | | | | | |
| 6 | | 0 | 0 | 0 | 0 0 |
| 7 | KOG1947 | | 0 | 0 | 0 AT2G42620.1 MAX2,ORE9,P |
| 8 | KOG1947 | | 0 | 0 | 0 AT2G42620.1 MAX2,ORE9,P |
| 9 | | | | | |
| 10 | | 0 | 0 | 0 | 0 AT4G04790.1 |
| 11 | | 0 | 0 | 0 | 0 AT4G04790.1 |
| 12 | | | | | |
| 13 | | | | | |
| 14 | | | | | |
| 15 | | | | | |
| 16 | | | | | |
| 17 | | | | | |
| 18 | | | | | |
| 19 | | | | | |
| 20 | | | | | |
| 21 | | | | | |
| 22 | | | | | |
| 23 | | | | | |
| 24 | | | | | |
| 25 | | | | | |
| 26 | | | | | |
| 27 | | | | | |
| 28 | | | | | |
| 29 | | | | | |
| 30 | | | | | |
| 31 | | | | | |
| 32 | | | | | |
| 33 | | | | | |
| 34 | | | | | |
| 35 | | | | | |
| 36 | | | | | |
| 37 | | | | | |
| 38 | | | | | |
| 39 | | | | | |
| 40 | | | | | |
| 41 | | | | | |
| 42 | | | | | |
| 43 | | | | | |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

Do not distribute

| arabi-defline | ID | Annot_defline | IDENTIFIER | NAME |
|---|--------------|----------------|--------------|-----------------------------|
| Insulinase (Peptidase family M16) family | Phvul.002G04 | PTHR11851:Sf | Phvul.002G04 | Protein modif |
| DHHC-type zinc finger family protein | Phvul.002G11 | PTHR22883:Sf | Phvul.002G11 | not assigned.a |
| DHHC-type zinc finger family protein | Phvul.002G11 | PTHR22883:Sf | Phvul.002G11 | not assigned.a |
| DHHC-type zinc finger family protein | Phvul.002G11 | PTHR22883:Sf | Phvul.002G11 | not assigned.a |
| DHHC-type zinc finger family protein | Phvul.002G11 | PTHR22883:Sf | Phvul.002G11 | not assigned.a |
| RNApolymerase 14 kDa subunit | Phvul.001G01 | PTHR13946:Sf | Phvul.001G01 | RNA biosynthe |
| RNApolymerase 14 kDa subunit | Phvul.001G01 | PTHR13946:Sf | Phvul.001G01 | RNA biosynthe |
| Major facilitator superfamily protein | Phvul.002G25 | KOG1330 - Su | Phvul.002G25 | Solute transpo |
| Major facilitator superfamily protein | Phvul.002G25 | KOG1330 - Su | Phvul.002G25 | Solute transpo |
| C2H2-like zinc finger protein | Phvul.002G33 | PTHR10593:Sf | Phvul.002G33 | RNA biosynthe |
| magnesium ion binding;thiamin pyrophc | Phvul.005G02 | K14759 - isocf | Phvul.005G02 | Coenzyme me |
| magnesium ion binding;thiamin pyrophc | Phvul.005G02 | K14759 - isocf | Phvul.005G02 | Coenzyme me |
| profilin 3 | Phvul.005G16 | K05759 - profi | Phvul.005G16 | Cytoskeleton |
| profilin 3 | Phvul.005G16 | K05759 - profi | Phvul.005G16 | Cytoskeleton |
| sequence-specific DNA binding transcrip | Phvul.006G17 | KOG4282 - Tr | Phvul.006G17 | RNA biosynthe |
| ribosome recycling factor, chloroplast pr | Phvul.007G17 | PTHR20982:Sf | Phvul.007G17 | Protein biosyr |
| carotenoid cleavage dioxygenase 1 | Phvul.009G10 | PTHR10543//I | Phvul.009G10 | Enzyme classif |
| carotenoid cleavage dioxygenase 1 | Phvul.009G10 | PTHR10543//I | Phvul.009G10 | Enzyme classif |
| carotenoid cleavage dioxygenase 1 | Phvul.009G10 | PTHR10543//I | Phvul.009G10 | Enzyme classif |
| carotenoid cleavage dioxygenase 1 | Phvul.009G10 | PTHR10543//I | Phvul.009G10 | Enzyme classif |
| carotenoid cleavage dioxygenase 1 | Phvul.009G10 | PTHR10543//I | Phvul.009G10 | Enzyme classif |
| carotenoid cleavage dioxygenase 1 | Phvul.009G10 | PTHR10543//I | Phvul.009G10 | Enzyme classif |
| dicer-like 1 | Phvul.009G26 | PTHR14950:Sf | Phvul.009G26 | RNA processir |
| S-adenosyl-L-methionine-dependent me | Phvul.003G05 | PTHR12176:Sf | Phvul.003G05 | not assigned.r |
| S-adenosyl-L-methionine-dependent me | Phvul.003G05 | PTHR12176:Sf | Phvul.003G05 | not assigned.r |
| Eukaryotic aspartyl protease family prot | Phvul.004G05 | PF13650 - Asp | Phvul.004G05 | not assigned.r |
| Eukaryotic aspartyl protease family prot | Phvul.004G05 | PF13650 - Asp | Phvul.004G05 | not assigned.r |
| syntaxin of plants 71 | Phvul.005G13 | K08506 - synt | Phvul.005G13 | Vesicle trafficl |
| Ankyrin repeat family protein | Phvul.006G10 | PTHR12447:Sf | Phvul.006G10 | not assigned.r |
| Ankyrin repeat family protein | Phvul.006G10 | PTHR12447:Sf | Phvul.006G10 | not assigned.r |
| cytochrome c oxidase 10 | Phvul.007G00 | K02257 - prot | Phvul.007G00 | not assigned.a |
| cytochrome c oxidase 10 | Phvul.007G00 | K02257 - prot | Phvul.007G00 | not assigned.a |
| Protein of unknown function (DUF1624) | Phvul.007G21 | K10532 - hep | Phvul.007G21 | not assigned.r |
| Protein of unknown function (DUF1624) | Phvul.007G21 | K10532 - hep | Phvul.007G21 | not assigned.r |
| Protein of unknown function (DUF1624) | Phvul.007G21 | K10532 - hep | Phvul.007G21 | not assigned.r |
| Protein of unknown function (DUF1624) | Phvul.007G21 | K10532 - hep | Phvul.007G21 | not assigned.r |
| Protein of unknown function (DUF1624) | Phvul.007G21 | K10532 - hep | Phvul.007G21 | not assigned.r |
| Protein of unknown function (DUF1624) | Phvul.007G21 | K10532 - hep | Phvul.007G21 | not assigned.r |
| Cystathionine beta-synthase (CBS) famil | Phvul.008G05 | PTHR13780:Sf | Phvul.008G05 | not assigned.a |
| Outer arm dynein light chain 1 protein | Phvul.008G17 | PTHR24365:Sf | Phvul.008G17 | not assigned.r |
| Outer arm dynein light chain 1 protein | Phvul.008G17 | PTHR24365:Sf | Phvul.008G17 | not assigned.r |
| Outer arm dynein light chain 1 protein | Phvul.008G17 | PTHR24365:Sf | Phvul.008G17 | not assigned.r |
| Outer arm dynein light chain 1 protein | Phvul.008G17 | PTHR24365:Sf | Phvul.008G17 | not assigned.r |
| | 0 | 0 | 0 | Phvul.011G13 not assigned.r |
| | 0 | 0 | 0 | Phvul.011G13 not assigned.r |

| | | | | |
|----|---|----------------------------|--------------|-----------------------------|
| 1 | | | | |
| 2 | Ubiquitin-conjugating enzyme family prc | Phvul.011G15PTHR24067:Sf | Phvul.011G15 | not assigned.r |
| 3 | Ubiquitin-conjugating enzyme family prc | Phvul.011G15PTHR24067:Sf | Phvul.011G15 | not assigned.r |
| 4 | Ubiquitin-conjugating enzyme family prc | Phvul.011G15PTHR24067:Sf | Phvul.011G15 | not assigned.r |
| 5 | Ubiquitin-conjugating enzyme family prc | Phvul.011G15PTHR24067:Sf | Phvul.011G15 | not assigned.r |
| 6 | Ubiquitin-conjugating enzyme family prc | Phvul.011G15PTHR24067:Sf | Phvul.011G15 | not assigned.r |
| 7 | Ubiquitin-conjugating enzyme family prc | Phvul.011G15PTHR24067:Sf | Phvul.011G15 | not assigned.r |
| 8 | Ubiquitin-conjugating enzyme family prc | Phvul.011G15PTHR24067:Sf | Phvul.011G15 | not assigned.r |
| 9 | Ubiquitin-conjugating enzyme family prc | Phvul.011G15PTHR24067:Sf | Phvul.011G15 | not assigned.r |
| 10 | acyl-CoA-binding domain 3 | Phvul.001G02PTHR23310:Sf | Phvul.001G02 | not assigned.a |
| 11 | acyl-CoA-binding domain 3 | Phvul.001G02PTHR23310:Sf | Phvul.001G02 | not assigned.a |
| 12 | RNA-binding (RRM/RBD/RNP motifs) fan | Phvul.001G14KOG0148//KC | Phvul.001G14 | not assigned.a |
| 13 | RNA-binding (RRM/RBD/RNP motifs) fan | Phvul.001G14KOG0148//KC | Phvul.001G14 | not assigned.a |
| 14 | RNA-binding (RRM/RBD/RNP motifs) fan | Phvul.001G14KOG0148//KC | Phvul.001G14 | not assigned.a |
| 15 | Pyridoxal-5'-phosphate-dependent enz | Phvul.001G25PTHR10314//I | Phvul.001G25 | not assigned.a |
| 16 | Pyridoxal-5'-phosphate-dependent enz | Phvul.001G25PTHR10314//I | Phvul.001G25 | not assigned.a |
| 17 | Pyridoxal-5'-phosphate-dependent enz | Phvul.001G25PTHR10314//I | Phvul.001G25 | not assigned.a |
| 18 | OSBP(oxysterol binding protein)-related | Phvul.001G25PTHR10972:Sf | Phvul.001G25 | not assigned.a |
| 19 | OSBP(oxysterol binding protein)-related | Phvul.001G25PTHR10972:Sf | Phvul.001G25 | not assigned.a |
| 20 | OSBP(oxysterol binding protein)-related | Phvul.001G25PTHR10972:Sf | Phvul.001G25 | not assigned.a |
| 21 | phosphoglucosamine mutase-related | Phvul.002G005.4.2.3 - Phos | Phvul.002G00 | Carbohydrate |
| 22 | phosphoglucosamine mutase-related | Phvul.002G005.4.2.3 - Phos | Phvul.002G00 | Carbohydrate |
| 23 | C2H2 and C2HC zinc fingers superfamily | 0 | 0 | Phvul.002G07RNA biosynthe |
| 24 | C2H2 and C2HC zinc fingers superfamily | 0 | 0 | Phvul.002G07RNA biosynthe |
| 25 | C2H2 and C2HC zinc fingers superfamily | 0 | 0 | Phvul.002G07RNA biosynthe |
| 26 | beta glucosidase 40 | Phvul.002G10PTHR10353:Sf | Phvul.002G10 | Enzyme classifi |
| 27 | beta glucosidase 40 | Phvul.002G10PTHR10353:Sf | Phvul.002G10 | Enzyme classifi |
| 28 | U-box domain-containing protein kinase | Phvul.002G14PTHR27003:Sf | Phvul.002G14 | not assigned.a |
| 29 | U-box domain-containing protein kinase | Phvul.002G14PTHR27003:Sf | Phvul.002G14 | not assigned.a |
| 30 | U-box domain-containing protein kinase | Phvul.002G14PTHR27003:Sf | Phvul.002G14 | not assigned.a |
| 31 | U-box domain-containing protein kinase | Phvul.002G14PTHR27003:Sf | Phvul.002G14 | not assigned.a |
| 32 | U-box domain-containing protein kinase | Phvul.002G14PTHR27003:Sf | Phvul.002G14 | not assigned.a |
| 33 | U-box domain-containing protein kinase | Phvul.002G14PTHR27003:Sf | Phvul.002G14 | not assigned.a |
| 34 | hydroxyproline-rich glycoprotein family | 0 | 0 | Phvul.002G15 not assigned.a |
| 35 | hydroxyproline-rich glycoprotein family | 0 | 0 | Phvul.002G15 not assigned.a |
| 36 | hydroxyproline-rich glycoprotein family | 0 | 0 | Phvul.002G15 not assigned.a |
| 37 | 2-oxoglutarate (2OG) and Fe(II)-depende | Phvul.003G01PTHR10209:Sf | Phvul.003G01 | Enzyme classifi |
| 38 | eukaryotic elongation factor 5A-1 | Phvul.003G15K03263 - tran | Phvul.003G15 | Protein biosyr |
| 39 | eukaryotic elongation factor 5A-1 | Phvul.003G15K03263 - tran | Phvul.003G15 | Protein biosyr |
| 40 | eukaryotic elongation factor 5A-1 | 0 | 0 | Phvul.003G17 not assigned.r |
| 41 | eukaryotic elongation factor 5A-1 | 0 | 0 | Phvul.003G17 not assigned.r |
| 42 | eukaryotic elongation factor 5A-1 | 0 | 0 | Phvul.003G17 not assigned.r |
| 43 | eukaryotic elongation factor 5A-1 | 0 | 0 | Phvul.003G17 not assigned.r |
| 44 | hydroxyproline-rich glycoprotein family | Phvul.003G26PTHR13208 - I | Phvul.003G26 | RNA biosynthe |
| 45 | hydroxyproline-rich glycoprotein family | Phvul.003G26PTHR13208 - I | Phvul.003G26 | RNA biosynthe |
| 46 | hydroxyproline-rich glycoprotein family | Phvul.003G26PTHR13208 - I | Phvul.003G26 | RNA biosynthe |
| 47 | hydroxyproline-rich glycoprotein family | Phvul.003G26PTHR13208 - I | Phvul.003G26 | RNA biosynthe |
| 48 | hydroxyproline-rich glycoprotein family | Phvul.003G26PTHR13208 - I | Phvul.003G26 | RNA biosynthe |
| 49 | 3-methylcrotonyl-CoA carboxylase | Phvul.003G29K01969 - 3-m | Phvul.003G29 | Amino acid m |
| 50 | 3-methylcrotonyl-CoA carboxylase | Phvul.003G29K01969 - 3-m | Phvul.003G29 | Amino acid m |
| 51 | 3-methylcrotonyl-CoA carboxylase | Phvul.003G29K01969 - 3-m | Phvul.003G29 | Amino acid m |
| 52 | 3-methylcrotonyl-CoA carboxylase | Phvul.003G29K01969 - 3-m | Phvul.003G29 | Amino acid m |
| 53 | 3-methylcrotonyl-CoA carboxylase | Phvul.003G29K01969 - 3-m | Phvul.003G29 | Amino acid m |
| 54 | 3-methylcrotonyl-CoA carboxylase | Phvul.003G29K01969 - 3-m | Phvul.003G29 | Amino acid m |
| 55 | Integrase-type DNA-binding superfamily | Phvul.004G06PTHR31677:Sf | Phvul.004G06 | RNA biosynthe |
| 56 | Integrase-type DNA-binding superfamily | Phvul.004G06PTHR31677:Sf | Phvul.004G06 | RNA biosynthe |
| 57 | Integrase-type DNA-binding superfamily | Phvul.004G06PTHR31677:Sf | Phvul.004G06 | RNA biosynthe |
| 58 | P-loop containing nucleoside triphospha | Phvul.005G06PTHR23069//I | Phvul.005G06 | DNA damage |
| 59 | Pentatricopeptide repeat (PPR) superfar | Phvul.007G15PF13041 - PP | Phvul.007G15 | not assigned.a |
| 60 | WD-40 repeat family protein / small nuc | Phvul.007G24K12662 - U4/L | Phvul.007G24 | RNA processir |
| | Werner syndrome-like exonuclease | Phvul.008G11PTHR13620 - | Phvul.008G11 | not assigned.a |

| | | | |
|----|---|-----------------------------------|------------------------------|
| 1 | Werner syndrome-like exonuclease | Phvul.008G11PTHR13620 - | Phvul.008G11 not assigned. |
| 2 | Pentatricopeptide repeat (PPR-like) superfamily protein | Phvul.008G23PF01535//PF1 | Phvul.008G23 not assigned. |
| 3 | | 0 Phvul.009G08PF02042 - RW | Phvul.009G08 not assigned. |
| 4 | | 0 Phvul.009G08PF02042 - RW | Phvul.009G08 not assigned. |
| 5 | HEAT repeat ;HECT-domain (ubiquitin-tr | Phvul.009G11PTHR11254:Sf | Phvul.009G11 Protein home |
| 6 | HEAT repeat ;HECT-domain (ubiquitin-tr | Phvul.009G11PTHR11254:Sf | Phvul.009G11 Protein home |
| 7 | RNA-binding (RRM/RBD/RNP motifs) fan | Phvul.010G11KOG0131//KC | Phvul.010G11 not assigned. |
| 8 | | 0 | 0 Phvul.011G00 not assigned. |
| 9 | | 0 | 0 Phvul.011G00 not assigned. |
| 10 | homolog of yeast autophagy 18 (ATG18) | Phvul.011G14PTHR13268:Sf | Phvul.011G14 Protein home |
| 11 | homolog of yeast autophagy 18 (ATG18) | Phvul.011G14PTHR13268:Sf | Phvul.011G14 Protein home |
| 12 | RING/U-box superfamily protein | Phvul.011G16PTHR14155:Sf | Phvul.011G16 not assigned. |
| 13 | dynamamin-like 3 | Phvul.011G21PTHR11566//I | Phvul.011G21 Vesicle traffi |
| 14 | dynamamin-like 3 | Phvul.011G21PTHR11566//I | Phvul.011G21 Vesicle traffi |
| 15 | | 0 Phvul.001G09KOG0508//KC | Phvul.001G09 not assigned. |
| 16 | cationic amino acid transporter 2 | Phvul.001G10K13863 - solu | Phvul.001G10 Solute transp |
| 17 | cationic amino acid transporter 2 | Phvul.001G10K13863 - solu | Phvul.001G10 Solute transp |
| 18 | cationic amino acid transporter 2 | Phvul.001G10K13863 - solu | Phvul.001G10 Solute transp |
| 19 | cationic amino acid transporter 2 | Phvul.001G10K13863 - solu | Phvul.001G10 Solute transp |
| 20 | cellulose synthase-like D5 | Phvul.001G21K00770 - 1,4- β | Phvul.001G21 Cell wall organ |
| 21 | cellulose synthase-like D5 | Phvul.001G21K00770 - 1,4- β | Phvul.001G21 Cell wall organ |
| 22 | Alkaline-phosphatase-like family protein | Phvul.002G14K05310 - etha | Phvul.002G14 not assigned. |
| 23 | Alkaline-phosphatase-like family protein | Phvul.002G14K05310 - etha | Phvul.002G14 not assigned. |
| 24 | Alkaline-phosphatase-like family protein | Phvul.002G14K05310 - etha | Phvul.002G14 not assigned. |
| 25 | Alkaline-phosphatase-like family protein | Phvul.002G14K05310 - etha | Phvul.002G14 not assigned. |
| 26 | cytochrome P450, family 77, subfamily 1 | Phvul.002G18PTHR13794 - I | Phvul.002G18 not assigned. |
| 27 | cytochrome P450, family 77, subfamily 1 | Phvul.002G18PTHR13794 - I | Phvul.002G18 not assigned. |
| 28 | Protein of unknown function (DUF1644) | Phvul.002G20PF07800 - Pro | Phvul.002G20 not assigned. |
| 29 | | 0 | 0 Phvul.002G23 not assigned. |
| 30 | | 0 | 0 Phvul.002G26 not assigned. |
| 31 | | 0 | 0 Phvul.002G26 not assigned. |
| 32 | F-box family protein | Phvul.002G27PF00646 - F-b | Phvul.002G27 not assigned. |
| 33 | F-box family protein | Phvul.002G27PF00646 - F-b | Phvul.002G27 not assigned. |
| 34 | F-box family protein | Phvul.002G27PF00646 - F-b | Phvul.002G27 not assigned. |
| 35 | F-box family protein | Phvul.002G27PF00646 - F-b | Phvul.002G27 not assigned. |
| 36 | Protein kinase protein with adenine nuc | Phvul.002G302.7.11.1 - Non | Phvul.002G30 Protein modif |
| 37 | Glutaredoxin family protein | Phvul.002G32PTHR10168:Sf | Phvul.002G32 not assigned. |
| 38 | Glutaredoxin family protein | Phvul.002G32PTHR10168:Sf | Phvul.002G32 not assigned. |
| 39 | allene oxide synthase | Phvul.003G01K01723 - hydr | Phvul.003G01 Phytohormon |
| 40 | amino acid transporter 1 | Phvul.003G02PTHR11785:Sf | Phvul.003G02 Solute transp |
| 41 | amino acid transporter 1 | Phvul.003G02PTHR11785:Sf | Phvul.003G02 Solute transp |
| 42 | Adenosylmethionine decarboxylase fam | Phvul.003G044.1.1.50 - Ade | Phvul.003G04 Polyamine me |
| 43 | Adenosylmethionine decarboxylase fam | Phvul.003G044.1.1.50 - Ade | Phvul.003G04 Polyamine me |
| 44 | SLAC1 homologue 1 | Phvul.003G08PF03595 - Vol | Phvul.003G08 Solute transp |
| 45 | Leucine-rich repeat protein kinase famil | Phvul.003G09PTHR27003:Sf | Phvul.003G09 Protein modif |
| 46 | Leucine-rich repeat protein kinase famil | Phvul.003G09PTHR27003:Sf | Phvul.003G09 Protein modif |

| | | | | |
|----|--|-----------------------------|--------------------------|------------------------------|
| 1 | | | | |
| 2 | multifunctional protein 2 | Phvul.003G091.1.1.35//4.2. | Phvul.003G09 | Lipid metaboli |
| 3 | Nucleic acid-binding proteins superfamil | Phvul.003G11PTHR36033:Sf | Phvul.003G11 | not assigned.r |
| 4 | Nucleic acid-binding proteins superfamil | Phvul.003G11PTHR36033:Sf | Phvul.003G11 | not assigned.r |
| 5 | MIF4G domain-containing protein / MA | Phvul.003G15PTHR23253//I | Phvul.003G15 | Protein biosyr |
| 6 | MIF4G domain-containing protein / MA | Phvul.003G15PTHR23253//I | Phvul.003G15 | Protein biosyr |
| 7 | MIF4G domain-containing protein / MA | Phvul.003G15PTHR23253//I | Phvul.003G15 | Protein biosyr |
| 8 | F-box/RNI-like superfamily protein | Phvul.003G20PF08387 - FB | Phvul.003G20 | not assigned.r |
| 9 | F-box/RNI-like superfamily protein | Phvul.003G20PF08387 - FB | Phvul.003G20 | not assigned.r |
| 10 | tubby like protein 2 | Phvul.003G25PTHR16517:Sf | Phvul.003G25 | RNA biosynthe |
| 11 | tubby like protein 2 | Phvul.003G25PTHR16517:Sf | Phvul.003G25 | RNA biosynthe |
| 12 | tubby like protein 2 | Phvul.003G25PTHR16517:Sf | Phvul.003G25 | RNA biosynthe |
| 13 | tubby like protein 2 | Phvul.003G25PTHR16517:Sf | Phvul.003G25 | RNA biosynthe |
| 14 | Tetratricopeptide repeat (TPR)-like supe | Phvul.003G29PF01535//PF1 | Phvul.003G29 | not assigned.a |
| 15 | Tetratricopeptide repeat (TPR)-like supe | Phvul.003G29PF01535//PF1 | Phvul.003G29 | not assigned.a |
| 16 | | 0 | 0 | 0 Phvul.005G08not assigned.a |
| 17 | | 0 | 0 | 0 Phvul.005G08not assigned.a |
| 18 | | | | |
| 19 | alpha/beta-Hydrolases superfamily prot | Phvul.006G11PTHR21493//I | Phvul.006G11 | Lipid metaboli |
| 20 | alpha/beta-Hydrolases superfamily prot | Phvul.006G11PTHR21493//I | Phvul.006G11 | Lipid metaboli |
| 21 | TCP family transcription factor | Phvul.007G01PTHR31072:Sf | Phvul.007G01 | Multi-process |
| 22 | glutamine-tRNA ligase, putative / glutan | Phvul.007G026.1.1.18 - Glut | Phvul.007G02 | Protein biosyr |
| 23 | Heavy metal transport/detoxification su | Phvul.007G03PTHR22814//I | Phvul.007G03 | not assigned.a |
| 24 | Heavy metal transport/detoxification su | Phvul.007G03PTHR22814//I | Phvul.007G03 | not assigned.a |
| 25 | ATP sulfurylase 1 | Phvul.007G062.7.7.4 - Sulfa | Phvul.007G06 | Nutrient uptal |
| 26 | ATP sulfurylase 1 | Phvul.007G062.7.7.4 - Sulfa | Phvul.007G06 | Nutrient uptal |
| 27 | AWPM-19-like family protein | Phvul.007G10PTHR33294:Sf | Phvul.007G10 | not assigned.a |
| 28 | AWPM-19-like family protein | Phvul.007G10PTHR33294:Sf | Phvul.007G10 | not assigned.a |
| 29 | | 0 | Phvul.007G14PF10270 - Me | Phvul.007G14Solute transpc |
| 30 | LETM1-like protein | Phvul.007G23PTHR14009:Sf | Phvul.007G23 | not assigned.r |
| 31 | Pentatricopeptide repeat (PPR-like) sup | Phvul.008G04PF01535//PF1 | Phvul.008G04 | RNA processir |
| 32 | | 0 | Phvul.008G17PTHR35689:Sf | Phvul.008G17not assigned.r |
| 33 | | 0 | Phvul.008G17PTHR35689:Sf | Phvul.008G17not assigned.r |
| 34 | | 0 | 0 | 0 Phvul.008G18not assigned.r |
| 35 | | 0 | 0 | 0 Phvul.008G18not assigned.r |
| 36 | zinc finger (CCCH-type) family protein | Phvul.008G26PTHR14493:Sf | Phvul.008G26 | RNA processir |
| 37 | zinc finger (CCCH-type) family protein | Phvul.008G26PTHR14493:Sf | Phvul.008G26 | RNA processir |
| 38 | zinc finger (CCCH-type) family protein | Phvul.008G26PTHR14493:Sf | Phvul.008G26 | RNA processir |
| 39 | zinc finger (CCCH-type) family protein | Phvul.008G26PTHR14493:Sf | Phvul.008G26 | RNA processir |
| 40 | Transducin/WD40 repeat-like superfami | 0 | 0 | 0 Phvul.009G04not assigned.r |
| 41 | Transducin/WD40 repeat-like superfami | 0 | 0 | 0 Phvul.009G04not assigned.r |
| 42 | Transducin/WD40 repeat-like superfami | 0 | 0 | 0 Phvul.009G04not assigned.r |
| 43 | Transducin/WD40 repeat-like superfami | 0 | 0 | 0 Phvul.009G04not assigned.r |
| 44 | Tetratricopeptide repeat (TPR)-like supe | Phvul.009G17PF01535//PF1 | Phvul.009G17 | not assigned.a |
| 45 | Tetratricopeptide repeat (TPR)-like supe | Phvul.009G17PF01535//PF1 | Phvul.009G17 | not assigned.a |
| 46 | Tetratricopeptide repeat (TPR)-like supe | Phvul.009G17PF01535//PF1 | Phvul.009G17 | not assigned.a |
| 47 | | 0 | Phvul.009G20PTHR13677:Sf | Phvul.009G20not assigned.r |
| 48 | | 0 | Phvul.009G20PTHR13677:Sf | Phvul.009G20not assigned.r |
| 49 | | 0 | Phvul.009G20PTHR13677:Sf | Phvul.009G20not assigned.r |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

0 Phvul.009G20PTHR13677:SfPhvul.009G20not assigned.r

GATA transcription factor 10 Phvul.011G08PTHR10071:SfPhvul.011G08RNA biosynthe

GATA transcription factor 10 Phvul.011G08PTHR10071:SfPhvul.011G08RNA biosynthe

cationic amino acid transporter 8 Phvul.011G17PTHR11785:SfPhvul.011G17Solute transp

cationic amino acid transporter 8 Phvul.011G17PTHR11785:SfPhvul.011G17Solute transp

H/ACA ribonucleoprotein complex, subuPhvul.001G11K11128 - H/A(Phvul.001G11Protein biosyr

VQ motif-containing protein Phvul.001G12PTHR33624:SfPhvul.001G12External stimu

VQ motif-containing protein Phvul.001G12PTHR33624:SfPhvul.001G12External stimu

heat shock transcription factor A6B Phvul.001G15PTHR10015//IPhvul.001G15RNA biosynthe

Pentatricopeptide repeat (PPR-like) supεPhvul.001G17PF01535//PF1Phvul.001G17not assigned.a

Pentatricopeptide repeat (PPR-like) supεPhvul.001G17PF01535//PF1Phvul.001G17not assigned.a

0 Phvul.001G18PTHR21737:SfPhvul.001G18not assigned.a

glyceraldehyde-3-phosphate dehydrogePhvul.001G25PTHR10836:SfPhvul.001G25Cellular respir

glyceraldehyde-3-phosphate dehydrogePhvul.001G25PTHR10836:SfPhvul.001G25Cellular respir

C2H2-like zinc finger protein Phvul.002G02PTHR10593:SfPhvul.002G02RNA biosynthe

C2H2-like zinc finger protein Phvul.002G02PTHR10593:SfPhvul.002G02RNA biosynthe

FORMS APLOID AND BINUCLEATE CELLS Phvul.002G09PTHR11353:SfPhvul.002G09Multi-process

FORMS APLOID AND BINUCLEATE CELLS Phvul.002G09PTHR11353:SfPhvul.002G09Multi-process

Transcription factor jumonji (jmj) family Phvul.002G13PTHR10694:SfPhvul.002G13RNA biosynthe

0 Phvul.002G13PF00076 - RN/Phvul.002G13not assigned.r

0 Phvul.002G13PF00076 - RN/Phvul.002G13not assigned.r

RNA-binding (RRM/RBD/RNP motifs) fanPhvul.002G13K14837 - nuclPhvul.002G13not assigned.r

RNA-binding (RRM/RBD/RNP motifs) fanPhvul.002G13K14837 - nuclPhvul.002G13not assigned.r

0 Phvul.002G15PF14111 - DorPhvul.002G15not assigned.r

Auxin efflux carrier family protein Phvul.003G03K13947 - auxiiPhvul.003G03Solute transp

Auxin efflux carrier family protein Phvul.003G03K13947 - auxiiPhvul.003G03Solute transp

C2H2-like zinc finger protein Phvul.003G25PTHR10593:SfPhvul.003G25RNA biosynthe

C2H2-like zinc finger protein Phvul.003G25PTHR10593:SfPhvul.003G25RNA biosynthe

F-box family protein 0 0 Phvul.003G26not assigned.a

3-methylcrotonyl-CoA carboxylase Phvul.003G29K01969 - 3-mεPhvul.003G29Amino acid m

3-methylcrotonyl-CoA carboxylase Phvul.003G29K01969 - 3-mεPhvul.003G29Amino acid m

3-methylcrotonyl-CoA carboxylase Phvul.003G29K01969 - 3-mεPhvul.003G29Amino acid m

3-methylcrotonyl-CoA carboxylase Phvul.003G29K01969 - 3-mεPhvul.003G29Amino acid m

chromomethylase 3 Phvul.004G17PTHR10629:SfPhvul.004G17Chromatin org

Thioredoxin family protein Phvul.005G00PTHR11260:SfPhvul.005G00not assigned.r

Thioredoxin family protein Phvul.005G00PTHR11260:SfPhvul.005G00not assigned.r

ATP-citrate lyase A-2 Phvul.005G04KOG1254 - ATPhvul.005G04Lipid metaboli

ATP-citrate lyase A-2 Phvul.005G04KOG1254 - ATPhvul.005G04Lipid metaboli

disease resistance protein (TIR-NBS-LRR Phvul.005G09PTHR11017//IPhvul.005G09not assigned.a

0 Phvul.005G13PF00076//PF1Phvul.005G13not assigned.r

tubby like protein 8 Phvul.005G18PTHR16517:SfPhvul.005G18RNA biosynthe

tubby like protein 8 Phvul.005G18PTHR16517:SfPhvul.005G18RNA biosynthe

HXXXD-type acyl-transferase family protPhvul.006G09PTHR31642:SfPhvul.006G09Enzyme classif

NPR1-like protein 3 Phvul.006G13PTHR24413:SfPhvul.006G13Phytohormon

NPR1-like protein 3 Phvul.006G13PTHR24413:SfPhvul.006G13Phytohormon

UDP-Glycosyltransferase superfamily prPhvul.006G20PTHR11926//IPhvul.006G20Enzyme classif

| | | | |
|----|--|----------------------------------|-------------------------------------|
| 1 | | | |
| 2 | UDP-Glycosyltransferase superfamily pr | Phvul.006G20PTHR11926//I | Phvul.006G20Enzyme classifi |
| 3 | Family of unknown function (DUF566) | Phvul.007G04PTHR31807:Sf | Phvul.007G04not assigned.a |
| 4 | Family of unknown function (DUF566) | Phvul.007G04PTHR31807:Sf | Phvul.007G04not assigned.a |
| 5 | Family of unknown function (DUF566) | Phvul.007G04PTHR31807:Sf | Phvul.007G04not assigned.a |
| 6 | Family of unknown function (DUF566) | Phvul.007G04PTHR31807:Sf | Phvul.007G04not assigned.a |
| 7 | Family of unknown function (DUF566) | Phvul.007G04PTHR31807:Sf | Phvul.007G04not assigned.a |
| 8 | NAD(P)-linked oxidoreductase superfam | Phvul.007G06PTHR11732//I | Phvul.007G06Enzyme classifi |
| 9 | heat shock transcription factor B2A | Phvul.007G06PTHR10015:Sf | Phvul.007G06RNA biosynthe |
| 10 | Protein of unknown function (DUF677) | Phvul.007G08PF05055 - Pro | Phvul.007G08not assigned.a |
| 11 | Protein of unknown function (DUF677) | Phvul.007G08PF05055 - Pro | Phvul.007G08not assigned.a |
| 12 | Protein of unknown function (DUF677) | Phvul.007G08PF05055 - Pro | Phvul.007G08not assigned.a |
| 13 | Protein of unknown function (DUF677) | Phvul.007G08PF05055 - Pro | Phvul.007G08not assigned.a |
| 14 | Protein of unknown function (DUF677) | Phvul.007G08PF05055 - Pro | Phvul.007G08not assigned.a |
| 15 | Homeodomain-like superfamily protein | Phvul.007G13PTHR31499:Sf | Phvul.007G13RNA biosynthe |
| 16 | Homeodomain-like superfamily protein | Phvul.007G13PTHR31499:Sf | Phvul.007G13RNA biosynthe |
| 17 | Protein of unknown function (DUF581) | Phvul.007G17PF04570 - zinc | Phvul.007G17Multi-process |
| 18 | Plant invertase/pectin methylesterase ir | Phvul.007G24PTHR31707:Sf | Phvul.007G24Cell wall organ |
| 19 | Ribosomal protein L7Ae/L30e/S12e/Gad | Phvul.007G27K02936 - large | Phvul.007G27Protein biosyr |
| 20 | Ribosomal protein L7Ae/L30e/S12e/Gad | Phvul.007G27K02936 - large | Phvul.007G27Protein biosyr |
| 21 | C-terminal domain phosphatase-like 3 | Phvul.008G01PTHR23081:Sf | Phvul.008G01Protein modif |
| 22 | non-intrinsic ABC protein 11 | Phvul.008G05PTHR24220:Sf | Phvul.008G05Lipid metaboli |
| 23 | non-intrinsic ABC protein 11 | Phvul.008G05PTHR24220:Sf | Phvul.008G05Lipid metaboli |
| 24 | GRAS family transcription factor | Phvul.008G07PTHR31636:Sf | Phvul.008G07External stimu |
| 25 | prenylated RAB acceptor 1.A1 | Phvul.008G11PTHR12859 - I | Phvul.008G11Vesicle trafficl |
| 26 | prenylated RAB acceptor 1.A1 | Phvul.008G11PTHR12859 - I | Phvul.008G11Vesicle trafficl |
| 27 | Lycopene beta/epsilon cyclase protein | Phvul.008G21PTHR32098:Sf | Phvul.008G21not assigned.r |
| 28 | Lycopene beta/epsilon cyclase protein | Phvul.008G21PTHR32098:Sf | Phvul.008G21not assigned.r |
| 29 | Lycopene beta/epsilon cyclase protein | Phvul.008G21PTHR32098:Sf | Phvul.008G21not assigned.r |
| 30 | Lycopene beta/epsilon cyclase protein | Phvul.008G21PTHR32098:Sf | Phvul.008G21not assigned.r |
| 31 | translocon at the inner envelope membe | Phvul.008G25PF16940 - Chl | Phvul.008G25Protein transla |
| 32 | translocon at the inner envelope membe | Phvul.008G25PF16940 - Chl | Phvul.008G25Protein transla |
| 33 | | 0 Phvul.009G08PF12776 - My | Phvul.009G08not assigned.a |
| 34 | | 0 Phvul.009G08PF12776 - My | Phvul.009G08not assigned.a |
| 35 | | 0 Phvul.009G08PF12776 - My | Phvul.009G08not assigned.a |
| 36 | | 0 Phvul.009G08PF12776 - My | Phvul.009G08not assigned.a |
| 37 | phosphatidylinositol 4-OH kinase beta1 | Phvul.009G14K00888 - phos | Phvul.009G14Multi-process |
| 38 | sirtuin 2 | Phvul.009G15PTHR11085:Sf | Phvul.009G15Protein modif |
| 39 | sirtuin 2 | Phvul.009G15PTHR11085:Sf | Phvul.009G15Protein modif |
| 40 | sirtuin 2 | Phvul.009G15PTHR11085:Sf | Phvul.009G15Protein modif |
| 41 | sirtuin 2 | Phvul.009G15PTHR11085:Sf | Phvul.009G15Protein modif |
| 42 | sirtuin 2 | Phvul.009G15PTHR11085:Sf | Phvul.009G15Protein modif |
| 43 | sirtuin 2 | Phvul.009G15PTHR11085:Sf | Phvul.009G15Protein modif |
| 44 | sirtuin 2 | Phvul.009G15PTHR11085:Sf | Phvul.009G15Protein modif |
| 45 | sirtuin 2 | Phvul.009G15PTHR11085:Sf | Phvul.009G15Protein modif |
| 46 | sirtuin 2 | Phvul.009G15PTHR11085:Sf | Phvul.009G15Protein modif |
| 47 | sirtuin 2 | Phvul.009G15PTHR11085:Sf | Phvul.009G15Protein modif |
| 48 | sirtuin 2 | Phvul.009G15PTHR11085:Sf | Phvul.009G15Protein modif |
| 49 | sirtuin 2 | Phvul.009G15PTHR11085:Sf | Phvul.009G15Protein modif |
| 50 | Protein kinase superfamily protein | Phvul.009G242.7.11.1 - Non | Phvul.009G24Multi-process |
| 51 | GPCR-type G protein 2 | Phvul.011G01PTHR15948 - (| Phvul.011G01External stimu |

1
2 GPCR-type G protein 2 Phvul.011G01PTHR15948 - (Phvul.011G01External stimu
3 0 0 0 Phvul.011G10not assigned.r
4 0 0 0 Phvul.011G10not assigned.r
5
6 0 Phvul.011G10PF14111 - DorPhvul.011G10not assigned.r
7 RNI-like superfamily protein Phvul.011G12PTHR24006:SfPhvul.011G12Phytohormon
8 RNI-like superfamily protein Phvul.011G12PTHR24006:SfPhvul.011G12Phytohormon
9
10 Tetratricopeptide repeat (TPR)-like supePhvul.011G14PF13041 - PPFPhvul.011G14not assigned.a
11 Tetratricopeptide repeat (TPR)-like supePhvul.011G14PF13041 - PPFPhvul.011G14not assigned.a
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

DESCRIPTION

stromal processing peptidase (SPP) (original description: pacid=37176362 transcript=Phvul.002G04
 (original description: pacid=37175092 transcript=Phvul.002G112900.2 locus=Phvul.002G112900 IC
 (original description: pacid=37175092 transcript=Phvul.002G112900.2 locus=Phvul.002G112900 IC
 (original description: pacid=37175092 transcript=Phvul.002G112900.2 locus=Phvul.002G112900 IC
 (original description: pacid=37175092 transcript=Phvul.002G112900.2 locus=Phvul.002G112900 IC
 subunit 11 of RNA polymerase (original description: pacid=37169148 transcript=Phvul.001G01645C
 subunit 11 of RNA polymerase (original description: pacid=37169148 transcript=Phvul.001G01645C
 MFS-type solute transporter (original description: pacid=37177177 transcript=Phvul.002G255100.1
 MFS-type solute transporter (original description: pacid=37177177 transcript=Phvul.002G255100.1
 C2H2 zinc finger transcription factor (original description: pacid=37177813 transcript=Phvul.002G3
 multifunctional phyloquinone biosynthesis protein (PHYLLO) (original description: pacid=37154118
 multifunctional phyloquinone biosynthesis protein (PHYLLO) (original description: pacid=37154118
 profilin actin nucleation protein (original description: pacid=37152607 transcript=Phvul.005G1653C
 profilin actin nucleation protein (original description: pacid=37152607 transcript=Phvul.005G1653C
transcription factor (Trihelix) (original description: pacid=37173860 transcript=Phvul.006G176000.:
 RRF translation ribosome recycling factor (original description: pacid=37164667 transcript=Phvul.0
 Carotenoid 9,10(9,10)-cleavage dioxygenase 1 OS=Pisum sativum (sp|q8lp17|ccd1_pea : 232.0) & |
 Carotenoid 9,10(9,10)-cleavage dioxygenase 1 OS=Pisum sativum (sp|q8lp17|ccd1_pea : 232.0) & |
 Carotenoid 9,10(9,10)-cleavage dioxygenase 1 OS=Pisum sativum (sp|q8lp17|ccd1_pea : 232.0) & |
 Carotenoid 9,10(9,10)-cleavage dioxygenase 1 OS=Pisum sativum (sp|q8lp17|ccd1_pea : 232.0) & |
 Carotenoid 9,10(9,10)-cleavage dioxygenase 1 OS=Pisum sativum (sp|q8lp17|ccd1_pea : 232.0) & |
 Carotenoid 9,10(9,10)-cleavage dioxygenase 1 OS=Pisum sativum (sp|q8lp17|ccd1_pea : 232.0) & |
 endoribonuclease component DCL1 of DCL1-HYL1 miRNA biogenesis complex (original description:
 no hits & (original description: pacid=37145987 transcript=Phvul.003G050000.1 locus=Phvul.003G
 no hits & (original description: pacid=37145987 transcript=Phvul.003G050000.1 locus=Phvul.003G
 no hits & (original description: pacid=37163227 transcript=Phvul.004G050550.1 locus=Phvul.004G
 no hits & (original description: pacid=37163227 transcript=Phvul.004G050550.1 locus=Phvul.004G
 SYP7 group Qc-type SNARE protein (original description: pacid=37152549 transcript=Phvul.005G13
 no hits & (original description: pacid=37171902 transcript=Phvul.006G105000.1 locus=Phvul.006G
 no hits & (original description: pacid=37171902 transcript=Phvul.006G105000.1 locus=Phvul.006G
 (original description: pacid=37166785 transcript=Phvul.007G006700.1 locus=Phvul.007G006700 IC
 (original description: pacid=37166785 transcript=Phvul.007G006700.1 locus=Phvul.007G006700 IC
 no hits & (original description: pacid=37165957 transcript=Phvul.007G216500.4 locus=Phvul.007G
 no hits & (original description: pacid=37165957 transcript=Phvul.007G216500.4 locus=Phvul.007G
 no hits & (original description: pacid=37165957 transcript=Phvul.007G216500.4 locus=Phvul.007G
 no hits & (original description: pacid=37165957 transcript=Phvul.007G216500.4 locus=Phvul.007G
 no hits & (original description: pacid=37165957 transcript=Phvul.007G216500.4 locus=Phvul.007G
 no hits & (original description: pacid=37165957 transcript=Phvul.007G216500.4 locus=Phvul.007G
 (original description: pacid=37160211 transcript=Phvul.008G055300.1 locus=Phvul.008G055300 IC
 no hits & (original description: pacid=37161166 transcript=Phvul.008G173900.2 locus=Phvul.008G
 no hits & (original description: pacid=37161166 transcript=Phvul.008G173900.2 locus=Phvul.008G
 no hits & (original description: pacid=37161166 transcript=Phvul.008G173900.2 locus=Phvul.008G
 no hits & (original description: pacid=37161166 transcript=Phvul.008G173900.2 locus=Phvul.008G
 no hits & (original description: pacid=37155165 transcript=Phvul.011G132801.1 locus=Phvul.011G
 no hits & (original description: pacid=37155165 transcript=Phvul.011G132801.1 locus=Phvul.011G

1 no hits & (original description: pacid=37155240 transcript=Phvul.011G157600.4 locus=Phvul.011G
2 no hits & (original description: pacid=37155240 transcript=Phvul.011G157600.4 locus=Phvul.011G
3 no hits & (original description: pacid=37155240 transcript=Phvul.011G157600.4 locus=Phvul.011G
4 no hits & (original description: pacid=37155240 transcript=Phvul.011G157600.4 locus=Phvul.011G
5 no hits & (original description: pacid=37155240 transcript=Phvul.011G157600.4 locus=Phvul.011G
6 no hits & (original description: pacid=37155240 transcript=Phvul.011G157600.4 locus=Phvul.011G
7 no hits & (original description: pacid=37155240 transcript=Phvul.011G157600.4 locus=Phvul.011G
8 no hits & (original description: pacid=37155240 transcript=Phvul.011G157600.4 locus=Phvul.011G
9 (original description: pacid=37167986 transcript=Phvul.001G026200.1 locus=Phvul.001G026200 IC
10 (original description: pacid=37167986 transcript=Phvul.001G026200.1 locus=Phvul.001G026200 IC
11 (original description: pacid=37167919 transcript=Phvul.001G141300.1 locus=Phvul.001G141300 IC
12 (original description: pacid=37167919 transcript=Phvul.001G141300.1 locus=Phvul.001G141300 IC
13 (original description: pacid=37167919 transcript=Phvul.001G141300.1 locus=Phvul.001G141300 IC
14 (original description: pacid=37168726 transcript=Phvul.001G256400.1 locus=Phvul.001G256400 IC
15 (original description: pacid=37168726 transcript=Phvul.001G256400.1 locus=Phvul.001G256400 IC
16 (original description: pacid=37168726 transcript=Phvul.001G256400.1 locus=Phvul.001G256400 IC
17 (original description: pacid=37168816 transcript=Phvul.001G256600.1 locus=Phvul.001G256600 IC
18 (original description: pacid=37168816 transcript=Phvul.001G256600.1 locus=Phvul.001G256600 IC
19 N-acetylglucosamine-phosphate mutase (original description: pacid=37177997 transcript=Phvul.00
20 N-acetylglucosamine-phosphate mutase (original description: pacid=37177997 transcript=Phvul.00
21 C2H2 zinc finger transcription factor (original description: pacid=37177254 transcript=Phvul.002G0
22 C2H2 zinc finger transcription factor (original description: pacid=37177254 transcript=Phvul.002G0
23 Beta-glucosidase 40 OS=Arabidopsis thaliana (sp|q9fze0|bgl40_arath : 833.0) & Enzyme classificati
24 Beta-glucosidase 40 OS=Arabidopsis thaliana (sp|q9fze0|bgl40_arath : 833.0) & Enzyme classificati
25 (original description: pacid=37174585 transcript=Phvul.002G146600.2 locus=Phvul.002G146600 IC
26 (original description: pacid=37174585 transcript=Phvul.002G146600.2 locus=Phvul.002G146600 IC
27 (original description: pacid=37174585 transcript=Phvul.002G146600.2 locus=Phvul.002G146600 IC
28 (original description: pacid=37174585 transcript=Phvul.002G146600.2 locus=Phvul.002G146600 IC
29 (original description: pacid=37174703 transcript=Phvul.002G158200.1 locus=Phvul.002G158200 IC
30 (original description: pacid=37174703 transcript=Phvul.002G158200.1 locus=Phvul.002G158200 IC
31 Probable 2-oxoglutarate/Fe(II)-dependent dioxygenase OS=Papaver somniferum (sp|d4n501|diox2
32 poly-P/G elongation factor (eEF5/eIF5A) (original description: pacid=37147810 transcript=Phvul.00
33 poly-P/G elongation factor (eEF5/eIF5A) (original description: pacid=37147810 transcript=Phvul.00
34 no hits & (original description: pacid=37145363 transcript=Phvul.003G179800.1 locus=Phvul.003G
35 no hits & (original description: pacid=37145363 transcript=Phvul.003G179800.1 locus=Phvul.003G
36 no hits & (original description: pacid=37145363 transcript=Phvul.003G179800.1 locus=Phvul.003G
37 component MED4 of middle module of MEDIATOR transcription co-activator complex (original des
38 component MED4 of middle module of MEDIATOR transcription co-activator complex (original des
39 component MED4 of middle module of MEDIATOR transcription co-activator complex (original des
40 component MED4 of middle module of MEDIATOR transcription co-activator complex (original des
41 subunit beta of methylcrotonoyl-CoA carboxylase complex (original description: pacid=37146169 t
42 subunit beta of methylcrotonoyl-CoA carboxylase complex (original description: pacid=37146169 t
43 subunit beta of methylcrotonoyl-CoA carboxylase complex (original description: pacid=37146169 t
44 transcription factor (ERF) (original description: pacid=37161639 transcript=Phvul.004G068900.2 loc
45 transcription factor (ERF) (original description: pacid=37161639 transcript=Phvul.004G068900.2 loc
46 component BRCA1|BARD1 of BRCA1,ÄBARD1 DNA-damage response heterodimer (original descrip
47 (original description: pacid=37166946 transcript=Phvul.007G157700.1 locus=Phvul.007G157700 IC
48 protein factor PRPF4 of U4/U6 small nuclear ribonucleoprotein particle (snRNP) (original descriptio
49 (original description: pacid=37160389 transcript=Phvul.008G111200.1 locus=Phvul.008G111200 IC
50
51
52
53
54
55
56
57
58
59
60

1 (original description: pacid=37160389 transcript=Phvul.008G111200.1 locus=Phvul.008G111200 IC
2 (original description: pacid=37157730 transcript=Phvul.008G230800.1 locus=Phvul.008G230800 IC
3 no hits & (original description: pacid=37148950 transcript=Phvul.009G080800.1 locus=Phvul.009G
4 no hits & (original description: pacid=37148950 transcript=Phvul.009G080800.1 locus=Phvul.009G
5 monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37148701 transcript=Phvul.009G
6 monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37148701 transcript=Phvul.009G
7 (original description: pacid=37143928 transcript=Phvul.010G119500.1 locus=Phvul.010G119500 IC
8 no hits & (original description: pacid=37157405 transcript=Phvul.011G008600.1 locus=Phvul.011G
9 no hits & (original description: pacid=37157405 transcript=Phvul.011G008600.1 locus=Phvul.011G
10 component ATG18 of autophagosome ATG9-2-18 membrane shuttling complex (original descriptio
11 component ATG18 of autophagosome ATG9-2-18 membrane shuttling complex (original descriptio
12 no hits & (original description: pacid=37155008 transcript=Phvul.011G169222.1 locus=Phvul.011G
13 DRP2-type clathrin coated vesicle dynamin (original description: pacid=37156922 transcript=Phvul.
14 DRP2-type clathrin coated vesicle dynamin (original description: pacid=37156922 transcript=Phvul.
15 no hits & (original description: pacid=37167898 transcript=Phvul.001G096200.1 locus=Phvul.001G
16 cationic amino acid transporter (CAT) (original description: pacid=37167733 transcript=Phvul.001G
17 cationic amino acid transporter (CAT) (original description: pacid=37167733 transcript=Phvul.001G
18 cationic amino acid transporter (CAT) (original description: pacid=37167733 transcript=Phvul.001G
19 cationic amino acid transporter (CAT) (original description: pacid=37167733 transcript=Phvul.001G
20 mannan synthase (CSLD) (original description: pacid=37168697 transcript=Phvul.001G211000.1 loc
21 mannan synthase (CSLD) (original description: pacid=37168697 transcript=Phvul.001G211000.1 loc
22 no hits & (original description: pacid=37175952 transcript=Phvul.002G147900.2 locus=Phvul.002G
23 no hits & (original description: pacid=37175952 transcript=Phvul.002G147900.2 locus=Phvul.002G
24 no hits & (original description: pacid=37175952 transcript=Phvul.002G147900.2 locus=Phvul.002G
25 no hits & (original description: pacid=37175952 transcript=Phvul.002G147900.2 locus=Phvul.002G
26 (original description: pacid=37177943 transcript=Phvul.002G182700.2 locus=Phvul.002G182700 IC
27 (original description: pacid=37177943 transcript=Phvul.002G182700.2 locus=Phvul.002G182700 IC
28 no hits & (original description: pacid=37178086 transcript=Phvul.002G202300.1 locus=Phvul.002G
29 (original description: pacid=37175275 transcript=Phvul.002G238000.1 locus=Phvul.002G238000 IC
30 no hits & (original description: pacid=37177790 transcript=Phvul.002G267100.1 locus=Phvul.002G
31 no hits & (original description: pacid=37177790 transcript=Phvul.002G267100.1 locus=Phvul.002G
32 (original description: pacid=37175452 transcript=Phvul.002G274400.2 locus=Phvul.002G274400 IC
33 (original description: pacid=37175452 transcript=Phvul.002G274400.2 locus=Phvul.002G274400 IC
34 (original description: pacid=37175452 transcript=Phvul.002G274400.2 locus=Phvul.002G274400 IC
35 (original description: pacid=37175452 transcript=Phvul.002G274400.2 locus=Phvul.002G274400 IC
36 protein kinase (PERK-related) (original description: pacid=37174973 transcript=Phvul.002G304500.
37 (original description: pacid=37178228 transcript=Phvul.002G327900.1 locus=Phvul.002G327900 IC
38 (original description: pacid=37178228 transcript=Phvul.002G327900.1 locus=Phvul.002G327900 IC
39 allene oxidase synthase (AOS) (original description: pacid=37146668 transcript=Phvul.003G010700
40 cationic amino acid transporter (CAT) (original description: pacid=37144797 transcript=Phvul.003G
41 cationic amino acid transporter (CAT) (original description: pacid=37144797 transcript=Phvul.003G
42 S-adenosyl methionine decarboxylase (original description: pacid=37148102 transcript=Phvul.003G
43 S-adenosyl methionine decarboxylase (original description: pacid=37148102 transcript=Phvul.003G
44 anion channel (SLAC) (original description: pacid=37147406 transcript=Phvul.003G080700.1 locus=
45 protein kinase (LRR-VIII-1) (original description: pacid=37148128 transcript=Phvul.003G090000.2 lc
46 protein kinase (LRR-VIII-1) (original description: pacid=37148128 transcript=Phvul.003G090000.2 lc

1 multifunctional enzyme (MFP) (original description: pacid=37146564 transcript=Phvul.003G09650C
2 no hits & (original description: pacid=37145474 transcript=Phvul.003G113900.1 locus=Phvul.003G
3 no hits & (original description: pacid=37145474 transcript=Phvul.003G113900.1 locus=Phvul.003G
4 component eIF-iso4G of eIF-iso4F unwinding complex (original description: pacid=37148389 transc
5 component eIF-iso4G of eIF-iso4F unwinding complex (original description: pacid=37148389 transc
6 no hits & (original description: pacid=37145370 transcript=Phvul.003G209900.1 locus=Phvul.003G
7 no hits & (original description: pacid=37145370 transcript=Phvul.003G209900.1 locus=Phvul.003G
8 transcription factor (TUB) (original description: pacid=37144375 transcript=Phvul.003G254900.2 lo
9 transcription factor (TUB) (original description: pacid=37144375 transcript=Phvul.003G254900.2 lo
10 transcription factor (TUB) (original description: pacid=37144375 transcript=Phvul.003G254900.2 lo
11 transcription factor (TUB) (original description: pacid=37144375 transcript=Phvul.003G254900.2 lo
12 (original description: pacid=37147652 transcript=Phvul.003G295700.2 locus=Phvul.003G295700 IC
13 (original description: pacid=37147652 transcript=Phvul.003G295700.2 locus=Phvul.003G295700 IC
14 (original description: pacid=37152396 transcript=Phvul.005G088636.1 locus=Phvul.005G088636 IC
15 (original description: pacid=37152396 transcript=Phvul.005G088636.1 locus=Phvul.005G088636 IC
16 phosphatidylglycerol lipase (PLIP1) (original description: pacid=37172685 transcript=Phvul.006G11.
17 phosphatidylglycerol lipase (PLIP1) (original description: pacid=37172685 transcript=Phvul.006G11.
18 CHE circadian clock repression factor (original description: pacid=37166457 transcript=Phvul.007G(
19 glutamine-tRNA ligase (original description: pacid=37166017 transcript=Phvul.007G028800.1 locus
20 (original description: pacid=37164910 transcript=Phvul.007G038000.1 locus=Phvul.007G038000 IC
21 (original description: pacid=37164910 transcript=Phvul.007G038000.1 locus=Phvul.007G038000 IC
22 ATP sulfurylase (original description: pacid=37166997 transcript=Phvul.007G062900.1 locus=Phvul.
23 ATP sulfurylase (original description: pacid=37166997 transcript=Phvul.007G062900.1 locus=Phvul.
24 (original description: pacid=37167447 transcript=Phvul.007G100700.1 locus=Phvul.007G100700 IC
25 (original description: pacid=37167447 transcript=Phvul.007G100700.1 locus=Phvul.007G100700 IC
26 magnesium cation transporter (MMgT) (original description: pacid=37164628 transcript=Phvul.007
27 no hits & (original description: pacid=37164585 transcript=Phvul.007G230450.1 locus=Phvul.007G
28 RNA editing factor (AHG11) (original description: pacid=37160213 transcript=Phvul.008G046100.1
29 no hits & (original description: pacid=37160926 transcript=Phvul.008G177200.2 locus=Phvul.008G
30 no hits & (original description: pacid=37160926 transcript=Phvul.008G177200.2 locus=Phvul.008G
31 no hits & (original description: pacid=37160761 transcript=Phvul.008G181900.2 locus=Phvul.008G
32 no hits & (original description: pacid=37160761 transcript=Phvul.008G181900.2 locus=Phvul.008G
33 mRNA-binding regulatory factor (TZF) (original description: pacid=37159289 transcript=Phvul.008G
34 mRNA-binding regulatory factor (TZF) (original description: pacid=37159289 transcript=Phvul.008G
35 mRNA-binding regulatory factor (TZF) (original description: pacid=37159289 transcript=Phvul.008G
36 mRNA-binding regulatory factor (TZF) (original description: pacid=37159289 transcript=Phvul.008G
37 no hits & (original description: pacid=37151386 transcript=Phvul.009G041100.2 locus=Phvul.009G
38 no hits & (original description: pacid=37151386 transcript=Phvul.009G041100.2 locus=Phvul.009G
39 no hits & (original description: pacid=37151386 transcript=Phvul.009G041100.2 locus=Phvul.009G
40 (original description: pacid=37150369 transcript=Phvul.009G175100.3 locus=Phvul.009G175100 IC
41 (original description: pacid=37150369 transcript=Phvul.009G175100.3 locus=Phvul.009G175100 IC
42 (original description: pacid=37150369 transcript=Phvul.009G175100.3 locus=Phvul.009G175100 IC
43 no hits & (original description: pacid=37151886 transcript=Phvul.009G200500.3 locus=Phvul.009G
44 no hits & (original description: pacid=37151886 transcript=Phvul.009G200500.3 locus=Phvul.009G
45 no hits & (original description: pacid=37151886 transcript=Phvul.009G200500.3 locus=Phvul.009G

1 no hits & (original description: pacid=37151886 transcript=Phvul.009G200500.3 locus=Phvul.009G
2 transcription factor (GATA) (original description: pacid=37156368 transcript=Phvul.011G080200.1 l
3 transcription factor (GATA) (original description: pacid=37156368 transcript=Phvul.011G080200.1 l
4 cationic amino acid transporter (CAT) (original description: pacid=37155925 transcript=Phvul.011G
5 cationic amino acid transporter (CAT) (original description: pacid=37155925 transcript=Phvul.011G
6 core component Gar1 of H/ACA small nucleolar ribonucleoprotein (snoRNP) RNA pseudouridylation
7 WRKY33-activating protein (SIB) (original description: pacid=37168270 transcript=Phvul.001G12340
8 WRKY33-activating protein (SIB) (original description: pacid=37168270 transcript=Phvul.001G12340
9 transcription factor (HSF) (original description: pacid=37170201 transcript=Phvul.001G154700.1 lo
10 (original description: pacid=37168659 transcript=Phvul.001G179800.1 locus=Phvul.001G179800 IC
11 (original description: pacid=37168659 transcript=Phvul.001G179800.1 locus=Phvul.001G179800 IC
12 (original description: pacid=37168299 transcript=Phvul.001G184000.1 locus=Phvul.001G184000 IC
13 NAD-dependent glyceraldehyde 3-phosphate dehydrogenase (original description: pacid=3717044;
14 NAD-dependent glyceraldehyde 3-phosphate dehydrogenase (original description: pacid=3717044;
15 C2H2 zinc finger transcription factor (original description: pacid=37177695 transcript=Phvul.002G0
16 C2H2 zinc finger transcription factor (original description: pacid=37177695 transcript=Phvul.002G0
17 phosphatidylinositol 3-phosphate 5-kinase (FAB1) (original description: pacid=37176675 transcript:
18 phosphatidylinositol 3-phosphate 5-kinase (FAB1) (original description: pacid=37176675 transcript:
19 transcription factor (JUMONJI) (original description: pacid=37177660 transcript=Phvul.002G137100
20 no hits & (original description: pacid=37178177 transcript=Phvul.002G137200.1 locus=Phvul.002G
21 no hits & (original description: pacid=37178177 transcript=Phvul.002G137200.1 locus=Phvul.002G
22 no hits & (original description: pacid=37178466 transcript=Phvul.002G139900.2 locus=Phvul.002G
23 no hits & (original description: pacid=37178466 transcript=Phvul.002G139900.2 locus=Phvul.002G
24 no hits & (original description: pacid=37175593 transcript=Phvul.002G156300.1 locus=Phvul.002G
25 auxin efflux transporter (PIN) (original description: pacid=37146616 transcript=Phvul.003G032500.
26 auxin efflux transporter (PIN) (original description: pacid=37146616 transcript=Phvul.003G032500.
27 C2H2 zinc finger transcription factor (original description: pacid=37145501 transcript=Phvul.003G2
28 C2H2 zinc finger transcription factor (original description: pacid=37145501 transcript=Phvul.003G2
29 (original description: pacid=37144586 transcript=Phvul.003G265700.1 locus=Phvul.003G265700 IC
30 subunit beta of methylcrotonoyl-CoA carboxylase complex (original description: pacid=37146169 tr
31 subunit beta of methylcrotonoyl-CoA carboxylase complex (original description: pacid=37146169 tr
32 subunit beta of methylcrotonoyl-CoA carboxylase complex (original description: pacid=37146169 tr
33 subunit beta of methylcrotonoyl-CoA carboxylase complex (original description: pacid=37146169 tr
34 DNA chromomethylase (CMT) (original description: pacid=37163557 transcript=Phvul.004G176100
35 no hits & (original description: pacid=37154097 transcript=Phvul.005G001500.2 locus=Phvul.005G
36 no hits & (original description: pacid=37154097 transcript=Phvul.005G001500.2 locus=Phvul.005G
37 alpha chain of ATP-dependent citrate lyase complex (original description: pacid=37153149 transcri
38 alpha chain of ATP-dependent citrate lyase complex (original description: pacid=37153149 transcri
39 (original description: pacid=37153683 transcript=Phvul.005G093400.1 locus=Phvul.005G093400 IC
40 no hits & (original description: pacid=37153235 transcript=Phvul.005G131700.1 locus=Phvul.005G
41 transcription factor (TUB) (original description: pacid=37154406 transcript=Phvul.005G183800.2 lo
42 transcription factor (TUB) (original description: pacid=37154406 transcript=Phvul.005G183800.2 lo
43 Benzyl alcohol O-benzoyltransferase OS=Nicotiana tabacum (sp|q8gt20|bebt_tobac : 533.0) & Enz
44 receptor protein (NPR3|4) (original description: pacid=37172197 transcript=Phvul.006G131400.1 l
45 receptor protein (NPR3|4) (original description: pacid=37172197 transcript=Phvul.006G131400.1 l
46 Soyasaponin III rhamnosyltransferase OS=Glycine max (sp|d4q9z5|sgt3_soybn : 536.0) & Enzyme c

1 Soyasaponin III rhamnosyltransferase OS=Glycine max (sp|d4q9z5|sgt3_soybn : 536.0) & Enzyme c
2 (original description: pacid=37165774 transcript=Phvul.007G043900.2 locus=Phvul.007G043900 IC
3 (original description: pacid=37165774 transcript=Phvul.007G043900.2 locus=Phvul.007G043900 IC
4 (original description: pacid=37165774 transcript=Phvul.007G043900.2 locus=Phvul.007G043900 IC
5 (original description: pacid=37165774 transcript=Phvul.007G043900.2 locus=Phvul.007G043900 IC
6 (original description: pacid=37165774 transcript=Phvul.007G043900.2 locus=Phvul.007G043900 IC
7 Perakine reductase OS=Rauvolfia serpentina (sp|q3l181|perr_ause : 490.0) & Enzyme classificatio
8 **transcription factor (HSF) (original description: pacid=37167531 transcript=Phvul.007G067800.1 lo**
9 (original description: pacid=37167319 transcript=Phvul.007G080900.2 locus=Phvul.007G080900 IC
10 (original description: pacid=37167319 transcript=Phvul.007G080900.2 locus=Phvul.007G080900 IC
11 (original description: pacid=37167319 transcript=Phvul.007G080900.2 locus=Phvul.007G080900 IC
12 (original description: pacid=37167319 transcript=Phvul.007G080900.2 locus=Phvul.007G080900 IC
13 G2-like GARP transcription factor (original description: pacid=37166422 transcript=Phvul.007G139:
14 G2-like GARP transcription factor (original description: pacid=37166422 transcript=Phvul.007G139:
15 SnRK1-interacting factor (FLZ) (original description: pacid=37167409 transcript=Phvul.007G173400
16 pectin methylesterase (original description: pacid=37164403 transcript=Phvul.007G246700.1 locus
17 component RPL7a of LSU proteome component (original description: pacid=37165435 transcript=P
18 component RPL7a of LSU proteome component (original description: pacid=37165435 transcript=P
19 subcluster H/CPL3-4 phosphatase (original description: pacid=37159302 transcript=Phvul.008G019
20 **ATPase component TGD3 of TGD lipid importer complex (original description: pacid=37160544 trar**
21 **ATPase component TGD3 of TGD lipid importer complex (original description: pacid=37160544 trar**
22 SCR gravity signalling transcription factor (original description: pacid=37158083 transcript=Phvul.00
23 **A-class Rab-GDF protein (original description: pacid=37160643 transcript=Phvul.008G114700.1 loci**
24 **A-class Rab-GDF protein (original description: pacid=37160643 transcript=Phvul.008G114700.1 loci**
25 no hits & (original description: pacid=37157723 transcript=Phvul.008G211500.4 locus=Phvul.008G
26 no hits & (original description: pacid=37157723 transcript=Phvul.008G211500.4 locus=Phvul.008G
27 no hits & (original description: pacid=37157723 transcript=Phvul.008G211500.4 locus=Phvul.008G
28 no hits & (original description: pacid=37157723 transcript=Phvul.008G211500.4 locus=Phvul.008G
29 component Tic110 of inner envelope TIC translocation system (original description: pacid=3715992
30 component Tic110 of inner envelope TIC translocation system (original description: pacid=3715992
31 (original description: pacid=37149910 transcript=Phvul.009G086300.2 locus=Phvul.009G086300 IC
32 (original description: pacid=37149910 transcript=Phvul.009G086300.2 locus=Phvul.009G086300 IC
33 (original description: pacid=37149910 transcript=Phvul.009G086300.2 locus=Phvul.009G086300 IC
34 (original description: pacid=37149910 transcript=Phvul.009G086300.2 locus=Phvul.009G086300 IC
35 phosphatidylinositol 4-kinase (PI4K-beta) (original description: pacid=37149528 transcript=Phvul.00
36 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
37 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
38 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
39 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
40 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
41 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
42 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
43 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
44 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
45 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
46 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
47 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
48 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
49 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
50 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
51 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
52 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
53 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
54 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
55 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
56 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
57 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
58 sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G154300
59 GTPase interactive protein kinase (RBK/RRK) (original description: pacid=37152122 transcript=Phv
60 cold sensor (COLD1) (original description: pacid=37156295 transcript=Phvul.011G017800.1 locus=F

1 cold sensor (COLD1) (original description: pacid=37156295 transcript=Phvul.011G017800.1 locus=F
2 no hits & (original description: pacid=37155821 transcript=Phvul.011G100200.2 locus=Phvul.011G
3 no hits & (original description: pacid=37155821 transcript=Phvul.011G100200.2 locus=Phvul.011G
4 no hits & (original description: pacid=37154697 transcript=Phvul.011G108300.1 locus=Phvul.011G
5 MAX2 strigolactone signal transducer (original description: pacid=37155383 transcript=Phvul.011G
6 MAX2 strigolactone signal transducer (original description: pacid=37155383 transcript=Phvul.011G
7 (original description: pacid=37155140 transcript=Phvul.011G140050.2 locus=Phvul.011G140050 IC
8 (original description: pacid=37155140 transcript=Phvul.011G140050.2 locus=Phvul.011G140050 IC
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1 i157600 ID=Phvul.011G157600.4.v2.1 annot-version=v2.1)
 2 i157600 ID=Phvul.011G157600.4.v2.1 annot-version=v2.1)
 3 i157600 ID=Phvul.011G157600.4.v2.1 annot-version=v2.1)
 4 i157600 ID=Phvul.011G157600.4.v2.1 annot-version=v2.1)
 5 i157600 ID=Phvul.011G157600.4.v2.1 annot-version=v2.1)
 6 i157600 ID=Phvul.011G157600.4.v2.1 annot-version=v2.1)
 7 i157600 ID=Phvul.011G157600.4.v2.1 annot-version=v2.1)
 8 i157600 ID=Phvul.011G157600.4.v2.1 annot-version=v2.1)
 9
 10)=Phvul.001G026200.1.v2.1 annot-version=v2.1) & Acyl-CoA-binding domain-containing protein 3 C
 11)=Phvul.001G026200.1.v2.1 annot-version=v2.1) & Acyl-CoA-binding domain-containing protein 3 C
 12)=Phvul.001G141300.1.v2.1 annot-version=v2.1) & UBP1-associated protein 2C OS=Arabidopsis tha
 13)=Phvul.001G141300.1.v2.1 annot-version=v2.1) & UBP1-associated protein 2C OS=Arabidopsis tha
 14)=Phvul.001G256400.1.v2.1 annot-version=v2.1) & D-cysteine desulfhydrase 2, mitochondrial OS=A
 15)=Phvul.001G256400.1.v2.1 annot-version=v2.1) & D-cysteine desulfhydrase 2, mitochondrial OS=A
 16)=Phvul.001G256600.1.v2.1 annot-version=v2.1) & Oxysterol-binding protein-related protein 1D OS
 17)=Phvul.001G256600.1.v2.1 annot-version=v2.1) & Oxysterol-binding protein-related protein 1D OS
 18)=Phvul.001G256600.1.v2.1 annot-version=v2.1) & Oxysterol-binding protein-related protein 1D OS
 19)2G003600.1 locus=Phvul.002G003600 ID=Phvul.002G003600.1.v2.1 annot-version=v2.1) &
 20)2G003600.1 locus=Phvul.002G003600 ID=Phvul.002G003600.1.v2.1 annot-version=v2.1) &
 21)75900.1 locus=Phvul.002G075900 ID=Phvul.002G075900.1.v2.1 annot-version=v2.1) &
 22)75900.1 locus=Phvul.002G075900 ID=Phvul.002G075900.1.v2.1 annot-version=v2.1) &
 23 ion.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2 : 434.9) (original description: pacid=37176972 transc
 24 ion.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2 : 434.9) (original description: pacid=37176972 transc
 25)=Phvul.002G146600.2.v2.1 annot-version=v2.1) & Putative U-box domain-containing protein 50 O'
 26)=Phvul.002G146600.2.v2.1 annot-version=v2.1) & Putative U-box domain-containing protein 50 O'
 27)=Phvul.002G146600.2.v2.1 annot-version=v2.1) & Putative U-box domain-containing protein 50 O'
 28)=Phvul.002G146600.2.v2.1 annot-version=v2.1) & Putative U-box domain-containing protein 50 O'
 29)=Phvul.002G158200.1.v2.1 annot-version=v2.1) & Uncharacterized protein At1g76660 OS=Arabidc
 30)=Phvul.002G158200.1.v2.1 annot-version=v2.1) & Uncharacterized protein At1g76660 OS=Arabidc
 31 2_papso : 230.0) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on p
 32)3G156333.1 locus=Phvul.003G156333 ID=Phvul.003G156333.1.v2.1 annot-version=v2.1) &
 33)3G156333.1 locus=Phvul.003G156333 ID=Phvul.003G156333.1.v2.1 annot-version=v2.1) &
 34 i179800 ID=Phvul.003G179800.1.v2.1 annot-version=v2.1)
 35 i179800 ID=Phvul.003G179800.1.v2.1 annot-version=v2.1)
 36 i179800 ID=Phvul.003G179800.1.v2.1 annot-version=v2.1)
 37 cription: pacid=37144783 transcript=Phvul.003G261400.2 locus=Phvul.003G261400 ID=Phvul.003G
 38 cription: pacid=37144783 transcript=Phvul.003G261400.2 locus=Phvul.003G261400 ID=Phvul.003G
 39 cription: pacid=37144783 transcript=Phvul.003G261400.2 locus=Phvul.003G261400 ID=Phvul.003G
 40 cription: pacid=37144783 transcript=Phvul.003G261400.2 locus=Phvul.003G261400 ID=Phvul.003G
 41 ranscript=Phvul.003G291600.2 locus=Phvul.003G291600 ID=Phvul.003G291600.2.v2.1 annot-versic
 42 ranscript=Phvul.003G291600.2 locus=Phvul.003G291600 ID=Phvul.003G291600.2.v2.1 annot-versic
 43 ranscript=Phvul.003G291600.2 locus=Phvul.003G291600 ID=Phvul.003G291600.2.v2.1 annot-versic
 44 ranscript=Phvul.003G291600.2 locus=Phvul.003G291600 ID=Phvul.003G291600.2.v2.1 annot-versic
 45 cus=Phvul.004G068900 ID=Phvul.004G068900.2.v2.1 annot-version=v2.1) &
 46 cus=Phvul.004G068900 ID=Phvul.004G068900.2.v2.1 annot-version=v2.1) &
 47 ption: pacid=37154570 transcript=Phvul.005G069600.1 locus=Phvul.005G069600 ID=Phvul.005G06'
 48)=Phvul.007G157700.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containing protein At:
 49 on: pacid=37166744 transcript=Phvul.007G249600.1 locus=Phvul.007G249600 ID=Phvul.007G24960
 50)=Phvul.008G111200.1.v2.1 annot-version=v2.1) & Werner Syndrome-like exonuclease OS=Arabido

1
2)=Phvul.008G111200.1.v2.1 annot-version=v2.1) & Werner Syndrome-like exonuclease OS=Arabido
3)=Phvul.008G230800.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containing protein At
4 i080800 ID=Phvul.009G080800.1.v2.1 annot-version=v2.1)
5 i080800 ID=Phvul.009G080800.1.v2.1 annot-version=v2.1)
6 i119700.1 locus=Phvul.009G119700 ID=Phvul.009G119700.1.v2.1 annot-version=v2.1) &
7 i119700.1 locus=Phvul.009G119700 ID=Phvul.009G119700.1.v2.1 annot-version=v2.1) &
8)=Phvul.010G119500.1.v2.1 annot-version=v2.1) & RNA-binding protein CP33, chloroplastic OS=Ara
9 i008600 ID=Phvul.011G008600.1.v2.1 annot-version=v2.1)
10 i008600 ID=Phvul.011G008600.1.v2.1 annot-version=v2.1)
11 in: pacid=37154904 transcript=Phvul.011G140900.1 locus=Phvul.011G140900 ID=Phvul.011G14090
12 in: pacid=37154904 transcript=Phvul.011G140900.1 locus=Phvul.011G140900 ID=Phvul.011G14090
13 i169222 ID=Phvul.011G169222.1.v2.1 annot-version=v2.1)
14 .011G215900.1 locus=Phvul.011G215900 ID=Phvul.011G215900.1.v2.1 annot-version=v2.1) &
15 .011G215900.1 locus=Phvul.011G215900 ID=Phvul.011G215900.1.v2.1 annot-version=v2.1) &
16 i096200 ID=Phvul.001G096200.1.v2.1 annot-version=v2.1)
17 i104700.2 locus=Phvul.001G104700 ID=Phvul.001G104700.2.v2.1 annot-version=v2.1) &
18 i104700.2 locus=Phvul.001G104700 ID=Phvul.001G104700.2.v2.1 annot-version=v2.1) &
19 i104700.2 locus=Phvul.001G104700 ID=Phvul.001G104700.2.v2.1 annot-version=v2.1) &
20 i104700.2 locus=Phvul.001G104700 ID=Phvul.001G104700.2.v2.1 annot-version=v2.1) &
21 cus=Phvul.001G211000 ID=Phvul.001G211000.1.v2.1 annot-version=v2.1) &
22 cus=Phvul.001G211000 ID=Phvul.001G211000.1.v2.1 annot-version=v2.1) &
23 i147900 ID=Phvul.002G147900.2.v2.1 annot-version=v2.1)
24 i147900 ID=Phvul.002G147900.2.v2.1 annot-version=v2.1)
25 i147900 ID=Phvul.002G147900.2.v2.1 annot-version=v2.1)
26 i147900 ID=Phvul.002G147900.2.v2.1 annot-version=v2.1)
27)=Phvul.002G182700.2.v2.1 annot-version=v2.1) & L-Ala-D/L-amino acid epimerase OS=Populus tric
28)=Phvul.002G182700.2.v2.1 annot-version=v2.1) & L-Ala-D/L-amino acid epimerase OS=Populus tric
29 i202300 ID=Phvul.002G202300.1.v2.1 annot-version=v2.1)
30)=Phvul.002G238000.1.v2.1 annot-version=v2.1) & Thioredoxin-like fold domain-containing protein
31 i267100 ID=Phvul.002G267100.1.v2.1 annot-version=v2.1)
32 i267100 ID=Phvul.002G267100.1.v2.1 annot-version=v2.1)
33)=Phvul.002G274400.2.v2.1 annot-version=v2.1) & F-box protein At5g39450 OS=Arabidopsis thaliar
34)=Phvul.002G274400.2.v2.1 annot-version=v2.1) & F-box protein At5g39450 OS=Arabidopsis thaliar
35)=Phvul.002G274400.2.v2.1 annot-version=v2.1) & F-box protein At5g39450 OS=Arabidopsis thaliar
36)=Phvul.002G274400.2.v2.1 annot-version=v2.1) & F-box protein At5g39450 OS=Arabidopsis thaliar
37 .1 locus=Phvul.002G304500 ID=Phvul.002G304500.1.v2.1 annot-version=v2.1) &
38)=Phvul.002G327900.1.v2.1 annot-version=v2.1) & Uncharacterized protein At5g39865 OS=Arabidc
39)=Phvul.002G327900.1.v2.1 annot-version=v2.1) & Uncharacterized protein At5g39865 OS=Arabidc
40).1 locus=Phvul.003G010700 ID=Phvul.003G010700.1.v2.1 annot-version=v2.1) &
41 i023101.2 locus=Phvul.003G023101 ID=Phvul.003G023101.2.v2.1 annot-version=v2.1) &
42 i023101.2 locus=Phvul.003G023101 ID=Phvul.003G023101.2.v2.1 annot-version=v2.1) &
43 i044200.1 locus=Phvul.003G044200 ID=Phvul.003G044200.1.v2.1 annot-version=v2.1) &
44 i044200.1 locus=Phvul.003G044200 ID=Phvul.003G044200.1.v2.1 annot-version=v2.1) &
45 :Phvul.003G080700 ID=Phvul.003G080700.1.v2.1 annot-version=v2.1) &
46 locus=Phvul.003G090000 ID=Phvul.003G090000.2.v2.1 annot-version=v2.1) &
47 locus=Phvul.003G090000 ID=Phvul.003G090000.2.v2.1 annot-version=v2.1) &

1
2)1 locus=Phvul.003G096500 ID=Phvul.003G096500.1.v2.1 annot-version=v2.1) &
3 i113900 ID=Phvul.003G113900.1.v2.1 annot-version=v2.1)
4 i113900 ID=Phvul.003G113900.1.v2.1 annot-version=v2.1)
5
6 ript=Phvul.003G154900.1 locus=Phvul.003G154900 ID=Phvul.003G154900.1.v2.1 annot-version=v2
7 ript=Phvul.003G154900.1 locus=Phvul.003G154900 ID=Phvul.003G154900.1.v2.1 annot-version=v2
8 i209900 ID=Phvul.003G209900.1.v2.1 annot-version=v2.1)
9 i209900 ID=Phvul.003G209900.1.v2.1 annot-version=v2.1)
10
11 ucus=Phvul.003G254900 ID=Phvul.003G254900.2.v2.1 annot-version=v2.1) &
12 ucus=Phvul.003G254900 ID=Phvul.003G254900.2.v2.1 annot-version=v2.1) &
13 ucus=Phvul.003G254900 ID=Phvul.003G254900.2.v2.1 annot-version=v2.1) &
14 ucus=Phvul.003G254900 ID=Phvul.003G254900.2.v2.1 annot-version=v2.1) &
15
16 D)=Phvul.003G295700.2.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containing protein At4
17 D)=Phvul.003G295700.2.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containing protein At4
18 D)=Phvul.005G088636.1.v2.1 annot-version=v2.1) & Ribosomal protein S1, mitochondrial OS=Marchi
19 D)=Phvul.005G088636.1.v2.1 annot-version=v2.1) & Ribosomal protein S1, mitochondrial OS=Marchi
20
21 2000.2 locus=Phvul.006G112000 ID=Phvul.006G112000.2.v2.1 annot-version=v2.1) &
22 2000.2 locus=Phvul.006G112000 ID=Phvul.006G112000.2.v2.1 annot-version=v2.1) &
23 015000.1 locus=Phvul.007G015000 ID=Phvul.007G015000.1.v2.1 annot-version=v2.1) &
24 i=Phvul.007G028800 ID=Phvul.007G028800.1.v2.1 annot-version=v2.1) &
25
26 D)=Phvul.007G038000.1.v2.1 annot-version=v2.1) & Heavy metal-associated isoprenylated plant pro
27 D)=Phvul.007G038000.1.v2.1 annot-version=v2.1) & Heavy metal-associated isoprenylated plant pro
28
29 .007G062900 ID=Phvul.007G062900.1.v2.1 annot-version=v2.1) &
30 .007G062900 ID=Phvul.007G062900.1.v2.1 annot-version=v2.1) &
31
32 D)=Phvul.007G100700.1.v2.1 annot-version=v2.1) & Membrane protein PM19L OS=Oryza sativa subs
33 D)=Phvul.007G100700.1.v2.1 annot-version=v2.1) & Membrane protein PM19L OS=Oryza sativa subs
34
35 'G149300.1 locus=Phvul.007G149300 ID=Phvul.007G149300.1.v2.1 annot-version=v2.1) &
36 i230450 ID=Phvul.007G230450.1.v2.1 annot-version=v2.1)
37 locus=Phvul.008G046100 ID=Phvul.008G046100.1.v2.1 annot-version=v2.1) &
38
39 i177200 ID=Phvul.008G177200.2.v2.1 annot-version=v2.1)
40 i177200 ID=Phvul.008G177200.2.v2.1 annot-version=v2.1)
41 i181900 ID=Phvul.008G181900.2.v2.1 annot-version=v2.1)
42 i181900 ID=Phvul.008G181900.2.v2.1 annot-version=v2.1)
43
44 i260900.2 locus=Phvul.008G260900 ID=Phvul.008G260900.2.v2.1 annot-version=v2.1) &
45 i260900.2 locus=Phvul.008G260900 ID=Phvul.008G260900.2.v2.1 annot-version=v2.1) &
46 i260900.2 locus=Phvul.008G260900 ID=Phvul.008G260900.2.v2.1 annot-version=v2.1) &
47 i260900.2 locus=Phvul.008G260900 ID=Phvul.008G260900.2.v2.1 annot-version=v2.1) &
48
49 i041100 ID=Phvul.009G041100.2.v2.1 annot-version=v2.1)
50 i041100 ID=Phvul.009G041100.2.v2.1 annot-version=v2.1)
51 i041100 ID=Phvul.009G041100.2.v2.1 annot-version=v2.1)
52 i041100 ID=Phvul.009G041100.2.v2.1 annot-version=v2.1)
53
54 D)=Phvul.009G175100.3.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat-containing pr
55 D)=Phvul.009G175100.3.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat-containing pr
56 D)=Phvul.009G175100.3.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat-containing pr
57
58 i200500 ID=Phvul.009G200500.3.v2.1 annot-version=v2.1)
59 i200500 ID=Phvul.009G200500.3.v2.1 annot-version=v2.1)
60 i200500 ID=Phvul.009G200500.3.v2.1 annot-version=v2.1)

1 i200500 ID=Phvul.009G200500.3.v2.1 annot-version=v2.1)
2 locus=Phvul.011G080200 ID=Phvul.011G080200.1.v2.1 annot-version=v2.1) &
3 locus=Phvul.011G080200 ID=Phvul.011G080200.1.v2.1 annot-version=v2.1) &
4 i174000.1 locus=Phvul.011G174000 ID=Phvul.011G174000.1.v2.1 annot-version=v2.1) &
5 i174000.1 locus=Phvul.011G174000 ID=Phvul.011G174000.1.v2.1 annot-version=v2.1) &
6 n complex (original description: pacid=37171084 transcript=Phvul.001G110400.1 locus=Phvul.001G
7 00.1 locus=Phvul.001G123400 ID=Phvul.001G123400.1.v2.1 annot-version=v2.1) &
8 00.1 locus=Phvul.001G123400 ID=Phvul.001G123400.1.v2.1 annot-version=v2.1) &
9 cus=Phvul.001G154700 ID=Phvul.001G154700.1.v2.1 annot-version=v2.1) &
10 D)=Phvul.001G179800.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat-containing pr
11 D)=Phvul.001G179800.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat-containing pr
12 D)=Phvul.001G184000.1.v2.1 annot-version=v2.1) & Cactin OS=Arabidopsis thaliana (sp|f4i2j8|catin_
13 2 transcript=Phvul.001G259000.1 locus=Phvul.001G259000 ID=Phvul.001G259000.1.v2.1 annot-ver
14 2 transcript=Phvul.001G259000.1 locus=Phvul.001G259000 ID=Phvul.001G259000.1.v2.1 annot-ver
15)28100.1 locus=Phvul.002G028100 ID=Phvul.002G028100.1.v2.1 annot-version=v2.1) &
16)28100.1 locus=Phvul.002G028100 ID=Phvul.002G028100.1.v2.1 annot-version=v2.1) &
17 =Phvul.002G092900.2 locus=Phvul.002G092900 ID=Phvul.002G092900.2.v2.1 annot-version=v2.1) &
18 =Phvul.002G092900.2 locus=Phvul.002G092900 ID=Phvul.002G092900.2.v2.1 annot-version=v2.1) &
19 0.1 locus=Phvul.002G137100 ID=Phvul.002G137100.1.v2.1 annot-version=v2.1) &
20 i137200 ID=Phvul.002G137200.1.v2.1 annot-version=v2.1)
21 i137200 ID=Phvul.002G137200.1.v2.1 annot-version=v2.1)
22 i139900 ID=Phvul.002G139900.2.v2.1 annot-version=v2.1)
23 i139900 ID=Phvul.002G139900.2.v2.1 annot-version=v2.1)
24 i156300 ID=Phvul.002G156300.1.v2.1 annot-version=v2.1)
25 .1 locus=Phvul.003G032500 ID=Phvul.003G032500.1.v2.1 annot-version=v2.1) &
26 .1 locus=Phvul.003G032500 ID=Phvul.003G032500.1.v2.1 annot-version=v2.1) &
27 !52400.1 locus=Phvul.003G252400 ID=Phvul.003G252400.1.v2.1 annot-version=v2.1) &
28 !52400.1 locus=Phvul.003G252400 ID=Phvul.003G252400.1.v2.1 annot-version=v2.1) &
29 D)=Phvul.003G265700.1.v2.1 annot-version=v2.1) & F-box protein At4g35930 OS=Arabidopsis thaliana
30 ranscript=Phvul.003G291600.2 locus=Phvul.003G291600 ID=Phvul.003G291600.2.v2.1 annot-versic
31 ranscript=Phvul.003G291600.2 locus=Phvul.003G291600 ID=Phvul.003G291600.2.v2.1 annot-versic
32 ranscript=Phvul.003G291600.2 locus=Phvul.003G291600 ID=Phvul.003G291600.2.v2.1 annot-versic
33 ranscript=Phvul.003G291600.2 locus=Phvul.003G291600 ID=Phvul.003G291600.2.v2.1 annot-versic
34).1 locus=Phvul.004G176100 ID=Phvul.004G176100.1.v2.1 annot-version=v2.1) &
35 i001500 ID=Phvul.005G001500.2.v2.1 annot-version=v2.1)
36 i001500 ID=Phvul.005G001500.2.v2.1 annot-version=v2.1)
37 pt=Phvul.005G043500.1 locus=Phvul.005G043500 ID=Phvul.005G043500.1.v2.1 annot-version=v2.1
38 pt=Phvul.005G043500.1 locus=Phvul.005G043500 ID=Phvul.005G043500.1.v2.1 annot-version=v2.1
39 D)=Phvul.005G093400.1.v2.1 annot-version=v2.1) & Disease resistance protein RPP5 OS=Arabidopsis
40 i131700 ID=Phvul.005G131700.1.v2.1 annot-version=v2.1)
41 locus=Phvul.005G183800 ID=Phvul.005G183800.2.v2.1 annot-version=v2.1) &
42 locus=Phvul.005G183800 ID=Phvul.005G183800.2.v2.1 annot-version=v2.1) &
43 yme classification.EC_2 transferases.EC_2.3 acyltransferase(50.2.3 : 37.5) (original description: paci
44 locus=Phvul.006G131400 ID=Phvul.006G131400.1.v2.1 annot-version=v2.1) &
45 locus=Phvul.006G131400 ID=Phvul.006G131400.1.v2.1 annot-version=v2.1) &
46 classification.EC_2 transferases.EC_2.4 glycosyltransferase(50.2.4 : 134.3) (original description: paci

1 classification.EC_2 transferases.EC_2.4 glycosyltransferase(50.2.4 : 134.3) (original description: paci
2)=Phvul.007G043900.2.v2.1 annot-version=v2.1) & Protein SNOWY COTYLEDON 3 OS=Arabidopsis t
3)=Phvul.007G043900.2.v2.1 annot-version=v2.1) & Protein SNOWY COTYLEDON 3 OS=Arabidopsis t
4)=Phvul.007G043900.2.v2.1 annot-version=v2.1) & Protein SNOWY COTYLEDON 3 OS=Arabidopsis t
5)=Phvul.007G043900.2.v2.1 annot-version=v2.1) & Protein SNOWY COTYLEDON 3 OS=Arabidopsis t
6)=Phvul.007G043900.2.v2.1 annot-version=v2.1) & Protein SNOWY COTYLEDON 3 OS=Arabidopsis t
7 on.EC_1 oxidoreductases.EC_1.1 oxidoreductase acting on CH-OH group of donor(50.1.1 : 438.7) (or
8 [cus=Phvul.007G067800 ID=Phvul.007G067800.1.v2.1 annot-version=v2.1](#)) &
9)=Phvul.007G080900.2.v2.1 annot-version=v2.1) & UPF0496 protein At1g20180 OS=Arabidopsis th
10)=Phvul.007G080900.2.v2.1 annot-version=v2.1) & UPF0496 protein At1g20180 OS=Arabidopsis th
11)=Phvul.007G080900.2.v2.1 annot-version=v2.1) & UPF0496 protein At1g20180 OS=Arabidopsis th
12)=Phvul.007G080900.2.v2.1 annot-version=v2.1) & UPF0496 protein At1g20180 OS=Arabidopsis th
13)=Phvul.007G080900.2.v2.1 annot-version=v2.1) & UPF0496 protein At1g20180 OS=Arabidopsis th
14)=Phvul.007G080900.2.v2.1 annot-version=v2.1) & UPF0496 protein At1g20180 OS=Arabidopsis th
15 300.1 locus=Phvul.007G139300 ID=Phvul.007G139300.1.v2.1 annot-version=v2.1) &
16 300.1 locus=Phvul.007G139300 ID=Phvul.007G139300.1.v2.1 annot-version=v2.1) &
17 1.1 locus=Phvul.007G173400 ID=Phvul.007G173400.1.v2.1 annot-version=v2.1) &
18 is=Phvul.007G246700 ID=Phvul.007G246700.1.v2.1 annot-version=v2.1) &
19 Phvul.007G274200.1 locus=Phvul.007G274200 ID=Phvul.007G274200.1.v2.1 annot-version=v2.1) &
20 Phvul.007G274200.1 locus=Phvul.007G274200 ID=Phvul.007G274200.1.v2.1 annot-version=v2.1) &
21 Phvul.007G274200.1 locus=Phvul.007G274200 ID=Phvul.007G274200.1.v2.1 annot-version=v2.1) &
22 Phvul.007G274200.1 locus=Phvul.007G274200 ID=Phvul.007G274200.1.v2.1 annot-version=v2.1) &
23 1000.1 locus=Phvul.008G019000 ID=Phvul.008G019000.1.v2.1 annot-version=v2.1) &
24 [nscript=Phvul.008G055500.1 locus=Phvul.008G055500 ID=Phvul.008G055500.1.v2.1 annot-version=](#)
25 [nscript=Phvul.008G055500.1 locus=Phvul.008G055500 ID=Phvul.008G055500.1.v2.1 annot-version=](#)
26 [08G077000.1 locus=Phvul.008G077000 ID=Phvul.008G077000.1.v2.1 annot-version=v2.1](#)) &
27 [us=Phvul.008G114700 ID=Phvul.008G114700.1.v2.1 annot-version=v2.1](#)) &
28 [us=Phvul.008G114700 ID=Phvul.008G114700.1.v2.1 annot-version=v2.1](#)) &
29 i211500 ID=Phvul.008G211500.4.v2.1 annot-version=v2.1)
30 i211500 ID=Phvul.008G211500.4.v2.1 annot-version=v2.1)
31 i211500 ID=Phvul.008G211500.4.v2.1 annot-version=v2.1)
32 i211500 ID=Phvul.008G211500.4.v2.1 annot-version=v2.1)
33 29 transcript=Phvul.008G250000.1 locus=Phvul.008G250000 ID=Phvul.008G250000.1.v2.1 annot-ve
34 29 transcript=Phvul.008G250000.1 locus=Phvul.008G250000 ID=Phvul.008G250000.1.v2.1 annot-ve
35)=Phvul.009G086300.2.v2.1 annot-version=v2.1) & L10-interacting MYB domain-containing protein
36)=Phvul.009G086300.2.v2.1 annot-version=v2.1) & L10-interacting MYB domain-containing protein
37)=Phvul.009G086300.2.v2.1 annot-version=v2.1) & L10-interacting MYB domain-containing protein
38)=Phvul.009G086300.2.v2.1 annot-version=v2.1) & L10-interacting MYB domain-containing protein
39 09G149800.1 locus=Phvul.009G149800 ID=Phvul.009G149800.1.v2.1 annot-version=v2.1) &
40 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
41 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
42 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
43 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
44 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
45 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
46 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
47 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
48 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
49 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
50 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
51 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
52 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
53 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
54 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
55 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
56 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
57 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
58 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
59 0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &
60 ul.009G240100.1 locus=Phvul.009G240100 ID=Phvul.009G240100.1.v2.1 annot-version=v2.1) &
Phvul.011G017800 ID=Phvul.011G017800.1.v2.1 annot-version=v2.1) &

1 Phvul.011G017800 ID=Phvul.011G017800.1.v2.1 annot-version=v2.1) &
2 i100200 ID=Phvul.011G100200.2.v2.1 annot-version=v2.1)
3 i100200 ID=Phvul.011G100200.2.v2.1 annot-version=v2.1)
4 i108300 ID=Phvul.011G108300.1.v2.1 annot-version=v2.1)
5 i129700.1 locus=Phvul.011G129700 ID=Phvul.011G129700.1.v2.1 annot-version=v2.1) &
6 i129700.1 locus=Phvul.011G129700 ID=Phvul.011G129700.1.v2.1 annot-version=v2.1) &
7 O=Phvul.011G140050.2.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containing protein At4
8 O=Phvul.011G140050.2.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containing protein At4
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4 *aliana* (sp|q7xa86|zdh11_arath : 318.0)
5 *aliana* (sp|q7xa86|zdh11_arath : 318.0)
6 *aliana* (sp|q7xa86|zdh11_arath : 318.0)
7 *aliana* (sp|q7xa86|zdh11_arath : 318.0)
8 *aliana* (sp|q7xa86|zdh11_arath : 318.0)
9

10
11
12
13
14
15
16 *sion=v2.1*) &
17 *sion=v2.1*) &
18
19

20
21
22
23
24 corporation of molecular oxygen (oxygenase)(50.1.12 : 199.5) (original description: pacid=37149575
25 corporation of molecular oxygen (oxygenase)(50.1.12 : 199.5) (original description: pacid=37149575
26 corporation of molecular oxygen (oxygenase)(50.1.12 : 199.5) (original description: pacid=37149575
27 corporation of molecular oxygen (oxygenase)(50.1.12 : 199.5) (original description: pacid=37149575
28 corporation of molecular oxygen (oxygenase)(50.1.12 : 199.5) (original description: pacid=37149575
29 corporation of molecular oxygen (oxygenase)(50.1.12 : 199.5) (original description: pacid=37149575
30 corporation of molecular oxygen (oxygenase)(50.1.12 : 199.5) (original description: pacid=37149575
31 corporation of molecular oxygen (oxygenase)(50.1.12 : 199.5) (original description: pacid=37149575
32 .1.v2.1 annot-version=v2.1) &
33
34
35
36
37
38
39
40
41

42 *al OS=Arabidopsis thaliana* (sp|o64886|cox10_arath : 442.0)
43 *al OS=Arabidopsis thaliana* (sp|o64886|cox10_arath : 442.0)
44
45
46
47
48
49
50
51
52

53 *idopsis thaliana* (sp|q8gza4|cbsx6_arath : 500.0)
54
55
56
57
58
59
60

OS=Arabidopsis thaliana (sp|q9stx1|acbp3_arath : 116.0)

OS=Arabidopsis thaliana (sp|q9stx1|acbp3_arath : 116.0)

thaliana (sp|q9lka4|uba2c_arath : 175.0)

thaliana (sp|q9lka4|uba2c_arath : 175.0)

Arabidopsis thaliana (sp|a1l4v7|dcyd2_arath : 443.0)

Arabidopsis thaliana (sp|a1l4v7|dcyd2_arath : 443.0)

S=Arabidopsis thaliana (sp|q9saf0|orp1d_arath : 1151.0)

S=Arabidopsis thaliana (sp|q9saf0|orp1d_arath : 1151.0)

cript=Phvul.002G102800.2 locus=Phvul.002G102800 ID=Phvul.002G102800.2.v2.1 annot-version=v2.1

cript=Phvul.002G102800.2 locus=Phvul.002G102800 ID=Phvul.002G102800.2.v2.1 annot-version=v2.1

S=Arabidopsis thaliana (sp|q9fgd7|pub50_arath : 342.0)

S=Arabidopsis thaliana (sp|q9fgd7|pub50_arath : 342.0)

S=Arabidopsis thaliana (sp|q9fgd7|pub50_arath : 342.0)

S=Arabidopsis thaliana (sp|q9fgd7|pub50_arath : 342.0)

Arabidopsis thaliana (sp|q9sre5|y1666_arath : 119.0)

Arabidopsis thaliana (sp|q9sre5|y1666_arath : 119.0)

paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 122.3) (original description)

i261400.2.v2.1 annot-version=v2.1) &

i261400.2.v2.1 annot-version=v2.1) &

i261400.2.v2.1 annot-version=v2.1) &

i261400.2.v2.1 annot-version=v2.1) &

on=v2.1) &

on=v2.1) &

on=v2.1) &

on=v2.1) &

9600.1.v2.1 annot-version=v2.1) &

3g53700, chloroplastic OS=Arabidopsis thaliana (sp|q9lff1|pp281_arath : 948.0)

0.1.v2.1 annot-version=v2.1) &

Arabidopsis thaliana (sp|q84lh3|wex_arath : 98.6)

1
2 *Arabidopsis thaliana* (sp|q84lh3|wex_arath : 98.6)
3 2g34400 OS=*Arabidopsis thaliana* (sp|o64705|pp184_arath : 608.0)
4

5
6
7
8
9
10 *Arabidopsis thaliana* (sp|q39061|cp33_arath : 102.0)
11

12
13
14 10.1.v2.1 annot-version=v2.1) &
15 10.1.v2.1 annot-version=v2.1) &
16

17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35 *Chocarpa* (sp|b9i2j6|axep_poptr : 565.0)
36 *Chocarpa* (sp|b9i2j6|axep_poptr : 565.0)
37

38
39 1 MRL7, chloroplastic OS=*Arabidopsis thaliana* (sp|f4jlc1|mrl7_arath : 334.0)
40

41
42
43 *Na* (sp|q8rwd6|fb271_arath : 511.0)
44 *Na* (sp|q8rwd6|fb271_arath : 511.0)
45 *Na* (sp|q8rwd6|fb271_arath : 511.0)
46 *Na* (sp|q8rwd6|fb271_arath : 511.0)
47
48

49 *Arabidopsis thaliana* (sp|q9fle8|y5986_arath : 127.0)
50 *Arabidopsis thaliana* (sp|q9fle8|y5986_arath : 127.0)
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6 2.1) &

7 2.1) &
8
9
10
11
12
13
14
15

16 4g04790, mitochondrial OS=Arabidopsis thaliana (sp|q6nq81|pp304_arath : 449.0)

17 4g04790, mitochondrial OS=Arabidopsis thaliana (sp|q6nq81|pp304_arath : 449.0)

18 antia polymorpha (sp|p26863|rt01_marpo : 94.7)

19 antia polymorpha (sp|p26863|rt01_marpo : 94.7)
20
21
22
23
24
25
26

27 rtein 37 OS=Arabidopsis thaliana (sp|a2rvm8|hip37_arath : 113.0)

28 rtein 37 OS=Arabidopsis thaliana (sp|a2rvm8|hip37_arath : 113.0)
29
30
31

32 sp. japonica (sp|q6l4d2|pm19l_orysj : 166.0)

33 sp. japonica (sp|q6l4d2|pm19l_orysj : 166.0)
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53

54 rotein At1g64310 OS=Arabidopsis thaliana (sp|q9c7v5|pp104_arath : 473.0)

55 rotein At1g64310 OS=Arabidopsis thaliana (sp|q9c7v5|pp104_arath : 473.0)

56 rotein At1g64310 OS=Arabidopsis thaliana (sp|q9c7v5|pp104_arath : 473.0)
57
58
59
60

1
2
3
4
5
6
7
8 i110400 ID=Phvul.001G110400.1.v2.1 annot-version=v2.1) &
9
10
11
12
13

14 rotein At5g37570 OS=Arabidopsis thaliana (sp|q9fhr3|pp403_arath : 574.0)

15 rotein At5g37570 OS=Arabidopsis thaliana (sp|q9fhr3|pp403_arath : 574.0)

16 _arath : 759.0)

17 rsion=v2.1) &

18 rsion=v2.1) &
19
20
21
22

23 &

24 &
25
26
27
28
29
30
31
32
33
34
35
36
37
38

39 na (sp|q5xf11|fb248_arath : 202.0)

40 n=v2.1) &

41 n=v2.1) &

42 n=v2.1) &

43 n=v2.1) &
44
45
46
47
48

49 1) &

50 1) &

51 s thaliana (sp|f4jnb7|rpp5_arath : 109.0)
52
53
54
55
56

57 id=37171403 transcript=Phvul.006G098700.1 locus=Phvul.006G098700 ID=Phvul.006G098700.1.v2.
58
59
60

d=37173062 transcript=Phvul.006G208400.1 locus=Phvul.006G208400 ID=Phvul.006G208400.1.v2.

1 id=37173062 transcript=Phvul.006G208400.1 locus=Phvul.006G208400 ID=Phvul.006G208400.1.v2.
2 thaliana (sp|q8gxd9|sco3_arath : 320.0)
3 thaliana (sp|q8gxd9|sco3_arath : 320.0)
4 thaliana (sp|q8gxd9|sco3_arath : 320.0)
5 thaliana (sp|q8gxd9|sco3_arath : 320.0)
6 original description: pacid=37166204 transcript=Phvul.007G062100.1 locus=Phvul.007G062100 ID=Phvul.007G062100.1.v2.
7 thaliana (sp|q6dye5|u496k_arath : 151.0)
8 thaliana (sp|q6dye5|u496k_arath : 151.0)
9 thaliana (sp|q6dye5|u496k_arath : 151.0)
10 thaliana (sp|q6dye5|u496k_arath : 151.0)

11 =v2.1) &
12 =v2.1) &
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36

37 version=v2.1) &
38 version=v2.1) &
39 OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
40 OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
41 OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
42 OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
43 OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
44 OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

4g04790, mitochondrial OS=Arabidopsis thaliana (sp|q6nq81|pp304_arath : 558.0)
4g04790, mitochondrial OS=Arabidopsis thaliana (sp|q6nq81|pp304_arath : 558.0)

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

2.1) &
2.1) &

ion: pacid=37145792 transcript=Phvul.003G013200.2 locus=Phvul.003G013200 ID=Phvul.003G0132

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

.1 annot-version=v2.1) &

.1 annot-version=v2.1) &

1
2 .1 annot-version=v2.1) &
3
4
5

6
7
8 hvul.007G062100.1.v2.1 annot-version=v2.1) &
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

·sion=v2.1) &
·sion=v2.1) &
·sion=v2.1) &
·sion=v2.1) &
·sion=v2.1) &
·sion=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

200.2.v2.1 annot-version=v2.1) &

Do not distribute

| | miRNA_Acc. | Target_Acc. | Expectation | UPE\$ | miRNA_start | miRNA_end |
|----|--------------|--------------------|-------------|-------|-------------|-----------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ggaaucuugauξ | Phvul.001G174400.1 | 0.5 | -1 | 1 | 21 |
| 4 | ggaaucuugauξ | Phvul.001G174400.1 | 0.5 | -1 | 1 | 21 |
| 5 | ggaaucuugauξ | Phvul.001G174400.1 | 0.5 | -1 | 1 | 21 |
| 6 | ggaaucuugauξ | Phvul.001G174400.1 | 0.5 | -1 | 1 | 21 |
| 7 | ggaaucuugauξ | Phvul.001G174400.1 | 0.5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξ | Phvul.001G174400.1 | 0.5 | -1 | 1 | 21 |
| 9 | ggaaucuugauξ | Phvul.001G174400.1 | 0.5 | -1 | 1 | 21 |
| 10 | ggaaucuugauξ | Phvul.001G174400.1 | 0.5 | -1 | 1 | 21 |
| 11 | ggaaucuugauξ | Phvul.001G174400.1 | 0.5 | -1 | 1 | 21 |
| 12 | ggaaucuugauξ | Phvul.001G174400.1 | 0.5 | -1 | 1 | 21 |
| 13 | ggaaucuugauξ | Phvul.001G174400.1 | 0.5 | -1 | 1 | 21 |
| 14 | ggaaucuugauξ | Phvul.001G174400.1 | 0.5 | -1 | 1 | 21 |
| 15 | ggaaucuugauξ | Phvul.001G174400.1 | 0.5 | -1 | 1 | 21 |
| 16 | ggaaucuugauξ | Phvul.001G174400.1 | 0.5 | -1 | 1 | 24 |
| 17 | ggaaucuugauξ | Phvul.002G016900.1 | 0.5 | -1 | 1 | 21 |
| 18 | ggaaucuugauξ | Phvul.002G016900.1 | 0.5 | -1 | 1 | 21 |
| 19 | ggaaucuugauξ | Phvul.002G016900.1 | 0.5 | -1 | 1 | 21 |
| 20 | ggaaucuugauξ | Phvul.002G016900.1 | 0.5 | -1 | 1 | 21 |
| 21 | ggaaucuugauξ | Phvul.002G016900.1 | 0.5 | -1 | 1 | 21 |
| 22 | ggaaucuugauξ | Phvul.002G016900.1 | 0.5 | -1 | 1 | 21 |
| 23 | ggaaucuugauξ | Phvul.002G016900.1 | 0.5 | -1 | 1 | 21 |
| 24 | ggaaucuugauξ | Phvul.002G016900.1 | 0.5 | -1 | 1 | 21 |
| 25 | ggaaucuugauξ | Phvul.002G016900.1 | 0.5 | -1 | 1 | 21 |
| 26 | ggaaucuugauξ | Phvul.002G016900.1 | 0.5 | -1 | 1 | 21 |
| 27 | ggaaucuugauξ | Phvul.002G016900.1 | 0.5 | -1 | 1 | 21 |
| 28 | ggaaucuugauξ | Phvul.002G016900.1 | 0.5 | -1 | 1 | 21 |
| 29 | ggaaucuugauξ | Phvul.002G016900.1 | 0.5 | -1 | 1 | 21 |
| 30 | ggaaucuugauξ | Phvul.002G016900.1 | 0.5 | -1 | 1 | 21 |
| 31 | ggaaucuugauξ | Phvul.002G016900.1 | 0.5 | -1 | 1 | 24 |
| 32 | ggaaucuugauξ | Phvul.003G241900.1 | 0.5 | -1 | 1 | 21 |
| 33 | ggaaucuugauξ | Phvul.003G241900.1 | 0.5 | -1 | 1 | 21 |
| 34 | ggaaucuugauξ | Phvul.003G241900.1 | 0.5 | -1 | 1 | 21 |
| 35 | ggaaucuugauξ | Phvul.003G241900.1 | 0.5 | -1 | 1 | 21 |
| 36 | ggaaucuugauξ | Phvul.003G241900.1 | 0.5 | -1 | 1 | 21 |
| 37 | ggaaucuugauξ | Phvul.003G241900.1 | 0.5 | -1 | 1 | 21 |
| 38 | ggaaucuugauξ | Phvul.003G241900.1 | 0.5 | -1 | 1 | 21 |
| 39 | ggaaucuugauξ | Phvul.003G241900.1 | 0.5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξ | Phvul.003G241900.1 | 0.5 | -1 | 1 | 21 |
| 41 | ggaaucuugauξ | Phvul.003G241900.1 | 0.5 | -1 | 1 | 21 |
| 42 | ggaaucuugauξ | Phvul.003G241900.1 | 0.5 | -1 | 1 | 21 |
| 43 | ggaaucuugauξ | Phvul.003G241900.1 | 0.5 | -1 | 1 | 21 |
| 44 | ggaaucuugauξ | Phvul.003G241900.1 | 0.5 | -1 | 1 | 21 |
| 45 | ggaaucuugauξ | Phvul.003G241900.1 | 0.5 | -1 | 1 | 24 |
| 46 | ggaaucuugauξ | Phvul.011G071100.2 | 1 | -1 | 1 | 21 |
| 47 | ggaaucuugauξ | Phvul.011G071100.1 | 1 | -1 | 1 | 21 |
| 48 | ggaaucuugauξ | Phvul.011G071100.1 | 1 | -1 | 1 | 21 |
| 49 | ggaaucuugauξ | Phvul.011G071100.2 | 1 | -1 | 1 | 21 |
| 50 | ggaaucuugauξ | Phvul.011G071100.2 | 1 | -1 | 1 | 21 |
| 51 | ggaaucuugauξ | Phvul.011G071100.1 | 1 | -1 | 1 | 21 |
| 52 | ggaaucuugauξ | Phvul.011G071100.2 | 1 | -1 | 1 | 21 |
| 53 | ggaaucuugauξ | Phvul.011G071100.1 | 1 | -1 | 1 | 21 |
| 54 | ggaaucuugauξ | Phvul.011G071100.1 | 1 | -1 | 1 | 21 |
| 55 | ggaaucuugauξ | Phvul.011G071100.2 | 1 | -1 | 1 | 21 |
| 56 | ggaaucuugauξ | Phvul.011G071100.1 | 1 | -1 | 1 | 21 |
| 57 | ggaaucuugauξ | Phvul.011G071100.2 | 1 | -1 | 1 | 21 |
| 58 | ggaaucuugauξ | Phvul.011G071100.2 | 1 | -1 | 1 | 21 |
| 59 | ggaaucuugauξ | Phvul.011G071100.1 | 1 | -1 | 1 | 21 |
| 60 | ggaaucuugauξ | Phvul.011G071100.2 | 1 | -1 | 1 | 21 |
| | ggaaucuugauξ | Phvul.011G071100.1 | 1 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.011G071100.2 | 1 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.011G071100.1 | 1 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.011G071100.2 | 1 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.011G071100.1 | 1 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.011G071100.2 | 1 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.011G071100.1 | 1 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.011G071100.2 | 1 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.011G071100.1 | 1 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.011G071100.2 | 1 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.011G071100.1 | 1 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.011G071100.2 | 1 | -1 | 1 | 24 |
| 13 | ggaaucuugauξPhvul.011G071100.1 | 1 | -1 | 1 | 24 |
| 14 | ggaaucuugauξPhvul.L000308.2 | 1 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.L000308.1 | 1 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.L000308.2 | 1 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.L000308.1 | 1 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.L000308.2 | 1 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.L000308.1 | 1 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.L000308.2 | 1 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.L000308.1 | 1 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.L000308.2 | 1 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.L000308.1 | 1 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.L000308.2 | 1 | -1 | 1 | 21 |
| 25 | ggaaucuugauξPhvul.L000308.1 | 1 | -1 | 1 | 21 |
| 26 | ggaaucuugauξPhvul.L000308.2 | 1 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.L000308.1 | 1 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.L000308.2 | 1 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.L000308.1 | 1 | -1 | 1 | 21 |
| 30 | ggaaucuugauξPhvul.L000308.2 | 1 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.L000308.1 | 1 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.L000308.2 | 1 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.L000308.1 | 1 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.L000308.2 | 1 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.L000308.1 | 1 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.L000308.2 | 1 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.L000308.1 | 1 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.L000308.2 | 1 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.L000308.1 | 1 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.L000308.2 | 1 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.L000308.1 | 1 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.L000308.2 | 1 | -1 | 1 | 24 |
| 43 | ggaaucuugauξPhvul.L000308.1 | 1 | -1 | 1 | 24 |
| 44 | uggaaucuugaI Phvul.001G174400.1 | 1.5 | -1 | 1 | 22 |
| 45 | uggaaucuugaI Phvul.002G016900.1 | 1.5 | -1 | 1 | 22 |
| 46 | uggaaucuugaI Phvul.003G241900.1 | 1.5 | -1 | 1 | 22 |
| 47 | ggaaucuugauξPhvul.005G132300.2 | 1.5 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.005G132300.1 | 1.5 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.005G132300.2 | 1.5 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.005G132300.1 | 1.5 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.005G132300.2 | 1.5 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.005G132300.1 | 1.5 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.005G132300.2 | 1.5 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.005G132300.1 | 1.5 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.005G132300.2 | 1.5 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.005G132300.1 | 1.5 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.005G132300.2 | 1.5 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.005G132300.1 | 1.5 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.005G132300.2 | 1.5 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.005G132300.1 | 1.5 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.005G132300.2 | 1.5 | -1 | 1 | 21 |

| | | | | | |
|----|--------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.005G132300.1 | 1.5 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.005G132300.2 | 1.5 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.005G132300.1 | 1.5 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.005G132300.2 | 1.5 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.005G132300.1 | 1.5 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.005G132300.2 | 1.5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.005G132300.1 | 1.5 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.005G132300.2 | 1.5 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.005G132300.1 | 1.5 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.005G132300.2 | 1.5 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.005G132300.1 | 1.5 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.005G132300.2 | 1.5 | -1 | 1 | 24 |
| 14 | ggaaucuugauξPhvul.005G132300.1 | 1.5 | -1 | 1 | 24 |
| 15 | ggaaucuugauξPhvul.007G240200.1 | 1.5 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.007G240200.1 | 1.5 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.007G240200.1 | 1.5 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.007G240200.1 | 1.5 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.007G240200.1 | 1.5 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.007G240200.1 | 1.5 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.007G240200.1 | 1.5 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.007G240200.1 | 1.5 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.007G240200.1 | 1.5 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.007G240200.1 | 1.5 | -1 | 1 | 21 |
| 25 | ggaaucuugauξPhvul.007G240200.1 | 1.5 | -1 | 1 | 21 |
| 26 | ggaaucuugauξPhvul.007G240200.1 | 1.5 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.007G240200.1 | 1.5 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.007G240200.1 | 1.5 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.007G240200.1 | 1.5 | -1 | 1 | 24 |
| 30 | ggaaucuugauξPhvul.011G082801.1 | 1.5 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.011G082801.1 | 1.5 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.011G082801.1 | 1.5 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.011G082801.1 | 1.5 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.011G082801.1 | 1.5 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.011G082801.1 | 1.5 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.011G082801.1 | 1.5 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.011G082801.1 | 1.5 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.011G082801.1 | 1.5 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.011G082801.1 | 1.5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.011G082801.1 | 1.5 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.011G082801.1 | 1.5 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.011G082801.1 | 1.5 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.011G082801.1 | 1.5 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.011G082801.1 | 1.5 | -1 | 1 | 24 |
| 45 | ggaaucuugauξPhvul.001G233200.2 | 2 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.001G233200.1 | 2 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.001G233200.2 | 2 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.001G233200.1 | 2 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.001G233200.2 | 2 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.001G233200.1 | 2 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.001G233200.2 | 2 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.001G233200.1 | 2 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.001G233200.2 | 2 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.001G233200.1 | 2 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.001G233200.2 | 2 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.001G233200.1 | 2 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.001G233200.2 | 2 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.001G233200.1 | 2 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.001G233200.2 | 2 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.001G233200.1 | 2 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.001G233200.2 | 2 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.001G233200.1 | 2 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.001G233200.2 | 2 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.001G233200.1 | 2 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.001G233200.2 | 2 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.001G233200.2 | 2 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.001G233200.1 | 2 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.001G233200.2 | 2 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.001G233200.1 | 2 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.001G233200.1 | 2 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.001G233200.2 | 2 | -1 | 1 | 24 |
| 12 | ggaaucuugauξPhvul.001G233200.1 | 2 | -1 | 1 | 24 |
| 13 | ggaaucuugauξPhvul.001G233200.1 | 2 | -1 | 1 | 24 |
| 14 | uggaaucuugaI Phvul.011G071100.2 | 2 | -1 | 1 | 22 |
| 15 | uggaaucuugaI Phvul.011G071100.1 | 2 | -1 | 1 | 22 |
| 16 | uggaaucuugaI Phvul.L000308.2 | 2 | -1 | 1 | 22 |
| 17 | uggaaucuugaI Phvul.L000308.1 | 2 | -1 | 1 | 22 |
| 18 | uggaaucuugaI Phvul.L000308.1 | 2 | -1 | 1 | 22 |
| 19 | uggaaucuugaI Phvul.003G111500.1 | 2.5 | -1 | 1 | 22 |
| 20 | uggaaucuugaI Phvul.005G118700.1 | 2.5 | -1 | 1 | 22 |
| 21 | uggaaucuugaI Phvul.005G118700.1 | 2.5 | -1 | 1 | 22 |
| 22 | uggaaucuugaI Phvul.008G058700.2 | 2.5 | -1 | 1 | 22 |
| 23 | uggaaucuugaI Phvul.008G058700.1 | 2.5 | -1 | 1 | 22 |
| 24 | uggaaucuugaI Phvul.011G150100.1 | 2.5 | -1 | 1 | 22 |
| 25 | uggaaucuugaI Phvul.011G150100.1 | 2.5 | -1 | 1 | 22 |
| 26 | ggaaucuugauξPhvul.001G033700.1 | 3 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.001G033700.2 | 3 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.001G033700.1 | 3 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.001G033700.1 | 3 | -1 | 1 | 21 |
| 30 | ggaaucuugauξPhvul.001G033700.2 | 3 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.001G033700.1 | 3 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.001G033700.2 | 3 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.001G033700.1 | 3 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.001G033700.1 | 3 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.001G033700.2 | 3 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.001G033700.1 | 3 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.001G033700.1 | 3 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.001G033700.2 | 3 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.001G033700.1 | 3 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.001G033700.2 | 3 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.001G033700.1 | 3 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.001G033700.1 | 3 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.001G033700.2 | 3 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.001G033700.1 | 3 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.001G033700.2 | 3 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.001G033700.1 | 3 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.001G033700.1 | 3 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.001G033700.2 | 3 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.001G033700.1 | 3 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.001G033700.1 | 3 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.001G033700.2 | 3 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.001G033700.1 | 3 | -1 | 1 | 24 |
| 53 | ggaaucuugauξPhvul.001G033700.2 | 3 | -1 | 1 | 24 |
| 54 | ggaaucuugauξPhvul.001G033700.2 | 3 | -1 | 1 | 24 |
| 55 | ggaaucuugauξPhvul.001G172501.1 | 3 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.001G172501.1 | 3 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.001G172501.1 | 3 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.001G172501.1 | 3 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.001G172501.1 | 3 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.001G172501.1 | 3 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.001G172501.1 | 3 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.001G172501.1 | 3 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.001G172501.1 | 3 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.001G172501.1 | 3 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.001G172501.1 | 3 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.001G172501.1 | 3 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.001G172501.1 | 3 | -1 | 1 | 24 |
| 8 | uggaaucuugaI Phvul.001G172501.1 | 3 | -1 | 1 | 22 |
| 9 | | | | | |
| 10 | uggaaucuugaI Phvul.001G212400.1 | 3 | -1 | 1 | 22 |
| 11 | uggaaucuugaI Phvul.001G212400.2 | 3 | -1 | 1 | 22 |
| 12 | ggaaucuugauξPhvul.002G012700.1 | 3 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.002G012700.1 | 3 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.002G012700.1 | 3 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.002G012700.1 | 3 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.002G012700.1 | 3 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.002G012700.1 | 3 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.002G012700.1 | 3 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.002G012700.1 | 3 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.002G012700.1 | 3 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.002G012700.1 | 3 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.002G012700.1 | 3 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.002G012700.1 | 3 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.002G012700.1 | 3 | -1 | 1 | 21 |
| 25 | uggaaucuugaI Phvul.002G197200.1 | 3 | -1 | 1 | 22 |
| 26 | uggaaucuugaI Phvul.002G218300.1 | 3 | -1 | 1 | 22 |
| 27 | uggaaucuugaI Phvul.002G330500.2 | 3 | -1 | 1 | 22 |
| 28 | uggaaucuugaI Phvul.002G330500.1 | 3 | -1 | 1 | 22 |
| 29 | uggaaucuugaI Phvul.003G262400.1 | 3 | -1 | 1 | 22 |
| 30 | uggaaucuugaI Phvul.003G262500.1 | 3 | -1 | 1 | 22 |
| 31 | ggaaucuugauξPhvul.005G030900.1 | 3 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.005G030900.1 | 3 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.005G030900.1 | 3 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.005G030900.1 | 3 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.005G030900.1 | 3 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.005G030900.1 | 3 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.005G030900.1 | 3 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.005G030900.1 | 3 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.005G030900.1 | 3 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.005G030900.1 | 3 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.005G030900.1 | 3 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.005G030900.1 | 3 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.005G030900.1 | 3 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.005G030900.1 | 3 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.005G030900.1 | 3 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.005G030900.1 | 3 | -1 | 1 | 24 |
| 47 | uggaaucuugaI Phvul.005G030900.1 | 3 | -1 | 1 | 22 |
| 48 | uggaaucuugaI Phvul.005G088700.3 | 3 | -1 | 1 | 22 |
| 49 | uggaaucuugaI Phvul.005G088700.2 | 3 | -1 | 1 | 22 |
| 50 | uggaaucuugaI Phvul.005G088700.1 | 3 | -1 | 1 | 22 |
| 51 | uggaaucuugaI Phvul.005G088800.1 | 3 | -1 | 1 | 22 |
| 52 | ggaaucuugauξPhvul.005G131000.1 | 3 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.005G131000.1 | 3 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.005G131000.1 | 3 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.005G131000.1 | 3 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.005G131000.1 | 3 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.005G131000.1 | 3 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.005G131000.1 | 3 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.005G131000.1 | 3 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.005G131000.1 | 3 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.005G131000.1 | 3 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.005G131000.1 | 3 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.005G131000.1 | 3 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.005G131000.1 | 3 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.005G131000.1 | 3 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.005G131000.1 | 3 | -1 | 1 | 24 |
| 8 | uggaaucuugaI Phvul.005G131000.1 | 3 | -1 | 1 | 22 |
| 9 | uggaaucuugaI Phvul.005G132300.2 | 3 | -1 | 1 | 22 |
| 10 | uggaaucuugaI Phvul.005G132300.1 | 3 | -1 | 1 | 22 |
| 11 | ggaaucuugauξPhvul.006G137900.1 | 3 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.006G137900.1 | 3 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.006G137900.1 | 3 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.006G137900.1 | 3 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.006G137900.1 | 3 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.006G137900.1 | 3 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.006G137900.1 | 3 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.006G137900.1 | 3 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.006G137900.1 | 3 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.006G137900.1 | 3 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.006G137900.1 | 3 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.006G137900.1 | 3 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.006G137900.1 | 3 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.006G137900.1 | 3 | -1 | 1 | 21 |
| 25 | ggaaucuugauξPhvul.006G137900.1 | 3 | -1 | 1 | 24 |
| 26 | ggaaucuugauξPhvul.006G137900.1 | 3 | -1 | 1 | 24 |
| 27 | uggaaucuugaI Phvul.007G240200.1 | 3 | -1 | 1 | 22 |
| 28 | ggaaucuugauξPhvul.008G033900.2 | 3 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.008G033900.3 | 3 | -1 | 1 | 21 |
| 30 | ggaaucuugauξPhvul.008G033900.1 | 3 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.008G033900.2 | 3 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.008G033900.3 | 3 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.008G033900.1 | 3 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.008G033900.2 | 3 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.008G033900.3 | 3 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.008G033900.1 | 3 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.008G033900.2 | 3 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.008G033900.3 | 3 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.008G033900.1 | 3 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.008G033900.2 | 3 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.008G033900.3 | 3 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.008G033900.1 | 3 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.008G033900.2 | 3 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.008G033900.3 | 3 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.008G033900.1 | 3 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.008G033900.2 | 3 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.008G033900.3 | 3 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.008G033900.1 | 3 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.008G033900.2 | 3 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.008G033900.3 | 3 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.008G033900.1 | 3 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.008G033900.2 | 3 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.008G033900.3 | 3 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.008G033900.1 | 3 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.008G033900.2 | 3 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.008G033900.3 | 3 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.008G033900.1 | 3 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.008G033900.2 | 3 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.008G033900.3 | 3 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.008G033900.1 | 3 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.008G033900.2 | 3 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.008G033900.3 | 3 | -1 | 1 | 21 |

| | | | | | | |
|----|--------------|--------------------|-----|----|---|----|
| 1 | | | | | | |
| 2 | ggaaucuugauξ | Phvul.008G033900.1 | 3 | -1 | 1 | 21 |
| 3 | ggaaucuugauξ | Phvul.008G033900.2 | 3 | -1 | 1 | 21 |
| 4 | ggaaucuugauξ | Phvul.008G033900.3 | 3 | -1 | 1 | 21 |
| 5 | | | | | | |
| 6 | ggaaucuugauξ | Phvul.008G033900.1 | 3 | -1 | 1 | 21 |
| 7 | ggaaucuugauξ | Phvul.008G033900.2 | 3 | -1 | 1 | 24 |
| 8 | ggaaucuugauξ | Phvul.008G033900.3 | 3 | -1 | 1 | 24 |
| 9 | | | | | | |
| 10 | ggaaucuugauξ | Phvul.008G033900.1 | 3 | -1 | 1 | 24 |
| 11 | uggaaucuugaτ | Phvul.008G033900.2 | 3 | -1 | 1 | 22 |
| 12 | uggaaucuugaτ | Phvul.008G033900.3 | 3 | -1 | 1 | 22 |
| 13 | | | | | | |
| 14 | uggaaucuugaτ | Phvul.008G033900.1 | 3 | -1 | 1 | 22 |
| 15 | ggaaucuugauξ | Phvul.009G130700.1 | 3 | -1 | 1 | 21 |
| 16 | ggaaucuugauξ | Phvul.009G130700.1 | 3 | -1 | 1 | 21 |
| 17 | | | | | | |
| 18 | ggaaucuugauξ | Phvul.009G130700.1 | 3 | -1 | 1 | 21 |
| 19 | ggaaucuugauξ | Phvul.009G130700.1 | 3 | -1 | 1 | 21 |
| 20 | ggaaucuugauξ | Phvul.009G130700.1 | 3 | -1 | 1 | 21 |
| 21 | | | | | | |
| 22 | ggaaucuugauξ | Phvul.009G130700.1 | 3 | -1 | 1 | 21 |
| 23 | ggaaucuugauξ | Phvul.009G130700.1 | 3 | -1 | 1 | 21 |
| 24 | ggaaucuugauξ | Phvul.009G130700.1 | 3 | -1 | 1 | 21 |
| 25 | | | | | | |
| 26 | ggaaucuugauξ | Phvul.009G130700.1 | 3 | -1 | 1 | 21 |
| 27 | ggaaucuugauξ | Phvul.009G130700.1 | 3 | -1 | 1 | 21 |
| 28 | ggaaucuugauξ | Phvul.009G130700.1 | 3 | -1 | 1 | 24 |
| 29 | | | | | | |
| 30 | uggaaucuugaτ | Phvul.009G249300.1 | 3 | -1 | 1 | 22 |
| 31 | uggaaucuugaτ | Phvul.011G082801.1 | 3 | -1 | 1 | 22 |
| 32 | uggaaucuugaτ | Phvul.011G150950.1 | 3 | -1 | 1 | 22 |
| 33 | | | | | | |
| 34 | uggaaucuugaτ | Phvul.011G152100.3 | 3 | -1 | 1 | 22 |
| 35 | uggaaucuugaτ | Phvul.011G152100.1 | 3 | -1 | 1 | 22 |
| 36 | uggaaucuugaτ | Phvul.011G152300.3 | 3 | -1 | 1 | 22 |
| 37 | uggaaucuugaτ | Phvul.011G152300.2 | 3 | -1 | 1 | 22 |
| 38 | | | | | | |
| 39 | uggaaucuugaτ | Phvul.011G152300.1 | 3 | -1 | 1 | 22 |
| 40 | uggaaucuugaτ | Phvul.011G152400.1 | 3 | -1 | 1 | 22 |
| 41 | | | | | | |
| 42 | uggaaucuugaτ | Phvul.011G168400.2 | 3 | -1 | 1 | 22 |
| 43 | uggaaucuugaτ | Phvul.001G033700.1 | 3.5 | -1 | 1 | 22 |
| 44 | uggaaucuugaτ | Phvul.001G033700.2 | 3.5 | -1 | 1 | 22 |
| 45 | | | | | | |
| 46 | ggaaucuugauξ | Phvul.001G187200.1 | 3.5 | -1 | 1 | 21 |
| 47 | ggaaucuugauξ | Phvul.001G187200.1 | 3.5 | -1 | 1 | 21 |
| 48 | ggaaucuugauξ | Phvul.001G187200.1 | 3.5 | -1 | 1 | 21 |
| 49 | ggaaucuugauξ | Phvul.001G187200.1 | 3.5 | -1 | 1 | 21 |
| 50 | | | | | | |
| 51 | ggaaucuugauξ | Phvul.001G187200.1 | 3.5 | -1 | 1 | 21 |
| 52 | ggaaucuugauξ | Phvul.001G187200.1 | 3.5 | -1 | 1 | 21 |
| 53 | ggaaucuugauξ | Phvul.001G187200.1 | 3.5 | -1 | 1 | 21 |
| 54 | | | | | | |
| 55 | ggaaucuugauξ | Phvul.001G187200.1 | 3.5 | -1 | 1 | 21 |
| 56 | ggaaucuugauξ | Phvul.001G187200.1 | 3.5 | -1 | 1 | 21 |
| 57 | ggaaucuugauξ | Phvul.001G187200.1 | 3.5 | -1 | 1 | 21 |
| 58 | | | | | | |
| 59 | ggaaucuugauξ | Phvul.001G187200.1 | 3.5 | -1 | 1 | 24 |
| 60 | uggaaucuugaτ | Phvul.001G187200.1 | 3.5 | -1 | 1 | 22 |
| | uggaaucuugaτ | Phvul.001G233200.2 | 3.5 | -1 | 1 | 22 |

| | | | | | |
|----|--------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggaaucuuga Phvul.001G233200.1 | 3.5 | -1 | 1 | 22 |
| 3 | uggaaucuuga Phvul.002G012700.1 | 3.5 | -1 | 1 | 22 |
| 4 | ggaaucuuga Phvul.002G083700.1 | 3.5 | -1 | 1 | 21 |
| 5 | ggaaucuuga Phvul.002G083700.1 | 3.5 | -1 | 1 | 21 |
| 6 | ggaaucuuga Phvul.002G083700.1 | 3.5 | -1 | 1 | 21 |
| 7 | ggaaucuuga Phvul.002G083700.1 | 3.5 | -1 | 1 | 21 |
| 8 | ggaaucuuga Phvul.002G083700.1 | 3.5 | -1 | 1 | 21 |
| 9 | ggaaucuuga Phvul.002G083700.1 | 3.5 | -1 | 1 | 21 |
| 10 | ggaaucuuga Phvul.002G083700.1 | 3.5 | -1 | 1 | 21 |
| 11 | ggaaucuuga Phvul.002G083700.1 | 3.5 | -1 | 1 | 21 |
| 12 | ggaaucuuga Phvul.002G083700.1 | 3.5 | -1 | 1 | 21 |
| 13 | ggaaucuuga Phvul.002G083700.1 | 3.5 | -1 | 1 | 21 |
| 14 | ggaaucuuga Phvul.002G083700.1 | 3.5 | -1 | 1 | 21 |
| 15 | ggaaucuuga Phvul.002G083700.1 | 3.5 | -1 | 1 | 21 |
| 16 | ggaaucuuga Phvul.002G083700.1 | 3.5 | -1 | 1 | 21 |
| 17 | ggaaucuuga Phvul.002G083700.1 | 3.5 | -1 | 1 | 21 |
| 18 | ggaaucuuga Phvul.002G276700.3 | 3.5 | -1 | 1 | 21 |
| 19 | ggaaucuuga Phvul.002G276700.2 | 3.5 | -1 | 1 | 21 |
| 20 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 21 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 22 | ggaaucuuga Phvul.002G276700.3 | 3.5 | -1 | 1 | 21 |
| 23 | ggaaucuuga Phvul.002G276700.2 | 3.5 | -1 | 1 | 21 |
| 24 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 25 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 26 | ggaaucuuga Phvul.002G276700.3 | 3.5 | -1 | 1 | 21 |
| 27 | ggaaucuuga Phvul.002G276700.2 | 3.5 | -1 | 1 | 21 |
| 28 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 29 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 30 | ggaaucuuga Phvul.002G276700.3 | 3.5 | -1 | 1 | 21 |
| 31 | ggaaucuuga Phvul.002G276700.2 | 3.5 | -1 | 1 | 21 |
| 32 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 33 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 34 | ggaaucuuga Phvul.002G276700.3 | 3.5 | -1 | 1 | 21 |
| 35 | ggaaucuuga Phvul.002G276700.2 | 3.5 | -1 | 1 | 21 |
| 36 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 37 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 38 | ggaaucuuga Phvul.002G276700.3 | 3.5 | -1 | 1 | 21 |
| 39 | ggaaucuuga Phvul.002G276700.2 | 3.5 | -1 | 1 | 21 |
| 40 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 41 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 42 | ggaaucuuga Phvul.002G276700.3 | 3.5 | -1 | 1 | 21 |
| 43 | ggaaucuuga Phvul.002G276700.2 | 3.5 | -1 | 1 | 21 |
| 44 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 45 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 46 | ggaaucuuga Phvul.002G276700.3 | 3.5 | -1 | 1 | 21 |
| 47 | ggaaucuuga Phvul.002G276700.2 | 3.5 | -1 | 1 | 21 |
| 48 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 49 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 50 | ggaaucuuga Phvul.002G276700.3 | 3.5 | -1 | 1 | 21 |
| 51 | ggaaucuuga Phvul.002G276700.2 | 3.5 | -1 | 1 | 21 |
| 52 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 53 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 54 | ggaaucuuga Phvul.002G276700.3 | 3.5 | -1 | 1 | 21 |
| 55 | ggaaucuuga Phvul.002G276700.2 | 3.5 | -1 | 1 | 21 |
| 56 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 57 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 21 |
| 58 | ggaaucuuga Phvul.002G276700.3 | 3.5 | -1 | 1 | 24 |
| 59 | ggaaucuuga Phvul.002G276700.2 | 3.5 | -1 | 1 | 24 |
| 60 | ggaaucuuga Phvul.002G276700.1 | 3.5 | -1 | 1 | 24 |
| | ggaaucuuga Phvul.002G313200.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|--------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.002G313200.1 | 3.5 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.002G313200.1 | 3.5 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.002G313200.1 | 3.5 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.002G313200.1 | 3.5 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.002G313200.1 | 3.5 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.002G313200.1 | 3.5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.002G313200.1 | 3.5 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.002G313200.1 | 3.5 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.002G313200.1 | 3.5 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.002G313200.1 | 3.5 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.002G313200.1 | 3.5 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.002G313200.1 | 3.5 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.003G053000.1 | 3.5 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.003G053000.1 | 3.5 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.003G053000.1 | 3.5 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.003G053000.1 | 3.5 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.003G053000.1 | 3.5 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.003G053000.1 | 3.5 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.003G053000.1 | 3.5 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.003G053000.1 | 3.5 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.003G053000.1 | 3.5 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.003G053000.1 | 3.5 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.003G053000.1 | 3.5 | -1 | 1 | 21 |
| 25 | ggaaucuugauξPhvul.003G053000.1 | 3.5 | -1 | 1 | 21 |
| 26 | ggaaucuugauξPhvul.003G053000.1 | 3.5 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.003G053000.1 | 3.5 | -1 | 1 | 24 |
| 28 | ggaaucuugauξPhvul.003G119100.2 | 3.5 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.003G119100.2 | 3.5 | -1 | 1 | 21 |
| 30 | ggaaucuugauξPhvul.003G119100.2 | 3.5 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.003G119100.2 | 3.5 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.003G119100.2 | 3.5 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.003G119100.2 | 3.5 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.003G119100.2 | 3.5 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.003G119100.2 | 3.5 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.003G119100.2 | 3.5 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.003G119100.2 | 3.5 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.003G119100.2 | 3.5 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.003G119100.2 | 3.5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.003G119100.2 | 3.5 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.003G119100.2 | 3.5 | -1 | 1 | 24 |
| 42 | ggaaucuugauξPhvul.003G119100.2 | 3.5 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.003G237100.1 | 3.5 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.003G237100.1 | 3.5 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.003G237100.1 | 3.5 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.003G237100.1 | 3.5 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.003G237100.1 | 3.5 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.003G237100.1 | 3.5 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.003G237100.1 | 3.5 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.003G237100.1 | 3.5 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.003G237100.1 | 3.5 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.003G237100.1 | 3.5 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.003G237100.1 | 3.5 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.003G237100.1 | 3.5 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.003G237100.1 | 3.5 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.003G262400.1 | 3.5 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.003G262400.1 | 3.5 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.003G262400.1 | 3.5 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.003G262400.1 | 3.5 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.003G262400.1 | 3.5 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.003G262400.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.003G262400.1 | 3.5 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.003G262400.1 | 3.5 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.003G262400.1 | 3.5 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.003G262400.1 | 3.5 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.003G262400.1 | 3.5 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.003G262400.1 | 3.5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.003G262500.1 | 3.5 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.003G262500.1 | 3.5 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.003G262500.1 | 3.5 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.003G262500.1 | 3.5 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.003G262500.1 | 3.5 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.003G262500.1 | 3.5 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.003G262500.1 | 3.5 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.003G262500.1 | 3.5 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.003G262500.1 | 3.5 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.003G262500.1 | 3.5 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.003G262500.1 | 3.5 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.003G262500.1 | 3.5 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.003G262500.1 | 3.5 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.003G262500.1 | 3.5 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.005G118700.1 | 3.5 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.005G118700.1 | 3.5 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.005G118700.1 | 3.5 | -1 | 1 | 21 |
| 25 | ggaaucuugauξPhvul.005G118700.1 | 3.5 | -1 | 1 | 21 |
| 26 | ggaaucuugauξPhvul.005G118700.1 | 3.5 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.005G118700.1 | 3.5 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.005G118700.1 | 3.5 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.005G118700.1 | 3.5 | -1 | 1 | 21 |
| 30 | ggaaucuugauξPhvul.005G118700.1 | 3.5 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.005G118700.1 | 3.5 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.005G118700.1 | 3.5 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.005G118700.1 | 3.5 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.005G118700.1 | 3.5 | -1 | 1 | 21 |
| 35 | uggaaucuugaI Phvul.006G136700.3 | 3.5 | -1 | 1 | 22 |
| 36 | uggaaucuugaI Phvul.006G136700.1 | 3.5 | -1 | 1 | 22 |
| 37 | ggaaucuugauξPhvul.006G151200.1 | 3.5 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.006G151200.1 | 3.5 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.006G151200.1 | 3.5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.006G151200.1 | 3.5 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.006G151200.1 | 3.5 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.006G151200.1 | 3.5 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.006G151200.1 | 3.5 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.006G151200.1 | 3.5 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.006G151200.1 | 3.5 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.006G151200.1 | 3.5 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.006G151200.1 | 3.5 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.006G151200.1 | 3.5 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.006G151200.1 | 3.5 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.006G151200.1 | 3.5 | -1 | 1 | 21 |
| 51 | uggaaucuugaI Phvul.006G172200.1 | 3.5 | -1 | 1 | 22 |
| 52 | ggaaucuugauξPhvul.006G181200.1 | 3.5 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.006G181200.1 | 3.5 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.006G181200.1 | 3.5 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.006G181200.1 | 3.5 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.006G181200.1 | 3.5 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.006G181200.1 | 3.5 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.006G181200.1 | 3.5 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.006G181200.1 | 3.5 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.006G181200.1 | 3.5 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.006G181200.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|--------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.006G181200.1 | 3.5 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.006G181200.1 | 3.5 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.007G234200.1 | 3.5 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.007G234200.1 | 3.5 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.007G234200.1 | 3.5 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.007G234200.1 | 3.5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.007G234200.1 | 3.5 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.007G234200.1 | 3.5 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.007G234200.1 | 3.5 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.007G234200.1 | 3.5 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.007G234200.1 | 3.5 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.007G234200.1 | 3.5 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.007G234200.1 | 3.5 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.007G234200.1 | 3.5 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.007G234200.1 | 3.5 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.007G234200.1 | 3.5 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.007G236400.1 | 3.5 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.007G236400.1 | 3.5 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.007G236400.1 | 3.5 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.007G236400.1 | 3.5 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.007G236400.1 | 3.5 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.007G236400.1 | 3.5 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.007G236400.1 | 3.5 | -1 | 1 | 21 |
| 25 | ggaaucuugauξPhvul.007G236400.1 | 3.5 | -1 | 1 | 21 |
| 26 | ggaaucuugauξPhvul.007G236400.1 | 3.5 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.007G236400.1 | 3.5 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.007G236400.1 | 3.5 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.007G236400.1 | 3.5 | -1 | 1 | 21 |
| 30 | ggaaucuugauξPhvul.007G236400.1 | 3.5 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.007G236400.1 | 3.5 | -1 | 1 | 24 |
| 32 | uggaaucuugaξPhvul.007G236400.1 | 3.5 | -1 | 1 | 22 |
| 33 | ggaaucuugauξPhvul.008G058700.2 | 3.5 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.008G058700.2 | 3.5 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.008G058700.1 | 3.5 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.008G058700.2 | 3.5 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.008G058700.1 | 3.5 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.008G058700.1 | 3.5 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.008G058700.2 | 3.5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.008G058700.1 | 3.5 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.008G058700.2 | 3.5 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.008G058700.2 | 3.5 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.008G058700.1 | 3.5 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.008G058700.2 | 3.5 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.008G058700.1 | 3.5 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.008G058700.1 | 3.5 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.008G058700.2 | 3.5 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.008G058700.1 | 3.5 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.008G058700.2 | 3.5 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.008G058700.2 | 3.5 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.008G058700.1 | 3.5 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.008G058700.2 | 3.5 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.008G058700.1 | 3.5 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.008G058700.1 | 3.5 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.008G058700.2 | 3.5 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.008G058700.1 | 3.5 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.008G058700.2 | 3.5 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.008G058700.2 | 3.5 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.008G058700.1 | 3.5 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.008G058700.2 | 3.5 | -1 | 1 | 24 |
| | ggaaucuugauξPhvul.008G058700.1 | 3.5 | -1 | 1 | 24 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξ Phvul.009G014600.2 | 3.5 | -1 | 1 | 21 |
| 3 | ggaaucuugauξ Phvul.009G014600.1 | 3.5 | -1 | 1 | 21 |
| 4 | ggaaucuugauξ Phvul.009G014600.2 | 3.5 | -1 | 1 | 21 |
| 5 | ggaaucuugauξ Phvul.009G014600.1 | 3.5 | -1 | 1 | 21 |
| 6 | ggaaucuugauξ Phvul.009G014600.2 | 3.5 | -1 | 1 | 21 |
| 7 | ggaaucuugauξ Phvul.009G014600.1 | 3.5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξ Phvul.009G014600.2 | 3.5 | -1 | 1 | 21 |
| 9 | ggaaucuugauξ Phvul.009G014600.1 | 3.5 | -1 | 1 | 21 |
| 10 | ggaaucuugauξ Phvul.009G014600.2 | 3.5 | -1 | 1 | 21 |
| 11 | ggaaucuugauξ Phvul.009G014600.1 | 3.5 | -1 | 1 | 21 |
| 12 | ggaaucuugauξ Phvul.009G014600.2 | 3.5 | -1 | 1 | 21 |
| 13 | ggaaucuugauξ Phvul.009G014600.1 | 3.5 | -1 | 1 | 21 |
| 14 | ggaaucuugauξ Phvul.009G014600.2 | 3.5 | -1 | 1 | 21 |
| 15 | ggaaucuugauξ Phvul.009G014600.1 | 3.5 | -1 | 1 | 21 |
| 16 | ggaaucuugauξ Phvul.009G014600.2 | 3.5 | -1 | 1 | 21 |
| 17 | ggaaucuugauξ Phvul.009G014600.1 | 3.5 | -1 | 1 | 21 |
| 18 | ggaaucuugauξ Phvul.009G014600.2 | 3.5 | -1 | 1 | 21 |
| 19 | ggaaucuugauξ Phvul.009G014600.1 | 3.5 | -1 | 1 | 21 |
| 20 | ggaaucuugauξ Phvul.009G014600.2 | 3.5 | -1 | 1 | 21 |
| 21 | ggaaucuugauξ Phvul.009G014600.1 | 3.5 | -1 | 1 | 21 |
| 22 | ggaaucuugauξ Phvul.009G014600.2 | 3.5 | -1 | 1 | 21 |
| 23 | ggaaucuugauξ Phvul.009G014600.1 | 3.5 | -1 | 1 | 21 |
| 24 | ggaaucuugauξ Phvul.009G014600.2 | 3.5 | -1 | 1 | 21 |
| 25 | ggaaucuugauξ Phvul.009G014600.1 | 3.5 | -1 | 1 | 21 |
| 26 | ggaaucuugauξ Phvul.009G014600.2 | 3.5 | -1 | 1 | 21 |
| 27 | ggaaucuugauξ Phvul.009G014600.1 | 3.5 | -1 | 1 | 21 |
| 28 | ggaaucuugauξ Phvul.009G117500.1 | 3.5 | -1 | 1 | 21 |
| 29 | ggaaucuugauξ Phvul.009G117500.1 | 3.5 | -1 | 1 | 21 |
| 30 | ggaaucuugauξ Phvul.009G117500.1 | 3.5 | -1 | 1 | 21 |
| 31 | ggaaucuugauξ Phvul.009G117500.1 | 3.5 | -1 | 1 | 21 |
| 32 | ggaaucuugauξ Phvul.009G117500.1 | 3.5 | -1 | 1 | 21 |
| 33 | ggaaucuugauξ Phvul.009G117500.1 | 3.5 | -1 | 1 | 21 |
| 34 | ggaaucuugauξ Phvul.009G117500.1 | 3.5 | -1 | 1 | 21 |
| 35 | ggaaucuugauξ Phvul.009G117500.1 | 3.5 | -1 | 1 | 21 |
| 36 | ggaaucuugauξ Phvul.009G117500.1 | 3.5 | -1 | 1 | 21 |
| 37 | ggaaucuugauξ Phvul.009G117500.1 | 3.5 | -1 | 1 | 21 |
| 38 | ggaaucuugauξ Phvul.009G117500.1 | 3.5 | -1 | 1 | 21 |
| 39 | ggaaucuugauξ Phvul.009G117500.1 | 3.5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξ Phvul.009G117500.1 | 3.5 | -1 | 1 | 21 |
| 41 | ggaaucuugauξ Phvul.009G117500.1 | 3.5 | -1 | 1 | 24 |
| 42 | ggaaucuugauξ Phvul.009G117500.1 | 3.5 | -1 | 1 | 21 |
| 43 | uggaaucuuga Phvul.009G130700.1 | 3.5 | -1 | 1 | 22 |
| 44 | ggaaucuugauξ Phvul.010G002600.1 | 3.5 | -1 | 1 | 21 |
| 45 | ggaaucuugauξ Phvul.010G002600.1 | 3.5 | -1 | 1 | 21 |
| 46 | ggaaucuugauξ Phvul.010G002600.1 | 3.5 | -1 | 1 | 21 |
| 47 | ggaaucuugauξ Phvul.010G002600.1 | 3.5 | -1 | 1 | 21 |
| 48 | ggaaucuugauξ Phvul.010G002600.1 | 3.5 | -1 | 1 | 21 |
| 49 | ggaaucuugauξ Phvul.010G002600.1 | 3.5 | -1 | 1 | 21 |
| 50 | ggaaucuugauξ Phvul.010G002600.1 | 3.5 | -1 | 1 | 21 |
| 51 | ggaaucuugauξ Phvul.010G002600.1 | 3.5 | -1 | 1 | 21 |
| 52 | ggaaucuugauξ Phvul.010G002600.1 | 3.5 | -1 | 1 | 21 |
| 53 | ggaaucuugauξ Phvul.010G002600.1 | 3.5 | -1 | 1 | 21 |
| 54 | ggaaucuugauξ Phvul.010G002600.1 | 3.5 | -1 | 1 | 21 |
| 55 | ggaaucuugauξ Phvul.010G002600.1 | 3.5 | -1 | 1 | 21 |
| 56 | ggaaucuugauξ Phvul.010G002600.1 | 3.5 | -1 | 1 | 21 |
| 57 | ggaaucuugauξ Phvul.010G002600.1 | 3.5 | -1 | 1 | 24 |
| 58 | uggaaucuuga Phvul.010G002600.1 | 3.5 | -1 | 1 | 22 |
| 59 | uggaaucuuga Phvul.011G067401.1 | 3.5 | -1 | 1 | 22 |
| 60 | ggaaucuugauξ Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.011G079800.1 | 3.5 | -1 | 1 | 24 |
| 15 | uggaaucuugaI Phvul.011G079800.1 | 3.5 | -1 | 1 | 22 |
| 16 | ggaaucuugauξPhvul.011G127400.1 | 3.5 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.011G127400.1 | 3.5 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.011G127400.1 | 3.5 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.011G127400.1 | 3.5 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.011G127400.1 | 3.5 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.011G127400.1 | 3.5 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.011G127400.1 | 3.5 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.011G127400.1 | 3.5 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.011G127400.1 | 3.5 | -1 | 1 | 21 |
| 25 | ggaaucuugauξPhvul.011G127400.1 | 3.5 | -1 | 1 | 21 |
| 26 | ggaaucuugauξPhvul.011G127400.1 | 3.5 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.011G127400.1 | 3.5 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.011G127400.1 | 3.5 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.011G127400.1 | 3.5 | -1 | 1 | 21 |
| 30 | uggaaucuugaI Phvul.011G127400.1 | 3.5 | -1 | 1 | 22 |
| 31 | ggaaucuugauξPhvul.011G147000.1 | 3.5 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.011G147000.1 | 3.5 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.011G147000.1 | 3.5 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.011G147000.1 | 3.5 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.011G147000.1 | 3.5 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.011G147000.1 | 3.5 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.011G147000.1 | 3.5 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.011G147000.1 | 3.5 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.011G147000.1 | 3.5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.011G147000.1 | 3.5 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.011G147000.1 | 3.5 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.011G147000.1 | 3.5 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.011G147000.1 | 3.5 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.011G150100.1 | 3.5 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.011G150100.1 | 3.5 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.011G150100.1 | 3.5 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.011G150100.1 | 3.5 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.011G150100.1 | 3.5 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.011G150100.1 | 3.5 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.011G150100.1 | 3.5 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.011G150100.1 | 3.5 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.011G150100.1 | 3.5 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.011G150100.1 | 3.5 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.011G150100.1 | 3.5 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.011G150100.1 | 3.5 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.011G150100.1 | 3.5 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.011G150100.1 | 3.5 | -1 | 1 | 24 |
| 58 | ggaaucuugauξPhvul.011G150100.1 | 3.5 | -1 | 1 | 24 |
| 59 | uggaaucuugaI Phvul.011G152200.3 | 3.5 | -1 | 1 | 22 |
| 60 | uggaaucuugaI Phvul.011G152200.1 | 3.5 | -1 | 1 | 22 |
| | ggaaucuugauξPhvul.L002332.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|--------------------------------|------|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.L002332.1 | 3.5 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.L002332.1 | 3.5 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.L002332.1 | 3.5 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.L002332.1 | 3.5 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.L002332.1 | 3.5 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.L002332.1 | 3.5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.L002332.1 | 3.5 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.L002332.1 | 3.5 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.L002332.1 | 3.5 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.L002332.1 | 3.5 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.L002332.1 | 3.5 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.L002332.1 | 3.5 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.L002332.1 | 3.5 | -1 | 1 | 24 |
| 15 | ggaaucuugauξPhvul.003G001200.1 | 3.75 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.003G001200.1 | 3.75 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.003G001200.1 | 3.75 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.003G001200.1 | 3.75 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.003G001200.1 | 3.75 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.003G001200.1 | 3.75 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.003G001200.1 | 3.75 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.003G001200.1 | 3.75 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.003G001200.1 | 3.75 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.003G001200.1 | 3.75 | -1 | 1 | 21 |
| 25 | ggaaucuugauξPhvul.003G001200.1 | 3.75 | -1 | 1 | 21 |
| 26 | ggaaucuugauξPhvul.003G001200.1 | 3.75 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.003G001200.1 | 3.75 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.003G001200.1 | 3.75 | -1 | 1 | 24 |
| 29 | ggaaucuugauξPhvul.003G001200.1 | 3.75 | -1 | 1 | 24 |
| 30 | uggaaucuuga Phvul.003G001200.1 | 3.75 | -1 | 1 | 22 |
| 31 | uggaaucuuga Phvul.001G147500.1 | 4 | -1 | 1 | 22 |
| 32 | ggaaucuugauξPhvul.001G169200.1 | 4 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.001G169200.1 | 4 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.001G169200.1 | 4 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.001G169200.1 | 4 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.001G169200.1 | 4 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.001G169200.1 | 4 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.001G169200.1 | 4 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.001G169200.1 | 4 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.001G169200.1 | 4 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.001G169200.1 | 4 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.001G169200.1 | 4 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.001G169200.1 | 4 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.001G169200.1 | 4 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.001G169200.1 | 4 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.001G174800.1 | 4 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.001G174800.1 | 4 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.001G174800.1 | 4 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.001G174800.1 | 4 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.001G174800.1 | 4 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.001G174800.1 | 4 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.001G174800.1 | 4 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.001G174800.1 | 4 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.001G174800.1 | 4 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.001G174800.1 | 4 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.001G174800.1 | 4 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.001G174800.1 | 4 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.001G174800.1 | 4 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.001G212400.1 | 4 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.001G212400.2 | 4 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.001G212400.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|--------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.001G212400.2 | 4 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.001G212400.1 | 4 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.001G212400.2 | 4 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.001G212400.1 | 4 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.001G212400.2 | 4 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.001G212400.1 | 4 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.001G212400.2 | 4 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.001G212400.1 | 4 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.001G212400.2 | 4 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.001G212400.1 | 4 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.001G212400.2 | 4 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.001G212400.1 | 4 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.001G212400.2 | 4 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.001G212400.1 | 4 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.001G212400.2 | 4 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.001G212400.1 | 4 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.001G212400.2 | 4 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.001G212400.1 | 4 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.001G212400.2 | 4 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.001G212400.1 | 4 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.001G212400.2 | 4 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.001G212400.1 | 4 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.001G216400.1 | 4 | -1 | 1 | 21 |
| 25 | ggaaucuugauξPhvul.001G216400.1 | 4 | -1 | 1 | 21 |
| 26 | ggaaucuugauξPhvul.001G216400.1 | 4 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.001G216400.1 | 4 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.001G216400.1 | 4 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.001G216400.1 | 4 | -1 | 1 | 21 |
| 30 | ggaaucuugauξPhvul.001G216400.1 | 4 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.001G216400.1 | 4 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.001G216400.1 | 4 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.001G216400.1 | 4 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.001G216400.1 | 4 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.001G216400.1 | 4 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.001G216400.1 | 4 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.001G216400.1 | 4 | -1 | 1 | 24 |
| 38 | ggaaucuugauξPhvul.001G216400.1 | 4 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.001G232300.2 | 4 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.001G232300.1 | 4 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.001G232300.2 | 4 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.001G232300.1 | 4 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.001G232300.2 | 4 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.001G232300.1 | 4 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.001G232300.2 | 4 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.001G232300.1 | 4 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.001G232300.2 | 4 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.001G232300.1 | 4 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.001G232300.2 | 4 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.001G232300.1 | 4 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.001G232300.2 | 4 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.001G232300.1 | 4 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.001G232300.2 | 4 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.001G232300.1 | 4 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.001G232300.2 | 4 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.001G232300.1 | 4 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.001G232300.2 | 4 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.001G232300.1 | 4 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.001G232300.2 | 4 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.001G232300.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.001G232300.2 | 4 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.001G232300.1 | 4 | -1 | 1 | 21 |
| 4 | uggaaucuugaI Phvul.001G232300.2 | 4 | -1 | 1 | 22 |
| 5 | uggaaucuugaI Phvul.001G232300.1 | 4 | -1 | 1 | 22 |
| 6 | ggaaucuugauξPhvul.001G269200.1 | 4 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.001G269200.1 | 4 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.001G269200.1 | 4 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.001G269200.1 | 4 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.001G269200.1 | 4 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.001G269200.1 | 4 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.001G269200.1 | 4 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.001G269200.1 | 4 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.001G269200.1 | 4 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.001G269200.1 | 4 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.001G269200.1 | 4 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.001G269200.1 | 4 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.001G269200.1 | 4 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.001G269200.1 | 4 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.001G269200.1 | 4 | -1 | 1 | 24 |
| 21 | ggaaucuugauξPhvul.001G269301.1 | 4 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.001G269301.1 | 4 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.001G269301.1 | 4 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.001G269301.1 | 4 | -1 | 1 | 21 |
| 25 | ggaaucuugauξPhvul.001G269301.1 | 4 | -1 | 1 | 21 |
| 26 | ggaaucuugauξPhvul.001G269301.1 | 4 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.001G269301.1 | 4 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.001G269301.1 | 4 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.001G269301.1 | 4 | -1 | 1 | 21 |
| 30 | ggaaucuugauξPhvul.001G269301.1 | 4 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.001G269301.1 | 4 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.001G269301.1 | 4 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.001G269301.1 | 4 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.001G269301.1 | 4 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.001G269301.1 | 4 | -1 | 1 | 24 |
| 36 | ggaaucuugauξPhvul.002G197200.1 | 4 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.002G197200.1 | 4 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.002G197200.1 | 4 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.002G197200.1 | 4 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.002G197200.1 | 4 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.002G197200.1 | 4 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.002G197200.1 | 4 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.002G197200.1 | 4 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.002G197200.1 | 4 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.002G197200.1 | 4 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.002G197200.1 | 4 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.002G197200.1 | 4 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.002G197200.1 | 4 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.002G218300.1 | 4 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.002G218300.1 | 4 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.002G218300.1 | 4 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.002G218300.1 | 4 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.002G218300.1 | 4 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.002G218300.1 | 4 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.002G218300.1 | 4 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.002G218300.1 | 4 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.002G218300.1 | 4 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.002G218300.1 | 4 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.002G218300.1 | 4 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.002G218300.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.002G218300.1 | 4 | -1 | 1 | 24 |
| 3 | uggaaucuugaI Phvul.002G264200.1 | 4 | -1 | 1 | 22 |
| 4 | ggaaucuugauξPhvul.002G330500.2 | 4 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.002G330500.1 | 4 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.002G330500.2 | 4 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.002G330500.1 | 4 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.002G330500.2 | 4 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.002G330500.1 | 4 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.002G330500.2 | 4 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.002G330500.1 | 4 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.002G330500.2 | 4 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.002G330500.1 | 4 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.002G330500.2 | 4 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.002G330500.1 | 4 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.002G330500.2 | 4 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.002G330500.1 | 4 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.002G330500.2 | 4 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.002G330500.1 | 4 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.002G330500.2 | 4 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.002G330500.1 | 4 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.002G330500.2 | 4 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.002G330500.1 | 4 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.002G330500.2 | 4 | -1 | 1 | 21 |
| 25 | ggaaucuugauξPhvul.002G330500.1 | 4 | -1 | 1 | 21 |
| 26 | ggaaucuugauξPhvul.002G330500.2 | 4 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.002G330500.1 | 4 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.002G330500.2 | 4 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.002G330500.1 | 4 | -1 | 1 | 21 |
| 30 | ggaaucuugauξPhvul.002G330500.2 | 4 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.003G111500.1 | 4 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.003G111500.1 | 4 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.003G111500.1 | 4 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.003G111500.1 | 4 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.003G111500.1 | 4 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.003G111500.1 | 4 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.003G111500.1 | 4 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.003G111500.1 | 4 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.003G111500.1 | 4 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.003G111500.1 | 4 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.003G111500.1 | 4 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.003G111500.1 | 4 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.003G111500.1 | 4 | -1 | 1 | 21 |
| 44 | uggaaucuugaI Phvul.003G119100.2 | 4 | -1 | 1 | 22 |
| 45 | ggaaucuugauξPhvul.003G203100.1 | 4 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.003G203100.1 | 4 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.003G203100.1 | 4 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.003G203100.1 | 4 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.003G203100.1 | 4 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.003G203100.1 | 4 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.003G203100.1 | 4 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.003G203100.1 | 4 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.003G203100.1 | 4 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.003G203100.1 | 4 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.003G203100.1 | 4 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.003G203100.1 | 4 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.003G203100.1 | 4 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.003G203100.1 | 4 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.003G203100.1 | 4 | -1 | 1 | 24 |
| 60 | ggaaucuugauξPhvul.003G229600.2 | 4 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.003G229600.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|--------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.003G229600.2 | 4 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.003G229600.1 | 4 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.003G229600.2 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | ggaaucuugauξPhvul.003G229600.1 | 4 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.003G229600.2 | 4 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.003G229600.1 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | ggaaucuugauξPhvul.003G229600.2 | 4 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.003G229600.1 | 4 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.003G229600.2 | 4 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | ggaaucuugauξPhvul.003G229600.1 | 4 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.003G229600.2 | 4 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.003G229600.1 | 4 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | ggaaucuugauξPhvul.003G229600.2 | 4 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.003G229600.1 | 4 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.003G229600.2 | 4 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | ggaaucuugauξPhvul.003G229600.1 | 4 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.003G229600.2 | 4 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.003G229600.1 | 4 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | ggaaucuugauξPhvul.003G229600.2 | 4 | -1 | 1 | 24 |
| 27 | ggaaucuugauξPhvul.003G229600.1 | 4 | -1 | 1 | 24 |
| 28 | uggaaucuuga Phvul.003G235900.1 | 4 | -1 | 1 | 22 |
| 29 | | | | | |
| 30 | ggaaucuugauξPhvul.003G259700.2 | 4 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.003G259700.2 | 4 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.003G259700.2 | 4 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | ggaaucuugauξPhvul.003G259700.2 | 4 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.003G259700.2 | 4 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.003G259700.2 | 4 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.003G259700.2 | 4 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | ggaaucuugauξPhvul.003G259700.2 | 4 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.003G259700.2 | 4 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.003G259700.2 | 4 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | ggaaucuugauξPhvul.003G260000.2 | 4 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.003G260000.1 | 4 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.003G260000.3 | 4 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | ggaaucuugauξPhvul.003G260000.2 | 4 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.003G260000.1 | 4 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.003G260000.3 | 4 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | ggaaucuugauξPhvul.003G260000.2 | 4 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.003G260000.1 | 4 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.003G260000.3 | 4 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | ggaaucuugauξPhvul.003G260000.2 | 4 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.003G260000.1 | 4 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.003G260000.3 | 4 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | ggaaucuugauξPhvul.003G260000.2 | 4 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.003G260000.1 | 4 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.003G260000.3 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|--------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.003G260000.2 | 4 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.003G260000.1 | 4 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.003G260000.3 | 4 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.003G260000.2 | 4 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.003G260000.1 | 4 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.003G260000.1 | 4 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.003G260000.3 | 4 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.003G260000.2 | 4 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.003G260000.1 | 4 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.003G260000.1 | 4 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.003G260000.3 | 4 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.003G260000.2 | 4 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.003G260000.1 | 4 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.003G260000.1 | 4 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.003G260000.3 | 4 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.003G260000.2 | 4 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.003G260000.1 | 4 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.003G260000.3 | 4 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.003G260000.3 | 4 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.003G268500.1 | 4 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.003G268500.1 | 4 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.003G268500.1 | 4 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.003G268500.1 | 4 | -1 | 1 | 21 |
| 25 | ggaaucuugauξPhvul.003G268500.1 | 4 | -1 | 1 | 21 |
| 26 | ggaaucuugauξPhvul.003G268500.1 | 4 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.003G268500.1 | 4 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.003G268500.1 | 4 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.003G268500.1 | 4 | -1 | 1 | 21 |
| 30 | ggaaucuugauξPhvul.003G268500.1 | 4 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.003G268500.1 | 4 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.003G268500.1 | 4 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.003G268500.1 | 4 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.003G268500.1 | 4 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.003G291200.1 | 4 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.003G291200.2 | 4 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.003G291200.1 | 4 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.003G291200.2 | 4 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.003G291200.1 | 4 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.003G291200.1 | 4 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.003G291200.2 | 4 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.003G291200.1 | 4 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.003G291200.2 | 4 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.003G291200.1 | 4 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.003G291200.2 | 4 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.003G291200.1 | 4 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.003G291200.2 | 4 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.003G291200.1 | 4 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.003G291200.2 | 4 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.003G291200.1 | 4 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.003G291200.2 | 4 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.003G291200.1 | 4 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.003G291200.2 | 4 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.003G291200.1 | 4 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.003G291200.2 | 4 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.003G291200.1 | 4 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.003G291200.2 | 4 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.003G291200.1 | 4 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.003G291200.2 | 4 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.004G031700.3 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.004G031700.3 | 4 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.004G031700.3 | 4 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.004G031700.3 | 4 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.004G031700.3 | 4 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.004G031700.3 | 4 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.004G031700.3 | 4 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.004G031700.3 | 4 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.004G031700.3 | 4 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.004G031700.3 | 4 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.004G031700.3 | 4 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.004G031700.3 | 4 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.004G031700.3 | 4 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.004G031700.3 | 4 | -1 | 1 | 24 |
| 15 | uggaaucuugaI Phvul.004G118500.5 | 4 | -1 | 1 | 22 |
| 16 | uggaaucuugaI Phvul.004G118500.2 | 4 | -1 | 1 | 22 |
| 17 | | | | | |
| 18 | ggaaucuugauξPhvul.005G068800.2 | 4 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.005G068800.1 | 4 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.005G068800.2 | 4 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.005G068800.1 | 4 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.005G068800.1 | 4 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.005G068800.2 | 4 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.005G068800.1 | 4 | -1 | 1 | 21 |
| 25 | ggaaucuugauξPhvul.005G068800.2 | 4 | -1 | 1 | 21 |
| 26 | ggaaucuugauξPhvul.005G068800.2 | 4 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.005G068800.1 | 4 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.005G068800.2 | 4 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.005G068800.1 | 4 | -1 | 1 | 21 |
| 30 | ggaaucuugauξPhvul.005G068800.1 | 4 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.005G068800.2 | 4 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.005G068800.1 | 4 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.005G068800.2 | 4 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.005G068800.2 | 4 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.005G068800.1 | 4 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.005G068800.2 | 4 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.005G068800.1 | 4 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.005G068800.1 | 4 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.005G068800.2 | 4 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.005G068800.1 | 4 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.005G068800.2 | 4 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.005G068800.1 | 4 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.005G088800.1 | 4 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.005G088800.1 | 4 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.005G088800.1 | 4 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.005G088800.1 | 4 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.005G088800.1 | 4 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.005G088800.1 | 4 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.005G088800.1 | 4 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.005G088800.1 | 4 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.005G088800.1 | 4 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.005G088800.1 | 4 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.005G088800.1 | 4 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.005G088800.1 | 4 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.005G088800.1 | 4 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.005G088800.1 | 4 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.005G088800.1 | 4 | -1 | 1 | 24 |
| 58 | ggaaucuugauξPhvul.005G171900.2 | 4 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.005G171900.1 | 4 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.005G171900.2 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.005G171900.1 | 4 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.005G171900.2 | 4 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.005G171900.1 | 4 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.005G171900.2 | 4 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.005G171900.1 | 4 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.005G171900.2 | 4 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.005G171900.1 | 4 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.005G171900.2 | 4 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.005G171900.1 | 4 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.005G171900.2 | 4 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.005G171900.1 | 4 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.005G171900.2 | 4 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.005G171900.1 | 4 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.005G171900.2 | 4 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.005G171900.1 | 4 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.005G171900.2 | 4 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.005G171900.1 | 4 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.005G171900.2 | 4 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.005G171900.1 | 4 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.005G171900.2 | 4 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.005G171900.1 | 4 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.005G171900.2 | 4 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.005G171900.1 | 4 | -1 | 1 | 24 |
| 25 | ggaaucuugauξPhvul.005G171900.2 | 4 | -1 | 1 | 24 |
| 26 | ggaaucuugauξPhvul.005G171900.1 | 4 | -1 | 1 | 24 |
| 27 | uggaaucuugaI Phvul.005G171900.2 | 4 | -1 | 1 | 22 |
| 28 | uggaaucuugaI Phvul.005G171900.1 | 4 | -1 | 1 | 22 |
| 29 | ggaaucuugauξPhvul.006G022400.1 | 4 | -1 | 1 | 24 |
| 30 | ggaaucuugauξPhvul.006G130200.1 | 4 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.006G130200.1 | 4 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.006G130200.1 | 4 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.006G130200.1 | 4 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.006G130200.1 | 4 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.006G130200.1 | 4 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.006G130200.1 | 4 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.006G130200.1 | 4 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.006G130200.1 | 4 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.006G130200.1 | 4 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.006G130200.1 | 4 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.006G130200.1 | 4 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.006G130200.1 | 4 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.006G130200.1 | 4 | -1 | 1 | 21 |
| 44 | uggaaucuugaI Phvul.006G130200.1 | 4 | -1 | 1 | 22 |
| 45 | uggaaucuugaI Phvul.006G137900.1 | 4 | -1 | 1 | 22 |
| 46 | uggaaucuugaI Phvul.006G181200.1 | 4 | -1 | 1 | 22 |
| 47 | ggaaucuugauξPhvul.007G029900.1 | 4 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.007G029900.1 | 4 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.007G029900.1 | 4 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.007G029900.1 | 4 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.007G029900.1 | 4 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.007G029900.1 | 4 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.007G029900.1 | 4 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.007G029900.1 | 4 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.007G029900.1 | 4 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.007G029900.1 | 4 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.007G029900.1 | 4 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.007G029900.1 | 4 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.007G029900.1 | 4 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.007G029900.1 | 4 | -1 | 1 | 21 |
| | uggaaucuugaI Phvul.007G046900.2 | 4 | -1 | 1 | 22 |

| | | | | | |
|----|--------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.007G089900.1 | 4 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.007G089900.1 | 4 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.007G089900.1 | 4 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.007G089900.1 | 4 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.007G089900.1 | 4 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.007G089900.1 | 4 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.007G089900.1 | 4 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.007G089900.1 | 4 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.007G089900.1 | 4 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.007G089900.1 | 4 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.007G089900.1 | 4 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.007G089900.1 | 4 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.007G089900.1 | 4 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.007G089900.1 | 4 | -1 | 1 | 24 |
| 16 | uggaaucuuga Phvul.007G089900.1 | 4 | -1 | 1 | 22 |
| 17 | ggaaucuugauξPhvul.007G199800.2 | 4 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.007G199800.1 | 4 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.007G199800.2 | 4 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.007G199800.1 | 4 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.007G199800.2 | 4 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.007G199800.1 | 4 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.007G199800.2 | 4 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.007G199800.1 | 4 | -1 | 1 | 21 |
| 25 | ggaaucuugauξPhvul.007G199800.2 | 4 | -1 | 1 | 21 |
| 26 | ggaaucuugauξPhvul.007G199800.1 | 4 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.007G199800.2 | 4 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.007G199800.1 | 4 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.007G199800.2 | 4 | -1 | 1 | 21 |
| 30 | ggaaucuugauξPhvul.007G199800.1 | 4 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.007G199800.2 | 4 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.007G199800.1 | 4 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.007G199800.2 | 4 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.007G199800.1 | 4 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.007G199800.2 | 4 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.007G199800.1 | 4 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.007G199800.2 | 4 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.007G199800.1 | 4 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.007G199800.2 | 4 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.007G199800.1 | 4 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.007G199800.2 | 4 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.007G199800.1 | 4 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.007G199800.2 | 4 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.008G081500.1 | 4 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.008G081500.1 | 4 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.008G081500.1 | 4 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.008G081500.1 | 4 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.008G081500.1 | 4 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.008G081500.1 | 4 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.008G081500.1 | 4 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.008G081500.1 | 4 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.008G081500.1 | 4 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.008G081500.1 | 4 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.008G081500.1 | 4 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.008G081500.1 | 4 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.008G081500.1 | 4 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.008G081500.1 | 4 | -1 | 1 | 24 |
| 58 | ggaaucuugauξPhvul.008G081500.1 | 4 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.008G089600.4 | 4 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.008G089600.3 | 4 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.008G089600.4 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.008G089600.3 | 4 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.008G089600.4 | 4 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.008G089600.3 | 4 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.008G089600.3 | 4 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.008G089600.4 | 4 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.008G089600.3 | 4 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.008G089600.4 | 4 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.008G089600.4 | 4 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.008G089600.3 | 4 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.008G089600.4 | 4 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.008G089600.3 | 4 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.008G089600.3 | 4 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.008G089600.4 | 4 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.008G089600.3 | 4 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.008G089600.4 | 4 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.008G089600.4 | 4 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.008G089600.3 | 4 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.008G089600.4 | 4 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.008G089600.3 | 4 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.008G089600.3 | 4 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.008G089600.4 | 4 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.008G089600.3 | 4 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.008G089600.4 | 4 | -1 | 1 | 24 |
| 25 | ggaaucuugauξPhvul.008G089600.3 | 4 | -1 | 1 | 24 |
| 26 | ggaaucuugauξPhvul.008G089600.3 | 4 | -1 | 1 | 24 |
| 27 | ggaaucuugauξPhvul.008G122700.1 | 4 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.008G122700.1 | 4 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.008G122700.1 | 4 | -1 | 1 | 21 |
| 30 | ggaaucuugauξPhvul.008G122700.1 | 4 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.008G122700.1 | 4 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.008G122700.1 | 4 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.008G122700.1 | 4 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.008G122700.1 | 4 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.008G122700.1 | 4 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.008G122700.1 | 4 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.008G122700.1 | 4 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.008G122700.1 | 4 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.008G122700.1 | 4 | -1 | 1 | 21 |
| 40 | uggaaucuugai Phvul.008G122700.1 | 4 | -1 | 1 | 22 |
| 41 | ggaaucuugauξPhvul.008G289900.1 | 4 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.008G289900.1 | 4 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.008G289900.1 | 4 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.008G289900.1 | 4 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.008G289900.1 | 4 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.008G289900.1 | 4 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.008G289900.1 | 4 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.008G289900.1 | 4 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.008G289900.1 | 4 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.008G289900.1 | 4 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.008G289900.1 | 4 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.008G289900.1 | 4 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.008G289900.1 | 4 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.008G289900.1 | 4 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.008G289900.1 | 4 | -1 | 1 | 24 |
| 56 | ggaaucuugauξPhvul.008G290600.1 | 4 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.008G290600.1 | 4 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.008G290600.1 | 4 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.008G290600.1 | 4 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.008G290600.1 | 4 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.008G290600.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξ Phvul.008G290600.1 | 4 | -1 | 1 | 21 |
| 3 | ggaaucuugauξ Phvul.008G290600.1 | 4 | -1 | 1 | 21 |
| 4 | ggaaucuugauξ Phvul.008G290600.1 | 4 | -1 | 1 | 21 |
| 5 | ggaaucuugauξ Phvul.008G290600.1 | 4 | -1 | 1 | 21 |
| 6 | ggaaucuugauξ Phvul.008G290600.1 | 4 | -1 | 1 | 21 |
| 7 | ggaaucuugauξ Phvul.008G290600.1 | 4 | -1 | 1 | 21 |
| 8 | ggaaucuugauξ Phvul.008G290600.1 | 4 | -1 | 1 | 24 |
| 9 | ggaaucuugauξ Phvul.008G290600.1 | 4 | -1 | 1 | 24 |
| 10 | uggaaucuugaι Phvul.009G117500.1 | 4 | -1 | 1 | 22 |
| 11 | ggaaucuugauξ Phvul.010G124800.1 | 4 | -1 | 1 | 21 |
| 12 | ggaaucuugauξ Phvul.010G124800.1 | 4 | -1 | 1 | 21 |
| 13 | ggaaucuugauξ Phvul.010G124800.1 | 4 | -1 | 1 | 21 |
| 14 | ggaaucuugauξ Phvul.010G124800.1 | 4 | -1 | 1 | 21 |
| 15 | ggaaucuugauξ Phvul.010G124800.1 | 4 | -1 | 1 | 21 |
| 16 | ggaaucuugauξ Phvul.010G124800.1 | 4 | -1 | 1 | 21 |
| 17 | ggaaucuugauξ Phvul.010G124800.1 | 4 | -1 | 1 | 21 |
| 18 | ggaaucuugauξ Phvul.010G124800.1 | 4 | -1 | 1 | 21 |
| 19 | ggaaucuugauξ Phvul.010G124800.1 | 4 | -1 | 1 | 21 |
| 20 | ggaaucuugauξ Phvul.010G124800.1 | 4 | -1 | 1 | 21 |
| 21 | ggaaucuugauξ Phvul.010G124800.1 | 4 | -1 | 1 | 21 |
| 22 | ggaaucuugauξ Phvul.010G124800.1 | 4 | -1 | 1 | 21 |
| 23 | ggaaucuugauξ Phvul.010G124800.1 | 4 | -1 | 1 | 21 |
| 24 | uggaaucuugaι Phvul.010G158100.1 | 4 | -1 | 1 | 22 |
| 25 | uggaaucuugaι Phvul.010G158100.1 | 4 | -1 | 1 | 22 |
| 26 | ggaaucuugauξ Phvul.011G013100.1 | 4 | -1 | 1 | 21 |
| 27 | ggaaucuugauξ Phvul.011G013100.1 | 4 | -1 | 1 | 21 |
| 28 | ggaaucuugauξ Phvul.011G013100.1 | 4 | -1 | 1 | 21 |
| 29 | ggaaucuugauξ Phvul.011G013100.1 | 4 | -1 | 1 | 21 |
| 30 | ggaaucuugauξ Phvul.011G013100.1 | 4 | -1 | 1 | 21 |
| 31 | ggaaucuugauξ Phvul.011G013100.1 | 4 | -1 | 1 | 21 |
| 32 | ggaaucuugauξ Phvul.011G013100.1 | 4 | -1 | 1 | 21 |
| 33 | ggaaucuugauξ Phvul.011G013100.1 | 4 | -1 | 1 | 21 |
| 34 | ggaaucuugauξ Phvul.011G013100.1 | 4 | -1 | 1 | 21 |
| 35 | ggaaucuugauξ Phvul.011G013100.1 | 4 | -1 | 1 | 21 |
| 36 | ggaaucuugauξ Phvul.011G013100.1 | 4 | -1 | 1 | 21 |
| 37 | ggaaucuugauξ Phvul.011G013100.1 | 4 | -1 | 1 | 21 |
| 38 | ggaaucuugauξ Phvul.011G013100.1 | 4 | -1 | 1 | 21 |
| 39 | uggaaucuugaι Phvul.011G013100.1 | 4 | -1 | 1 | 22 |
| 40 | uggaaucuugaι Phvul.011G047800.2 | 4 | -1 | 1 | 22 |
| 41 | uggaaucuugaι Phvul.011G047800.1 | 4 | -1 | 1 | 22 |
| 42 | uggaaucuugaι Phvul.011G047800.1 | 4 | -1 | 1 | 22 |
| 43 | ggaaucuugauξ Phvul.011G067401.1 | 4 | -1 | 1 | 21 |
| 44 | ggaaucuugauξ Phvul.011G067401.1 | 4 | -1 | 1 | 21 |
| 45 | ggaaucuugauξ Phvul.011G067401.1 | 4 | -1 | 1 | 21 |
| 46 | ggaaucuugauξ Phvul.011G067401.1 | 4 | -1 | 1 | 21 |
| 47 | ggaaucuugauξ Phvul.011G067401.1 | 4 | -1 | 1 | 21 |
| 48 | ggaaucuugauξ Phvul.011G067401.1 | 4 | -1 | 1 | 21 |
| 49 | ggaaucuugauξ Phvul.011G067401.1 | 4 | -1 | 1 | 21 |
| 50 | ggaaucuugauξ Phvul.011G067401.1 | 4 | -1 | 1 | 21 |
| 51 | ggaaucuugauξ Phvul.011G067401.1 | 4 | -1 | 1 | 21 |
| 52 | ggaaucuugauξ Phvul.011G067401.1 | 4 | -1 | 1 | 21 |
| 53 | ggaaucuugauξ Phvul.011G067401.1 | 4 | -1 | 1 | 21 |
| 54 | ggaaucuugauξ Phvul.011G067401.1 | 4 | -1 | 1 | 21 |
| 55 | ggaaucuugauξ Phvul.011G067401.1 | 4 | -1 | 1 | 21 |
| 56 | ggaaucuugauξ Phvul.011G127100.1 | 4 | -1 | 1 | 21 |
| 57 | ggaaucuugauξ Phvul.011G127100.1 | 4 | -1 | 1 | 21 |
| 58 | ggaaucuugauξ Phvul.011G127100.1 | 4 | -1 | 1 | 21 |
| 59 | ggaaucuugauξ Phvul.011G127100.1 | 4 | -1 | 1 | 21 |
| 60 | ggaaucuugauξ Phvul.011G127100.1 | 4 | -1 | 1 | 21 |
| | ggaaucuugauξ Phvul.011G127100.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|--------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.011G127100.1 | 4 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.011G127100.1 | 4 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.011G127100.1 | 4 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.011G127100.1 | 4 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.011G127100.1 | 4 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.011G127100.1 | 4 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.011G150950.1 | 4 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.011G150950.1 | 4 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.011G150950.1 | 4 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.011G150950.1 | 4 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.011G150950.1 | 4 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.011G150950.1 | 4 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.011G150950.1 | 4 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.011G150950.1 | 4 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.011G150950.1 | 4 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.011G150950.1 | 4 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.011G150950.1 | 4 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.011G150950.1 | 4 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.011G150950.1 | 4 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.011G150950.1 | 4 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.011G150950.1 | 4 | -1 | 1 | 24 |
| 23 | ggaaucuugauξPhvul.011G152100.3 | 4 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.011G152100.1 | 4 | -1 | 1 | 21 |
| 25 | ggaaucuugauξPhvul.011G152100.3 | 4 | -1 | 1 | 21 |
| 26 | ggaaucuugauξPhvul.011G152100.3 | 4 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.011G152100.1 | 4 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.011G152100.3 | 4 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.011G152100.1 | 4 | -1 | 1 | 21 |
| 30 | ggaaucuugauξPhvul.011G152100.1 | 4 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.011G152100.3 | 4 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.011G152100.1 | 4 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.011G152100.3 | 4 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.011G152100.3 | 4 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.011G152100.1 | 4 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.011G152100.3 | 4 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.011G152100.1 | 4 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.011G152100.1 | 4 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.011G152100.3 | 4 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.011G152100.1 | 4 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.011G152100.3 | 4 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.011G152100.3 | 4 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.011G152100.1 | 4 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.011G152100.3 | 4 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.011G152100.1 | 4 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.011G152100.3 | 4 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.011G152100.3 | 4 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.011G152100.1 | 4 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.011G152100.3 | 4 | -1 | 1 | 24 |
| 50 | ggaaucuugauξPhvul.011G152100.1 | 4 | -1 | 1 | 24 |
| 51 | ggaaucuugauξPhvul.011G152100.1 | 4 | -1 | 1 | 24 |
| 52 | ggaaucuugauξPhvul.011G152300.3 | 4 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.011G152300.2 | 4 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.011G152300.1 | 4 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.011G152300.3 | 4 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.011G152300.3 | 4 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.011G152300.2 | 4 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.011G152300.2 | 4 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.011G152300.1 | 4 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.011G152300.3 | 4 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.011G152300.2 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|--------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.011G152300.1 | 4 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.011G152300.3 | 4 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.011G152300.2 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | ggaaucuugauξPhvul.011G152300.1 | 4 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.011G152300.3 | 4 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.011G152300.2 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | ggaaucuugauξPhvul.011G152300.1 | 4 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.011G152300.3 | 4 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.011G152300.2 | 4 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | ggaaucuugauξPhvul.011G152300.1 | 4 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.011G152300.3 | 4 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.011G152300.2 | 4 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | ggaaucuugauξPhvul.011G152300.1 | 4 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.011G152300.3 | 4 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.011G152300.2 | 4 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | ggaaucuugauξPhvul.011G152300.1 | 4 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.011G152300.3 | 4 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.011G152300.2 | 4 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | ggaaucuugauξPhvul.011G152300.1 | 4 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.011G152300.3 | 4 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.011G152300.2 | 4 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | ggaaucuugauξPhvul.011G152300.1 | 4 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.011G152300.3 | 4 | -1 | 1 | 24 |
| 32 | ggaaucuugauξPhvul.011G152300.2 | 4 | -1 | 1 | 24 |
| 33 | | | | | |
| 34 | ggaaucuugauξPhvul.011G152300.1 | 4 | -1 | 1 | 24 |
| 35 | ggaaucuugauξPhvul.011G152400.1 | 4 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.011G152400.1 | 4 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.011G152400.1 | 4 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | ggaaucuugauξPhvul.011G152400.1 | 4 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.011G152400.1 | 4 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.011G152400.1 | 4 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | ggaaucuugauξPhvul.011G152400.1 | 4 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.011G152400.1 | 4 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.011G152400.1 | 4 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | ggaaucuugauξPhvul.011G152400.1 | 4 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.011G152400.1 | 4 | -1 | 1 | 24 |
| 49 | uggaaucuugaξPhvul.011G156200.1 | 4 | -1 | 1 | 22 |
| 50 | | | | | |
| 51 | ggaaucuugauξPhvul.011G168400.2 | 4 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.011G168400.2 | 4 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.011G168400.2 | 4 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | ggaaucuugauξPhvul.011G168400.2 | 4 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.011G168400.2 | 4 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.011G168400.2 | 4 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | ggaaucuugauξPhvul.011G168400.2 | 4 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.011G168400.2 | 4 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.011G168400.2 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.011G168400.2 | 4 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.011G168400.2 | 4 | -1 | 1 | 24 |
| 4 | ggaaucuugauξPhvul.011G202200.1 | 4 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.011G202200.1 | 4 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.011G202200.1 | 4 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.011G202200.1 | 4 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.011G202200.1 | 4 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.011G202200.1 | 4 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.011G202200.1 | 4 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.011G202200.1 | 4 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.011G202200.1 | 4 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.011G202200.1 | 4 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.011G202200.1 | 4 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.011G202200.1 | 4 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.011G202200.1 | 4 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.011G202200.1 | 4 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.011G202200.1 | 4 | -1 | 1 | 24 |
| 19 | ggaaucuugauξPhvul.001G152400.1 | 4.5 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.001G152400.1 | 4.5 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.001G152400.1 | 4.5 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.001G152400.1 | 4.5 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.001G152400.1 | 4.5 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.001G152400.1 | 4.5 | -1 | 1 | 21 |
| 25 | ggaaucuugauξPhvul.001G152400.1 | 4.5 | -1 | 1 | 21 |
| 26 | ggaaucuugauξPhvul.001G152400.1 | 4.5 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.001G152400.1 | 4.5 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.001G152400.1 | 4.5 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.001G152400.1 | 4.5 | -1 | 1 | 21 |
| 30 | ggaaucuugauξPhvul.001G152400.1 | 4.5 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.001G152400.1 | 4.5 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.001G152400.1 | 4.5 | -1 | 1 | 24 |
| 33 | ggaaucuugauξPhvul.001G176200.1 | 4.5 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.001G176200.1 | 4.5 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.001G176200.1 | 4.5 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.001G176200.1 | 4.5 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.001G176200.1 | 4.5 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.001G176200.1 | 4.5 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.001G176200.1 | 4.5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.001G176200.1 | 4.5 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.001G176200.1 | 4.5 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.001G176200.1 | 4.5 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.001G176200.1 | 4.5 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.001G176200.1 | 4.5 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.001G176200.1 | 4.5 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.001G176200.1 | 4.5 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.001G176200.1 | 4.5 | -1 | 1 | 24 |
| 48 | uggaaucuugaI Phvul.001G269200.1 | 4.5 | -1 | 1 | 22 |
| 49 | uggaaucuugaI Phvul.001G269301.1 | 4.5 | -1 | 1 | 22 |
| 50 | ggaaucuugauξPhvul.002G010800.1 | 4.5 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.002G010800.1 | 4.5 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.002G010800.1 | 4.5 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.002G010800.1 | 4.5 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.002G010800.1 | 4.5 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.002G010800.1 | 4.5 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.002G010800.1 | 4.5 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.002G010800.1 | 4.5 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.002G010800.1 | 4.5 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.002G010800.1 | 4.5 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.002G010800.1 | 4.5 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.002G010800.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.002G010800.1 | 4.5 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.002G010800.1 | 4.5 | -1 | 1 | 24 |
| 4 | uggaaucuugaI Phvul.002G010800.1 | 4.5 | -1 | 1 | 22 |
| 5 | | | | | |
| 6 | ggaaucuugauξPhvul.002G199800.1 | 4.5 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.002G199800.1 | 4.5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.002G199800.1 | 4.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | ggaaucuugauξPhvul.002G199800.1 | 4.5 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.002G199800.1 | 4.5 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.002G199800.1 | 4.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | ggaaucuugauξPhvul.002G199800.1 | 4.5 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.002G199800.1 | 4.5 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.002G199800.1 | 4.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | ggaaucuugauξPhvul.002G199800.1 | 4.5 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.002G199800.1 | 4.5 | -1 | 1 | 24 |
| 20 | ggaaucuugauξPhvul.002G214900.1 | 4.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | ggaaucuugauξPhvul.002G214900.1 | 4.5 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.002G214900.1 | 4.5 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.002G214900.1 | 4.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | ggaaucuugauξPhvul.002G214900.1 | 4.5 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.002G214900.1 | 4.5 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.002G214900.1 | 4.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | ggaaucuugauξPhvul.002G214900.1 | 4.5 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.002G214900.1 | 4.5 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.002G214900.1 | 4.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | ggaaucuugauξPhvul.002G215000.1 | 4.5 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.002G215000.1 | 4.5 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.002G215000.1 | 4.5 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.002G215000.1 | 4.5 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | ggaaucuugauξPhvul.002G215000.1 | 4.5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.002G215000.1 | 4.5 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.002G215000.1 | 4.5 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | ggaaucuugauξPhvul.002G215000.1 | 4.5 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.002G215000.1 | 4.5 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.002G215000.1 | 4.5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | ggaaucuugauξPhvul.002G264200.1 | 4.5 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.002G264200.1 | 4.5 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.002G264200.1 | 4.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | ggaaucuugauξPhvul.002G264200.1 | 4.5 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.002G264200.1 | 4.5 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.002G264200.1 | 4.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | ggaaucuugauξPhvul.002G264200.1 | 4.5 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.002G264200.1 | 4.5 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.002G264200.1 | 4.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | ggaaucuugauξPhvul.002G264200.1 | 4.5 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.002G264200.1 | 4.5 | -1 | 1 | 24 |
| | uggaaucuugaI Phvul.002G276700.3 | 4.5 | -1 | 1 | 22 |

| | | | | | |
|----|--------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggaaucuuga Phvul.002G276700.2 | 4.5 | -1 | 1 | 22 |
| 3 | uggaaucuuga Phvul.002G276700.1 | 4.5 | -1 | 1 | 22 |
| 4 | uggaaucuuga Phvul.002G308800.1 | 4.5 | -1 | 1 | 22 |
| 5 | ggaaucuuga Phvul.002G326600.1 | 4.5 | -1 | 1 | 21 |
| 6 | ggaaucuuga Phvul.002G326600.2 | 4.5 | -1 | 1 | 21 |
| 7 | ggaaucuuga Phvul.002G326600.1 | 4.5 | -1 | 1 | 21 |
| 8 | ggaaucuuga Phvul.002G326600.2 | 4.5 | -1 | 1 | 21 |
| 9 | ggaaucuuga Phvul.002G326600.1 | 4.5 | -1 | 1 | 21 |
| 10 | ggaaucuuga Phvul.002G326600.2 | 4.5 | -1 | 1 | 21 |
| 11 | ggaaucuuga Phvul.002G326600.1 | 4.5 | -1 | 1 | 21 |
| 12 | ggaaucuuga Phvul.002G326600.2 | 4.5 | -1 | 1 | 21 |
| 13 | ggaaucuuga Phvul.002G326600.1 | 4.5 | -1 | 1 | 21 |
| 14 | ggaaucuuga Phvul.002G326600.2 | 4.5 | -1 | 1 | 21 |
| 15 | ggaaucuuga Phvul.002G326600.1 | 4.5 | -1 | 1 | 21 |
| 16 | ggaaucuuga Phvul.002G326600.2 | 4.5 | -1 | 1 | 21 |
| 17 | ggaaucuuga Phvul.002G326600.1 | 4.5 | -1 | 1 | 21 |
| 18 | ggaaucuuga Phvul.002G326600.2 | 4.5 | -1 | 1 | 21 |
| 19 | ggaaucuuga Phvul.002G326600.1 | 4.5 | -1 | 1 | 21 |
| 20 | ggaaucuuga Phvul.002G326600.2 | 4.5 | -1 | 1 | 21 |
| 21 | ggaaucuuga Phvul.002G326600.1 | 4.5 | -1 | 1 | 21 |
| 22 | ggaaucuuga Phvul.002G326600.2 | 4.5 | -1 | 1 | 21 |
| 23 | ggaaucuuga Phvul.002G326600.1 | 4.5 | -1 | 1 | 21 |
| 24 | ggaaucuuga Phvul.002G326600.2 | 4.5 | -1 | 1 | 21 |
| 25 | ggaaucuuga Phvul.002G326600.1 | 4.5 | -1 | 1 | 21 |
| 26 | ggaaucuuga Phvul.002G326600.2 | 4.5 | -1 | 1 | 21 |
| 27 | ggaaucuuga Phvul.002G326600.1 | 4.5 | -1 | 1 | 21 |
| 28 | ggaaucuuga Phvul.002G326600.2 | 4.5 | -1 | 1 | 21 |
| 29 | ggaaucuuga Phvul.002G326600.1 | 4.5 | -1 | 1 | 21 |
| 30 | ggaaucuuga Phvul.002G326600.2 | 4.5 | -1 | 1 | 21 |
| 31 | ggaaucuuga Phvul.002G326600.1 | 4.5 | -1 | 1 | 21 |
| 32 | uggaaucuuga Phvul.002G326600.1 | 4.5 | -1 | 1 | 22 |
| 33 | uggaaucuuga Phvul.002G326600.2 | 4.5 | -1 | 1 | 22 |
| 34 | ggaaucuuga Phvul.003G170000.1 | 4.5 | -1 | 1 | 21 |
| 35 | ggaaucuuga Phvul.003G170000.1 | 4.5 | -1 | 1 | 21 |
| 36 | ggaaucuuga Phvul.003G170000.1 | 4.5 | -1 | 1 | 21 |
| 37 | ggaaucuuga Phvul.003G170000.1 | 4.5 | -1 | 1 | 21 |
| 38 | ggaaucuuga Phvul.003G170000.1 | 4.5 | -1 | 1 | 21 |
| 39 | ggaaucuuga Phvul.003G170000.1 | 4.5 | -1 | 1 | 21 |
| 40 | ggaaucuuga Phvul.003G170000.1 | 4.5 | -1 | 1 | 21 |
| 41 | ggaaucuuga Phvul.003G170000.1 | 4.5 | -1 | 1 | 21 |
| 42 | ggaaucuuga Phvul.003G170000.1 | 4.5 | -1 | 1 | 21 |
| 43 | ggaaucuuga Phvul.003G170000.1 | 4.5 | -1 | 1 | 21 |
| 44 | ggaaucuuga Phvul.003G170000.1 | 4.5 | -1 | 1 | 21 |
| 45 | ggaaucuuga Phvul.003G170000.1 | 4.5 | -1 | 1 | 21 |
| 46 | ggaaucuuga Phvul.003G170000.1 | 4.5 | -1 | 1 | 21 |
| 47 | ggaaucuuga Phvul.003G170000.1 | 4.5 | -1 | 1 | 21 |
| 48 | ggaaucuuga Phvul.003G189300.1 | 4.5 | -1 | 1 | 21 |
| 49 | ggaaucuuga Phvul.003G189300.2 | 4.5 | -1 | 1 | 21 |
| 50 | ggaaucuuga Phvul.003G189300.1 | 4.5 | -1 | 1 | 21 |
| 51 | ggaaucuuga Phvul.003G189300.2 | 4.5 | -1 | 1 | 21 |
| 52 | ggaaucuuga Phvul.003G189300.1 | 4.5 | -1 | 1 | 21 |
| 53 | ggaaucuuga Phvul.003G189300.2 | 4.5 | -1 | 1 | 21 |
| 54 | ggaaucuuga Phvul.003G189300.1 | 4.5 | -1 | 1 | 21 |
| 55 | ggaaucuuga Phvul.003G189300.2 | 4.5 | -1 | 1 | 21 |
| 56 | ggaaucuuga Phvul.003G189300.1 | 4.5 | -1 | 1 | 21 |
| 57 | ggaaucuuga Phvul.003G189300.2 | 4.5 | -1 | 1 | 21 |
| 58 | ggaaucuuga Phvul.003G189300.1 | 4.5 | -1 | 1 | 21 |
| 59 | ggaaucuuga Phvul.003G189300.2 | 4.5 | -1 | 1 | 21 |
| 60 | ggaaucuuga Phvul.003G189300.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.003G189300.2 | 4.5 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.003G189300.1 | 4.5 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.003G189300.2 | 4.5 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.003G189300.1 | 4.5 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.003G189300.1 | 4.5 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.003G189300.2 | 4.5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.003G189300.1 | 4.5 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.003G189300.2 | 4.5 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.003G189300.2 | 4.5 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.003G189300.1 | 4.5 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.003G189300.2 | 4.5 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.003G202100.1 | 4.5 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.003G202100.1 | 4.5 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.003G202100.1 | 4.5 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.003G202100.1 | 4.5 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.003G202100.1 | 4.5 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.003G202100.1 | 4.5 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.003G202100.1 | 4.5 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.003G202100.1 | 4.5 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.003G202100.1 | 4.5 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.003G202100.1 | 4.5 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.003G202100.1 | 4.5 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.003G202100.1 | 4.5 | -1 | 1 | 21 |
| 25 | ggaaucuugauξPhvul.003G202100.1 | 4.5 | -1 | 1 | 21 |
| 26 | ggaaucuugauξPhvul.003G202100.1 | 4.5 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.003G206500.1 | 4.5 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.003G206500.1 | 4.5 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.003G206500.1 | 4.5 | -1 | 1 | 21 |
| 30 | ggaaucuugauξPhvul.003G206500.1 | 4.5 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.003G206500.1 | 4.5 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.003G206500.1 | 4.5 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.003G206500.1 | 4.5 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.003G206500.1 | 4.5 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.003G206500.1 | 4.5 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.003G206500.1 | 4.5 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.003G206500.1 | 4.5 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.003G206500.1 | 4.5 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.003G206500.1 | 4.5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.003G206500.1 | 4.5 | -1 | 1 | 24 |
| 41 | uggaaucuugaI Phvul.003G229600.2 | 4.5 | -1 | 1 | 22 |
| 42 | uggaaucuugaI Phvul.003G229600.1 | 4.5 | -1 | 1 | 22 |
| 43 | ggaaucuugauξPhvul.003G235900.1 | 4.5 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.003G235900.1 | 4.5 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.003G235900.1 | 4.5 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.003G235900.1 | 4.5 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.003G235900.1 | 4.5 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.003G235900.1 | 4.5 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.003G235900.1 | 4.5 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.003G235900.1 | 4.5 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.003G235900.1 | 4.5 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.003G235900.1 | 4.5 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.003G235900.1 | 4.5 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.003G235900.1 | 4.5 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.003G235900.1 | 4.5 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.003G235900.1 | 4.5 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.004G046400.1 | 4.5 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.004G046400.1 | 4.5 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.004G046400.1 | 4.5 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.004G046400.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|--------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.004G046400.1 | 4.5 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.004G046400.1 | 4.5 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.004G046400.1 | 4.5 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.004G046400.1 | 4.5 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.004G046400.1 | 4.5 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.004G046400.1 | 4.5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.004G046400.1 | 4.5 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.004G046400.1 | 4.5 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.004G046400.1 | 4.5 | -1 | 1 | 24 |
| 11 | ggaaucuugauξPhvul.005G057900.1 | 4.5 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.005G057900.1 | 4.5 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.005G057900.1 | 4.5 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.005G057900.1 | 4.5 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.005G057900.1 | 4.5 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.005G057900.1 | 4.5 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.005G057900.1 | 4.5 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.005G057900.1 | 4.5 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.005G057900.1 | 4.5 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.005G057900.1 | 4.5 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.005G057900.1 | 4.5 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.005G057900.1 | 4.5 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.005G057900.1 | 4.5 | -1 | 1 | 21 |
| 24 | uggaaucuugaξPhvul.005G168700.1 | 4.5 | -1 | 1 | 22 |
| 25 | ggaaucuugauξPhvul.006G106300.1 | 4.5 | -1 | 1 | 21 |
| 26 | ggaaucuugauξPhvul.006G106300.1 | 4.5 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.006G106300.1 | 4.5 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.006G106300.1 | 4.5 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.006G106300.1 | 4.5 | -1 | 1 | 21 |
| 30 | ggaaucuugauξPhvul.006G106300.1 | 4.5 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.006G106300.1 | 4.5 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.006G106300.1 | 4.5 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.006G106300.1 | 4.5 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.006G106300.1 | 4.5 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.006G106300.1 | 4.5 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.006G106300.1 | 4.5 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.006G106300.1 | 4.5 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.006G106300.1 | 4.5 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.006G106400.2 | 4.5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.006G106400.1 | 4.5 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.006G106400.2 | 4.5 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.006G106400.1 | 4.5 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.006G106400.1 | 4.5 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.006G106400.2 | 4.5 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.006G106400.1 | 4.5 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.006G106400.1 | 4.5 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.006G106400.2 | 4.5 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.006G106400.1 | 4.5 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.006G106400.2 | 4.5 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.006G106400.2 | 4.5 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.006G106400.1 | 4.5 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.006G106400.2 | 4.5 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.006G106400.1 | 4.5 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.006G106400.1 | 4.5 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.006G106400.2 | 4.5 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.006G106400.1 | 4.5 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.006G106400.2 | 4.5 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.006G106400.2 | 4.5 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.006G106400.1 | 4.5 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.006G106400.2 | 4.5 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.006G106400.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.006G106400.2 | 4.5 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.006G106400.1 | 4.5 | -1 | 1 | 21 |
| 4 | uggaaucuugau Phvul.006G112211.1 | 4.5 | -1 | 1 | 22 |
| 5 | | | | | |
| 6 | ggaaucuugauξPhvul.006G133600.1 | 4.5 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.006G133600.1 | 4.5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.006G133600.1 | 4.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | ggaaucuugauξPhvul.006G133600.1 | 4.5 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.006G133600.1 | 4.5 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.006G133600.1 | 4.5 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.006G133600.1 | 4.5 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.006G133600.1 | 4.5 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.006G133600.1 | 4.5 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.006G133600.1 | 4.5 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.006G133600.1 | 4.5 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.006G133600.1 | 4.5 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.006G136700.3 | 4.5 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.006G136700.1 | 4.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | ggaaucuugauξPhvul.006G136700.3 | 4.5 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.006G136700.1 | 4.5 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.006G136700.3 | 4.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | ggaaucuugauξPhvul.006G136700.1 | 4.5 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.006G136700.3 | 4.5 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.006G136700.1 | 4.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | ggaaucuugauξPhvul.006G136700.3 | 4.5 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.006G136700.1 | 4.5 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.006G136700.3 | 4.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | ggaaucuugauξPhvul.006G136700.1 | 4.5 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.006G136700.3 | 4.5 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.006G136700.1 | 4.5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | ggaaucuugauξPhvul.006G136700.3 | 4.5 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.006G136700.1 | 4.5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.006G136700.3 | 4.5 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | ggaaucuugauξPhvul.006G136700.1 | 4.5 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.006G136700.3 | 4.5 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.006G136700.1 | 4.5 | -1 | 1 | 21 |
| 45 | | | | | |
| 46 | ggaaucuugauξPhvul.006G139100.1 | 4.5 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.006G139100.1 | 4.5 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.006G139100.1 | 4.5 | -1 | 1 | 21 |
| 49 | | | | | |
| 50 | ggaaucuugauξPhvul.006G139100.1 | 4.5 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.006G139100.1 | 4.5 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.006G139100.1 | 4.5 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.006G139100.1 | 4.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | ggaaucuugauξPhvul.006G139100.1 | 4.5 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.006G139100.1 | 4.5 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.006G139100.1 | 4.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | ggaaucuugauξPhvul.006G139100.1 | 4.5 | -1 | 1 | 24 |
| 60 | ggaaucuugauξPhvul.006G151200.1 | 4.5 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.006G151200.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.006G151200.1 | 4.5 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.006G151200.1 | 4.5 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.006G151200.1 | 4.5 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.006G151200.1 | 4.5 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.006G151200.1 | 4.5 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.006G151200.1 | 4.5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.006G151200.1 | 4.5 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.006G151200.1 | 4.5 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.006G151200.1 | 4.5 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.006G151200.1 | 4.5 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.006G172200.1 | 4.5 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.006G172200.1 | 4.5 | -1 | 1 | 21 |
| 14 | ggaaucuugauξPhvul.006G172200.1 | 4.5 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.006G172200.1 | 4.5 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.006G172200.1 | 4.5 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.006G172200.1 | 4.5 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.006G172200.1 | 4.5 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.006G172200.1 | 4.5 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.006G172200.1 | 4.5 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.006G172200.1 | 4.5 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.006G172200.1 | 4.5 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.006G172200.1 | 4.5 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.006G172200.1 | 4.5 | -1 | 1 | 21 |
| 25 | ggaaucuugauξPhvul.006G172200.1 | 4.5 | -1 | 1 | 21 |
| 26 | uggaaucuugai Phvul.007G199800.2 | 4.5 | -1 | 1 | 22 |
| 27 | uggaaucuugai Phvul.007G199800.1 | 4.5 | -1 | 1 | 22 |
| 28 | uggaaucuugai Phvul.007G280600.1 | 4.5 | -1 | 1 | 22 |
| 29 | ggaaucuugauξPhvul.008G048600.3 | 4.5 | -1 | 1 | 21 |
| 30 | ggaaucuugauξPhvul.008G048600.4 | 4.5 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.008G048600.2 | 4.5 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.008G048600.1 | 4.5 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.008G048600.3 | 4.5 | -1 | 1 | 21 |
| 34 | ggaaucuugauξPhvul.008G048600.4 | 4.5 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.008G048600.2 | 4.5 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.008G048600.1 | 4.5 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.008G048600.3 | 4.5 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.008G048600.4 | 4.5 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.008G048600.2 | 4.5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.008G048600.1 | 4.5 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.008G048600.3 | 4.5 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.008G048600.4 | 4.5 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.008G048600.2 | 4.5 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.008G048600.1 | 4.5 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.008G048600.3 | 4.5 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.008G048600.4 | 4.5 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.008G048600.2 | 4.5 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.008G048600.1 | 4.5 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.008G048600.3 | 4.5 | -1 | 1 | 21 |
| 50 | ggaaucuugauξPhvul.008G048600.4 | 4.5 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.008G048600.2 | 4.5 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.008G048600.1 | 4.5 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.008G048600.3 | 4.5 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.008G048600.4 | 4.5 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.008G048600.2 | 4.5 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.008G048600.1 | 4.5 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.008G048600.3 | 4.5 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.008G048600.4 | 4.5 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.008G048600.2 | 4.5 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.008G048600.1 | 4.5 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.008G048600.3 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|--------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.008G048600.4 | 4.5 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.008G048600.2 | 4.5 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.008G048600.1 | 4.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | ggaaucuugauξPhvul.008G048600.3 | 4.5 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.008G048600.4 | 4.5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.008G048600.2 | 4.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | ggaaucuugauξPhvul.008G048600.1 | 4.5 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.008G048600.3 | 4.5 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.008G048600.4 | 4.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | ggaaucuugauξPhvul.008G048600.2 | 4.5 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.008G048600.1 | 4.5 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.008G048600.3 | 4.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | ggaaucuugauξPhvul.008G048600.4 | 4.5 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.008G048600.2 | 4.5 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.008G048600.1 | 4.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | ggaaucuugauξPhvul.008G048600.3 | 4.5 | -1 | 1 | 24 |
| 23 | ggaaucuugauξPhvul.008G048600.4 | 4.5 | -1 | 1 | 24 |
| 24 | ggaaucuugauξPhvul.008G048600.2 | 4.5 | -1 | 1 | 24 |
| 25 | | | | | |
| 26 | ggaaucuugauξPhvul.008G048600.1 | 4.5 | -1 | 1 | 24 |
| 27 | uggaaucuuga Phvul.008G048600.3 | 4.5 | -1 | 1 | 22 |
| 28 | uggaaucuuga Phvul.008G048600.4 | 4.5 | -1 | 1 | 22 |
| 29 | | | | | |
| 30 | uggaaucuuga Phvul.008G048600.2 | 4.5 | -1 | 1 | 22 |
| 31 | uggaaucuuga Phvul.008G048600.1 | 4.5 | -1 | 1 | 22 |
| 32 | ggaaucuugauξPhvul.008G049000.1 | 4.5 | -1 | 1 | 21 |
| 33 | ggaaucuugauξPhvul.008G049000.1 | 4.5 | -1 | 1 | 21 |
| 34 | | | | | |
| 35 | ggaaucuugauξPhvul.008G049000.1 | 4.5 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.008G049000.1 | 4.5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | ggaaucuugauξPhvul.008G049000.1 | 4.5 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.008G049000.1 | 4.5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.008G049000.1 | 4.5 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | ggaaucuugauξPhvul.008G049000.1 | 4.5 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.008G049000.1 | 4.5 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.008G049000.1 | 4.5 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.008G049000.1 | 4.5 | -1 | 1 | 24 |
| 46 | | | | | |
| 47 | ggaaucuugauξPhvul.008G049400.1 | 4.5 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.008G049400.1 | 4.5 | -1 | 1 | 21 |
| 49 | | | | | |
| 50 | ggaaucuugauξPhvul.008G049400.1 | 4.5 | -1 | 1 | 21 |
| 51 | ggaaucuugauξPhvul.008G049400.1 | 4.5 | -1 | 1 | 21 |
| 52 | ggaaucuugauξPhvul.008G049400.1 | 4.5 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.008G049400.1 | 4.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | ggaaucuugauξPhvul.008G049400.1 | 4.5 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.008G049400.1 | 4.5 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.008G049400.1 | 4.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | ggaaucuugauξPhvul.008G049400.1 | 4.5 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.008G093200.1 | 4.5 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.008G093200.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξ Phvul.008G093200.1 | 4.5 | -1 | 1 | 21 |
| 3 | ggaaucuugauξ Phvul.008G093200.1 | 4.5 | -1 | 1 | 21 |
| 4 | ggaaucuugauξ Phvul.008G093200.1 | 4.5 | -1 | 1 | 21 |
| 5 | ggaaucuugauξ Phvul.008G093200.1 | 4.5 | -1 | 1 | 21 |
| 6 | ggaaucuugauξ Phvul.008G093200.1 | 4.5 | -1 | 1 | 21 |
| 7 | ggaaucuugauξ Phvul.008G093200.1 | 4.5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξ Phvul.008G093200.1 | 4.5 | -1 | 1 | 21 |
| 9 | ggaaucuugauξ Phvul.008G093200.1 | 4.5 | -1 | 1 | 21 |
| 10 | ggaaucuugauξ Phvul.008G093200.1 | 4.5 | -1 | 1 | 21 |
| 11 | ggaaucuugauξ Phvul.008G093200.1 | 4.5 | -1 | 1 | 21 |
| 12 | ggaaucuugauξ Phvul.008G093200.1 | 4.5 | -1 | 1 | 24 |
| 13 | ggaaucuugauξ Phvul.008G145800.1 | 4.5 | -1 | 1 | 21 |
| 14 | ggaaucuugauξ Phvul.008G145800.1 | 4.5 | -1 | 1 | 21 |
| 15 | ggaaucuugauξ Phvul.008G145800.1 | 4.5 | -1 | 1 | 21 |
| 16 | ggaaucuugauξ Phvul.008G145800.1 | 4.5 | -1 | 1 | 21 |
| 17 | ggaaucuugauξ Phvul.008G145800.1 | 4.5 | -1 | 1 | 21 |
| 18 | ggaaucuugauξ Phvul.008G145800.1 | 4.5 | -1 | 1 | 21 |
| 19 | ggaaucuugauξ Phvul.008G145800.1 | 4.5 | -1 | 1 | 21 |
| 20 | ggaaucuugauξ Phvul.008G145800.1 | 4.5 | -1 | 1 | 21 |
| 21 | ggaaucuugauξ Phvul.008G145800.1 | 4.5 | -1 | 1 | 21 |
| 22 | ggaaucuugauξ Phvul.008G145800.1 | 4.5 | -1 | 1 | 21 |
| 23 | ggaaucuugauξ Phvul.008G145800.1 | 4.5 | -1 | 1 | 21 |
| 24 | ggaaucuugauξ Phvul.008G145800.1 | 4.5 | -1 | 1 | 21 |
| 25 | ggaaucuugauξ Phvul.008G145800.1 | 4.5 | -1 | 1 | 21 |
| 26 | ggaaucuugauξ Phvul.008G145800.1 | 4.5 | -1 | 1 | 21 |
| 27 | ggaaucuugauξ Phvul.008G145800.1 | 4.5 | -1 | 1 | 24 |
| 28 | uggaaucuugaξ Phvul.008G145800.1 | 4.5 | -1 | 1 | 22 |
| 29 | ggaaucuugauξ Phvul.008G260200.2 | 4.5 | -1 | 1 | 21 |
| 30 | ggaaucuugauξ Phvul.008G260200.2 | 4.5 | -1 | 1 | 21 |
| 31 | ggaaucuugauξ Phvul.008G260200.2 | 4.5 | -1 | 1 | 21 |
| 32 | ggaaucuugauξ Phvul.008G260200.2 | 4.5 | -1 | 1 | 21 |
| 33 | ggaaucuugauξ Phvul.008G260200.2 | 4.5 | -1 | 1 | 21 |
| 34 | ggaaucuugauξ Phvul.008G260200.2 | 4.5 | -1 | 1 | 21 |
| 35 | ggaaucuugauξ Phvul.008G260200.2 | 4.5 | -1 | 1 | 21 |
| 36 | ggaaucuugauξ Phvul.008G260200.2 | 4.5 | -1 | 1 | 21 |
| 37 | ggaaucuugauξ Phvul.008G260200.2 | 4.5 | -1 | 1 | 21 |
| 38 | ggaaucuugauξ Phvul.008G260200.2 | 4.5 | -1 | 1 | 21 |
| 39 | ggaaucuugauξ Phvul.008G260200.2 | 4.5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξ Phvul.008G260200.2 | 4.5 | -1 | 1 | 21 |
| 41 | ggaaucuugauξ Phvul.008G260200.2 | 4.5 | -1 | 1 | 21 |
| 42 | ggaaucuugauξ Phvul.008G260200.2 | 4.5 | -1 | 1 | 21 |
| 43 | uggaaucuugaξ Phvul.008G290600.1 | 4.5 | -1 | 1 | 22 |
| 44 | uggaaucuugaξ Phvul.009G014600.2 | 4.5 | -1 | 1 | 22 |
| 45 | uggaaucuugaξ Phvul.009G014600.1 | 4.5 | -1 | 1 | 22 |
| 46 | uggaaucuugaξ Phvul.009G149200.1 | 4.5 | -1 | 1 | 22 |
| 47 | ggaaucuugauξ Phvul.009G198000.1 | 4.5 | -1 | 1 | 21 |
| 48 | ggaaucuugauξ Phvul.009G198000.1 | 4.5 | -1 | 1 | 21 |
| 49 | ggaaucuugauξ Phvul.009G198000.1 | 4.5 | -1 | 1 | 21 |
| 50 | ggaaucuugauξ Phvul.009G198000.1 | 4.5 | -1 | 1 | 21 |
| 51 | ggaaucuugauξ Phvul.009G198000.1 | 4.5 | -1 | 1 | 21 |
| 52 | ggaaucuugauξ Phvul.009G198000.1 | 4.5 | -1 | 1 | 21 |
| 53 | ggaaucuugauξ Phvul.009G198000.1 | 4.5 | -1 | 1 | 21 |
| 54 | ggaaucuugauξ Phvul.009G198000.1 | 4.5 | -1 | 1 | 21 |
| 55 | ggaaucuugauξ Phvul.009G198000.1 | 4.5 | -1 | 1 | 21 |
| 56 | ggaaucuugauξ Phvul.009G198000.1 | 4.5 | -1 | 1 | 21 |
| 57 | ggaaucuugauξ Phvul.009G198000.1 | 4.5 | -1 | 1 | 21 |
| 58 | ggaaucuugauξ Phvul.009G198000.1 | 4.5 | -1 | 1 | 21 |
| 59 | ggaaucuugauξ Phvul.009G198000.1 | 4.5 | -1 | 1 | 21 |
| 60 | ggaaucuugauξ Phvul.009G198000.1 | 4.5 | -1 | 1 | 21 |
| | uggaaucuugaξ Phvul.010G124800.1 | 4.5 | -1 | 1 | 22 |

| | | | | | |
|----|--------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggaaucuuga Phvul.011G053200.1 | 4.5 | -1 | 1 | 22 |
| 3 | uggaaucuuga Phvul.011G152100.3 | 4.5 | -1 | 1 | 22 |
| 4 | uggaaucuuga Phvul.011G152100.1 | 4.5 | -1 | 1 | 22 |
| 5 | | | | | |
| 6 | uggaaucuuga Phvul.L002332.1 | 4.5 | -1 | 1 | 22 |
| 7 | uggaaucuuga Phvul.001G013800.1 | 5 | -1 | 1 | 22 |
| 8 | ggaaucuuga Phvul.001G126800.1 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | ggaaucuuga Phvul.001G126800.1 | 5 | -1 | 1 | 21 |
| 11 | ggaaucuuga Phvul.001G126800.1 | 5 | -1 | 1 | 21 |
| 12 | ggaaucuuga Phvul.001G126800.1 | 5 | -1 | 1 | 21 |
| 13 | ggaaucuuga Phvul.001G126800.1 | 5 | -1 | 1 | 21 |
| 14 | ggaaucuuga Phvul.001G126800.1 | 5 | -1 | 1 | 21 |
| 15 | ggaaucuuga Phvul.001G126800.1 | 5 | -1 | 1 | 21 |
| 16 | ggaaucuuga Phvul.001G126800.1 | 5 | -1 | 1 | 21 |
| 17 | ggaaucuuga Phvul.001G126800.1 | 5 | -1 | 1 | 21 |
| 18 | ggaaucuuga Phvul.001G126800.1 | 5 | -1 | 1 | 21 |
| 19 | ggaaucuuga Phvul.001G126800.1 | 5 | -1 | 1 | 21 |
| 20 | ggaaucuuga Phvul.001G126800.1 | 5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggaaucuuga Phvul.001G131700.3 | 5 | -1 | 1 | 22 |
| 23 | uggaaucuuga Phvul.001G131700.2 | 5 | -1 | 1 | 22 |
| 24 | uggaaucuuga Phvul.001G131700.1 | 5 | -1 | 1 | 22 |
| 25 | | | | | |
| 26 | uggaaucuuga Phvul.001G216400.1 | 5 | -1 | 1 | 22 |
| 27 | ggaaucuuga Phvul.002G134400.1 | 5 | -1 | 1 | 21 |
| 28 | ggaaucuuga Phvul.002G134400.1 | 5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | ggaaucuuga Phvul.002G134400.1 | 5 | -1 | 1 | 21 |
| 31 | ggaaucuuga Phvul.002G134400.1 | 5 | -1 | 1 | 21 |
| 32 | ggaaucuuga Phvul.002G134400.1 | 5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | ggaaucuuga Phvul.002G134400.1 | 5 | -1 | 1 | 21 |
| 35 | ggaaucuuga Phvul.002G134400.1 | 5 | -1 | 1 | 21 |
| 36 | ggaaucuuga Phvul.002G134400.1 | 5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | ggaaucuuga Phvul.002G134400.1 | 5 | -1 | 1 | 21 |
| 39 | ggaaucuuga Phvul.002G134400.1 | 5 | -1 | 1 | 21 |
| 40 | uggaaucuuga Phvul.002G134400.1 | 5 | -1 | 1 | 22 |
| 41 | | | | | |
| 42 | ggaaucuuga Phvul.002G134700.1 | 5 | -1 | 1 | 21 |
| 43 | ggaaucuuga Phvul.002G134700.1 | 5 | -1 | 1 | 21 |
| 44 | ggaaucuuga Phvul.002G134700.1 | 5 | -1 | 1 | 21 |
| 45 | ggaaucuuga Phvul.002G134700.1 | 5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | ggaaucuuga Phvul.002G134700.1 | 5 | -1 | 1 | 21 |
| 48 | ggaaucuuga Phvul.002G134700.1 | 5 | -1 | 1 | 21 |
| 49 | | | | | |
| 50 | ggaaucuuga Phvul.002G134700.1 | 5 | -1 | 1 | 21 |
| 51 | ggaaucuuga Phvul.002G134700.1 | 5 | -1 | 1 | 21 |
| 52 | ggaaucuuga Phvul.002G134700.1 | 5 | -1 | 1 | 21 |
| 53 | ggaaucuuga Phvul.002G134700.1 | 5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggaaucuuga Phvul.002G134700.1 | 5 | -1 | 1 | 22 |
| 56 | ggaaucuuga Phvul.002G135500.1 | 5 | -1 | 1 | 21 |
| 57 | ggaaucuuga Phvul.002G135500.1 | 5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | ggaaucuuga Phvul.002G135500.1 | 5 | -1 | 1 | 21 |
| 60 | ggaaucuuga Phvul.002G135500.1 | 5 | -1 | 1 | 21 |
| | ggaaucuuga Phvul.002G135500.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξ Phvul.002G135500.1 | 5 | -1 | 1 | 21 |
| 3 | ggaaucuugauξ Phvul.002G135500.1 | 5 | -1 | 1 | 21 |
| 4 | ggaaucuugauξ Phvul.002G135500.1 | 5 | -1 | 1 | 21 |
| 5 | ggaaucuugauξ Phvul.002G135500.1 | 5 | -1 | 1 | 21 |
| 6 | ggaaucuugauξ Phvul.002G135500.1 | 5 | -1 | 1 | 21 |
| 7 | ggaaucuugauξ Phvul.002G135500.1 | 5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξ Phvul.002G135500.1 | 5 | -1 | 1 | 24 |
| 9 | ggaaucuugauξ Phvul.002G135500.1 | 5 | -1 | 1 | 22 |
| 10 | uggaaucuugaι Phvul.002G135500.1 | 5 | -1 | 1 | 22 |
| 11 | ggaaucuugauξ Phvul.002G166200.3 | 5 | -1 | 1 | 24 |
| 12 | ggaaucuugauξ Phvul.002G166200.2 | 5 | -1 | 1 | 24 |
| 13 | ggaaucuugauξ Phvul.002G166200.1 | 5 | -1 | 1 | 24 |
| 14 | ggaaucuugauξ Phvul.002G166200.1 | 5 | -1 | 1 | 24 |
| 15 | ggaaucuugauξ Phvul.002G285400.1 | 5 | -1 | 1 | 21 |
| 16 | ggaaucuugauξ Phvul.002G285400.1 | 5 | -1 | 1 | 21 |
| 17 | ggaaucuugauξ Phvul.002G285400.1 | 5 | -1 | 1 | 21 |
| 18 | ggaaucuugauξ Phvul.002G285400.1 | 5 | -1 | 1 | 21 |
| 19 | ggaaucuugauξ Phvul.002G285400.1 | 5 | -1 | 1 | 21 |
| 20 | ggaaucuugauξ Phvul.002G285400.1 | 5 | -1 | 1 | 21 |
| 21 | ggaaucuugauξ Phvul.002G285400.1 | 5 | -1 | 1 | 21 |
| 22 | ggaaucuugauξ Phvul.002G285400.1 | 5 | -1 | 1 | 21 |
| 23 | ggaaucuugauξ Phvul.002G285400.1 | 5 | -1 | 1 | 21 |
| 24 | ggaaucuugauξ Phvul.002G285400.1 | 5 | -1 | 1 | 21 |
| 25 | ggaaucuugauξ Phvul.002G285400.1 | 5 | -1 | 1 | 21 |
| 26 | ggaaucuugauξ Phvul.002G285400.1 | 5 | -1 | 1 | 21 |
| 27 | ggaaucuugauξ Phvul.002G285400.1 | 5 | -1 | 1 | 21 |
| 28 | ggaaucuugauξ Phvul.002G285400.1 | 5 | -1 | 1 | 24 |
| 29 | ggaaucuugauξ Phvul.002G285400.1 | 5 | -1 | 1 | 24 |
| 30 | uggaaucuugaι Phvul.003G053000.1 | 5 | -1 | 1 | 22 |
| 31 | ggaaucuugauξ Phvul.003G192500.1 | 5 | -1 | 1 | 21 |
| 32 | ggaaucuugauξ Phvul.003G192500.1 | 5 | -1 | 1 | 21 |
| 33 | ggaaucuugauξ Phvul.003G192500.1 | 5 | -1 | 1 | 21 |
| 34 | ggaaucuugauξ Phvul.003G192500.1 | 5 | -1 | 1 | 21 |
| 35 | ggaaucuugauξ Phvul.003G192500.1 | 5 | -1 | 1 | 21 |
| 36 | ggaaucuugauξ Phvul.003G192500.1 | 5 | -1 | 1 | 21 |
| 37 | ggaaucuugauξ Phvul.003G192500.1 | 5 | -1 | 1 | 21 |
| 38 | ggaaucuugauξ Phvul.003G192500.1 | 5 | -1 | 1 | 21 |
| 39 | ggaaucuugauξ Phvul.003G192500.1 | 5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξ Phvul.003G192500.1 | 5 | -1 | 1 | 21 |
| 41 | ggaaucuugauξ Phvul.003G192500.1 | 5 | -1 | 1 | 21 |
| 42 | ggaaucuugauξ Phvul.003G192500.1 | 5 | -1 | 1 | 21 |
| 43 | ggaaucuugauξ Phvul.003G192500.1 | 5 | -1 | 1 | 21 |
| 44 | ggaaucuugauξ Phvul.003G223934.1 | 5 | -1 | 1 | 21 |
| 45 | ggaaucuugauξ Phvul.003G223934.1 | 5 | -1 | 1 | 21 |
| 46 | ggaaucuugauξ Phvul.003G223934.1 | 5 | -1 | 1 | 21 |
| 47 | ggaaucuugauξ Phvul.003G223934.1 | 5 | -1 | 1 | 21 |
| 48 | ggaaucuugauξ Phvul.003G223934.1 | 5 | -1 | 1 | 21 |
| 49 | ggaaucuugauξ Phvul.003G223934.1 | 5 | -1 | 1 | 21 |
| 50 | ggaaucuugauξ Phvul.003G223934.1 | 5 | -1 | 1 | 21 |
| 51 | ggaaucuugauξ Phvul.003G223934.1 | 5 | -1 | 1 | 21 |
| 52 | ggaaucuugauξ Phvul.003G223934.1 | 5 | -1 | 1 | 21 |
| 53 | ggaaucuugauξ Phvul.003G223934.1 | 5 | -1 | 1 | 21 |
| 54 | ggaaucuugauξ Phvul.003G223934.1 | 5 | -1 | 1 | 21 |
| 55 | ggaaucuugauξ Phvul.003G223934.1 | 5 | -1 | 1 | 21 |
| 56 | ggaaucuugauξ Phvul.003G223934.1 | 5 | -1 | 1 | 21 |
| 57 | ggaaucuugauξ Phvul.003G223934.1 | 5 | -1 | 1 | 24 |
| 58 | ggaaucuugauξ Phvul.003G223934.1 | 5 | -1 | 1 | 24 |
| 59 | uggaaucuugaι Phvul.003G223934.1 | 5 | -1 | 1 | 22 |
| 60 | ggaaucuugauξ Phvul.003G274500.1 | 5 | -1 | 1 | 21 |
| | ggaaucuugauξ Phvul.003G274500.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξ Phvul.003G274500.1 | 5 | -1 | 1 | 21 |
| 3 | ggaaucuugauξ Phvul.003G274500.1 | 5 | -1 | 1 | 21 |
| 4 | ggaaucuugauξ Phvul.003G274500.1 | 5 | -1 | 1 | 21 |
| 5 | ggaaucuugauξ Phvul.003G274500.1 | 5 | -1 | 1 | 21 |
| 6 | ggaaucuugauξ Phvul.003G274500.1 | 5 | -1 | 1 | 21 |
| 7 | ggaaucuugauξ Phvul.003G274500.1 | 5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξ Phvul.003G274500.1 | 5 | -1 | 1 | 21 |
| 9 | ggaaucuugauξ Phvul.003G274500.1 | 5 | -1 | 1 | 21 |
| 10 | ggaaucuugauξ Phvul.003G274500.1 | 5 | -1 | 1 | 21 |
| 11 | ggaaucuugauξ Phvul.003G274500.1 | 5 | -1 | 1 | 21 |
| 12 | ggaaucuugauξ Phvul.003G274500.1 | 5 | -1 | 1 | 24 |
| 13 | ggaaucuugauξ Phvul.004G118500.5 | 5 | -1 | 1 | 21 |
| 14 | ggaaucuugauξ Phvul.004G118500.5 | 5 | -1 | 1 | 21 |
| 15 | ggaaucuugauξ Phvul.004G118500.2 | 5 | -1 | 1 | 21 |
| 16 | ggaaucuugauξ Phvul.004G118500.5 | 5 | -1 | 1 | 21 |
| 17 | ggaaucuugauξ Phvul.004G118500.5 | 5 | -1 | 1 | 21 |
| 18 | ggaaucuugauξ Phvul.004G118500.2 | 5 | -1 | 1 | 21 |
| 19 | ggaaucuugauξ Phvul.004G118500.5 | 5 | -1 | 1 | 21 |
| 20 | ggaaucuugauξ Phvul.004G118500.2 | 5 | -1 | 1 | 21 |
| 21 | ggaaucuugauξ Phvul.004G118500.2 | 5 | -1 | 1 | 21 |
| 22 | ggaaucuugauξ Phvul.004G118500.5 | 5 | -1 | 1 | 21 |
| 23 | ggaaucuugauξ Phvul.004G118500.2 | 5 | -1 | 1 | 21 |
| 24 | ggaaucuugauξ Phvul.004G118500.5 | 5 | -1 | 1 | 21 |
| 25 | ggaaucuugauξ Phvul.004G118500.5 | 5 | -1 | 1 | 21 |
| 26 | ggaaucuugauξ Phvul.004G118500.2 | 5 | -1 | 1 | 21 |
| 27 | ggaaucuugauξ Phvul.004G118500.5 | 5 | -1 | 1 | 21 |
| 28 | ggaaucuugauξ Phvul.004G118500.2 | 5 | -1 | 1 | 21 |
| 29 | ggaaucuugauξ Phvul.004G118500.5 | 5 | -1 | 1 | 21 |
| 30 | ggaaucuugauξ Phvul.004G118500.5 | 5 | -1 | 1 | 21 |
| 31 | ggaaucuugauξ Phvul.004G118500.2 | 5 | -1 | 1 | 21 |
| 32 | ggaaucuugauξ Phvul.004G118500.5 | 5 | -1 | 1 | 21 |
| 33 | ggaaucuugauξ Phvul.004G118500.2 | 5 | -1 | 1 | 21 |
| 34 | ggaaucuugauξ Phvul.004G118500.2 | 5 | -1 | 1 | 21 |
| 35 | ggaaucuugauξ Phvul.004G118500.5 | 5 | -1 | 1 | 21 |
| 36 | ggaaucuugauξ Phvul.004G118500.2 | 5 | -1 | 1 | 21 |
| 37 | ggaaucuugauξ Phvul.004G118500.5 | 5 | -1 | 1 | 21 |
| 38 | ggaaucuugauξ Phvul.004G118500.5 | 5 | -1 | 1 | 21 |
| 39 | ggaaucuugauξ Phvul.004G118500.2 | 5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξ Phvul.004G118500.5 | 5 | -1 | 1 | 24 |
| 41 | ggaaucuugauξ Phvul.004G118500.2 | 5 | -1 | 1 | 24 |
| 42 | ggaaucuugauξ Phvul.004G176200.1 | 5 | -1 | 1 | 21 |
| 43 | ggaaucuugauξ Phvul.004G176200.1 | 5 | -1 | 1 | 21 |
| 44 | ggaaucuugauξ Phvul.004G176200.1 | 5 | -1 | 1 | 21 |
| 45 | ggaaucuugauξ Phvul.004G176200.1 | 5 | -1 | 1 | 21 |
| 46 | ggaaucuugauξ Phvul.004G176200.1 | 5 | -1 | 1 | 21 |
| 47 | ggaaucuugauξ Phvul.004G176200.1 | 5 | -1 | 1 | 21 |
| 48 | ggaaucuugauξ Phvul.004G176200.1 | 5 | -1 | 1 | 21 |
| 49 | ggaaucuugauξ Phvul.004G176200.1 | 5 | -1 | 1 | 21 |
| 50 | ggaaucuugauξ Phvul.004G176200.1 | 5 | -1 | 1 | 21 |
| 51 | ggaaucuugauξ Phvul.004G176200.1 | 5 | -1 | 1 | 21 |
| 52 | ggaaucuugauξ Phvul.004G176200.1 | 5 | -1 | 1 | 21 |
| 53 | ggaaucuugauξ Phvul.004G176200.1 | 5 | -1 | 1 | 21 |
| 54 | ggaaucuugauξ Phvul.004G176200.1 | 5 | -1 | 1 | 21 |
| 55 | ggaaucuugauξ Phvul.004G176200.1 | 5 | -1 | 1 | 21 |
| 56 | ggaaucuugauξ Phvul.004G176200.1 | 5 | -1 | 1 | 24 |
| 57 | uggaaucuuga Phvul.004G176200.1 | 5 | -1 | 1 | 22 |
| 58 | uggaaucuuga Phvul.005G057900.1 | 5 | -1 | 1 | 22 |
| 59 | uggaaucuuga Phvul.005G057900.1 | 5 | -1 | 1 | 22 |
| 60 | uggaaucuuga Phvul.005G068800.2 | 5 | -1 | 1 | 22 |
| | uggaaucuuga Phvul.005G068800.1 | 5 | -1 | 1 | 22 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξ Phvul.006G055700.1 | 5 | -1 | 1 | 21 |
| 3 | ggaaucuugauξ Phvul.006G055700.1 | 5 | -1 | 1 | 21 |
| 4 | ggaaucuugauξ Phvul.006G055700.1 | 5 | -1 | 1 | 21 |
| 5 | ggaaucuugauξ Phvul.006G055700.1 | 5 | -1 | 1 | 21 |
| 6 | ggaaucuugauξ Phvul.006G055700.1 | 5 | -1 | 1 | 21 |
| 7 | ggaaucuugauξ Phvul.006G055700.1 | 5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξ Phvul.006G055700.1 | 5 | -1 | 1 | 21 |
| 9 | ggaaucuugauξ Phvul.006G055700.1 | 5 | -1 | 1 | 21 |
| 10 | ggaaucuugauξ Phvul.006G055700.1 | 5 | -1 | 1 | 21 |
| 11 | ggaaucuugauξ Phvul.006G055700.1 | 5 | -1 | 1 | 21 |
| 12 | ggaaucuugauξ Phvul.006G055700.1 | 5 | -1 | 1 | 21 |
| 13 | ggaaucuugauξ Phvul.006G055700.1 | 5 | -1 | 1 | 21 |
| 14 | ggaaucuugauξ Phvul.006G055700.1 | 5 | -1 | 1 | 21 |
| 15 | uggaaucuugaι Phvul.006G106300.1 | 5 | -1 | 1 | 22 |
| 16 | uggaaucuugaι Phvul.006G106400.1 | 5 | -1 | 1 | 22 |
| 17 | uggaaucuugaι Phvul.006G106400.2 | 5 | -1 | 1 | 22 |
| 18 | uggaaucuugaι Phvul.006G106400.2 | 5 | -1 | 1 | 22 |
| 19 | ggaaucuugauξ Phvul.006G112211.1 | 5 | -1 | 1 | 21 |
| 20 | ggaaucuugauξ Phvul.006G112211.1 | 5 | -1 | 1 | 21 |
| 21 | ggaaucuugauξ Phvul.006G112211.1 | 5 | -1 | 1 | 21 |
| 22 | ggaaucuugauξ Phvul.006G112211.1 | 5 | -1 | 1 | 21 |
| 23 | ggaaucuugauξ Phvul.006G112211.1 | 5 | -1 | 1 | 21 |
| 24 | ggaaucuugauξ Phvul.006G112211.1 | 5 | -1 | 1 | 21 |
| 25 | ggaaucuugauξ Phvul.006G112211.1 | 5 | -1 | 1 | 21 |
| 26 | ggaaucuugauξ Phvul.006G112211.1 | 5 | -1 | 1 | 21 |
| 27 | ggaaucuugauξ Phvul.006G112211.1 | 5 | -1 | 1 | 21 |
| 28 | ggaaucuugauξ Phvul.006G112211.1 | 5 | -1 | 1 | 21 |
| 29 | ggaaucuugauξ Phvul.006G112211.1 | 5 | -1 | 1 | 21 |
| 30 | ggaaucuugauξ Phvul.006G112211.1 | 5 | -1 | 1 | 21 |
| 31 | ggaaucuugauξ Phvul.006G112211.1 | 5 | -1 | 1 | 21 |
| 32 | ggaaucuugauξ Phvul.006G112211.1 | 5 | -1 | 1 | 24 |
| 33 | ggaaucuugauξ Phvul.006G117900.1 | 5 | -1 | 1 | 21 |
| 34 | ggaaucuugauξ Phvul.006G117900.1 | 5 | -1 | 1 | 21 |
| 35 | ggaaucuugauξ Phvul.006G117900.1 | 5 | -1 | 1 | 21 |
| 36 | ggaaucuugauξ Phvul.006G117900.1 | 5 | -1 | 1 | 21 |
| 37 | ggaaucuugauξ Phvul.006G117900.1 | 5 | -1 | 1 | 21 |
| 38 | ggaaucuugauξ Phvul.006G117900.1 | 5 | -1 | 1 | 21 |
| 39 | ggaaucuugauξ Phvul.006G117900.1 | 5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξ Phvul.006G117900.1 | 5 | -1 | 1 | 21 |
| 41 | ggaaucuugauξ Phvul.006G117900.1 | 5 | -1 | 1 | 21 |
| 42 | ggaaucuugauξ Phvul.006G117900.1 | 5 | -1 | 1 | 21 |
| 43 | ggaaucuugauξ Phvul.006G117900.1 | 5 | -1 | 1 | 21 |
| 44 | ggaaucuugauξ Phvul.006G117900.1 | 5 | -1 | 1 | 21 |
| 45 | ggaaucuugauξ Phvul.006G117900.1 | 5 | -1 | 1 | 21 |
| 46 | ggaaucuugauξ Phvul.006G117900.1 | 5 | -1 | 1 | 21 |
| 47 | uggaaucuugaι Phvul.006G139100.1 | 5 | -1 | 1 | 22 |
| 48 | ggaaucuugauξ Phvul.007G199700.2 | 5 | -1 | 1 | 21 |
| 49 | ggaaucuugauξ Phvul.007G199700.2 | 5 | -1 | 1 | 21 |
| 50 | ggaaucuugauξ Phvul.007G199700.2 | 5 | -1 | 1 | 21 |
| 51 | ggaaucuugauξ Phvul.007G199700.2 | 5 | -1 | 1 | 21 |
| 52 | ggaaucuugauξ Phvul.007G199700.2 | 5 | -1 | 1 | 21 |
| 53 | ggaaucuugauξ Phvul.007G199700.2 | 5 | -1 | 1 | 21 |
| 54 | ggaaucuugauξ Phvul.007G199700.2 | 5 | -1 | 1 | 21 |
| 55 | ggaaucuugauξ Phvul.007G199700.2 | 5 | -1 | 1 | 21 |
| 56 | ggaaucuugauξ Phvul.007G199700.2 | 5 | -1 | 1 | 21 |
| 57 | ggaaucuugauξ Phvul.007G199700.2 | 5 | -1 | 1 | 21 |
| 58 | ggaaucuugauξ Phvul.007G199700.2 | 5 | -1 | 1 | 21 |
| 59 | ggaaucuugauξ Phvul.007G199700.2 | 5 | -1 | 1 | 21 |
| 60 | ggaaucuugauξ Phvul.007G199700.2 | 5 | -1 | 1 | 21 |
| | ggaaucuugauξ Phvul.007G227900.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.007G227900.1 | 5 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.007G227900.1 | 5 | -1 | 1 | 21 |
| 4 | ggaaucuugauξPhvul.007G227900.1 | 5 | -1 | 1 | 21 |
| 5 | ggaaucuugauξPhvul.007G227900.1 | 5 | -1 | 1 | 21 |
| 6 | ggaaucuugauξPhvul.007G227900.1 | 5 | -1 | 1 | 21 |
| 7 | ggaaucuugauξPhvul.007G227900.1 | 5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.007G227900.1 | 5 | -1 | 1 | 21 |
| 9 | ggaaucuugauξPhvul.007G227900.1 | 5 | -1 | 1 | 21 |
| 10 | ggaaucuugauξPhvul.007G227900.1 | 5 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.007G227900.1 | 5 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.007G227900.1 | 5 | -1 | 1 | 21 |
| 13 | ggaaucuugauξPhvul.007G227900.1 | 5 | -1 | 1 | 21 |
| 14 | uggaaucuugaI Phvul.007G252700.1 | 5 | -1 | 1 | 22 |
| 15 | ggaaucuugauξPhvul.008G003900.1 | 5 | -1 | 1 | 24 |
| 16 | uggaaucuugaI Phvul.008G003900.1 | 5 | -1 | 1 | 22 |
| 17 | ggaaucuugauξPhvul.008G041600.1 | 5 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.008G041600.1 | 5 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.008G041600.1 | 5 | -1 | 1 | 21 |
| 20 | ggaaucuugauξPhvul.008G041600.1 | 5 | -1 | 1 | 21 |
| 21 | ggaaucuugauξPhvul.008G041600.1 | 5 | -1 | 1 | 21 |
| 22 | ggaaucuugauξPhvul.008G041600.1 | 5 | -1 | 1 | 21 |
| 23 | ggaaucuugauξPhvul.008G041600.1 | 5 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.008G041600.1 | 5 | -1 | 1 | 21 |
| 25 | ggaaucuugauξPhvul.008G041600.1 | 5 | -1 | 1 | 21 |
| 26 | ggaaucuugauξPhvul.008G041600.1 | 5 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.008G041600.1 | 5 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.008G041600.1 | 5 | -1 | 1 | 21 |
| 29 | ggaaucuugauξPhvul.008G041600.1 | 5 | -1 | 1 | 21 |
| 30 | ggaaucuugauξPhvul.008G041600.1 | 5 | -1 | 1 | 21 |
| 31 | uggaaucuugaI Phvul.008G041600.1 | 5 | -1 | 1 | 22 |
| 32 | uggaaucuugaI Phvul.008G081500.1 | 5 | -1 | 1 | 22 |
| 33 | uggaaucuugaI Phvul.008G093200.1 | 5 | -1 | 1 | 22 |
| 34 | uggaaucuugaI Phvul.008G093200.1 | 5 | -1 | 1 | 22 |
| 35 | ggaaucuugauξPhvul.008G176200.1 | 5 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.008G176200.1 | 5 | -1 | 1 | 21 |
| 37 | ggaaucuugauξPhvul.008G176200.1 | 5 | -1 | 1 | 21 |
| 38 | ggaaucuugauξPhvul.008G176200.1 | 5 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.008G176200.1 | 5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.008G176200.1 | 5 | -1 | 1 | 21 |
| 41 | ggaaucuugauξPhvul.008G176200.1 | 5 | -1 | 1 | 21 |
| 42 | ggaaucuugauξPhvul.008G176200.1 | 5 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.008G176200.1 | 5 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.008G176200.1 | 5 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.008G176200.1 | 5 | -1 | 1 | 21 |
| 46 | ggaaucuugauξPhvul.008G176200.1 | 5 | -1 | 1 | 21 |
| 47 | ggaaucuugauξPhvul.008G176200.1 | 5 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.008G199500.1 | 5 | -1 | 1 | 24 |
| 49 | uggaaucuugaI Phvul.008G199500.1 | 5 | -1 | 1 | 22 |
| 50 | uggaaucuugaI Phvul.008G199500.1 | 5 | -1 | 1 | 22 |
| 51 | ggaaucuugauξPhvul.008G257400.1 | 5 | -1 | 1 | 24 |
| 52 | ggaaucuugauξPhvul.009G092600.1 | 5 | -1 | 1 | 21 |
| 53 | ggaaucuugauξPhvul.009G092600.1 | 5 | -1 | 1 | 21 |
| 54 | ggaaucuugauξPhvul.009G092600.1 | 5 | -1 | 1 | 21 |
| 55 | ggaaucuugauξPhvul.009G092600.1 | 5 | -1 | 1 | 21 |
| 56 | ggaaucuugauξPhvul.009G092600.1 | 5 | -1 | 1 | 21 |
| 57 | ggaaucuugauξPhvul.009G092600.1 | 5 | -1 | 1 | 21 |
| 58 | ggaaucuugauξPhvul.009G092600.1 | 5 | -1 | 1 | 21 |
| 59 | ggaaucuugauξPhvul.009G092600.1 | 5 | -1 | 1 | 21 |
| 60 | ggaaucuugauξPhvul.009G092600.1 | 5 | -1 | 1 | 21 |
| | ggaaucuugauξPhvul.009G092600.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ggaaucuugauξPhvul.009G092600.1 | 5 | -1 | 1 | 21 |
| 3 | ggaaucuugauξPhvul.009G092600.1 | 5 | -1 | 1 | 21 |
| 4 | uggaaucuugaI Phvul.009G092600.1 | 5 | -1 | 1 | 22 |
| 5 | | | | | |
| 6 | ggaaucuugauξPhvul.010G053600.1 | 5 | -1 | 1 | 24 |
| 7 | ggaaucuugauξPhvul.011G035700.2 | 5 | -1 | 1 | 21 |
| 8 | ggaaucuugauξPhvul.011G035700.2 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | ggaaucuugauξPhvul.011G035700.2 | 5 | -1 | 1 | 21 |
| 11 | ggaaucuugauξPhvul.011G035700.2 | 5 | -1 | 1 | 21 |
| 12 | ggaaucuugauξPhvul.011G035700.2 | 5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | ggaaucuugauξPhvul.011G035700.2 | 5 | -1 | 1 | 21 |
| 15 | ggaaucuugauξPhvul.011G035700.2 | 5 | -1 | 1 | 21 |
| 16 | ggaaucuugauξPhvul.011G035700.2 | 5 | -1 | 1 | 21 |
| 17 | ggaaucuugauξPhvul.011G035700.2 | 5 | -1 | 1 | 21 |
| 18 | ggaaucuugauξPhvul.011G035700.2 | 5 | -1 | 1 | 21 |
| 19 | ggaaucuugauξPhvul.011G035700.2 | 5 | -1 | 1 | 21 |
| 20 | uggaaucuugaI Phvul.011G082801.1 | 5 | -1 | 1 | 22 |
| 21 | | | | | |
| 22 | uggaaucuugaI Phvul.011G147000.1 | 5 | -1 | 1 | 22 |
| 23 | ggaaucuugauξPhvul.011G152100.3 | 5 | -1 | 1 | 21 |
| 24 | ggaaucuugauξPhvul.011G152100.1 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | ggaaucuugauξPhvul.011G152100.3 | 5 | -1 | 1 | 21 |
| 27 | ggaaucuugauξPhvul.011G152100.1 | 5 | -1 | 1 | 21 |
| 28 | ggaaucuugauξPhvul.011G152100.3 | 5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | ggaaucuugauξPhvul.011G152100.1 | 5 | -1 | 1 | 21 |
| 31 | ggaaucuugauξPhvul.011G152100.3 | 5 | -1 | 1 | 21 |
| 32 | ggaaucuugauξPhvul.011G152100.1 | 5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | ggaaucuugauξPhvul.011G152100.3 | 5 | -1 | 1 | 21 |
| 35 | ggaaucuugauξPhvul.011G152100.1 | 5 | -1 | 1 | 21 |
| 36 | ggaaucuugauξPhvul.011G152100.3 | 5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | ggaaucuugauξPhvul.011G152100.1 | 5 | -1 | 1 | 21 |
| 39 | ggaaucuugauξPhvul.011G152100.3 | 5 | -1 | 1 | 21 |
| 40 | ggaaucuugauξPhvul.011G152100.1 | 5 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | ggaaucuugauξPhvul.011G152100.3 | 5 | -1 | 1 | 21 |
| 43 | ggaaucuugauξPhvul.011G152100.1 | 5 | -1 | 1 | 21 |
| 44 | ggaaucuugauξPhvul.011G152100.3 | 5 | -1 | 1 | 21 |
| 45 | ggaaucuugauξPhvul.011G152100.1 | 5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | ggaaucuugauξPhvul.011G152100.3 | 5 | -1 | 1 | 21 |
| 48 | ggaaucuugauξPhvul.011G152100.1 | 5 | -1 | 1 | 21 |
| 49 | ggaaucuugauξPhvul.011G152100.3 | 5 | -1 | 1 | 24 |
| 50 | ggaaucuugauξPhvul.011G152100.3 | 5 | -1 | 1 | 24 |
| 51 | ggaaucuugauξPhvul.011G152100.1 | 5 | -1 | 1 | 24 |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|------|----------------|------------------|---------------|--------------|
| 1 | | | | | |
| 2 | 13 | 33 GGAAUCUUG | CCUCAGCAUC | Translation | pacid=371693 |
| 3 | 13 | 33 GGAAUCUUG | CCUCAGCAUC | Translation | pacid=371693 |
| 4 | 13 | 33 GGAAUCUUG | CCUCAGCAUC | Translation | pacid=371693 |
| 5 | 13 | 33 GGAAUCUUG | CCUCAGCAUC | Translation | pacid=371693 |
| 6 | 13 | 33 GGAAUCUUG | CCUCAGCAUC | Translation | pacid=371693 |
| 7 | 10 | 33 GGAAUCUUG | UUUCCUCAG | (Translation) | pacid=371693 |
| 8 | 13 | 34 UGGAUCUU | CCUCAGCAUC | Translation | pacid=371693 |
| 9 | | | | | |
| 10 | 657 | 678 UGGAUCUU |AGUCAGCAG | Cleavage | pacid=371678 |
| 11 | 725 | 746 UGGAUCUU |AGUCAGCAG | Cleavage | pacid=371678 |
| 12 | 460 | 480 GGAAUCUUG | ::: GCGCUGCAU | / Cleavage | pacid=371786 |
| 13 | 460 | 480 GGAAUCUUG | ::: GCGCUGCAU | / Cleavage | pacid=371786 |
| 14 | 460 | 480 GGAAUCUUG | ::: GCGCUGCAU | / Cleavage | pacid=371786 |
| 15 | 460 | 480 GGAAUCUUG | ::: GCGCUGCAU | / Cleavage | pacid=371786 |
| 16 | 460 | 480 GGAAUCUUG | ::: GCGCUGCAU | / Cleavage | pacid=371786 |
| 17 | 460 | 480 GGAAUCUUG | ::: GCGCUGCAU | / Cleavage | pacid=371786 |
| 18 | 460 | 480 GGAAUCUUG | ::: GCGCUGCAU | / Cleavage | pacid=371786 |
| 19 | 460 | 480 GGAAUCUUG | ::: GCGCUGCAU | / Cleavage | pacid=371786 |
| 20 | 460 | 480 GGAAUCUUG | ::: GCGCUGCAU | / Cleavage | pacid=371786 |
| 21 | 460 | 480 GGAAUCUUG | ::: GCGCUGCAU | / Cleavage | pacid=371786 |
| 22 | 460 | 480 GGAAUCUUG | ::: GCGCUGCAU | / Cleavage | pacid=371786 |
| 23 | 460 | 480 GGAAUCUUG | ::: GCGCUGCAU | / Cleavage | pacid=371786 |
| 24 | 460 | 480 GGAAUCUUG | ::: GCGCUGCAU | / Cleavage | pacid=371786 |
| 25 | 460 | 480 GGAAUCUUG | ::: GCGCUGCAU | / Cleavage | pacid=371786 |
| 26 | 637 | 658 UGGAUCUU | ::: GAUCAGCAU | (Translation) | pacid=371757 |
| 27 | 251 | 272 UGGAUCUU | ::: UUCGGCGU | (Translation) | pacid=371760 |
| 28 | 446 | 467 UGGAUCUU | ::: UCCAGCUU | (Translation) | pacid=371756 |
| 29 | 672 | 693 UGGAUCUU | ::: UCCAGCUU | (Translation) | pacid=371756 |
| 30 | | | | | |
| 31 | 186 | 207 UGGAUCUU |CACCAGCGUC | Cleavage | pacid=371456 |
| 32 | 165 | 186 UGGAUCUU |CACCAGCGUC | Cleavage | pacid=371462 |
| 33 | 1854 | 1874 GGAAUCUUG | ::: AUGUAUCUU | (Cleavage) | pacid=371541 |
| 34 | 1854 | 1874 GGAAUCUUG | ::: AUGUAUCUU | (Cleavage) | pacid=371541 |
| 35 | 1854 | 1874 GGAAUCUUG | ::: AUGUAUCUU | (Cleavage) | pacid=371541 |
| 36 | 1854 | 1874 GGAAUCUUG | ::: AUGUAUCUU | (Cleavage) | pacid=371541 |
| 37 | 1854 | 1874 GGAAUCUUG | ::: AUGUAUCUU | (Cleavage) | pacid=371541 |
| 38 | 1854 | 1874 GGAAUCUUG | ::: AUGUAUCUU | (Cleavage) | pacid=371541 |
| 39 | 1854 | 1874 GGAAUCUUG | ::: AUGUAUCUU | (Cleavage) | pacid=371541 |
| 40 | 1854 | 1874 GGAAUCUUG | ::: AUGUAUCUU | (Cleavage) | pacid=371541 |
| 41 | 1854 | 1874 GGAAUCUUG | ::: AUGUAUCUU | (Cleavage) | pacid=371541 |
| 42 | 1854 | 1874 GGAAUCUUG | ::: AUGUAUCUU | (Cleavage) | pacid=371541 |
| 43 | 1854 | 1874 GGAAUCUUG | ::: AUGUAUCUU | (Cleavage) | pacid=371541 |
| 44 | 1854 | 1874 GGAAUCUUG | ::: AUGUAUCUU | (Cleavage) | pacid=371541 |
| 45 | 1854 | 1874 GGAAUCUUG | ::: AUGUAUCUU | (Cleavage) | pacid=371541 |
| 46 | 1854 | 1874 GGAAUCUUG | ::: AUGUAUCUU | (Cleavage) | pacid=371541 |
| 47 | 1851 | 1874 GGAAUCUUG | ::: CUUAUGUAU | (Cleavage) | pacid=371541 |
| 48 | 1854 | 1875 UGGAUCUU | ::: AUGUAUCUU | (Cleavage) | pacid=371541 |
| 49 | 1903 | 1924 UGGAUCUU | ::: UUUUAUCUU | Cleavage | pacid=371531 |
| 50 | 2017 | 2038 UGGAUCUU | ::: UUUUAUCUU | Cleavage | pacid=371531 |
| 51 | 2016 | 2037 UGGAUCUU | ::: UUUUAUCUU | Cleavage | pacid=371531 |
| 52 | 1836 | 1857 UGGAUCUU | ::: CUCUACCUUC | Cleavage | pacid=371538 |
| 53 | | | | | |
| 54 | 18 | 38 GGAAUCUUG | ::: CAUCAUCAUC | Cleavage | pacid=371523 |
| 55 | 18 | 38 GGAAUCUUG | ::: CAUCAUCAUC | Cleavage | pacid=371523 |
| 56 | 18 | 38 GGAAUCUUG | ::: CAUCAUCAUC | Cleavage | pacid=371523 |
| 57 | 18 | 38 GGAAUCUUG | ::: CAUCAUCAUC | Cleavage | pacid=371523 |
| 58 | 18 | 38 GGAAUCUUG | ::: CAUCAUCAUC | Cleavage | pacid=371523 |
| 59 | 18 | 38 GGAAUCUUG | ::: CAUCAUCAUC | Cleavage | pacid=371523 |
| 60 | 18 | 38 GGAAUCUUG | ::: CAUCAUCAUC | Cleavage | pacid=371523 |

| | | | | |
|----|------|------|---|--------------|
| 1 | | | | |
| 2 | 18 | 38 | GGAAUCUUG, :: ::::: CAUCAUCAUC Cleavage | pacid=371523 |
| 3 | 18 | 38 | GGAAUCUUG, :: ::::: CAUCAUCAUC Cleavage | pacid=371523 |
| 4 | 18 | 38 | GGAAUCUUG, :: ::::: CAUCAUCAUC Cleavage | pacid=371523 |
| 5 | 18 | 38 | GGAAUCUUG, :: ::::: CAUCAUCAUC Cleavage | pacid=371523 |
| 6 | 18 | 38 | GGAAUCUUG, :: ::::: CAUCAUCAUC Cleavage | pacid=371523 |
| 7 | 15 | 38 | GGAAUCUUG, :: : ::::: UGGCAUCAUC Cleavage | pacid=371523 |
| 8 | 18 | 39 | UGGAAUCUUG, :: ::::: CAUCAUCAUC Cleavage | pacid=371523 |
| 9 | | | | |
| 10 | 764 | 785 | UGGAAUCUUG, ::::: AUGUAGCAUC Cleavage | pacid=371539 |
| 11 | 764 | 785 | UGGAAUCUUG, ::::: AUGUAGCAUC Cleavage | pacid=371539 |
| 12 | 604 | 623 | GGAAUCUUG, ::::: GUGCAGU-UC Cleavage | pacid=371730 |
| 13 | 604 | 623 | GGAAUCUUG, ::::: GUGCAGU-UC Cleavage | pacid=371730 |
| 14 | 604 | 623 | GGAAUCUUG, ::::: GUGCAGU-UC Cleavage | pacid=371730 |
| 15 | 604 | 623 | GGAAUCUUG, ::::: GUGCAGU-UC Cleavage | pacid=371730 |
| 16 | 604 | 623 | GGAAUCUUG, ::::: GUGCAGU-UC Cleavage | pacid=371730 |
| 17 | 604 | 623 | GGAAUCUUG, ::::: GUGCAGU-UC Cleavage | pacid=371730 |
| 18 | 604 | 623 | GGAAUCUUG, ::::: GUGCAGU-UC Cleavage | pacid=371730 |
| 19 | 604 | 623 | GGAAUCUUG, ::::: GUGCAGU-UC Cleavage | pacid=371730 |
| 20 | 604 | 623 | GGAAUCUUG, ::::: GUGCAGU-UC Cleavage | pacid=371730 |
| 21 | 604 | 623 | GGAAUCUUG, ::::: GUGCAGU-UC Cleavage | pacid=371730 |
| 22 | 604 | 623 | GGAAUCUUG, ::::: GUGCAGU-UC Cleavage | pacid=371730 |
| 23 | 604 | 623 | GGAAUCUUG, ::::: GUGCAGU-UC Cleavage | pacid=371730 |
| 24 | 604 | 623 | GGAAUCUUG, ::::: GUGCAGU-UC Cleavage | pacid=371730 |
| 25 | 604 | 623 | GGAAUCUUG, ::::: GUGCAGU-UC Cleavage | pacid=371730 |
| 26 | 601 | 623 | GGAAUCUUG, : ::::: AAGGUGCAGI Cleavage | pacid=371730 |
| 27 | 1503 | 1524 | UGGAAUCUUG, ::::: CAGCAGCAUC Cleavage | pacid=371641 |
| 28 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 29 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 30 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 31 | 339 | 359 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 32 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 33 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 34 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 35 | 339 | 359 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 36 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 37 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 38 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 39 | 339 | 359 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 40 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 41 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 42 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 43 | 339 | 359 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 44 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 45 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 46 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 47 | 339 | 359 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 48 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 49 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 50 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 51 | 339 | 359 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 52 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 53 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 54 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 55 | 339 | 359 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 56 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 57 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 58 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 59 | 339 | 359 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| 60 | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |
| | 342 | 362 | GGAAUCUUG, :: : ::::: CUCCGCCAUC Cleavage | pacid=371597 |

| | | | | |
|----|------|-------------------------------------|------------------------|--------------|
| 1 | | | | |
| 2 | 339 | 359 GGAAUCUUG) :: . ::::::::::::::: | CUCCGCCAUC Cleavage | pacid=371597 |
| 3 | 342 | 362 GGAAUCUUG) :: . ::::::::::::::: | CUCCGCCAUC Cleavage | pacid=371597 |
| 4 | 342 | 362 GGAAUCUUG) :: . ::::::::::::::: | CUCCGCCAUC Cleavage | pacid=371597 |
| 5 | 342 | 362 GGAAUCUUG) :: . ::::::::::::::: | CUCCGCCAUC Cleavage | pacid=371597 |
| 6 | 339 | 359 GGAAUCUUG) :: . ::::::::::::::: | CUCCGCCAUC Cleavage | pacid=371597 |
| 7 | 339 | 362 GGAAUCUUG) :: . ::::::::::::::: | AUCCUCCGCC Cleavage | pacid=371597 |
| 8 | 339 | 362 GGAAUCUUG) :: . ::::::::::::::: | AUCCUCCGCC Cleavage | pacid=371597 |
| 9 | 339 | 362 GGAAUCUUG) :: . ::::::::::::::: | AUCCUCCGCC Cleavage | pacid=371597 |
| 10 | 336 | 359 GGAAUCUUG) :: . ::::::::::::::: | AUCCUCCGCC Cleavage | pacid=371597 |
| 11 | 342 | 363 UGGAUCUU) :: . ::::::::::::::: | CUCCGCCAUC Cleavage | pacid=371597 |
| 12 | 342 | 363 UGGAUCUU) :: . ::::::::::::::: | CUCCGCCAUC Cleavage | pacid=371597 |
| 13 | 342 | 363 UGGAUCUU) :: . ::::::::::::::: | CUCCGCCAUC Cleavage | pacid=371597 |
| 14 | 339 | 360 UGGAUCUU) :: . ::::::::::::::: | CUCCGCCAUC Cleavage | pacid=371597 |
| 15 | 467 | 487 GGAAUCUUG) :: . ::::::::::::::: | GAGUGGCAC(Cleavage | pacid=371506 |
| 16 | 467 | 487 GGAAUCUUG) :: . ::::::::::::::: | GAGUGGCAC(Cleavage | pacid=371506 |
| 17 | 467 | 487 GGAAUCUUG) :: . ::::::::::::::: | GAGUGGCAC(Cleavage | pacid=371506 |
| 18 | 467 | 487 GGAAUCUUG) :: . ::::::::::::::: | GAGUGGCAC(Cleavage | pacid=371506 |
| 19 | 467 | 487 GGAAUCUUG) :: . ::::::::::::::: | GAGUGGCAC(Cleavage | pacid=371506 |
| 20 | 467 | 487 GGAAUCUUG) :: . ::::::::::::::: | GAGUGGCAC(Cleavage | pacid=371506 |
| 21 | 467 | 487 GGAAUCUUG) :: . ::::::::::::::: | GAGUGGCAC(Cleavage | pacid=371506 |
| 22 | 467 | 487 GGAAUCUUG) :: . ::::::::::::::: | GAGUGGCAC(Cleavage | pacid=371506 |
| 23 | 467 | 487 GGAAUCUUG) :: . ::::::::::::::: | GAGUGGCAC(Cleavage | pacid=371506 |
| 24 | 467 | 487 GGAAUCUUG) :: . ::::::::::::::: | GAGUGGCAC(Cleavage | pacid=371506 |
| 25 | 467 | 487 GGAAUCUUG) :: . ::::::::::::::: | GAGUGGCAC(Cleavage | pacid=371506 |
| 26 | 467 | 487 GGAAUCUUG) :: . ::::::::::::::: | GAGUGGCAC(Cleavage | pacid=371506 |
| 27 | 467 | 487 GGAAUCUUG) :: . ::::::::::::::: | GAGUGGCAC(Cleavage | pacid=371506 |
| 28 | 464 | 487 GGAAUCUUG) :: . ::::::::::::::: | GCGGAGUGG(Cleavage | pacid=371506 |
| 29 | 151 | 172 UGGAUCUU) :: . ::::::::::::::: | CAUCAUCAUC Cleavage | pacid=371511 |
| 30 | 151 | 172 UGGAUCUU) :: . ::::::::::::::: | CAUCAUCAUC Cleavage | pacid=371511 |
| 31 | 873 | 894 UGGAUCUU) :: . ::::::::::::::: | AUGUAGCAU(Cleavage | pacid=371559 |
| 32 | 1868 | 1889 UGGAUCUU) :: . ::::::::::::::: | CUUUAUCUU(Cleavage | pacid=371556 |
| 33 | 1850 | 1871 UGGAUCUU) :: . ::::::::::::::: | CUUUAUCUU(Cleavage | pacid=371565 |
| 34 | 1850 | 1871 UGGAUCUU) :: . ::::::::::::::: | CUUUAUCUU(Cleavage | pacid=371565 |
| 35 | 1850 | 1871 UGGAUCUU) :: . ::::::::::::::: | CUUUAUCUU(Cleavage | pacid=371565 |
| 36 | 1832 | 1853 UGGAUCUU) :: . ::::::::::::::: | CUAUAUCUU(Cleavage | pacid=371556 |
| 37 | 1914 | 1935 UGGAUCUU) :: . ::::::::::::::: | CUAUAUCUU(Cleavage | pacid=371556 |
| 38 | 1914 | 1935 UGGAUCUU) :: . ::::::::::::::: | CUAUAUCUU(Cleavage | pacid=371556 |
| 39 | 1917 | 1938 UGGAUCUU) :: . ::::::::::::::: | CUAUAUCUU(Cleavage | pacid=371556 |
| 40 | 1935 | 1956 UGGAUCUU) :: . ::::::::::::::: | CUUUAUCUU(Cleavage | pacid=371563 |
| 41 | 1935 | 1956 UGGAUCUU) :: . ::::::::::::::: | CUUUAUCUU(Cleavage | pacid=371563 |
| 42 | 1839 | 1860 UGGAUCUU) :: . ::::::::::::::: | CUUUAUCUU(Cleavage | pacid=371559 |
| 43 | 147 | 168 UGGAUCUU) :: . ::::::::::::::: | GUGGAGCAU(Cleavage | pacid=371678 |
| 44 | 403 | 424 UGGAUCUU) :: . ::::::::::::::: | GUGGAGCAU(Cleavage | pacid=371678 |
| 45 | 132 | 152 GGAAUCUUG) :: . ::::::::::::::: | GUGCUGCAU(Translation | pacid=371702 |
| 46 | 132 | 152 GGAAUCUUG) :: . ::::::::::::::: | GUGCUGCAU(Translation | pacid=371702 |
| 47 | 132 | 152 GGAAUCUUG) :: . ::::::::::::::: | GUGCUGCAU(Translation | pacid=371702 |
| 48 | 132 | 152 GGAAUCUUG) :: . ::::::::::::::: | GUGCUGCAU(Translation | pacid=371702 |
| 49 | 132 | 152 GGAAUCUUG) :: . ::::::::::::::: | GUGCUGCAU(Translation | pacid=371702 |
| 50 | 132 | 152 GGAAUCUUG) :: . ::::::::::::::: | GUGCUGCAU(Translation | pacid=371702 |
| 51 | 132 | 152 GGAAUCUUG) :: . ::::::::::::::: | GUGCUGCAU(Translation | pacid=371702 |
| 52 | 132 | 152 GGAAUCUUG) :: . ::::::::::::::: | GUGCUGCAU(Translation | pacid=371702 |
| 53 | 132 | 152 GGAAUCUUG) :: . ::::::::::::::: | GUGCUGCAU(Translation | pacid=371702 |
| 54 | 132 | 152 GGAAUCUUG) :: . ::::::::::::::: | GUGCUGCAU(Translation | pacid=371702 |
| 55 | 132 | 152 GGAAUCUUG) :: . ::::::::::::::: | GUGCUGCAU(Translation | pacid=371702 |
| 56 | 132 | 152 GGAAUCUUG) :: . ::::::::::::::: | GUGCUGCAU(Translation | pacid=371702 |
| 57 | 132 | 152 GGAAUCUUG) :: . ::::::::::::::: | GUGCUGCAU(Translation | pacid=371702 |
| 58 | 132 | 152 GGAAUCUUG) :: . ::::::::::::::: | GUGCUGCAU(Translation | pacid=371702 |
| 59 | 129 | 152 GGAAUCUUG) :: . ::::::::::::::: | AUCGUGCUG(Translation | pacid=371702 |
| 60 | 132 | 153 UGGAUCUU) :: . ::::::::::::::: | GUGCUGCAU(Cleavage | pacid=371702 |
| | 445 | 466 UGGAUCUU) :: . ::::::::::::::: | GUGGAGCAU(Cleavage | pacid=371703 |

| | | | | | |
|----|------|-----------------|------------------------|----------|--------------|
| 1 | | | | | |
| 2 | 186 | 206 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371456 |
| 3 | 186 | 206 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371456 |
| 4 | 186 | 206 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371456 |
| 5 | 186 | 206 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371456 |
| 6 | 186 | 206 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371456 |
| 7 | 186 | 206 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371456 |
| 8 | 165 | 185 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371462 |
| 9 | 165 | 185 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371462 |
| 10 | 165 | 185 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371462 |
| 11 | 165 | 185 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371462 |
| 12 | 165 | 185 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371462 |
| 13 | 165 | 185 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371462 |
| 14 | 165 | 185 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371462 |
| 15 | 165 | 185 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371462 |
| 16 | 165 | 185 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371462 |
| 17 | 165 | 185 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371462 |
| 18 | 165 | 185 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371462 |
| 19 | 165 | 185 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371462 |
| 20 | 165 | 185 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371462 |
| 21 | 165 | 185 GGAAUCUUG, |: CACCAGCGUC | Cleavage | pacid=371462 |
| 22 | 1430 | 1450 GGAAUCUUG, | ::: UCUCACCAUC | Cleavage | pacid=371544 |
| 23 | 1430 | 1450 GGAAUCUUG, | ::: UCUCACCAUC | Cleavage | pacid=371544 |
| 24 | 1430 | 1450 GGAAUCUUG, | ::: UCUCACCAUC | Cleavage | pacid=371544 |
| 25 | 1430 | 1450 GGAAUCUUG, | ::: UCUCACCAUC | Cleavage | pacid=371544 |
| 26 | 1430 | 1450 GGAAUCUUG, | ::: UCUCACCAUC | Cleavage | pacid=371544 |
| 27 | 1430 | 1450 GGAAUCUUG, | ::: UCUCACCAUC | Cleavage | pacid=371544 |
| 28 | 1430 | 1450 GGAAUCUUG, | ::: UCUCACCAUC | Cleavage | pacid=371544 |
| 29 | 1430 | 1450 GGAAUCUUG, | ::: UCUCACCAUC | Cleavage | pacid=371544 |
| 30 | 1430 | 1450 GGAAUCUUG, | ::: UCUCACCAUC | Cleavage | pacid=371544 |
| 31 | 1430 | 1450 GGAAUCUUG, | ::: UCUCACCAUC | Cleavage | pacid=371544 |
| 32 | 1430 | 1450 GGAAUCUUG, | ::: UCUCACCAUC | Cleavage | pacid=371544 |
| 33 | 1430 | 1450 GGAAUCUUG, | ::: UCUCACCAUC | Cleavage | pacid=371544 |
| 34 | 1430 | 1450 GGAAUCUUG, | ::: UCUCACCAUC | Cleavage | pacid=371544 |
| 35 | 1096 | 1117 UGGAUCUU: | :: :: CUUCACUACC | Cleavage | pacid=371722 |
| 36 | 1247 | 1268 UGGAUCUU: | :: :: CUUCACUACC | Cleavage | pacid=371722 |
| 37 | 1203 | 1223 GGAAUCUUG, | ...:: GGGUGGCCUI | Cleavage | pacid=371734 |
| 38 | 1203 | 1223 GGAAUCUUG, | ...:: GGGUGGCCUI | Cleavage | pacid=371734 |
| 39 | 1203 | 1223 GGAAUCUUG, | ...:: GGGUGGCCUI | Cleavage | pacid=371734 |
| 40 | 1203 | 1223 GGAAUCUUG, | ...:: GGGUGGCCUI | Cleavage | pacid=371734 |
| 41 | 1203 | 1223 GGAAUCUUG, | ...:: GGGUGGCCUI | Cleavage | pacid=371734 |
| 42 | 1203 | 1223 GGAAUCUUG, | ...:: GGGUGGCCUI | Cleavage | pacid=371734 |
| 43 | 1203 | 1223 GGAAUCUUG, | ...:: GGGUGGCCUI | Cleavage | pacid=371734 |
| 44 | 1203 | 1223 GGAAUCUUG, | ...:: GGGUGGCCUI | Cleavage | pacid=371734 |
| 45 | 1203 | 1223 GGAAUCUUG, | ...:: GGGUGGCCUI | Cleavage | pacid=371734 |
| 46 | 1203 | 1223 GGAAUCUUG, | ...:: GGGUGGCCUI | Cleavage | pacid=371734 |
| 47 | 1203 | 1223 GGAAUCUUG, | ...:: GGGUGGCCUI | Cleavage | pacid=371734 |
| 48 | 1203 | 1223 GGAAUCUUG, | ...:: GGGUGGCCUI | Cleavage | pacid=371734 |
| 49 | 1203 | 1223 GGAAUCUUG, | ...:: GGGUGGCCUI | Cleavage | pacid=371734 |
| 50 | 1203 | 1223 GGAAUCUUG, | ...:: GGGUGGCCUI | Cleavage | pacid=371734 |
| 51 | 195 | 216 UGGAUCUU: |:UCAAGACAUC | Cleavage | pacid=371729 |
| 52 | 1892 | 1912 GGAAUCUUG, | :: :: UUGGGGAAU | Cleavage | pacid=371729 |
| 53 | 1892 | 1912 GGAAUCUUG, | :: :: UUGGGGAAU | Cleavage | pacid=371729 |
| 54 | 1892 | 1912 GGAAUCUUG, | :: :: UUGGGGAAU | Cleavage | pacid=371729 |
| 55 | 1892 | 1912 GGAAUCUUG, | :: :: UUGGGGAAU | Cleavage | pacid=371729 |
| 56 | 1892 | 1912 GGAAUCUUG, | :: :: UUGGGGAAU | Cleavage | pacid=371729 |
| 57 | 1892 | 1912 GGAAUCUUG, | :: :: UUGGGGAAU | Cleavage | pacid=371729 |
| 58 | 1892 | 1912 GGAAUCUUG, | :: :: UUGGGGAAU | Cleavage | pacid=371729 |
| 59 | 1892 | 1912 GGAAUCUUG, | :: :: UUGGGGAAU | Cleavage | pacid=371729 |
| 60 | 1892 | 1912 GGAAUCUUG, | :: :: UUGGGGAAU | Cleavage | pacid=371729 |
| | 1892 | 1912 GGAAUCUUG, | :: :: UUGGGGAAU | Cleavage | pacid=371729 |

| | | | | |
|----|------|-----------------------|-----------------------------|--------------|
| 1 | | | | |
| 2 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 3 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 4 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 5 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 6 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 7 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 8 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 9 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 10 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 11 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 12 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 13 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 14 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 15 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 16 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 17 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 18 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 19 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 20 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 21 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 22 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 23 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 24 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 25 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 26 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 27 | 1154 | 1174 GGAAUCUUG, ... | AUGCGAAAUC Cleavage | pacid=371505 |
| 28 | 1044 | 1064 GGAAUCUUG, | CUGCAAUAU Cleavage | pacid=371487 |
| 29 | 1044 | 1064 GGAAUCUUG, | CUGCAAUAU Cleavage | pacid=371487 |
| 30 | 1044 | 1064 GGAAUCUUG, | CUGCAAUAU Cleavage | pacid=371487 |
| 31 | 1044 | 1064 GGAAUCUUG, | CUGCAAUAU Cleavage | pacid=371487 |
| 32 | 1044 | 1064 GGAAUCUUG, | CUGCAAUAU Cleavage | pacid=371487 |
| 33 | 1044 | 1064 GGAAUCUUG, | CUGCAAUAU Cleavage | pacid=371487 |
| 34 | 1044 | 1064 GGAAUCUUG, | CUGCAAUAU Cleavage | pacid=371487 |
| 35 | 1044 | 1064 GGAAUCUUG, | CUGCAAUAU Cleavage | pacid=371487 |
| 36 | 1044 | 1064 GGAAUCUUG, | CUGCAAUAU Cleavage | pacid=371487 |
| 37 | 1044 | 1064 GGAAUCUUG, | CUGCAAUAU Cleavage | pacid=371487 |
| 38 | 1044 | 1064 GGAAUCUUG, | CUGCAAUAU Cleavage | pacid=371487 |
| 39 | 1044 | 1064 GGAAUCUUG, | CUGCAAUAU Cleavage | pacid=371487 |
| 40 | 1044 | 1064 GGAAUCUUG, | CUGCAAUAU Cleavage | pacid=371487 |
| 41 | 1041 | 1064 GGAAUCUUG, | UGCCUGCAAL Cleavage | pacid=371487 |
| 42 | 467 | 488 UGGAUCUU, | GAGUGGCAC Cleavage | pacid=371506 |
| 43 | 286 | 306 GGAAUCUUG, | AUGCAGCAU Translation | pacid=371433 |
| 44 | 286 | 306 GGAAUCUUG, | AUGCAGCAU Translation | pacid=371433 |
| 45 | 286 | 306 GGAAUCUUG, | AUGCAGCAU Translation | pacid=371433 |
| 46 | 286 | 306 GGAAUCUUG, | AUGCAGCAU Translation | pacid=371433 |
| 47 | 286 | 306 GGAAUCUUG, | AUGCAGCAU Translation | pacid=371433 |
| 48 | 286 | 306 GGAAUCUUG, | AUGCAGCAU Translation | pacid=371433 |
| 49 | 286 | 306 GGAAUCUUG, | AUGCAGCAU Translation | pacid=371433 |
| 50 | 286 | 306 GGAAUCUUG, | AUGCAGCAU Translation | pacid=371433 |
| 51 | 286 | 306 GGAAUCUUG, | AUGCAGCAU Translation | pacid=371433 |
| 52 | 286 | 306 GGAAUCUUG, | AUGCAGCAU Translation | pacid=371433 |
| 53 | 286 | 306 GGAAUCUUG, | AUGCAGCAU Translation | pacid=371433 |
| 54 | 286 | 306 GGAAUCUUG, | AUGCAGCAU Translation | pacid=371433 |
| 55 | 286 | 306 GGAAUCUUG, | AUGCAGCAU Translation | pacid=371433 |
| 56 | 286 | 306 GGAAUCUUG, | AUGCAGCAU Translation | pacid=371433 |
| 57 | 283 | 306 GGAAUCUUG, | AGCAUGCAG Translation | pacid=371433 |
| 58 | 286 | 307 UGGAUCUU, | AUGCAGCAU Translation | pacid=371433 |
| 59 | 1306 | 1327 UGGAUCUU, | AUGCAGGAC Translation | pacid=371570 |
| 60 | 2984 | 3004 GGAAUCUUG, | CUGUGGCAU Cleavage | pacid=371569 |

| | | | | |
|----|------|---|--------------|--|
| 1 | | | | |
| 2 | 1397 | 1417 GGAAUCUUG,..... UUGCACCGU Cleavage | pacid=371485 | |
| 3 | 1397 | 1417 GGAAUCUUG,..... UUGCACCGU Cleavage | pacid=371485 | |
| 4 | 1397 | 1417 GGAAUCUUG,..... UUGCACCGU Cleavage | pacid=371485 | |
| 5 | 1397 | 1417 GGAAUCUUG,..... UUGCACCGU Cleavage | pacid=371485 | |
| 6 | 1397 | 1417 GGAAUCUUG,..... UUGCACCGU Cleavage | pacid=371485 | |
| 7 | 1397 | 1417 GGAAUCUUG,..... UUGCACCGU Cleavage | pacid=371485 | |
| 8 | 1397 | 1417 GGAAUCUUG,..... UUGCACCGU Cleavage | pacid=371485 | |
| 9 | 1397 | 1417 GGAAUCUUG,..... UUGCACCGU Cleavage | pacid=371485 | |
| 10 | 1397 | 1417 GGAAUCUUG,..... UUGCACCGU Cleavage | pacid=371485 | |
| 11 | 1397 | 1417 GGAAUCUUG,..... UUGCACCGU Cleavage | pacid=371485 | |
| 12 | 1397 | 1417 GGAAUCUUG,..... UUGCACCGU Cleavage | pacid=371485 | |
| 13 | 1397 | 1417 GGAAUCUUG,..... UUGCACCGU Cleavage | pacid=371485 | |
| 14 | 1394 | 1417 GGAAUCUUG,..... UUAUUGCAC(Cleavage | pacid=371485 | |
| 15 | 249 | 271 GGAAUCUUG-AAGCAGCAUC Cleavage | pacid=371446 | |
| 16 | 249 | 271 GGAAUCUUG-AAGCAGCAUC Cleavage | pacid=371446 | |
| 17 | 249 | 271 GGAAUCUUG-AAGCAGCAUC Cleavage | pacid=371446 | |
| 18 | 249 | 271 GGAAUCUUG-AAGCAGCAUC Cleavage | pacid=371446 | |
| 19 | 249 | 271 GGAAUCUUG-AAGCAGCAUC Cleavage | pacid=371446 | |
| 20 | 249 | 271 GGAAUCUUG-AAGCAGCAUC Cleavage | pacid=371446 | |
| 21 | 249 | 271 GGAAUCUUG-AAGCAGCAUC Cleavage | pacid=371446 | |
| 22 | 249 | 271 GGAAUCUUG-AAGCAGCAUC Cleavage | pacid=371446 | |
| 23 | 249 | 271 GGAAUCUUG-AAGCAGCAUC Cleavage | pacid=371446 | |
| 24 | 249 | 271 GGAAUCUUG-AAGCAGCAUC Cleavage | pacid=371446 | |
| 25 | 249 | 271 GGAAUCUUG-AAGCAGCAUC Cleavage | pacid=371446 | |
| 26 | 249 | 271 GGAAUCUUG-AAGCAGCAUC Cleavage | pacid=371446 | |
| 27 | 249 | 271 GGAAUCUUG-AAGCAGCAUC Cleavage | pacid=371446 | |
| 28 | 246 | 271 GGAAUCUUG-AGAAAGCAGC Cleavage | pacid=371446 | |
| 29 | 249 | 272 UGGAUCUUGAAGCAGCAUC Translation | pacid=371446 | |
| 30 | | | | |
| 31 | 1104 | 1125 UGGAUCUUGAUUUUGUAU Cleavage | pacid=371685 | |
| 32 | 311 | 331 GGAAUCUUG,..... UCGCGGUGU(Translation | pacid=371712 | |
| 33 | 311 | 331 GGAAUCUUG,..... UCGCGGUGU(Translation | pacid=371712 | |
| 34 | 311 | 331 GGAAUCUUG,..... UCGCGGUGU(Translation | pacid=371712 | |
| 35 | 311 | 331 GGAAUCUUG,..... UCGCGGUGU(Translation | pacid=371712 | |
| 36 | 311 | 331 GGAAUCUUG,..... UCGCGGUGU(Translation | pacid=371712 | |
| 37 | 311 | 331 GGAAUCUUG,..... UCGCGGUGU(Translation | pacid=371712 | |
| 38 | 311 | 331 GGAAUCUUG,..... UCGCGGUGU(Translation | pacid=371712 | |
| 39 | 311 | 331 GGAAUCUUG,..... UCGCGGUGU(Translation | pacid=371712 | |
| 40 | 311 | 331 GGAAUCUUG,..... UCGCGGUGU(Translation | pacid=371712 | |
| 41 | 311 | 331 GGAAUCUUG,..... UCGCGGUGU(Translation | pacid=371712 | |
| 42 | 311 | 331 GGAAUCUUG,..... UCGCGGUGU(Translation | pacid=371712 | |
| 43 | 311 | 331 GGAAUCUUG,..... UCGCGGUGU(Translation | pacid=371712 | |
| 44 | 311 | 331 GGAAUCUUG,..... UCGCGGUGU(Translation | pacid=371712 | |
| 45 | 154 | 174 GGAAUCUUG,..... CCUCAGCAUC Cleavage | pacid=371703 | |
| 46 | 154 | 174 GGAAUCUUG,..... CCUCAGCAUC Cleavage | pacid=371703 | |
| 47 | 154 | 174 GGAAUCUUG,..... CCUCAGCAUC Cleavage | pacid=371703 | |
| 48 | 154 | 174 GGAAUCUUG,..... CCUCAGCAUC Cleavage | pacid=371703 | |
| 49 | 154 | 174 GGAAUCUUG,..... CCUCAGCAUC Cleavage | pacid=371703 | |
| 50 | 154 | 174 GGAAUCUUG,..... CCUCAGCAUC Cleavage | pacid=371703 | |
| 51 | 154 | 174 GGAAUCUUG,..... CCUCAGCAUC Cleavage | pacid=371703 | |
| 52 | 154 | 174 GGAAUCUUG,..... CCUCAGCAUC Cleavage | pacid=371703 | |
| 53 | 154 | 174 GGAAUCUUG,..... CCUCAGCAUC Cleavage | pacid=371703 | |
| 54 | 154 | 174 GGAAUCUUG,..... CCUCAGCAUC Cleavage | pacid=371703 | |
| 55 | 154 | 174 GGAAUCUUG,..... CCUCAGCAUC Cleavage | pacid=371703 | |
| 56 | 154 | 174 GGAAUCUUG,..... CCUCAGCAUC Cleavage | pacid=371703 | |
| 57 | 154 | 174 GGAAUCUUG,..... CCUCAGCAUC Cleavage | pacid=371703 | |
| 58 | 657 | 677 GGAAUCUUG,..... AGUCAGCAGI Cleavage | pacid=371678 | |
| 59 | 725 | 745 GGAAUCUUG,..... AGUCAGCAGI Cleavage | pacid=371678 | |
| 60 | 657 | 677 GGAAUCUUG,..... AGUCAGCAGI Cleavage | pacid=371678 | |

| | | | | |
|----|-------|------------------|---------------------------|--------------------------|
| 1 | | | | |
| 2 | 248 | 271 GGAAUCUUG/ | :: ::::: ::::UCGUUUCGG | Translation pacid=371760 |
| 3 | 1999 | 2020 UGGAUCUU(: | :: ::::: ::::CUAGAGUI | Cleavage pacid=371787 |
| 4 | 446 | 466 GGAAUCUUG/ | :: ::::: ::::UCCAGCUU | Cleavage pacid=371756 |
| 5 | 672 | 692 GGAAUCUUG/ | :: ::::: ::::UCCAGCUU | Cleavage pacid=371756 |
| 6 | 446 | 466 GGAAUCUUG/ | :: ::::: ::::UCCAGCUU | Cleavage pacid=371756 |
| 7 | 672 | 692 GGAAUCUUG/ | :: ::::: ::::UCCAGCUU | Cleavage pacid=371756 |
| 8 | 446 | 466 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 9 | 672 | 692 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 10 | 446 | 466 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 11 | 672 | 692 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 12 | 446 | 466 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 13 | 672 | 692 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 14 | 446 | 466 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 15 | 672 | 692 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 16 | 446 | 466 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 17 | 672 | 692 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 18 | 446 | 466 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 19 | 672 | 692 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 20 | 446 | 466 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 21 | 672 | 692 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 22 | 446 | 466 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 23 | 672 | 692 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 24 | 446 | 466 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 25 | 672 | 692 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 26 | 446 | 466 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 27 | 672 | 692 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 28 | 446 | 466 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 29 | 672 | 692 GGAAUCUUG/ | :: ::::: :~::~:UCCAGCUU | Cleavage pacid=371756 |
| 30 | 261 | 281 GGAAUCUUG/ | :: ::::: :~::~:CAAAGCAGC | Cleavage pacid=371448 |
| 31 | 261 | 281 GGAAUCUUG/ | :: ::::: :~::~:CAAAGCAGC | Cleavage pacid=371448 |
| 32 | 261 | 281 GGAAUCUUG/ | :: ::::: :~::~:CAAAGCAGC | Cleavage pacid=371448 |
| 33 | 261 | 281 GGAAUCUUG/ | :: ::::: :~::~:CAAAGCAGC | Cleavage pacid=371448 |
| 34 | 261 | 281 GGAAUCUUG/ | :: ::::: :~::~:CAAAGCAGC | Cleavage pacid=371448 |
| 35 | 261 | 281 GGAAUCUUG/ | :: ::::: :~::~:CAAAGCAGC | Cleavage pacid=371448 |
| 36 | 261 | 281 GGAAUCUUG/ | :: ::::: :~::~:CAAAGCAGC | Cleavage pacid=371448 |
| 37 | 261 | 281 GGAAUCUUG/ | :: ::::: :~::~:CAAAGCAGC | Cleavage pacid=371448 |
| 38 | 261 | 281 GGAAUCUUG/ | :: ::::: :~::~:CAAAGCAGC | Cleavage pacid=371448 |
| 39 | 261 | 281 GGAAUCUUG/ | :: ::::: :~::~:CAAAGCAGC | Cleavage pacid=371448 |
| 40 | 261 | 281 GGAAUCUUG/ | :: ::::: :~::~:CAAAGCAGC | Cleavage pacid=371448 |
| 41 | 261 | 281 GGAAUCUUG/ | :: ::::: :~::~:CAAAGCAGC | Cleavage pacid=371448 |
| 42 | 261 | 281 GGAAUCUUG/ | :: ::::: :~::~:CAAAGCAGC | Cleavage pacid=371448 |
| 43 | 12225 | 12246 UGGAUCUU(: | :: ::::: :~::~:CAGCGCUU | Translation pacid=371454 |
| 44 | 2133 | 2153 GGAAUCUUG/ | :: ::::: :~::~:CGGCAGCAU | Translation pacid=371445 |
| 45 | 2133 | 2153 GGAAUCUUG/ | :: ::::: :~::~:CGGCAGCAU | Translation pacid=371445 |
| 46 | 2133 | 2153 GGAAUCUUG/ | :: ::::: :~::~:CGGCAGCAU | Translation pacid=371445 |
| 47 | 2133 | 2153 GGAAUCUUG/ | :: ::::: :~::~:CGGCAGCAU | Translation pacid=371445 |
| 48 | 2133 | 2153 GGAAUCUUG/ | :: ::::: :~::~:CGGCAGCAU | Translation pacid=371445 |
| 49 | 2133 | 2153 GGAAUCUUG/ | :: ::::: :~::~:CGGCAGCAU | Translation pacid=371445 |
| 50 | 2133 | 2153 GGAAUCUUG/ | :: ::::: :~::~:CGGCAGCAU | Translation pacid=371445 |
| 51 | 2133 | 2153 GGAAUCUUG/ | :: ::::: :~::~:CGGCAGCAU | Translation pacid=371445 |
| 52 | 2133 | 2153 GGAAUCUUG/ | :: ::::: :~::~:CGGCAGCAU | Translation pacid=371445 |
| 53 | 2133 | 2153 GGAAUCUUG/ | :: ::::: :~::~:CGGCAGCAU | Translation pacid=371445 |
| 54 | 2133 | 2153 GGAAUCUUG/ | :: ::::: :~::~:CGGCAGCAU | Translation pacid=371445 |
| 55 | 2133 | 2153 GGAAUCUUG/ | :: ::::: :~::~:CGGCAGCAU | Translation pacid=371445 |
| 56 | 2133 | 2153 GGAAUCUUG/ | :: ::::: :~::~:CGGCAGCAU | Translation pacid=371445 |
| 57 | 2133 | 2153 GGAAUCUUG/ | :: ::::: :~::~:CGGCAGCAU | Translation pacid=371445 |
| 58 | 2130 | 2153 GGAAUCUUG/ | :: ::::: :~::~:CCCCGGCAGC | Translation pacid=371445 |
| 59 | 1083 | 1103 GGAAUCUUG/ | :: ::::: :~::~:GUGUGGCAU | Cleavage pacid=371476 |
| 60 | 1216 | 1236 GGAAUCUUG/ | :: ::::: :~::~:GUGUGGCAU | Cleavage pacid=371476 |

| | | | | |
|----|------|--|--------------|--|
| 1 | | | | |
| 2 | 381 | 401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation | pacid=371633 | |
| 3 | 381 | 401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation | pacid=371633 | |
| 4 | 381 | 401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation | pacid=371633 | |
| 5 | 381 | 401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation | pacid=371633 | |
| 6 | 381 | 401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation | pacid=371633 | |
| 7 | 381 | 401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation | pacid=371633 | |
| 8 | 381 | 401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation | pacid=371633 | |
| 9 | 381 | 401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation | pacid=371633 | |
| 10 | 381 | 401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation | pacid=371633 | |
| 11 | 381 | 401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation | pacid=371633 | |
| 12 | 381 | 401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation | pacid=371633 | |
| 13 | 381 | 401 GGAAUCUUG,::: :::: ::::: UUGCUCU(Translation | pacid=371633 | |
| 14 | 378 | 401 GGAAUCUUG,::: :::: ::::: CUUUUGCUU(Translation | pacid=371633 | |
| 15 | 1146 | 1167 UGGAUCUU(: :::: : ::::: UUCCAGUACC Cleavage | pacid=371632 | |
| 16 | 1151 | 1172 UGGAUCUU(: :::: : ::::: UUCCAGUACC Cleavage | pacid=371631 | |
| 17 | | | | |
| 18 | 1181 | 1201 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 19 | 1262 | 1282 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 20 | 1181 | 1201 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 21 | 1262 | 1282 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 22 | 1181 | 1201 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 23 | 1262 | 1282 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 24 | 1181 | 1201 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 25 | 1262 | 1282 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 26 | 1181 | 1201 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 27 | 1262 | 1282 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 28 | 1181 | 1201 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 29 | 1262 | 1282 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 30 | 1181 | 1201 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 31 | 1262 | 1282 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 32 | 1181 | 1201 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 33 | 1262 | 1282 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 34 | 1181 | 1201 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 35 | 1262 | 1282 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 36 | 1181 | 1201 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 37 | 1262 | 1282 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 38 | 1181 | 1201 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 39 | 1262 | 1282 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 40 | 1181 | 1201 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 41 | 1262 | 1282 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 42 | 1181 | 1201 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 43 | 1262 | 1282 GGAAUCUUG, ::::: : : : GUGCAGCAU(Cleavage | pacid=371529 | |
| 44 | 1836 | 1856 GGAAUCUUG,::: : : ::::: CUCUACCUUC Cleavage | pacid=371538 | |
| 45 | 1836 | 1856 GGAAUCUUG,::: : : ::::: CUCUACCUUC Cleavage | pacid=371538 | |
| 46 | 1836 | 1856 GGAAUCUUG,::: : : ::::: CUCUACCUUC Cleavage | pacid=371538 | |
| 47 | 1836 | 1856 GGAAUCUUG,::: : : ::::: CUCUACCUUC Cleavage | pacid=371538 | |
| 48 | 1836 | 1856 GGAAUCUUG,::: : : ::::: CUCUACCUUC Cleavage | pacid=371538 | |
| 49 | 1836 | 1856 GGAAUCUUG,::: : : ::::: CUCUACCUUC Cleavage | pacid=371538 | |
| 50 | 1836 | 1856 GGAAUCUUG,::: : : ::::: CUCUACCUUC Cleavage | pacid=371538 | |
| 51 | 1836 | 1856 GGAAUCUUG,::: : : ::::: CUCUACCUUC Cleavage | pacid=371538 | |
| 52 | 1836 | 1856 GGAAUCUUG,::: : : ::::: CUCUACCUUC Cleavage | pacid=371538 | |
| 53 | 1836 | 1856 GGAAUCUUG,::: : : ::::: CUCUACCUUC Cleavage | pacid=371538 | |
| 54 | 1836 | 1856 GGAAUCUUG,::: : : ::::: CUCUACCUUC Cleavage | pacid=371538 | |
| 55 | 1836 | 1856 GGAAUCUUG,::: : : ::::: CUCUACCUUC Cleavage | pacid=371538 | |
| 56 | 1836 | 1856 GGAAUCUUG,::: : : ::::: CUCUACCUUC Cleavage | pacid=371538 | |
| 57 | 1833 | 1856 GGAAUCUUG,::: : : ::::: CUUCUCUACC Cleavage | pacid=371538 | |
| 58 | 888 | 908 GGAAUCUUG,::: . ::::: CUUCGUCAU(Cleavage | pacid=371540 | |
| 59 | 899 | 919 GGAAUCUUG,::: . ::::: CUUCGUCAU(Cleavage | pacid=371540 | |
| 60 | 888 | 908 GGAAUCUUG,::: . ::::: CUUCGUCAU(Cleavage | pacid=371540 | |

| | | | | |
|----|-----|-------------------------------------|-------------|--------------|
| 1 | | | | |
| 2 | 249 | 270 GGAAU-CUUG:::: ::::: CUGCUGCAUC | Cleavage | pacid=371645 |
| 3 | 249 | 270 GGAAU-CUUG:::: ::::: CUGCUGCAUC | Cleavage | pacid=371645 |
| 4 | 249 | 270 GGAAU-CUUG:::: ::::: CUGCUGCAUC | Cleavage | pacid=371645 |
| 5 | 249 | 270 GGAAU-CUUG:::: ::::: CUGCUGCAUC | Cleavage | pacid=371645 |
| 6 | 249 | 270 GGAAU-CUUG:::: ::::: CUGCUGCAUC | Cleavage | pacid=371645 |
| 7 | 249 | 270 GGAAU-CUUG:::: ::::: CUGCUGCAUC | Cleavage | pacid=371645 |
| 8 | 249 | 270 GGAAU-CUUG:::: ::::: CUGCUGCAUC | Cleavage | pacid=371645 |
| 9 | 249 | 270 GGAAU-CUUG:::: ::::: CUGCUGCAUC | Cleavage | pacid=371645 |
| 10 | 249 | 270 GGAAU-CUUG:::: ::::: CUGCUGCAUC | Cleavage | pacid=371645 |
| 11 | 249 | 270 GGAAU-CUUG:::: ::::: CUGCUGCAUC | Cleavage | pacid=371645 |
| 12 | 249 | 270 GGAAU-CUUG:::: ::::: CUGCUGCAUC | Cleavage | pacid=371645 |
| 13 | 249 | 270 GGAAU-CUUG:::: ::::: CUGCUGCAUC | Cleavage | pacid=371645 |
| 14 | 249 | 270 GGAAU-CUUG:::: ::::: CUGCUGCAUC | Cleavage | pacid=371645 |
| 15 | 246 | 270 GGAAU-CUUG:::: ::::: UUGCUGCUG | Cleavage | pacid=371645 |
| 16 | 249 | 271 UGGAU-CUU:::: ::::: CUGCUGCAUC | Cleavage | pacid=371645 |
| 17 | 143 | 163 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 18 | 204 | 224 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 19 | 143 | 163 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 20 | 204 | 224 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 21 | 143 | 163 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 22 | 204 | 224 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 23 | 143 | 163 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 24 | 204 | 224 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 25 | 143 | 163 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 26 | 204 | 224 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 27 | 143 | 163 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 28 | 204 | 224 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 29 | 143 | 163 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 30 | 204 | 224 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 31 | 143 | 163 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 32 | 204 | 224 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 33 | 143 | 163 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 34 | 204 | 224 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 35 | 143 | 163 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 36 | 204 | 224 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 37 | 143 | 163 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 38 | 204 | 224 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 39 | 143 | 163 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 40 | 204 | 224 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 41 | 143 | 163 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 42 | 204 | 224 GGAAUCUUG, ::::: AUGUAGUUU | Cleavage | pacid=371666 |
| 43 | 230 | 250 GGAAUCUUG, ::::: CUGCAGAAUC | Translation | pacid=371577 |
| 44 | 230 | 250 GGAAUCUUG, ::::: CUGCAGAAUC | Translation | pacid=371577 |
| 45 | 230 | 250 GGAAUCUUG, ::::: CUGCAGAAUC | Translation | pacid=371577 |
| 46 | 230 | 250 GGAAUCUUG, ::::: CUGCAGAAUC | Translation | pacid=371577 |
| 47 | 230 | 250 GGAAUCUUG, ::::: CUGCAGAAUC | Translation | pacid=371577 |
| 48 | 230 | 250 GGAAUCUUG, ::::: CUGCAGAAUC | Translation | pacid=371577 |
| 49 | 230 | 250 GGAAUCUUG, ::::: CUGCAGAAUC | Translation | pacid=371577 |
| 50 | 230 | 250 GGAAUCUUG, ::::: CUGCAGAAUC | Translation | pacid=371577 |
| 51 | 230 | 250 GGAAUCUUG, ::::: CUGCAGAAUC | Translation | pacid=371577 |
| 52 | 230 | 250 GGAAUCUUG, ::::: CUGCAGAAUC | Translation | pacid=371577 |
| 53 | 230 | 250 GGAAUCUUG, ::::: CUGCAGAAUC | Translation | pacid=371577 |
| 54 | 230 | 250 GGAAUCUUG, ::::: CUGCAGAAUC | Translation | pacid=371577 |
| 55 | 230 | 250 GGAAUCUUG, ::::: CUGCAGAAUC | Translation | pacid=371577 |
| 56 | 230 | 250 GGAAUCUUG, ::::: CUGCAGAAUC | Translation | pacid=371577 |
| 57 | 227 | 250 GGAAUCUUG, ::::: CAGCUGCAGA | Translation | pacid=371577 |
| 58 | 741 | 761 GGAAUCUUG, ::::: UUGGAGCGU | Cleavage | pacid=371604 |
| 59 | 741 | 761 GGAAUCUUG, ::::: UUGGAGCGU | Cleavage | pacid=371604 |
| 60 | 741 | 761 GGAAUCUUG, ::::: UUGGAGCGU | Cleavage | pacid=371604 |

| | | | | |
|----|------|--|--|--------------|
| 1 | | | | |
| 2 | 1448 | 1469 GGAAUCUUG,.....: ..:.....:UUGUAUGUA Cleavage | | pacid=371614 |
| 3 | 1448 | 1469 GGAAUCUUG,.....: ..:.....:UUGUAUGUA Cleavage | | pacid=371614 |
| 4 | 1448 | 1469 GGAAUCUUG,.....: ..:.....:UUGUAUGUA Cleavage | | pacid=371614 |
| 5 | 1448 | 1469 GGAAUCUUG,.....: ..:.....:UUGUAUGUA Cleavage | | pacid=371614 |
| 6 | 1448 | 1469 GGAAUCUUG,.....: ..:.....:UUGUAUGUA Cleavage | | pacid=371614 |
| 7 | 1448 | 1469 GGAAUCUUG,.....: ..:.....:UUGUAUGUA Cleavage | | pacid=371614 |
| 8 | 1445 | 1469 GGAAUCUUG,: ..:.....:UACUUGUAU Cleavage | | pacid=371614 |
| 9 | 1044 | 1065 UGGAUCUU.....: ..:.....:CUGCAAUAU Cleavage | | pacid=371487 |
| 10 | | | | |
| 11 | 65 | 85 GGAAUCUUG,: ..:.....:UGAUAGCAU Cleavage | | pacid=371423 |
| 12 | 65 | 85 GGAAUCUUG,: ..:.....:UGAUAGCAU Cleavage | | pacid=371423 |
| 13 | 65 | 85 GGAAUCUUG,: ..:.....:UGAUAGCAU Cleavage | | pacid=371423 |
| 14 | 65 | 85 GGAAUCUUG,: ..:.....:UGAUAGCAU Cleavage | | pacid=371423 |
| 15 | 65 | 85 GGAAUCUUG,: ..:.....:UGAUAGCAU Cleavage | | pacid=371423 |
| 16 | 65 | 85 GGAAUCUUG,: ..:.....:UGAUAGCAU Cleavage | | pacid=371423 |
| 17 | 65 | 85 GGAAUCUUG,: ..:.....:UGAUAGCAU Cleavage | | pacid=371423 |
| 18 | 65 | 85 GGAAUCUUG,: ..:.....:UGAUAGCAU Cleavage | | pacid=371423 |
| 19 | 65 | 85 GGAAUCUUG,: ..:.....:UGAUAGCAU Cleavage | | pacid=371423 |
| 20 | 65 | 85 GGAAUCUUG,: ..:.....:UGAUAGCAU Cleavage | | pacid=371423 |
| 21 | 65 | 85 GGAAUCUUG,: ..:.....:UGAUAGCAU Cleavage | | pacid=371423 |
| 22 | 65 | 85 GGAAUCUUG,: ..:.....:UGAUAGCAU Cleavage | | pacid=371423 |
| 23 | 65 | 85 GGAAUCUUG,: ..:.....:UGAUAGCAU Cleavage | | pacid=371423 |
| 24 | 329 | 350 UGGAUCUU.....: ..:.....:UUGCAGCAG Cleavage | | pacid=371436 |
| 25 | | | | |
| 26 | 102 | 122 GGAAUCUUG,: ..:.....:CAGCAGCAGC Cleavage | | pacid=371568 |
| 27 | 102 | 122 GGAAUCUUG,: ..:.....:CAGCAGCAGC Cleavage | | pacid=371568 |
| 28 | 102 | 122 GGAAUCUUG,: ..:.....:CAGCAGCAGC Cleavage | | pacid=371568 |
| 29 | 102 | 122 GGAAUCUUG,: ..:.....:CAGCAGCAGC Cleavage | | pacid=371568 |
| 30 | 102 | 122 GGAAUCUUG,: ..:.....:CAGCAGCAGC Cleavage | | pacid=371568 |
| 31 | 102 | 122 GGAAUCUUG,: ..:.....:CAGCAGCAGC Cleavage | | pacid=371568 |
| 32 | 102 | 122 GGAAUCUUG,: ..:.....:CAGCAGCAGC Cleavage | | pacid=371568 |
| 33 | 102 | 122 GGAAUCUUG,: ..:.....:CAGCAGCAGC Cleavage | | pacid=371568 |
| 34 | 102 | 122 GGAAUCUUG,: ..:.....:CAGCAGCAGC Cleavage | | pacid=371568 |
| 35 | 102 | 122 GGAAUCUUG,: ..:.....:CAGCAGCAGC Cleavage | | pacid=371568 |
| 36 | 102 | 122 GGAAUCUUG,: ..:.....:CAGCAGCAGC Cleavage | | pacid=371568 |
| 37 | 102 | 122 GGAAUCUUG,: ..:.....:CAGCAGCAGC Cleavage | | pacid=371568 |
| 38 | 102 | 122 GGAAUCUUG,: ..:.....:CAGCAGCAGC Cleavage | | pacid=371568 |
| 39 | 102 | 123 UGGAUCUU.....: ..:.....:CAGCAGCAGC Cleavage | | pacid=371568 |
| 40 | 695 | 716 UGGAUCUU.....: ..:.....:ACUCCCAUC Cleavage | | pacid=371547 |
| 41 | 695 | 716 UGGAUCUU.....: ..:.....:ACUCCCAUC Cleavage | | pacid=371547 |
| 42 | | | | |
| 43 | 1306 | 1326 GGAAUCUUG,: ..:.....:AUGCAGGACC Translation | | pacid=371570 |
| 44 | 1306 | 1326 GGAAUCUUG,: ..:.....:AUGCAGGACC Translation | | pacid=371570 |
| 45 | 1306 | 1326 GGAAUCUUG,: ..:.....:AUGCAGGACC Translation | | pacid=371570 |
| 46 | 1306 | 1326 GGAAUCUUG,: ..:.....:AUGCAGGACC Translation | | pacid=371570 |
| 47 | 1306 | 1326 GGAAUCUUG,: ..:.....:AUGCAGGACC Translation | | pacid=371570 |
| 48 | 1306 | 1326 GGAAUCUUG,: ..:.....:AUGCAGGACC Translation | | pacid=371570 |
| 49 | 1306 | 1326 GGAAUCUUG,: ..:.....:AUGCAGGACC Translation | | pacid=371570 |
| 50 | 1306 | 1326 GGAAUCUUG,: ..:.....:AUGCAGGACC Translation | | pacid=371570 |
| 51 | 1306 | 1326 GGAAUCUUG,: ..:.....:AUGCAGGACC Translation | | pacid=371570 |
| 52 | 1306 | 1326 GGAAUCUUG,: ..:.....:AUGCAGGACC Translation | | pacid=371570 |
| 53 | 1306 | 1326 GGAAUCUUG,: ..:.....:AUGCAGGACC Translation | | pacid=371570 |
| 54 | 1306 | 1326 GGAAUCUUG,: ..:.....:AUGCAGGACC Translation | | pacid=371570 |
| 55 | 1306 | 1326 GGAAUCUUG,: ..:.....:AUGCAGGACC Translation | | pacid=371570 |
| 56 | 426 | 446 GGAAUCUUG,: ..:.....:UGACAGUGU Translation | | pacid=371553 |
| 57 | 426 | 446 GGAAUCUUG,: ..:.....:UGACAGUGU Translation | | pacid=371553 |
| 58 | 426 | 446 GGAAUCUUG,: ..:.....:UGACAGUGU Translation | | pacid=371553 |
| 59 | 426 | 446 GGAAUCUUG,: ..:.....:UGACAGUGU Translation | | pacid=371553 |
| 60 | 426 | 446 GGAAUCUUG,: ..:.....:UGACAGUGU Translation | | pacid=371553 |

| | | | | |
|----|------|---|--|--------------|
| 1 | | | | |
| 2 | 1731 | 1751 GGAAUCUUG, ::::: : : : : : CUGCAGCUUL Cleavage | | pacid=371468 |
| 3 | 1542 | 1562 GGAAUCUUG, ::::: : : : : : CUGCAGCUUL Cleavage | | pacid=371468 |
| 4 | 1731 | 1751 GGAAUCUUG, ::::: : : : : : CUGCAGCUUL Cleavage | | pacid=371468 |
| 5 | 1542 | 1562 GGAAUCUUG, ::::: : : : : : CUGCAGCUUL Cleavage | | pacid=371468 |
| 6 | 1542 | 1562 GGAAUCUUG, ::::: : : : : : CUGCAGCUUL Cleavage | | pacid=371468 |
| 7 | 1731 | 1751 GGAAUCUUG, ::::: : : : : : CUGCAGCUUL Cleavage | | pacid=371468 |
| 8 | 1542 | 1562 GGAAUCUUG, ::::: : : : : : CUGCAGCUUL Cleavage | | pacid=371468 |
| 9 | | | | |
| 10 | 1731 | 1751 GGAAUCUUG, ::::: : : : : : CUGCAGCUUL Cleavage | | pacid=371468 |
| 11 | 1542 | 1562 GGAAUCUUG, ::::: : : : : : CUGCAGCUUL Cleavage | | pacid=371468 |
| 12 | 1731 | 1751 GGAAUCUUG, ::::: : : : : : CUGCAGCUUL Cleavage | | pacid=371468 |
| 13 | | | | |
| 14 | 2495 | 2515 GGAAUCUUG, : : : : : : CUCCAACAUU Translation | | pacid=371476 |
| 15 | 2495 | 2515 GGAAUCUUG, : : : : : : CUCCAACAUU Translation | | pacid=371476 |
| 16 | 2495 | 2515 GGAAUCUUG, : : : : : : CUCCAACAUU Translation | | pacid=371476 |
| 17 | 2495 | 2515 GGAAUCUUG, : : : : : : CUCCAACAUU Translation | | pacid=371476 |
| 18 | 2495 | 2515 GGAAUCUUG, : : : : : : CUCCAACAUU Translation | | pacid=371476 |
| 19 | 2495 | 2515 GGAAUCUUG, : : : : : : CUCCAACAUU Translation | | pacid=371476 |
| 20 | 2495 | 2515 GGAAUCUUG, : : : : : : CUCCAACAUU Translation | | pacid=371476 |
| 21 | | | | |
| 22 | 2495 | 2515 GGAAUCUUG, : : : : : : CUCCAACAUU Translation | | pacid=371476 |
| 23 | 2495 | 2515 GGAAUCUUG, : : : : : : CUCCAACAUU Translation | | pacid=371476 |
| 24 | 2495 | 2515 GGAAUCUUG, : : : : : : CUCCAACAUU Translation | | pacid=371476 |
| 25 | 2495 | 2515 GGAAUCUUG, : : : : : : CUCCAACAUU Translation | | pacid=371476 |
| 26 | 2495 | 2515 GGAAUCUUG, : : : : : : CUCCAACAUU Translation | | pacid=371476 |
| 27 | 128 | 148 GGAAUCUUG, ::::: : : : : : UUGCAGCAUI Translation | | pacid=371454 |
| 28 | 128 | 148 GGAAUCUUG, ::::: : : : : : UUGCAGCAUI Translation | | pacid=371454 |
| 29 | 128 | 148 GGAAUCUUG, ::::: : : : : : UUGCAGCAUI Translation | | pacid=371454 |
| 30 | 128 | 148 GGAAUCUUG, ::::: : : : : : UUGCAGCAUI Translation | | pacid=371454 |
| 31 | 128 | 148 GGAAUCUUG, ::::: : : : : : UUGCAGCAUI Translation | | pacid=371454 |
| 32 | 128 | 148 GGAAUCUUG, ::::: : : : : : UUGCAGCAUI Translation | | pacid=371454 |
| 33 | 128 | 148 GGAAUCUUG, ::::: : : : : : UUGCAGCAUI Translation | | pacid=371454 |
| 34 | 128 | 148 GGAAUCUUG, ::::: : : : : : UUGCAGCAUI Translation | | pacid=371454 |
| 35 | 128 | 148 GGAAUCUUG, ::::: : : : : : UUGCAGCAUI Translation | | pacid=371454 |
| 36 | 128 | 148 GGAAUCUUG, ::::: : : : : : UUGCAGCAUI Translation | | pacid=371454 |
| 37 | 128 | 148 GGAAUCUUG, ::::: : : : : : UUGCAGCAUI Translation | | pacid=371454 |
| 38 | 128 | 148 GGAAUCUUG, ::::: : : : : : UUGCAGCAUI Translation | | pacid=371454 |
| 39 | 128 | 148 GGAAUCUUG, ::::: : : : : : UUGCAGCAUI Translation | | pacid=371454 |
| 40 | 125 | 148 GGAAUCUUG, ::::: : : : : : GUGUUGCAG Translation | | pacid=371454 |
| 41 | | | | |
| 42 | 1083 | 1104 UGGAUCUUI, ::::: : : : : : GUGUGGCAU Translation | | pacid=371476 |
| 43 | 1216 | 1237 UGGAUCUUI, ::::: : : : : : GUGUGGCAU Translation | | pacid=371476 |
| 44 | 485 | 505 GGAAUCUUG, : : : : : : GAA AUGUAU Cleavage | | pacid=371481 |
| 45 | 485 | 505 GGAAUCUUG, : : : : : : GAA AUGUAU Cleavage | | pacid=371481 |
| 46 | 485 | 505 GGAAUCUUG, : : : : : : GAA AUGUAU Cleavage | | pacid=371481 |
| 47 | 485 | 505 GGAAUCUUG, : : : : : : GAA AUGUAU Cleavage | | pacid=371481 |
| 48 | 485 | 505 GGAAUCUUG, : : : : : : GAA AUGUAU Cleavage | | pacid=371481 |
| 49 | 485 | 505 GGAAUCUUG, : : : : : : GAA AUGUAU Cleavage | | pacid=371481 |
| 50 | 485 | 505 GGAAUCUUG, : : : : : : GAA AUGUAU Cleavage | | pacid=371481 |
| 51 | 485 | 505 GGAAUCUUG, : : : : : : GAA AUGUAU Cleavage | | pacid=371481 |
| 52 | 485 | 505 GGAAUCUUG, : : : : : : GAA AUGUAU Cleavage | | pacid=371481 |
| 53 | 485 | 505 GGAAUCUUG, : : : : : : GAA AUGUAU Cleavage | | pacid=371481 |
| 54 | 485 | 505 GGAAUCUUG, : : : : : : GAA AUGUAU Cleavage | | pacid=371481 |
| 55 | 485 | 505 GGAAUCUUG, : : : : : : GAA AUGUAU Cleavage | | pacid=371481 |
| 56 | 485 | 505 GGAAUCUUG, : : : : : : GAA AUGUAU Cleavage | | pacid=371481 |
| 57 | 718 | 738 GGAAUCUUG, : : : : : : UUUUGGCAU Translation | | pacid=371621 |
| 58 | 718 | 738 GGAAUCUUG, : : : : : : UUUUGGCAU Translation | | pacid=371621 |
| 59 | 718 | 738 GGAAUCUUG, : : : : : : UUUUGGCAU Translation | | pacid=371621 |
| 60 | 718 | 738 GGAAUCUUG, : : : : : : UUUUGGCAU Translation | | pacid=371621 |

| | | | | |
|----|-----|---|--------------|--|
| 1 | | | | |
| 2 | 836 | 856 GGAAUCUUG)..... UUGCUGCAG(Cleavage | pacid=371610 | |
| 3 | 938 | 958 GGAAUCUUG)..... UUGCUGCAG(Cleavage | pacid=371610 | |
| 4 | 941 | 961 GGAAUCUUG)..... UUGCUGCAG(Cleavage | pacid=371609 | |
| 5 | 833 | 853 GGAAUCUUG)..... UUGCUGCAG(Cleavage | pacid=371610 | |
| 6 | 836 | 856 GGAAUCUUG)..... UUGCUGCAG(Cleavage | pacid=371610 | |
| 7 | 938 | 958 GGAAUCUUG)..... UUGCUGCAG(Cleavage | pacid=371610 | |
| 8 | 941 | 961 GGAAUCUUG)..... UUGCUGCAG(Cleavage | pacid=371609 | |
| 9 | 833 | 853 GGAAUCUUG)..... UUGCUGCAG(Cleavage | pacid=371610 | |
| 10 | 836 | 856 GGAAUCUUG)..... UUGCUGCAG(Cleavage | pacid=371610 | |
| 11 | 938 | 958 GGAAUCUUG)..... UUGCUGCAG(Cleavage | pacid=371610 | |
| 12 | 941 | 961 GGAAUCUUG)..... UUGCUGCAG(Cleavage | pacid=371609 | |
| 13 | 833 | 853 GGAAUCUUG)..... UUGCUGCAG(Cleavage | pacid=371610 | |
| 14 | 836 | 856 GGAAUCUUG)..... UUGCUGCAG(Cleavage | pacid=371610 | |
| 15 | 938 | 958 GGAAUCUUG)..... UUGCUGCAG(Cleavage | pacid=371610 | |
| 16 | 941 | 961 GGAAUCUUG)..... UUGCUGCAG(Cleavage | pacid=371609 | |
| 17 | 833 | 853 GGAAUCUUG)..... UUGCUGCAG(Cleavage | pacid=371610 | |
| 18 | 836 | 856 GGAAUCUUG)..... UUGCUGCAG(Cleavage | pacid=371610 | |
| 19 | 938 | 958 GGAAUCUUG)..... UUGCUGCAG(Cleavage | pacid=371610 | |
| 20 | 941 | 961 GGAAUCUUG)..... UUGCUGCAG(Cleavage | pacid=371609 | |
| 21 | 830 | 853 GGAAUCUUG).....UGGUUGCUG Cleavage | pacid=371610 | |
| 22 | 833 | 856 GGAAUCUUG).....UGGUUGCUG Cleavage | pacid=371610 | |
| 23 | 935 | 958 GGAAUCUUG).....UGGUUGCUG Cleavage | pacid=371610 | |
| 24 | 938 | 961 GGAAUCUUG).....UGGUUGCUG Cleavage | pacid=371609 | |
| 25 | 833 | 854 UGGAUCUU)..... :UUGCUGCAG(Cleavage | pacid=371610 | |
| 26 | 836 | 857 UGGAUCUU)..... :UUGCUGCAG(Cleavage | pacid=371610 | |
| 27 | 938 | 959 UGGAUCUU)..... :UUGCUGCAG(Cleavage | pacid=371610 | |
| 28 | 941 | 962 UGGAUCUU)..... :UUGCUGCAG(Cleavage | pacid=371609 | |
| 29 | 504 | 525 GGAAUCUUG).....UUGCAGAUAI Cleavage | pacid=371614 | |
| 30 | 504 | 525 GGAAUCUUG).....UUGCAGAUAI Cleavage | pacid=371614 | |
| 31 | 504 | 525 GGAAUCUUG).....UUGCAGAUAI Cleavage | pacid=371614 | |
| 32 | 504 | 525 GGAAUCUUG).....UUGCAGAUAI Cleavage | pacid=371614 | |
| 33 | 504 | 525 GGAAUCUUG).....UUGCAGAUAI Cleavage | pacid=371614 | |
| 34 | 504 | 525 GGAAUCUUG).....UUGCAGAUAI Cleavage | pacid=371614 | |
| 35 | 504 | 525 GGAAUCUUG).....UUGCAGAUAI Cleavage | pacid=371614 | |
| 36 | 504 | 525 GGAAUCUUG).....UUGCAGAUAI Cleavage | pacid=371614 | |
| 37 | 504 | 525 GGAAUCUUG).....UUGCAGAUAI Cleavage | pacid=371614 | |
| 38 | 504 | 525 GGAAUCUUG).....UUGCAGAUAI Cleavage | pacid=371614 | |
| 39 | 504 | 525 GGAAUCUUG).....UUGCAGAUAI Cleavage | pacid=371614 | |
| 40 | 504 | 525 GGAAUCUUG).....UUGCAGAUAI Cleavage | pacid=371614 | |
| 41 | 504 | 525 GGAAUCUUG).....UUGCAGAUAI Cleavage | pacid=371614 | |
| 42 | 504 | 525 GGAAUCUUG).....UUGCAGAUAI Cleavage | pacid=371614 | |
| 43 | 504 | 525 GGAAUCUUG).....UUGCAGAUAI Cleavage | pacid=371614 | |
| 44 | 504 | 525 GGAAUCUUG).....UUGCAGAUAI Cleavage | pacid=371614 | |
| 45 | 501 | 525 GGAAUCUUG).....GAGUUGCAG/ Cleavage | pacid=371614 | |
| 46 | 746 | 766 GGAAUCUUG)..... UUGUGGCAU Translation | pacid=371578 | |
| 47 | 746 | 766 GGAAUCUUG)..... UUGUGGCAU Translation | pacid=371578 | |
| 48 | 746 | 766 GGAAUCUUG)..... UUGUGGCAU Translation | pacid=371578 | |
| 49 | 746 | 766 GGAAUCUUG)..... UUGUGGCAU Translation | pacid=371578 | |
| 50 | 746 | 766 GGAAUCUUG)..... UUGUGGCAU Translation | pacid=371578 | |
| 51 | 746 | 766 GGAAUCUUG)..... UUGUGGCAU Translation | pacid=371578 | |
| 52 | 746 | 766 GGAAUCUUG)..... UUGUGGCAU Translation | pacid=371578 | |
| 53 | 746 | 766 GGAAUCUUG)..... UUGUGGCAU Translation | pacid=371578 | |
| 54 | 746 | 766 GGAAUCUUG)..... UUGUGGCAU Translation | pacid=371578 | |
| 55 | 746 | 766 GGAAUCUUG)..... UUGUGGCAU Translation | pacid=371578 | |
| 56 | 746 | 766 GGAAUCUUG)..... UUGUGGCAU Translation | pacid=371578 | |
| 57 | 746 | 766 GGAAUCUUG)..... UUGUGGCAU Translation | pacid=371578 | |
| 58 | 746 | 766 GGAAUCUUG)..... UUGUGGCAU Translation | pacid=371578 | |
| 59 | 20 | 40 GGAAUCUUG)..... CUGCAGCAAC Translation | pacid=371576 | |
| 60 | 20 | 40 GGAAUCUUG)..... CUGCAGCAAC Translation | pacid=371576 | |

| | | | |
|----|------|--|--------------|
| 1 | | | |
| 2 | 20 | 40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation | pacid=371576 |
| 3 | 20 | 40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation | pacid=371576 |
| 4 | 20 | 40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation | pacid=371576 |
| 5 | 20 | 40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation | pacid=371576 |
| 6 | 20 | 40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation | pacid=371576 |
| 7 | 20 | 40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation | pacid=371576 |
| 8 | 20 | 40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation | pacid=371576 |
| 9 | 20 | 40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation | pacid=371576 |
| 10 | 20 | 40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation | pacid=371576 |
| 11 | 20 | 40 GGAAUCUUG, :::::::::: : ::::::::::.. CUGCAGCAAC Translation | pacid=371576 |
| 12 | 17 | 40 GGAAUCUUG, : :::::::::: : ::::::::::UUUCUGCAG(Translation | pacid=371576 |
| 13 | | | |
| 14 | 567 | 587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage | pacid=371598 |
| 15 | 567 | 587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage | pacid=371598 |
| 16 | 567 | 587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage | pacid=371598 |
| 17 | 567 | 587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage | pacid=371598 |
| 18 | 567 | 587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage | pacid=371598 |
| 19 | 567 | 587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage | pacid=371598 |
| 20 | 567 | 587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage | pacid=371598 |
| 21 | 567 | 587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage | pacid=371598 |
| 22 | 567 | 587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage | pacid=371598 |
| 23 | 567 | 587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage | pacid=371598 |
| 24 | 567 | 587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage | pacid=371598 |
| 25 | 567 | 587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage | pacid=371598 |
| 26 | 567 | 587 GGAAUCUUG, :: ::::::::::: :::: CUGGAGCAUI Cleavage | pacid=371598 |
| 27 | 564 | 587 GGAAUCUUG, :: ::::::::::: ::::AGGCUGGAG(Cleavage | pacid=371598 |
| 28 | 567 | 588 UGGAUCUU, : ::::::::::: :::::CUGGAGCAUI Cleavage | pacid=371598 |
| 29 | 627 | 646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage | pacid=371604 |
| 30 | 627 | 646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage | pacid=371604 |
| 31 | 627 | 646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage | pacid=371604 |
| 32 | 627 | 646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage | pacid=371604 |
| 33 | 627 | 646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage | pacid=371604 |
| 34 | 627 | 646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage | pacid=371604 |
| 35 | 627 | 646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage | pacid=371604 |
| 36 | 627 | 646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage | pacid=371604 |
| 37 | 627 | 646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage | pacid=371604 |
| 38 | 627 | 646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage | pacid=371604 |
| 39 | 627 | 646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage | pacid=371604 |
| 40 | 627 | 646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage | pacid=371604 |
| 41 | 627 | 646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage | pacid=371604 |
| 42 | 627 | 646 GGAAUCUUG, :: ::::::::::: :::: UUGAAGCAU(Cleavage | pacid=371604 |
| 43 | 1448 | 1470 UGGAUCUU, : ::::::::::: :::::UUGUAUGUA Cleavage | pacid=371614 |
| 44 | 1154 | 1175 UGGAUCUU, : ::::::::::: ::::: AUGCGAAAUCleavage | pacid=371505 |
| 45 | 1154 | 1175 UGGAUCUU, : ::::::::::: ::::: AUGCGAAAUCleavage | pacid=371505 |
| 46 | | | |
| 47 | 94 | 114 UGGAUCUU, : ::::::::::: :::::CAGCAGCAUC Translation | pacid=371511 |
| 48 | 1001 | 1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage | pacid=371502 |
| 49 | 1001 | 1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage | pacid=371502 |
| 50 | 1001 | 1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage | pacid=371502 |
| 51 | 1001 | 1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage | pacid=371502 |
| 52 | 1001 | 1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage | pacid=371502 |
| 53 | 1001 | 1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage | pacid=371502 |
| 54 | 1001 | 1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage | pacid=371502 |
| 55 | 1001 | 1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage | pacid=371502 |
| 56 | 1001 | 1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage | pacid=371502 |
| 57 | 1001 | 1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage | pacid=371502 |
| 58 | 1001 | 1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage | pacid=371502 |
| 59 | 1001 | 1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage | pacid=371502 |
| 60 | 1001 | 1021 GGAAUCUUG, :: ::::::::::: ::::: UUACAGCAUI Cleavage | pacid=371502 |
| | 65 | 86 UGGAUCUU, : ::::::::::: :::::UGAUAGCAU(Cleavage | pacid=371423 |

| | | | | | |
|----|------|------|---|--|--------------|
| 1 | | | | | |
| 2 | 441 | 462 | UGGAAUCUU(:::: ::::: : :::::GUGCAACAUL Cleavage | | pacid=371565 |
| 3 | 1075 | 1096 | UGGAAUCUU(:::: ::::: : ::::: GGUUAGUAA Translation | | pacid=371565 |
| 4 | 1075 | 1096 | UGGAAUCUU(:::: ::::: : ::::: GGUUAGUAA Translation | | pacid=371565 |
| 5 | | | | | |
| 6 | 1397 | 1418 | UGGAAUCUU(:::: ::::: : ::::: UUGCACCGUL Cleavage | | pacid=371485 |
| 7 | 119 | 141 | UGGAAUCUU(::::: : : :::::GUGCAGCAGI Cleavage | | pacid=371694 |
| 8 | 1408 | 1428 | GGAAUCUUG) ::::: ::::: : ::::: UUGCACCAUL Cleavage | | pacid=371688 |
| 9 | | | | | |
| 10 | 1408 | 1428 | GGAAUCUUG) ::::: ::::: : ::::: UUGCACCAUL Cleavage | | pacid=371688 |
| 11 | 1408 | 1428 | GGAAUCUUG) ::::: ::::: : ::::: UUGCACCAUL Cleavage | | pacid=371688 |
| 12 | 1408 | 1428 | GGAAUCUUG) ::::: ::::: : ::::: UUGCACCAUL Cleavage | | pacid=371688 |
| 13 | | | | | |
| 14 | 1408 | 1428 | GGAAUCUUG) ::::: ::::: : ::::: UUGCACCAUL Cleavage | | pacid=371688 |
| 15 | 1408 | 1428 | GGAAUCUUG) ::::: ::::: : ::::: UUGCACCAUL Cleavage | | pacid=371688 |
| 16 | 1408 | 1428 | GGAAUCUUG) ::::: ::::: : ::::: UUGCACCAUL Cleavage | | pacid=371688 |
| 17 | | | | | |
| 18 | 1408 | 1428 | GGAAUCUUG) ::::: ::::: : ::::: UUGCACCAUL Cleavage | | pacid=371688 |
| 19 | 1408 | 1428 | GGAAUCUUG) ::::: ::::: : ::::: UUGCACCAUL Cleavage | | pacid=371688 |
| 20 | 1408 | 1428 | GGAAUCUUG) ::::: ::::: : ::::: UUGCACCAUL Cleavage | | pacid=371688 |
| 21 | | | | | |
| 22 | 1981 | 2001 | UGGAAUCUU(::::: : : :::::UUGCAGCAU(Cleavage | | pacid=371683 |
| 23 | 1989 | 2009 | UGGAAUCUU(::::: : : :::::UUGCAGCAU(Cleavage | | pacid=371683 |
| 24 | 1996 | 2016 | UGGAAUCUU(::::: : : :::::UUGCAGCAU(Cleavage | | pacid=371683 |
| 25 | | | | | |
| 26 | 1546 | 1567 | UGGAAUCUU(::::: ::::: : : CUGAAGCAU(Cleavage | | pacid=371686 |
| 27 | 1061 | 1080 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371777 |
| 28 | 1061 | 1080 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371777 |
| 29 | | | | | |
| 30 | 1061 | 1080 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371777 |
| 31 | 1061 | 1080 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371777 |
| 32 | 1061 | 1080 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371777 |
| 33 | | | | | |
| 34 | 1061 | 1080 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371777 |
| 35 | 1061 | 1080 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371777 |
| 36 | 1061 | 1080 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371777 |
| 37 | | | | | |
| 38 | 1061 | 1080 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371777 |
| 39 | 1061 | 1080 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371777 |
| 40 | 1061 | 1081 | UGGAAUCUU(::::: : : :::::CUGC GGCAUL Cleavage | | pacid=371777 |
| 41 | | | | | |
| 42 | 1230 | 1249 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371779 |
| 43 | 1230 | 1249 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371779 |
| 44 | 1230 | 1249 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371779 |
| 45 | 1230 | 1249 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371779 |
| 46 | | | | | |
| 47 | 1230 | 1249 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371779 |
| 48 | 1230 | 1249 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371779 |
| 49 | 1230 | 1249 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371779 |
| 50 | | | | | |
| 51 | 1230 | 1249 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371779 |
| 52 | 1230 | 1249 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371779 |
| 53 | 1230 | 1249 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371779 |
| 54 | | | | | |
| 55 | 1230 | 1250 | UGGAAUCUU(::::: : : :::::CUGC GGCAUL Cleavage | | pacid=371779 |
| 56 | 1216 | 1235 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371765 |
| 57 | 1216 | 1235 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371765 |
| 58 | | | | | |
| 59 | 1216 | 1235 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371765 |
| 60 | 1216 | 1235 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371765 |
| | 1216 | 1235 | GGAAUCUUG) ::::: ::::: : : CUGC GGCAUL Cleavage | | pacid=371765 |

| | | | | |
|----|------|--|--|--------------|
| 1 | | | | |
| 2 | 764 | 784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage | | pacid=371673 |
| 3 | 764 | 784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage | | pacid=371673 |
| 4 | 764 | 784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage | | pacid=371673 |
| 5 | 764 | 784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage | | pacid=371673 |
| 6 | 764 | 784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage | | pacid=371673 |
| 7 | 764 | 784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage | | pacid=371673 |
| 8 | 764 | 784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage | | pacid=371673 |
| 9 | 764 | 784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage | | pacid=371673 |
| 10 | 764 | 784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage | | pacid=371673 |
| 11 | 764 | 784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage | | pacid=371673 |
| 12 | 764 | 784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage | | pacid=371673 |
| 13 | 764 | 784 GGAAUCUUG)..... : : : : UUGCAGCAU(Cleavage | | pacid=371673 |
| 14 | 1518 | 1539 UGGAUCUU)..... : : : : UUGCAGUAC(Cleavage | | pacid=371650 |
| 15 | 2961 | 2984 GGAAUCUUG)..... : : : : UUAUGCAG(Cleavage | | pacid=371581 |
| 16 | 2964 | 2985 UGGAUCUU)..... : : : : AUGCAGCAU(Cleavage | | pacid=371581 |
| 17 | 1687 | 1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage | | pacid=371596 |
| 18 | 1687 | 1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage | | pacid=371596 |
| 19 | 1687 | 1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage | | pacid=371596 |
| 20 | 1687 | 1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage | | pacid=371596 |
| 21 | 1687 | 1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage | | pacid=371596 |
| 22 | 1687 | 1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage | | pacid=371596 |
| 23 | 1687 | 1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage | | pacid=371596 |
| 24 | 1687 | 1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage | | pacid=371596 |
| 25 | 1687 | 1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage | | pacid=371596 |
| 26 | 1687 | 1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage | | pacid=371596 |
| 27 | 1687 | 1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage | | pacid=371596 |
| 28 | 1687 | 1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage | | pacid=371596 |
| 29 | 1687 | 1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage | | pacid=371596 |
| 30 | 1687 | 1707 GGAAUCUUG)..... : : : : CUGUGGAA(Cleavage | | pacid=371596 |
| 31 | 1687 | 1708 UGGAUCUU)..... : : : : CUGUGGAA(Cleavage | | pacid=371596 |
| 32 | 230 | 251 UGGAUCUU)..... : : : : CUGCAGAAU(Translation | | pacid=371577 |
| 33 | 20 | 41 UGGAUCUU)..... : : : : CUGCAGCAAC Cleavage | | pacid=371576 |
| 34 | 203 | 223 GGAAUCUUG)..... : : : : CUGCAACAUC Cleavage | | pacid=371610 |
| 35 | 203 | 223 GGAAUCUUG)..... : : : : CUGCAACAUC Cleavage | | pacid=371610 |
| 36 | 203 | 223 GGAAUCUUG)..... : : : : CUGCAACAUC Cleavage | | pacid=371610 |
| 37 | 203 | 223 GGAAUCUUG)..... : : : : CUGCAACAUC Cleavage | | pacid=371610 |
| 38 | 203 | 223 GGAAUCUUG)..... : : : : CUGCAACAUC Cleavage | | pacid=371610 |
| 39 | 203 | 223 GGAAUCUUG)..... : : : : CUGCAACAUC Cleavage | | pacid=371610 |
| 40 | 203 | 223 GGAAUCUUG)..... : : : : CUGCAACAUC Cleavage | | pacid=371610 |
| 41 | 203 | 223 GGAAUCUUG)..... : : : : CUGCAACAUC Cleavage | | pacid=371610 |
| 42 | 203 | 223 GGAAUCUUG)..... : : : : CUGCAACAUC Cleavage | | pacid=371610 |
| 43 | 203 | 223 GGAAUCUUG)..... : : : : CUGCAACAUC Cleavage | | pacid=371610 |
| 44 | 203 | 223 GGAAUCUUG)..... : : : : CUGCAACAUC Cleavage | | pacid=371610 |
| 45 | 203 | 223 GGAAUCUUG)..... : : : : CUGCAACAUC Cleavage | | pacid=371610 |
| 46 | 203 | 223 GGAAUCUUG)..... : : : : CUGCAACAUC Cleavage | | pacid=371610 |
| 47 | 203 | 223 GGAAUCUUG)..... : : : : CUGCAACAUC Cleavage | | pacid=371610 |
| 48 | 471 | 493 GGAAUCUUG)..... : : : : UUGCUGCAG- Cleavage | | pacid=371584 |
| 49 | 474 | 494 UGGAUCUU)..... : : : : CUGCAG-AUU Cleavage | | pacid=371584 |
| 50 | 163 | 186 GGAAUCUUG)..... : : : : CUGCAGCAAL Cleavage | | pacid=371613 |
| 51 | 1986 | 2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage | | pacid=371498 |
| 52 | 1986 | 2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage | | pacid=371498 |
| 53 | 1986 | 2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage | | pacid=371498 |
| 54 | 1986 | 2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage | | pacid=371498 |
| 55 | 1986 | 2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage | | pacid=371498 |
| 56 | 1986 | 2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage | | pacid=371498 |
| 57 | 1986 | 2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage | | pacid=371498 |
| 58 | 1986 | 2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage | | pacid=371498 |
| 59 | 1986 | 2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage | | pacid=371498 |
| 60 | 1986 | 2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage | | pacid=371498 |
| | 1986 | 2007 GGAAU-CUUG)..... : : : : UUGCUGCAU(Cleavage | | pacid=371498 |

| | | | | |
|----|------|-----------------|-----------|--------------|
| 1 | | | | |
| 2 | 1986 | 2007 GGAAU-CUUG | UUGCUGCAU | pacid=371498 |
| 3 | 1986 | 2007 GGAAU-CUUG | UUGCUGCAU | pacid=371498 |
| 4 | 1986 | 2008 UGGAU-CUU | UUGCUGCAU | pacid=371498 |
| 5 | 3055 | 3078 GGAAUCUUG | UUGAUGCAA | pacid=371424 |
| 6 | 1147 | 1167 GGAAUCUUG | CUGCUGCAU | pacid=371560 |
| 7 | 1147 | 1167 GGAAUCUUG | CUGCUGCAU | pacid=371560 |
| 8 | 1147 | 1167 GGAAUCUUG | CUGCUGCAU | pacid=371560 |
| 9 | 1147 | 1167 GGAAUCUUG | CUGCUGCAU | pacid=371560 |
| 10 | 1147 | 1167 GGAAUCUUG | CUGCUGCAU | pacid=371560 |
| 11 | 1147 | 1167 GGAAUCUUG | CUGCUGCAU | pacid=371560 |
| 12 | 1147 | 1167 GGAAUCUUG | CUGCUGCAU | pacid=371560 |
| 13 | 1147 | 1167 GGAAUCUUG | CUGCUGCAU | pacid=371560 |
| 14 | 1147 | 1167 GGAAUCUUG | CUGCUGCAU | pacid=371560 |
| 15 | 1147 | 1167 GGAAUCUUG | CUGCUGCAU | pacid=371560 |
| 16 | 1147 | 1167 GGAAUCUUG | CUGCUGCAU | pacid=371560 |
| 17 | 1147 | 1167 GGAAUCUUG | CUGCUGCAU | pacid=371560 |
| 18 | 1147 | 1167 GGAAUCUUG | CUGCUGCAU | pacid=371560 |
| 19 | 1147 | 1167 GGAAUCUUG | CUGCUGCAU | pacid=371560 |
| 20 | 2140 | 2162 UGGAUCUU | CUAUAGCUA | pacid=371559 |
| 21 | 1941 | 1962 UGGAUCUU | AUGUACCUU | pacid=371568 |
| 22 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 23 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 24 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 25 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 26 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 27 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 28 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 29 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 30 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 31 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 32 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 33 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 34 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 35 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 36 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 37 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 38 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 39 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 40 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 41 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 42 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 43 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 44 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 45 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 46 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 47 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 48 | 1075 | 1095 GGAAUCUUG | GGUUAGUAA | pacid=371565 |
| 49 | 1072 | 1095 GGAAUCUUG | UAAGGUUAG | pacid=371565 |
| 50 | 1072 | 1095 GGAAUCUUG | UAAGGUUAG | pacid=371565 |
| 51 | 1072 | 1095 GGAAUCUUG | UAAGGUUAG | pacid=371565 |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

| | | | | | |
|----|---|--------------------|------------------|---------------------------|-------------|
| 1 | | | | | |
| 2 | 1 | Phvul.001G233200.1 | Phvul.001G233200 | Phvul.001G23 | 0 0 |
| 3 | 1 | Phvul.001G233200.2 | Phvul.001G233200 | Phvul.001G23 | 0 0 |
| 4 | 1 | Phvul.001G233200.1 | Phvul.001G233200 | Phvul.001G23 | 0 0 |
| 5 | 1 | Phvul.001G233200.2 | Phvul.001G233200 | Phvul.001G23 | 0 0 |
| 6 | 1 | Phvul.001G233200.1 | Phvul.001G233200 | Phvul.001G23 | 0 0 |
| 7 | 1 | Phvul.001G233200.2 | Phvul.001G233200 | Phvul.001G23 | 0 0 |
| 8 | 1 | Phvul.001G233200.1 | Phvul.001G233200 | Phvul.001G23 | 0 0 |
| 9 | 1 | Phvul.001G233200.2 | Phvul.001G233200 | Phvul.001G23 | 0 0 |
| 10 | 1 | Phvul.001G233200.1 | Phvul.001G233200 | Phvul.001G23 | 0 0 |
| 11 | 1 | Phvul.001G233200.2 | Phvul.001G233200 | Phvul.001G23 | 0 0 |
| 12 | 1 | Phvul.001G233200.1 | Phvul.001G233200 | Phvul.001G23 | 0 0 |
| 13 | 1 | Phvul.011G071100.2 | Phvul.011G071100 | Phvul.011G07 PF00847 | PTHR32467,P |
| 14 | 1 | Phvul.011G071100.1 | Phvul.011G071100 | Phvul.011G07 PF00847 | PTHR32467,P |
| 15 | 1 | Phvul.L000308.2 | Phvul.L000308 | Phvul.L000308 PF00847 | PTHR32467,P |
| 16 | 1 | Phvul.L000308.1 | Phvul.L000308 | Phvul.L000308 PF00847 | PTHR32467,P |
| 17 | 1 | Phvul.003G111500.1 | Phvul.003G111500 | Phvul.003G11 PF06351 | PTHR31843,P |
| 18 | 1 | Phvul.005G118700.1 | Phvul.005G118700 | Phvul.005G11 PF07646,PF13 | PTHR11668,P |
| 19 | 1 | Phvul.008G058700.2 | Phvul.008G058700 | Phvul.008G05 PF01657,PF07 | PTHR27002,P |
| 20 | 1 | Phvul.008G058700.1 | Phvul.008G058700 | Phvul.008G05 PF01657,PF07 | PTHR27002,P |
| 21 | 1 | Phvul.011G150100.1 | Phvul.011G150100 | Phvul.011G15 PF00954,PF08 | PTHR27002,P |
| 22 | 1 | Phvul.001G033700.1 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 23 | 1 | Phvul.001G033700.2 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 24 | 1 | Phvul.001G033700.1 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 25 | 1 | Phvul.001G033700.2 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 26 | 1 | Phvul.001G033700.1 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 27 | 1 | Phvul.001G033700.2 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 28 | 1 | Phvul.001G033700.1 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 29 | 1 | Phvul.001G033700.2 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 30 | 1 | Phvul.001G033700.1 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 31 | 1 | Phvul.001G033700.2 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 32 | 1 | Phvul.001G033700.1 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 33 | 1 | Phvul.001G033700.2 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 34 | 1 | Phvul.001G033700.1 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 35 | 1 | Phvul.001G033700.2 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 36 | 1 | Phvul.001G033700.1 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 37 | 1 | Phvul.001G033700.2 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 38 | 1 | Phvul.001G033700.1 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 39 | 1 | Phvul.001G033700.2 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 40 | 1 | Phvul.001G033700.1 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 41 | 1 | Phvul.001G033700.2 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 42 | 1 | Phvul.001G033700.1 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 43 | 1 | Phvul.001G033700.2 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 44 | 1 | Phvul.001G033700.1 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 45 | 1 | Phvul.001G033700.2 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 46 | 1 | Phvul.001G033700.1 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 47 | 1 | Phvul.001G033700.2 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 48 | 1 | Phvul.001G033700.1 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 49 | 1 | Phvul.001G033700.2 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 50 | 1 | Phvul.001G033700.1 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 51 | 1 | Phvul.001G033700.2 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 52 | 1 | Phvul.001G033700.1 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 53 | 1 | Phvul.001G033700.2 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 54 | 1 | Phvul.001G172501.1 | Phvul.001G172501 | Phvul.001G17 | 0 0 |
| 55 | 1 | Phvul.001G172501.1 | Phvul.001G172501 | Phvul.001G17 | 0 0 |
| 56 | 1 | Phvul.001G172501.1 | Phvul.001G172501 | Phvul.001G17 | 0 0 |
| 57 | 1 | Phvul.001G172501.1 | Phvul.001G172501 | Phvul.001G17 | 0 0 |
| 58 | 1 | Phvul.001G172501.1 | Phvul.001G172501 | Phvul.001G17 | 0 0 |
| 59 | 1 | Phvul.001G172501.1 | Phvul.001G172501 | Phvul.001G17 | 0 0 |
| 60 | 1 | Phvul.001G172501.1 | Phvul.001G172501 | Phvul.001G17 | 0 0 |

| | | | | | |
|----|---|--------------------|------------------|--------------------------------------|-------------|
| 1 | | | | | |
| 2 | 1 | Phvul.001G172501.1 | Phvul.001G172501 | Phvul.001G17 | 0 0 |
| 3 | 1 | Phvul.001G172501.1 | Phvul.001G172501 | Phvul.001G17 | 0 0 |
| 4 | 1 | Phvul.001G172501.1 | Phvul.001G172501 | Phvul.001G17 | 0 0 |
| 5 | 1 | Phvul.001G172501.1 | Phvul.001G172501 | Phvul.001G17 | 0 0 |
| 6 | 1 | Phvul.001G172501.1 | Phvul.001G172501 | Phvul.001G17 | 0 0 |
| 7 | 1 | Phvul.001G172501.1 | Phvul.001G172501 | Phvul.001G17 | 0 0 |
| 8 | 1 | Phvul.001G172501.1 | Phvul.001G172501 | Phvul.001G17 | 0 0 |
| 9 | 1 | Phvul.001G172501.1 | Phvul.001G172501 | Phvul.001G17 | 0 0 |
| 10 | 1 | Phvul.001G212400.1 | Phvul.001G212400 | Phvul.001G21 PF12428 | PTHR23012,P |
| 11 | 1 | Phvul.001G212400.2 | Phvul.001G212400 | Phvul.001G21 PF12428 | PTHR23012,P |
| 12 | 1 | Phvul.002G012700.1 | Phvul.002G012700 | Phvul.002G01 PF07714 | PTHR24054,P |
| 13 | 1 | Phvul.002G012700.1 | Phvul.002G012700 | Phvul.002G01 PF07714 | PTHR24054,P |
| 14 | 1 | Phvul.002G012700.1 | Phvul.002G012700 | Phvul.002G01 PF07714 | PTHR24054,P |
| 15 | 1 | Phvul.002G012700.1 | Phvul.002G012700 | Phvul.002G01 PF07714 | PTHR24054,P |
| 16 | 1 | Phvul.002G012700.1 | Phvul.002G012700 | Phvul.002G01 PF07714 | PTHR24054,P |
| 17 | 1 | Phvul.002G012700.1 | Phvul.002G012700 | Phvul.002G01 PF07714 | PTHR24054,P |
| 18 | 1 | Phvul.002G012700.1 | Phvul.002G012700 | Phvul.002G01 PF07714 | PTHR24054,P |
| 19 | 1 | Phvul.002G012700.1 | Phvul.002G012700 | Phvul.002G01 PF07714 | PTHR24054,P |
| 20 | 1 | Phvul.002G012700.1 | Phvul.002G012700 | Phvul.002G01 PF07714 | PTHR24054,P |
| 21 | 1 | Phvul.002G012700.1 | Phvul.002G012700 | Phvul.002G01 PF07714 | PTHR24054,P |
| 22 | 1 | Phvul.002G012700.1 | Phvul.002G012700 | Phvul.002G01 PF07714 | PTHR24054,P |
| 23 | 1 | Phvul.002G012700.1 | Phvul.002G012700 | Phvul.002G01 PF07714 | PTHR24054,P |
| 24 | 1 | Phvul.002G012700.1 | Phvul.002G012700 | Phvul.002G01 PF07714 | PTHR24054,P |
| 25 | 1 | Phvul.002G012700.1 | Phvul.002G012700 | Phvul.002G01 PF07714 | PTHR24054,P |
| 26 | 1 | Phvul.002G197200.1 | Phvul.002G197200 | Phvul.002G19 PF07779 | PTHR13533,P |
| 27 | 1 | Phvul.002G218300.1 | Phvul.002G218300 | Phvul.002G21 PF02679 | 0 |
| 28 | 1 | Phvul.002G330500.2 | Phvul.002G330500 | Phvul.002G33 | 0 PTHR14513 |
| 29 | 1 | Phvul.002G330500.1 | Phvul.002G330500 | Phvul.002G33 | 0 PTHR14513 |
| 30 | 1 | Phvul.003G262400.1 | Phvul.003G262400 | Phvul.003G26 PF02535 | PTHR11040,P |
| 31 | 1 | Phvul.003G262500.1 | Phvul.003G262500 | Phvul.003G26 PF02535 | PTHR11040,P |
| 32 | 1 | Phvul.005G030900.1 | Phvul.005G030900 | Phvul.005G03 PF08276,PF00PTHR27002,P | |
| 33 | 1 | Phvul.005G030900.1 | Phvul.005G030900 | Phvul.005G03 PF08276,PF00PTHR27002,P | |
| 34 | 1 | Phvul.005G030900.1 | Phvul.005G030900 | Phvul.005G03 PF08276,PF00PTHR27002,P | |
| 35 | 1 | Phvul.005G030900.1 | Phvul.005G030900 | Phvul.005G03 PF08276,PF00PTHR27002,P | |
| 36 | 1 | Phvul.005G030900.1 | Phvul.005G030900 | Phvul.005G03 PF08276,PF00PTHR27002,P | |
| 37 | 1 | Phvul.005G030900.1 | Phvul.005G030900 | Phvul.005G03 PF08276,PF00PTHR27002,P | |
| 38 | 1 | Phvul.005G030900.1 | Phvul.005G030900 | Phvul.005G03 PF08276,PF00PTHR27002,P | |
| 39 | 1 | Phvul.005G030900.1 | Phvul.005G030900 | Phvul.005G03 PF08276,PF00PTHR27002,P | |
| 40 | 1 | Phvul.005G030900.1 | Phvul.005G030900 | Phvul.005G03 PF08276,PF00PTHR27002,P | |
| 41 | 1 | Phvul.005G030900.1 | Phvul.005G030900 | Phvul.005G03 PF08276,PF00PTHR27002,P | |
| 42 | 1 | Phvul.005G030900.1 | Phvul.005G030900 | Phvul.005G03 PF08276,PF00PTHR27002,P | |
| 43 | 1 | Phvul.005G030900.1 | Phvul.005G030900 | Phvul.005G03 PF08276,PF00PTHR27002,P | |
| 44 | 1 | Phvul.005G030900.1 | Phvul.005G030900 | Phvul.005G03 PF08276,PF00PTHR27002,P | |
| 45 | 1 | Phvul.005G030900.1 | Phvul.005G030900 | Phvul.005G03 PF08276,PF00PTHR27002,P | |
| 46 | 1 | Phvul.005G030900.1 | Phvul.005G030900 | Phvul.005G03 PF08276,PF00PTHR27002,P | |
| 47 | 1 | Phvul.005G030900.1 | Phvul.005G030900 | Phvul.005G03 PF08276,PF00PTHR27002,P | |
| 48 | 1 | Phvul.005G030900.1 | Phvul.005G030900 | Phvul.005G03 PF08276,PF00PTHR27002,P | |
| 49 | 1 | Phvul.005G088700.3 | Phvul.005G088700 | Phvul.005G08 PF08276,PF01PTHR27002,P | |
| 50 | 1 | Phvul.005G088700.2 | Phvul.005G088700 | Phvul.005G08 PF08276,PF01PTHR27002,P | |
| 51 | 1 | Phvul.005G088700.1 | Phvul.005G088700 | Phvul.005G08 PF08276,PF01PTHR27002,P | |
| 52 | 1 | Phvul.005G088800.1 | Phvul.005G088800 | Phvul.005G08 PF11883,PF08PTHR27002,P | |
| 53 | 1 | Phvul.005G131000.1 | Phvul.005G131000 | Phvul.005G13 PF00450 | PTHR11802,P |
| 54 | 1 | Phvul.005G131000.1 | Phvul.005G131000 | Phvul.005G13 PF00450 | PTHR11802,P |
| 55 | 1 | Phvul.005G131000.1 | Phvul.005G131000 | Phvul.005G13 PF00450 | PTHR11802,P |
| 56 | 1 | Phvul.005G131000.1 | Phvul.005G131000 | Phvul.005G13 PF00450 | PTHR11802,P |
| 57 | 1 | Phvul.005G131000.1 | Phvul.005G131000 | Phvul.005G13 PF00450 | PTHR11802,P |
| 58 | 1 | Phvul.005G131000.1 | Phvul.005G131000 | Phvul.005G13 PF00450 | PTHR11802,P |
| 59 | 1 | Phvul.005G131000.1 | Phvul.005G131000 | Phvul.005G13 PF00450 | PTHR11802,P |
| 60 | 1 | Phvul.005G131000.1 | Phvul.005G131000 | Phvul.005G13 PF00450 | PTHR11802,P |

| | | | | | |
|----|---|--------------------|------------------|--------------------------|---------------|
| 1 | | | | | |
| 2 | 1 | Phvul.008G033900.1 | Phvul.008G033900 | Phvul.008G03 | 0 PTHR13890,P |
| 3 | 1 | Phvul.008G033900.2 | Phvul.008G033900 | Phvul.008G03 | 0 PTHR13890,P |
| 4 | 1 | Phvul.008G033900.3 | Phvul.008G033900 | Phvul.008G03 | 0 PTHR13890,P |
| 5 | 1 | Phvul.008G033900.1 | Phvul.008G033900 | Phvul.008G03 | 0 PTHR13890,P |
| 6 | 1 | Phvul.008G033900.2 | Phvul.008G033900 | Phvul.008G03 | 0 PTHR13890,P |
| 7 | 1 | Phvul.008G033900.3 | Phvul.008G033900 | Phvul.008G03 | 0 PTHR13890,P |
| 8 | 1 | Phvul.008G033900.1 | Phvul.008G033900 | Phvul.008G03 | 0 PTHR13890,P |
| 9 | 1 | Phvul.008G033900.2 | Phvul.008G033900 | Phvul.008G03 | 0 PTHR13890,P |
| 10 | 1 | Phvul.008G033900.3 | Phvul.008G033900 | Phvul.008G03 | 0 PTHR13890,P |
| 11 | 1 | Phvul.008G033900.1 | Phvul.008G033900 | Phvul.008G03 | 0 PTHR13890,P |
| 12 | 1 | Phvul.008G033900.2 | Phvul.008G033900 | Phvul.008G03 | 0 PTHR13890,P |
| 13 | 1 | Phvul.008G033900.3 | Phvul.008G033900 | Phvul.008G03 | 0 PTHR13890,P |
| 14 | 1 | Phvul.008G033900.1 | Phvul.008G033900 | Phvul.008G03 | 0 PTHR13890,P |
| 15 | 1 | Phvul.009G130700.1 | Phvul.009G130700 | Phvul.009G13 PF00651 | PTHR24413,P |
| 16 | 1 | Phvul.009G130700.1 | Phvul.009G130700 | Phvul.009G13 PF00651 | PTHR24413,P |
| 17 | 1 | Phvul.009G130700.1 | Phvul.009G130700 | Phvul.009G13 PF00651 | PTHR24413,P |
| 18 | 1 | Phvul.009G130700.1 | Phvul.009G130700 | Phvul.009G13 PF00651 | PTHR24413,P |
| 19 | 1 | Phvul.009G130700.1 | Phvul.009G130700 | Phvul.009G13 PF00651 | PTHR24413,P |
| 20 | 1 | Phvul.009G130700.1 | Phvul.009G130700 | Phvul.009G13 PF00651 | PTHR24413,P |
| 21 | 1 | Phvul.009G130700.1 | Phvul.009G130700 | Phvul.009G13 PF00651 | PTHR24413,P |
| 22 | 1 | Phvul.009G130700.1 | Phvul.009G130700 | Phvul.009G13 PF00651 | PTHR24413,P |
| 23 | 1 | Phvul.009G130700.1 | Phvul.009G130700 | Phvul.009G13 PF00651 | PTHR24413,P |
| 24 | 1 | Phvul.009G130700.1 | Phvul.009G130700 | Phvul.009G13 PF00651 | PTHR24413,P |
| 25 | 1 | Phvul.009G130700.1 | Phvul.009G130700 | Phvul.009G13 PF00651 | PTHR24413,P |
| 26 | 1 | Phvul.009G130700.1 | Phvul.009G130700 | Phvul.009G13 PF00651 | PTHR24413,P |
| 27 | 1 | Phvul.009G130700.1 | Phvul.009G130700 | Phvul.009G13 PF00651 | PTHR24413,P |
| 28 | 1 | Phvul.009G130700.1 | Phvul.009G130700 | Phvul.009G13 PF00651 | PTHR24413,P |
| 29 | 1 | Phvul.009G249300.1 | Phvul.009G249300 | Phvul.009G24PF13041,PF14 | PTHR24015,P |
| 30 | 2 | Phvul.011G082801.1 | Phvul.011G082801 | Phvul.011G08 | 0 0 |
| 31 | 1 | Phvul.011G150950.1 | Phvul.011G150950 | Phvul.011G15PF11883,PF00 | PTHR27002,P |
| 32 | 2 | Phvul.011G152100.3 | Phvul.011G152100 | Phvul.011G15PF08276,PF00 | PTHR27002,P |
| 33 | 2 | Phvul.011G152100.1 | Phvul.011G152100 | Phvul.011G15PF08276,PF00 | PTHR27002,P |
| 34 | 1 | Phvul.011G152300.3 | Phvul.011G152300 | Phvul.011G15PF08276,PF00 | PTHR27002,P |
| 35 | 1 | Phvul.011G152300.2 | Phvul.011G152300 | Phvul.011G15PF08276,PF00 | PTHR27002,P |
| 36 | 1 | Phvul.011G152300.1 | Phvul.011G152300 | Phvul.011G15PF08276,PF00 | PTHR27002,P |
| 37 | 1 | Phvul.011G152400.1 | Phvul.011G152400 | Phvul.011G15PF11883,PF08 | PTHR27002,P |
| 38 | 1 | Phvul.011G168400.2 | Phvul.011G168400 | Phvul.011G16PF08276,PF00 | PTHR27002,P |
| 39 | 1 | Phvul.001G033700.1 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 40 | 1 | Phvul.001G033700.2 | Phvul.001G033700 | Phvul.001G03 PF10258 | PTHR13135 |
| 41 | 1 | Phvul.001G187200.1 | Phvul.001G187200 | Phvul.001G18 PF03140 | PTHR31549,P |
| 42 | 1 | Phvul.001G187200.1 | Phvul.001G187200 | Phvul.001G18 PF03140 | PTHR31549,P |
| 43 | 1 | Phvul.001G187200.1 | Phvul.001G187200 | Phvul.001G18 PF03140 | PTHR31549,P |
| 44 | 1 | Phvul.001G187200.1 | Phvul.001G187200 | Phvul.001G18 PF03140 | PTHR31549,P |
| 45 | 1 | Phvul.001G187200.1 | Phvul.001G187200 | Phvul.001G18 PF03140 | PTHR31549,P |
| 46 | 1 | Phvul.001G187200.1 | Phvul.001G187200 | Phvul.001G18 PF03140 | PTHR31549,P |
| 47 | 1 | Phvul.001G187200.1 | Phvul.001G187200 | Phvul.001G18 PF03140 | PTHR31549,P |
| 48 | 1 | Phvul.001G187200.1 | Phvul.001G187200 | Phvul.001G18 PF03140 | PTHR31549,P |
| 49 | 1 | Phvul.001G187200.1 | Phvul.001G187200 | Phvul.001G18 PF03140 | PTHR31549,P |
| 50 | 1 | Phvul.001G187200.1 | Phvul.001G187200 | Phvul.001G18 PF03140 | PTHR31549,P |
| 51 | 1 | Phvul.001G187200.1 | Phvul.001G187200 | Phvul.001G18 PF03140 | PTHR31549,P |
| 52 | 1 | Phvul.001G187200.1 | Phvul.001G187200 | Phvul.001G18 PF03140 | PTHR31549,P |
| 53 | 1 | Phvul.001G187200.1 | Phvul.001G187200 | Phvul.001G18 PF03140 | PTHR31549,P |
| 54 | 1 | Phvul.001G187200.1 | Phvul.001G187200 | Phvul.001G18 PF03140 | PTHR31549,P |
| 55 | 1 | Phvul.001G187200.1 | Phvul.001G187200 | Phvul.001G18 PF03140 | PTHR31549,P |
| 56 | 1 | Phvul.001G187200.1 | Phvul.001G187200 | Phvul.001G18 PF03140 | PTHR31549,P |
| 57 | 1 | Phvul.001G187200.1 | Phvul.001G187200 | Phvul.001G18 PF03140 | PTHR31549,P |
| 58 | 1 | Phvul.001G187200.1 | Phvul.001G187200 | Phvul.001G18 PF03140 | PTHR31549,P |
| 59 | 1 | Phvul.001G187200.1 | Phvul.001G187200 | Phvul.001G18 PF03140 | PTHR31549,P |
| 60 | 1 | Phvul.001G233200.2 | Phvul.001G233200 | Phvul.001G23 | 0 0 |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | |
|----------------------|------------------|-------------------------------------|-------------|
| 1 Phvul.009G014600.2 | Phvul.009G014600 | Phvul.009G01 PF00561 | PTHR10992,P |
| 1 Phvul.009G014600.1 | Phvul.009G014600 | Phvul.009G01 PF00561 | PTHR10992,P |
| 1 Phvul.009G014600.2 | Phvul.009G014600 | Phvul.009G01 PF00561 | PTHR10992,P |
| 1 Phvul.009G014600.1 | Phvul.009G014600 | Phvul.009G01 PF00561 | PTHR10992,P |
| 1 Phvul.009G014600.2 | Phvul.009G014600 | Phvul.009G01 PF00561 | PTHR10992,P |
| 1 Phvul.009G014600.1 | Phvul.009G014600 | Phvul.009G01 PF00561 | PTHR10992,P |
| 1 Phvul.009G014600.2 | Phvul.009G014600 | Phvul.009G01 PF00561 | PTHR10992,P |
| 1 Phvul.009G014600.1 | Phvul.009G014600 | Phvul.009G01 PF00561 | PTHR10992,P |
| 1 Phvul.009G014600.2 | Phvul.009G014600 | Phvul.009G01 PF00561 | PTHR10992,P |
| 1 Phvul.009G014600.1 | Phvul.009G014600 | Phvul.009G01 PF00561 | PTHR10992,P |
| 1 Phvul.009G014600.2 | Phvul.009G014600 | Phvul.009G01 PF00561 | PTHR10992,P |
| 1 Phvul.009G014600.1 | Phvul.009G014600 | Phvul.009G01 PF00561 | PTHR10992,P |
| 1 Phvul.009G014600.2 | Phvul.009G014600 | Phvul.009G01 PF00561 | PTHR10992,P |
| 1 Phvul.009G014600.1 | Phvul.009G014600 | Phvul.009G01 PF00561 | PTHR10992,P |
| 1 Phvul.009G014600.2 | Phvul.009G014600 | Phvul.009G01 PF00561 | PTHR10992,P |
| 1 Phvul.009G014600.1 | Phvul.009G014600 | Phvul.009G01 PF00561 | PTHR10992,P |
| 1 Phvul.009G014600.2 | Phvul.009G014600 | Phvul.009G01 PF00561 | PTHR10992,P |
| 1 Phvul.009G117500.1 | Phvul.009G117500 | Phvul.009G11 PF00385 | PTHR22812 |
| 1 Phvul.009G117500.1 | Phvul.009G117500 | Phvul.009G11 PF00385 | PTHR22812 |
| 1 Phvul.009G117500.1 | Phvul.009G117500 | Phvul.009G11 PF00385 | PTHR22812 |
| 1 Phvul.009G117500.1 | Phvul.009G117500 | Phvul.009G11 PF00385 | PTHR22812 |
| 1 Phvul.009G117500.1 | Phvul.009G117500 | Phvul.009G11 PF00385 | PTHR22812 |
| 1 Phvul.009G117500.1 | Phvul.009G117500 | Phvul.009G11 PF00385 | PTHR22812 |
| 1 Phvul.009G117500.1 | Phvul.009G117500 | Phvul.009G11 PF00385 | PTHR22812 |
| 1 Phvul.009G117500.1 | Phvul.009G117500 | Phvul.009G11 PF00385 | PTHR22812 |
| 1 Phvul.009G117500.1 | Phvul.009G117500 | Phvul.009G11 PF00385 | PTHR22812 |
| 1 Phvul.009G117500.1 | Phvul.009G117500 | Phvul.009G11 PF00385 | PTHR22812 |
| 1 Phvul.009G117500.1 | Phvul.009G117500 | Phvul.009G11 PF00385 | PTHR22812 |
| 1 Phvul.009G117500.1 | Phvul.009G117500 | Phvul.009G11 PF00385 | PTHR22812 |
| 1 Phvul.009G130700.1 | Phvul.009G130700 | Phvul.009G13 PF00651 | PTHR24413,P |
| 1 Phvul.010G002600.1 | Phvul.010G002600 | Phvul.010G00 PF03140 | PTHR31549,P |
| 1 Phvul.010G002600.1 | Phvul.010G002600 | Phvul.010G00 PF03140 | PTHR31549,P |
| 1 Phvul.010G002600.1 | Phvul.010G002600 | Phvul.010G00 PF03140 | PTHR31549,P |
| 1 Phvul.010G002600.1 | Phvul.010G002600 | Phvul.010G00 PF03140 | PTHR31549,P |
| 1 Phvul.010G002600.1 | Phvul.010G002600 | Phvul.010G00 PF03140 | PTHR31549,P |
| 1 Phvul.010G002600.1 | Phvul.010G002600 | Phvul.010G00 PF03140 | PTHR31549,P |
| 1 Phvul.010G002600.1 | Phvul.010G002600 | Phvul.010G00 PF03140 | PTHR31549,P |
| 1 Phvul.010G002600.1 | Phvul.010G002600 | Phvul.010G00 PF03140 | PTHR31549,P |
| 1 Phvul.010G002600.1 | Phvul.010G002600 | Phvul.010G00 PF03140 | PTHR31549,P |
| 1 Phvul.010G002600.1 | Phvul.010G002600 | Phvul.010G00 PF03140 | PTHR31549,P |
| 1 Phvul.010G002600.1 | Phvul.010G002600 | Phvul.010G00 PF03140 | PTHR31549,P |
| 1 Phvul.010G002600.1 | Phvul.010G002600 | Phvul.010G00 PF03140 | PTHR31549,P |
| 1 Phvul.010G002600.1 | Phvul.010G002600 | Phvul.010G00 PF03140 | PTHR31549,P |
| 1 Phvul.010G002600.1 | Phvul.010G002600 | Phvul.010G00 PF03140 | PTHR31549,P |
| 1 Phvul.011G067401.1 | Phvul.011G067401 | Phvul.011G06PF11721,PF00PTHR27006,P | |
| 1 Phvul.011G079800.1 | Phvul.011G079800 | Phvul.011G07PF00046,PF08PTHR24326,P | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | |
|----------------------|------------------|--|----------------------------|
| 1 Phvul.003G189300.2 | Phvul.003G189300 | Phvul.003G18 PF02701 | PTHR31089,P ⁻ |
| 1 Phvul.003G189300.1 | Phvul.003G189300 | Phvul.003G18 PF02701 | PTHR31089,P ⁻ |
| 1 Phvul.003G189300.2 | Phvul.003G189300 | Phvul.003G18 PF02701 | PTHR31089,P ⁻ |
| 1 Phvul.003G189300.1 | Phvul.003G189300 | Phvul.003G18 PF02701 | PTHR31089,P ⁻ |
| 1 Phvul.003G189300.2 | Phvul.003G189300 | Phvul.003G18 PF02701 | PTHR31089,P ⁻ |
| 1 Phvul.003G189300.1 | Phvul.003G189300 | Phvul.003G18 PF02701 | PTHR31089,P ⁻ |
| 1 Phvul.003G189300.2 | Phvul.003G189300 | Phvul.003G18 PF02701 | PTHR31089,P ⁻ |
| 1 Phvul.003G189300.1 | Phvul.003G189300 | Phvul.003G18 PF02701 | PTHR31089,P ⁻ |
| 1 Phvul.003G189300.2 | Phvul.003G189300 | Phvul.003G18 PF02701 | PTHR31089,P ⁻ |
| 1 Phvul.003G202100.1 | Phvul.003G202100 | Phvul.003G20PF08263,PF00PTHR27000,P ⁻ | |
| 1 Phvul.003G202100.1 | Phvul.003G202100 | Phvul.003G20PF08263,PF00PTHR27000,P ⁻ | |
| 1 Phvul.003G202100.1 | Phvul.003G202100 | Phvul.003G20PF08263,PF00PTHR27000,P ⁻ | |
| 1 Phvul.003G202100.1 | Phvul.003G202100 | Phvul.003G20PF08263,PF00PTHR27000,P ⁻ | |
| 1 Phvul.003G202100.1 | Phvul.003G202100 | Phvul.003G20PF08263,PF00PTHR27000,P ⁻ | |
| 1 Phvul.003G202100.1 | Phvul.003G202100 | Phvul.003G20PF08263,PF00PTHR27000,P ⁻ | |
| 1 Phvul.003G202100.1 | Phvul.003G202100 | Phvul.003G20PF08263,PF00PTHR27000,P ⁻ | |
| 1 Phvul.003G202100.1 | Phvul.003G202100 | Phvul.003G20PF08263,PF00PTHR27000,P ⁻ | |
| 1 Phvul.003G202100.1 | Phvul.003G202100 | Phvul.003G20PF08263,PF00PTHR27000,P ⁻ | |
| 1 Phvul.003G202100.1 | Phvul.003G202100 | Phvul.003G20PF08263,PF00PTHR27000,P ⁻ | |
| 1 Phvul.003G202100.1 | Phvul.003G202100 | Phvul.003G20PF08263,PF00PTHR27000,P ⁻ | |
| 1 Phvul.003G206500.1 | Phvul.003G206500 | Phvul.003G20 | 0 PTHR36795,P ⁻ |
| 1 Phvul.003G206500.1 | Phvul.003G206500 | Phvul.003G20 | 0 PTHR36795,P ⁻ |
| 1 Phvul.003G206500.1 | Phvul.003G206500 | Phvul.003G20 | 0 PTHR36795,P ⁻ |
| 1 Phvul.003G206500.1 | Phvul.003G206500 | Phvul.003G20 | 0 PTHR36795,P ⁻ |
| 1 Phvul.003G206500.1 | Phvul.003G206500 | Phvul.003G20 | 0 PTHR36795,P ⁻ |
| 1 Phvul.003G206500.1 | Phvul.003G206500 | Phvul.003G20 | 0 PTHR36795,P ⁻ |
| 1 Phvul.003G206500.1 | Phvul.003G206500 | Phvul.003G20 | 0 PTHR36795,P ⁻ |
| 1 Phvul.003G206500.1 | Phvul.003G206500 | Phvul.003G20 | 0 PTHR36795,P ⁻ |
| 1 Phvul.003G206500.1 | Phvul.003G206500 | Phvul.003G20 | 0 PTHR36795,P ⁻ |
| 1 Phvul.003G206500.1 | Phvul.003G206500 | Phvul.003G20 | 0 PTHR36795,P ⁻ |
| 1 Phvul.003G206500.1 | Phvul.003G206500 | Phvul.003G20 | 0 PTHR36795,P ⁻ |
| 1 Phvul.003G229600.2 | Phvul.003G229600 | Phvul.003G22 PF02365 | PTHR31989,P ⁻ |
| 1 Phvul.003G229600.1 | Phvul.003G229600 | Phvul.003G22 PF02365 | PTHR31989,P ⁻ |
| 1 Phvul.003G235900.1 | Phvul.003G235900 | Phvul.003G23 PF07714 | PTHR24054,P ⁻ |
| 1 Phvul.003G235900.1 | Phvul.003G235900 | Phvul.003G23 PF07714 | PTHR24054,P ⁻ |
| 1 Phvul.003G235900.1 | Phvul.003G235900 | Phvul.003G23 PF07714 | PTHR24054,P ⁻ |
| 1 Phvul.003G235900.1 | Phvul.003G235900 | Phvul.003G23 PF07714 | PTHR24054,P ⁻ |
| 1 Phvul.003G235900.1 | Phvul.003G235900 | Phvul.003G23 PF07714 | PTHR24054,P ⁻ |
| 1 Phvul.003G235900.1 | Phvul.003G235900 | Phvul.003G23 PF07714 | PTHR24054,P ⁻ |
| 1 Phvul.003G235900.1 | Phvul.003G235900 | Phvul.003G23 PF07714 | PTHR24054,P ⁻ |
| 1 Phvul.003G235900.1 | Phvul.003G235900 | Phvul.003G23 PF07714 | PTHR24054,P ⁻ |
| 1 Phvul.003G235900.1 | Phvul.003G235900 | Phvul.003G23 PF07714 | PTHR24054,P ⁻ |
| 1 Phvul.003G235900.1 | Phvul.003G235900 | Phvul.003G23 PF07714 | PTHR24054,P ⁻ |
| 1 Phvul.004G046400.1 | Phvul.004G046400 | Phvul.004G04PF13676,PF00PTHR11017,P ⁻ | |
| 1 Phvul.004G046400.1 | Phvul.004G046400 | Phvul.004G04PF13676,PF00PTHR11017,P ⁻ | |
| 1 Phvul.004G046400.1 | Phvul.004G046400 | Phvul.004G04PF13676,PF00PTHR11017,P ⁻ | |
| 1 Phvul.004G046400.1 | Phvul.004G046400 | Phvul.004G04PF13676,PF00PTHR11017,P ⁻ | |

| | | | | |
|----|---|--------------------|------------------|--------------------------------------|
| 1 | | | | |
| 2 | 1 | Phvul.009G092600.1 | Phvul.009G092600 | Phvul.009G09 PF07651 PTHR22951,P |
| 3 | 1 | Phvul.009G092600.1 | Phvul.009G092600 | Phvul.009G09 PF07651 PTHR22951,P |
| 4 | 1 | Phvul.009G092600.1 | Phvul.009G092600 | Phvul.009G09 PF07651 PTHR22951,P |
| 5 | 1 | Phvul.009G092600.1 | Phvul.009G092600 | Phvul.009G09 PF07651 PTHR22951,P |
| 6 | 1 | Phvul.010G053600.1 | Phvul.010G053600 | Phvul.010G05 PF00780,PF10PTHR12894,P |
| 7 | 1 | Phvul.011G035700.2 | Phvul.011G035700 | Phvul.011G03 PF07716 PTHR23334,P |
| 8 | 1 | Phvul.011G035700.2 | Phvul.011G035700 | Phvul.011G03 PF07716 PTHR23334,P |
| 9 | 1 | Phvul.011G035700.2 | Phvul.011G035700 | Phvul.011G03 PF07716 PTHR23334,P |
| 10 | 1 | Phvul.011G035700.2 | Phvul.011G035700 | Phvul.011G03 PF07716 PTHR23334,P |
| 11 | 1 | Phvul.011G035700.2 | Phvul.011G035700 | Phvul.011G03 PF07716 PTHR23334,P |
| 12 | 1 | Phvul.011G035700.2 | Phvul.011G035700 | Phvul.011G03 PF07716 PTHR23334,P |
| 13 | 1 | Phvul.011G035700.2 | Phvul.011G035700 | Phvul.011G03 PF07716 PTHR23334,P |
| 14 | 1 | Phvul.011G035700.2 | Phvul.011G035700 | Phvul.011G03 PF07716 PTHR23334,P |
| 15 | 1 | Phvul.011G035700.2 | Phvul.011G035700 | Phvul.011G03 PF07716 PTHR23334,P |
| 16 | 1 | Phvul.011G035700.2 | Phvul.011G035700 | Phvul.011G03 PF07716 PTHR23334,P |
| 17 | 1 | Phvul.011G035700.2 | Phvul.011G035700 | Phvul.011G03 PF07716 PTHR23334,P |
| 18 | 1 | Phvul.011G035700.2 | Phvul.011G035700 | Phvul.011G03 PF07716 PTHR23334,P |
| 19 | 1 | Phvul.011G035700.2 | Phvul.011G035700 | Phvul.011G03 PF07716 PTHR23334,P |
| 20 | 2 | Phvul.011G082801.1 | Phvul.011G082801 | Phvul.011G08 0 0 |
| 21 | | | | |
| 22 | 1 | Phvul.011G147000.1 | Phvul.011G147000 | Phvul.011G14 PF08276,PF00PTHR27002,P |
| 23 | 2 | Phvul.011G152100.3 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 24 | 2 | Phvul.011G152100.1 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 25 | 2 | Phvul.011G152100.3 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 26 | 2 | Phvul.011G152100.3 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 27 | 2 | Phvul.011G152100.1 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 28 | 2 | Phvul.011G152100.3 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 29 | 2 | Phvul.011G152100.1 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 30 | 2 | Phvul.011G152100.3 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 31 | 2 | Phvul.011G152100.3 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 32 | 2 | Phvul.011G152100.1 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 33 | 2 | Phvul.011G152100.3 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 34 | 2 | Phvul.011G152100.3 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 35 | 2 | Phvul.011G152100.1 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 36 | 2 | Phvul.011G152100.3 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 37 | 2 | Phvul.011G152100.1 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 38 | 2 | Phvul.011G152100.3 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 39 | 2 | Phvul.011G152100.3 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 40 | 2 | Phvul.011G152100.1 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 41 | 2 | Phvul.011G152100.3 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 42 | 2 | Phvul.011G152100.3 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 43 | 2 | Phvul.011G152100.1 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 44 | 2 | Phvul.011G152100.3 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 45 | 2 | Phvul.011G152100.1 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 46 | 2 | Phvul.011G152100.3 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 47 | 2 | Phvul.011G152100.3 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 48 | 2 | Phvul.011G152100.1 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 49 | 2 | Phvul.011G152100.3 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 50 | 2 | Phvul.011G152100.3 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 51 | 2 | Phvul.011G152100.1 | Phvul.011G152100 | Phvul.011G15 PF08276,PF00PTHR27002,P |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

| | KOG | KEGG | KOG | GO | Best-hit-arabi-arabi-symbol |
|----|-----|------|----------|--------------------------------------|-----------------------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.3 RAP2.7,TOE1 | |
| 4 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.3 RAP2.7,TOE1 | |
| 5 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.3 RAP2.7,TOE1 | |
| 6 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.3 RAP2.7,TOE1 | |
| 7 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.3 RAP2.7,TOE1 | |
| 8 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.3 RAP2.7,TOE1 | |
| 9 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.3 RAP2.7,TOE1 | |
| 10 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.3 RAP2.7,TOE1 | |
| 11 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.3 RAP2.7,TOE1 | |
| 12 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.3 RAP2.7,TOE1 | |
| 13 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.3 RAP2.7,TOE1 | |
| 14 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.3 RAP2.7,TOE1 | |
| 15 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.3 RAP2.7,TOE1 | |
| 16 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.3 RAP2.7,TOE1 | |
| 17 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.3 RAP2.7,TOE1 | |
| 18 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 19 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 20 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 21 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 22 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 23 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 24 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 25 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 26 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 27 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 28 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 29 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 30 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 31 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 32 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 33 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 34 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 35 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 36 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 37 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 38 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 39 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 40 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 41 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 42 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 43 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 44 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 45 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 46 | | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 AP2,FL1,FLO2 | |
| 47 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 RAP2.7,TOE1 | |
| 48 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 RAP2.7,TOE1 | |
| 49 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 RAP2.7,TOE1 | |
| 50 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 RAP2.7,TOE1 | |
| 51 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 RAP2.7,TOE1 | |
| 52 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 RAP2.7,TOE1 | |
| 53 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 RAP2.7,TOE1 | |
| 54 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 RAP2.7,TOE1 | |
| 55 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 RAP2.7,TOE1 | |
| 56 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 RAP2.7,TOE1 | |
| 57 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 RAP2.7,TOE1 | |
| 58 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 RAP2.7,TOE1 | |
| 59 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 RAP2.7,TOE1 | |
| 60 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 RAP2.7,TOE1 | |

| | | | | | | |
|----|---|----------|-------------------------|--------------|---|---|
| 1 | | | | | | |
| 2 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 3 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 4 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 5 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 6 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 7 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 8 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 9 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 10 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 11 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 12 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 13 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 14 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 15 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 16 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 17 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 18 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 19 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 20 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 21 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 22 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 23 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 24 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 25 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 26 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 27 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 28 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 29 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 30 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 31 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 32 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 33 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 34 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 35 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 36 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 37 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 38 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 39 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 40 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 41 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 42 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 43 | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 | RAP2.7,TOE1 | | |
| 44 | 0 | 0 K09284 | GO:0006355,(AT2G28550.3 | RAP2.7,TOE1 | | |
| 45 | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 | AP2,FL1,FLO2 | | |
| 46 | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 | AP2,FL1,FLO2 | | |
| 47 | 0 | 0 K09284 | GO:0006355,(AT4G36920.2 | AP2,FL1,FLO2 | | |
| 48 | 0 | 0 | 0 | 0 | 0 | 0 |
| 49 | 0 | 0 | 0 | 0 | 0 | 0 |
| 50 | 0 | 0 | 0 | 0 | 0 | 0 |
| 51 | 0 | 0 | 0 | 0 | 0 | 0 |
| 52 | 0 | 0 | 0 | 0 | 0 | 0 |
| 53 | 0 | 0 | 0 | 0 | 0 | 0 |
| 54 | 0 | 0 | 0 | 0 | 0 | 0 |
| 55 | 0 | 0 | 0 | 0 | 0 | 0 |
| 56 | 0 | 0 | 0 | 0 | 0 | 0 |
| 57 | 0 | 0 | 0 | 0 | 0 | 0 |
| 58 | 0 | 0 | 0 | 0 | 0 | 0 |
| 59 | 0 | 0 | 0 | 0 | 0 | 0 |
| 60 | 0 | 0 | 0 | 0 | 0 | 0 |
| | 0 | 0 | 0 | 0 | 0 | 0 |

| | | | | | | | |
|----|---|----------|-------------------------------------|---|---|---|---|
| 1 | | | | | | | |
| 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 7 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 8 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 9 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 15 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 16 | 0 | 0 K09284 | GO:0006355,(AT2G28550.2 RAP2.7,TOE1 | | | | |
| 17 | 0 | 0 K09284 | GO:0006355,(AT2G28550.2 RAP2.7,TOE1 | | | | |
| 18 | 0 | 0 K09284 | GO:0006355,(AT2G28550.2 RAP2.7,TOE1 | | | | |
| 19 | 0 | 0 K09284 | GO:0006355,(AT2G28550.2 RAP2.7,TOE1 | | | | |
| 20 | 0 | 0 K09284 | GO:0006355,(AT2G28550.2 RAP2.7,TOE1 | | | | |
| 21 | 0 | 0 K09284 | GO:0006355,(AT2G28550.2 RAP2.7,TOE1 | | | | |
| 22 | 0 | 0 K09284 | GO:0006355,(AT2G28550.2 RAP2.7,TOE1 | | | | |
| 23 | 0 | 0 K09284 | GO:0006355,(AT2G28550.2 RAP2.7,TOE1 | | | | |
| 24 | 0 | 0 K09284 | GO:0006355,(AT2G28550.2 RAP2.7,TOE1 | | | | |
| 25 | 0 | 0 K09284 | GO:0006355,(AT2G28550.2 RAP2.7,TOE1 | | | | |
| 26 | 0 | 0 K09284 | GO:0006355,(AT2G28550.2 RAP2.7,TOE1 | | | | |
| 27 | 0 | 0 K09284 | GO:0006355,(AT2G28550.2 RAP2.7,TOE1 | | | | |
| 28 | 0 | 0 K09284 | GO:0006355,(AT2G28550.2 RAP2.7,TOE1 | | | | |
| 29 | 0 | 0 K09284 | GO:0006355,(AT2G28550.2 RAP2.7,TOE1 | | | | |
| 30 | 0 | 0 K09284 | GO:0006355,(AT2G28550.2 RAP2.7,TOE1 | | | | |
| 31 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 32 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 33 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 34 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 35 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 36 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 37 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 38 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 39 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 40 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 41 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 42 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 43 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 44 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 45 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 46 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 47 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 48 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 49 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 50 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 51 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 52 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 53 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 54 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 55 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 56 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 57 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 58 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 59 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 60 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

| | | | | | | | |
|----|---------|------------|----------|-------------------------------------|---------------|---|---|
| 1 | | | | | | | |
| 2 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 3 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 4 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 5 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 6 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 7 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 8 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 9 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 10 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 11 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 12 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 13 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 14 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 RAP2.7,TOE1 | | | |
| 15 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 RAP2.7,TOE1 | | | |
| 16 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 RAP2.7,TOE1 | | | |
| 17 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 RAP2.7,TOE1 | | | |
| 18 | | 0 | 0 K09284 | GO:0006355,(AT2G28550.1 RAP2.7,TOE1 | | | |
| 19 | | 0 5.3.99.6 | K10525 | GO:0016853,(AT3G25780.1 AOC3 | | | |
| 20 | KOG0374 | 3.1.3.16 | | 0 GO:0005515,(AT2G27210.1 BSL3 | | | |
| 21 | | | | | | | |
| 22 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | | | |
| 23 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | | | |
| 24 | KOG1187 | 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | | | 0 |
| 25 | | | | | | | |
| 26 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 27 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 28 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 29 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 30 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 31 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 32 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 33 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 34 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 35 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 36 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 37 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 38 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 39 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 40 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 41 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 42 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 43 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 44 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 45 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 46 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 47 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 48 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 49 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 50 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 51 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 52 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 53 | | 0 | 0 K14291 | 0 AT3G20430.1 | | | 0 |
| 54 | | 0 | 0 | 0 | | | 0 |
| 55 | | 0 | 0 | 0 | 0 AT1G06590.1 | | 0 |
| 56 | | 0 | 0 | 0 | 0 AT1G06590.1 | | 0 |
| 57 | | 0 | 0 | 0 | 0 AT1G06590.1 | | 0 |
| 58 | | 0 | 0 | 0 | 0 AT1G06590.1 | | 0 |
| 59 | | 0 | 0 | 0 | 0 AT1G06590.1 | | 0 |
| 60 | | 0 | 0 | 0 | 0 AT1G06590.1 | | 0 |
| | | 0 | 0 | 0 | 0 AT1G06590.1 | | 0 |

| | | | | | |
|----|------------|-----------------|-------------------------------------|---------------|---|
| 1 | | | | | |
| 2 | 0 | 0 | 0 | 0 AT1G06590.1 | 0 |
| 3 | 0 | 0 | 0 | 0 AT1G06590.1 | 0 |
| 4 | 0 | 0 | 0 | 0 AT1G06590.1 | 0 |
| 5 | 0 | 0 | 0 | 0 AT1G06590.1 | 0 |
| 6 | 0 | 0 | 0 | 0 AT1G06590.1 | 0 |
| 7 | 0 | 0 | 0 | 0 AT1G06590.1 | 0 |
| 8 | 0 | 0 | 0 | 0 AT1G06590.1 | 0 |
| 9 | 0 | 0 | 0 | 0 AT1G06590.1 | 0 |
| 10 | 0 | 0 | 0 | 0 AT1G02610.1 | 0 |
| 11 | 0 | 0 | 0 | 0 AT1G02610.1 | 0 |
| 12 | 0 2.7.11.1 | K03097 | GO:0006468,(AT5G67380.1 ATCKA1,CKA1 | | |
| 13 | 0 2.7.11.1 | K03097 | GO:0006468,(AT5G67380.1 ATCKA1,CKA1 | | |
| 14 | 0 2.7.11.1 | K03097 | GO:0006468,(AT5G67380.1 ATCKA1,CKA1 | | |
| 15 | 0 2.7.11.1 | K03097 | GO:0006468,(AT5G67380.1 ATCKA1,CKA1 | | |
| 16 | 0 2.7.11.1 | K03097 | GO:0006468,(AT5G67380.1 ATCKA1,CKA1 | | |
| 17 | 0 2.7.11.1 | K03097 | GO:0006468,(AT5G67380.1 ATCKA1,CKA1 | | |
| 18 | 0 2.7.11.1 | K03097 | GO:0006468,(AT5G67380.1 ATCKA1,CKA1 | | |
| 19 | 0 2.7.11.1 | K03097 | GO:0006468,(AT5G67380.1 ATCKA1,CKA1 | | |
| 20 | 0 2.7.11.1 | K03097 | GO:0006468,(AT5G67380.1 ATCKA1,CKA1 | | |
| 21 | 0 2.7.11.1 | K03097 | GO:0006468,(AT5G67380.1 ATCKA1,CKA1 | | |
| 22 | 0 2.7.11.1 | K03097 | GO:0006468,(AT5G67380.1 ATCKA1,CKA1 | | |
| 23 | 0 2.7.11.1 | K03097 | GO:0006468,(AT5G67380.1 ATCKA1,CKA1 | | |
| 24 | 0 2.7.11.1 | K03097 | GO:0006468,(AT5G67380.1 ATCKA1,CKA1 | | |
| 25 | 0 2.3.1.45 | | 0 0 AT2G34410.2 | | 0 |
| 26 | 0 4.4.1.19 | | 0 GO:0019295 AT4G21320.1 HSA32 | | |
| 27 | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | | |
| 28 | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | | |
| 29 | | | | | |
| 30 | | | | | |
| 31 | KOG1558 | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | |
| 32 | KOG1558 | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | |
| 33 | | | | | |
| 34 | 0 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | | 0 |
| 35 | 0 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | | 0 |
| 36 | 0 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | | 0 |
| 37 | 0 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | | 0 |
| 38 | 0 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | | 0 |
| 39 | 0 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | | 0 |
| 40 | 0 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | | 0 |
| 41 | 0 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | | 0 |
| 42 | 0 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | | 0 |
| 43 | 0 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | | 0 |
| 44 | 0 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | | 0 |
| 45 | 0 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | | 0 |
| 46 | 0 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | | 0 |
| 47 | 0 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | | 0 |
| 48 | 0 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | | 0 |
| 49 | KOG1187 | 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | | 0 |
| 50 | KOG1187 | 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | | 0 |
| 51 | KOG1187 | 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | | 0 |
| 52 | KOG1187 | 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | | 0 |
| 53 | KOG1187 | 2.7.11.1 | 0 GO:0004674,(AT4G21380.1 ARK3,RK3 | | |
| 54 | | | | | |
| 55 | KOG1282 | 3.4.16.5 K16298 | GO:0006508,(AT3G45010.1 scpl48 | | |
| 56 | KOG1282 | 3.4.16.5 K16298 | GO:0006508,(AT3G45010.1 scpl48 | | |
| 57 | KOG1282 | 3.4.16.5 K16298 | GO:0006508,(AT3G45010.1 scpl48 | | |
| 58 | KOG1282 | 3.4.16.5 K16298 | GO:0006508,(AT3G45010.1 scpl48 | | |
| 59 | KOG1282 | 3.4.16.5 K16298 | GO:0006508,(AT3G45010.1 scpl48 | | |
| 60 | KOG1282 | 3.4.16.5 K16298 | GO:0006508,(AT3G45010.1 scpl48 | | |
| | KOG1282 | 3.4.16.5 K16298 | GO:0006508,(AT3G45010.1 scpl48 | | |

| | | | | | | | |
|----|---------|----------|--------|-------------------------|-------------------------|-------------|-------------|
| 1 | | | | | | | |
| 2 | KOG1282 | 3.4.16.5 | K16298 | GO:0006508,(AT3G45010.1 | scpl48 | | |
| 3 | KOG1282 | 3.4.16.5 | K16298 | GO:0006508,(AT3G45010.1 | scpl48 | | |
| 4 | KOG1282 | 3.4.16.5 | K16298 | GO:0006508,(AT3G45010.1 | scpl48 | | |
| 5 | KOG1282 | 3.4.16.5 | K16298 | GO:0006508,(AT3G45010.1 | scpl48 | | |
| 6 | KOG1282 | 3.4.16.5 | K16298 | GO:0006508,(AT3G45010.1 | scpl48 | | |
| 7 | KOG1282 | 3.4.16.5 | K16298 | GO:0006508,(AT3G45010.1 | scpl48 | | |
| 8 | KOG1282 | 3.4.16.5 | K16298 | GO:0006508,(AT3G45010.1 | scpl48 | | |
| 9 | | | | | | | |
| 10 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 11 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 12 | KOG1441 | | 0 | 0 | GO:0055085 | AT3G11320.1 | 0 |
| 13 | KOG1441 | | 0 | 0 | GO:0055085 | AT3G11320.1 | 0 |
| 14 | KOG1441 | | 0 | 0 | GO:0055085 | AT3G11320.1 | 0 |
| 15 | KOG1441 | | 0 | 0 | GO:0055085 | AT3G11320.1 | 0 |
| 16 | KOG1441 | | 0 | 0 | GO:0055085 | AT3G11320.1 | 0 |
| 17 | KOG1441 | | 0 | 0 | GO:0055085 | AT3G11320.1 | 0 |
| 18 | KOG1441 | | 0 | 0 | GO:0055085 | AT3G11320.1 | 0 |
| 19 | KOG1441 | | 0 | 0 | GO:0055085 | AT3G11320.1 | 0 |
| 20 | KOG1441 | | 0 | 0 | GO:0055085 | AT3G11320.1 | 0 |
| 21 | KOG1441 | | 0 | 0 | GO:0055085 | AT3G11320.1 | 0 |
| 22 | KOG1441 | | 0 | 0 | GO:0055085 | AT3G11320.1 | 0 |
| 23 | KOG1441 | | 0 | 0 | GO:0055085 | AT3G11320.1 | 0 |
| 24 | KOG1441 | | 0 | 0 | GO:0055085 | AT3G11320.1 | 0 |
| 25 | KOG1441 | | 0 | 0 | GO:0055085 | AT3G11320.1 | 0 |
| 26 | KOG1441 | | 0 | 0 | GO:0055085 | AT3G11320.1 | 0 |
| 27 | | 0 | 0 | K09284 | GO:0006355,(AT2G28550.2 | RAP2.7,TOE1 | |
| 28 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 29 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 30 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 31 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 32 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 33 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 34 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 35 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 36 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 37 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 38 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 39 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 40 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 41 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 42 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 43 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 44 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 45 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 46 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 47 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 48 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 49 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 50 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 51 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 52 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 53 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 54 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 55 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 56 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 57 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 58 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 59 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 60 | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| | | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |

| | | | | | | |
|----|---------|------------|--------|------------|-------------------------|-------------|
| 1 | | | | | | |
| 2 | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 3 | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 4 | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 5 | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 6 | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 7 | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 8 | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 9 | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 10 | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 11 | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 12 | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 13 | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 14 | 0 | 0 | 0 | 0 | AT3G19640.1 | MGT4,MRS2-3 |
| 15 | 0 | 0 | K10523 | GO:0005515 | AT4G08455.1 | 0 |
| 16 | 0 | 0 | K10523 | GO:0005515 | AT4G08455.1 | 0 |
| 17 | 0 | 0 | K10523 | GO:0005515 | AT4G08455.1 | 0 |
| 18 | 0 | 0 | K10523 | GO:0005515 | AT4G08455.1 | 0 |
| 19 | 0 | 0 | K10523 | GO:0005515 | AT4G08455.1 | 0 |
| 20 | 0 | 0 | K10523 | GO:0005515 | AT4G08455.1 | 0 |
| 21 | 0 | 0 | K10523 | GO:0005515 | AT4G08455.1 | 0 |
| 22 | 0 | 0 | K10523 | GO:0005515 | AT4G08455.1 | 0 |
| 23 | 0 | 0 | K10523 | GO:0005515 | AT4G08455.1 | 0 |
| 24 | 0 | 0 | K10523 | GO:0005515 | AT4G08455.1 | 0 |
| 25 | 0 | 0 | K10523 | GO:0005515 | AT4G08455.1 | 0 |
| 26 | 0 | 0 | K10523 | GO:0005515 | AT4G08455.1 | 0 |
| 27 | 0 | 0 | K10523 | GO:0005515 | AT4G08455.1 | 0 |
| 28 | 0 | 0 | K10523 | GO:0005515 | AT4G08455.1 | 0 |
| 29 | 0 | 0 | 0 | 0 | AT5G50990.1 | 0 |
| 30 | 0 | 0 | 0 | 0 | 0 | 0 |
| 31 | 0 | 0 | 0 | 0 | 0 | 0 |
| 32 | KOG1187 | 2.7.11.1 | | 0 | GO:0004674,(AT4G27290.1 | 0 |
| 33 | | 0 2.7.11.1 | | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 34 | | 0 2.7.11.1 | | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 35 | | 0 2.7.11.1 | | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 36 | KOG1187 | 2.7.11.1 | | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 37 | KOG1187 | 2.7.11.1 | | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 38 | KOG1187 | 2.7.11.1 | | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 39 | KOG1187 | 2.7.11.1 | | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 40 | KOG1187 | 2.7.11.1 | | 0 | GO:0004674,(AT4G27290.1 | 0 |
| 41 | KOG1187 | 2.7.11.1 | | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 42 | | | | | | |
| 43 | 0 | 0 | K14291 | | AT3G20430.1 | 0 |
| 44 | 0 | 0 | K14291 | | AT3G20430.1 | 0 |
| 45 | 0 | 0 | 0 | 0 | AT2G36430.1 | 0 |
| 46 | 0 | 0 | 0 | 0 | AT2G36430.1 | 0 |
| 47 | 0 | 0 | 0 | 0 | AT2G36430.1 | 0 |
| 48 | 0 | 0 | 0 | 0 | AT2G36430.1 | 0 |
| 49 | 0 | 0 | 0 | 0 | AT2G36430.1 | 0 |
| 50 | 0 | 0 | 0 | 0 | AT2G36430.1 | 0 |
| 51 | 0 | 0 | 0 | 0 | AT2G36430.1 | 0 |
| 52 | 0 | 0 | 0 | 0 | AT2G36430.1 | 0 |
| 53 | 0 | 0 | 0 | 0 | AT2G36430.1 | 0 |
| 54 | 0 | 0 | 0 | 0 | AT2G36430.1 | 0 |
| 55 | 0 | 0 | 0 | 0 | AT2G36430.1 | 0 |
| 56 | 0 | 0 | 0 | 0 | AT2G36430.1 | 0 |
| 57 | 0 | 0 | 0 | 0 | AT2G36430.1 | 0 |
| 58 | 0 | 0 | 0 | 0 | AT2G36430.1 | 0 |
| 59 | 0 | 0 | 0 | 0 | AT2G36430.1 | 0 |
| 60 | 0 | 0 | 0 | 0 | AT2G36430.1 | 0 |
| | 0 | 0 | 0 | 0 | 0 | 0 |

| | | | | | | | |
|----|---------|-------------|----------|---------------------------|----------------|---|---|
| 1 | | | | | | | |
| 2 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 3 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT5G67380.1 | ATCKA1,CKA1 | | |
| 4 | | 0 | 0 K15032 | GO:0006355,(AT2G03050.1 | EMB93,SOLDAT1(| | |
| 5 | | 0 | 0 K15032 | GO:0006355,(AT2G03050.1 | EMB93,SOLDAT1(| | |
| 6 | | 0 | 0 K15032 | GO:0006355,(AT2G03050.1 | EMB93,SOLDAT1(| | |
| 7 | | 0 | 0 K15032 | GO:0006355,(AT2G03050.1 | EMB93,SOLDAT1(| | |
| 8 | | 0 | 0 K15032 | GO:0006355,(AT2G03050.1 | EMB93,SOLDAT1(| | |
| 9 | | 0 | 0 K15032 | GO:0006355,(AT2G03050.1 | EMB93,SOLDAT1(| | |
| 10 | | 0 | 0 K15032 | GO:0006355,(AT2G03050.1 | EMB93,SOLDAT1(| | |
| 11 | | 0 | 0 K15032 | GO:0006355,(AT2G03050.1 | EMB93,SOLDAT1(| | |
| 12 | | 0 | 0 K15032 | GO:0006355,(AT2G03050.1 | EMB93,SOLDAT1(| | |
| 13 | | 0 | 0 K15032 | GO:0006355,(AT2G03050.1 | EMB93,SOLDAT1(| | |
| 14 | | 0 | 0 K15032 | GO:0006355,(AT2G03050.1 | EMB93,SOLDAT1(| | |
| 15 | | 0 | 0 K15032 | GO:0006355,(AT2G03050.1 | EMB93,SOLDAT1(| | |
| 16 | | 0 | 0 K15032 | GO:0006355,(AT2G03050.1 | EMB93,SOLDAT1(| | |
| 17 | | 0 | 0 K15032 | GO:0006355,(AT2G03050.1 | EMB93,SOLDAT1(| | |
| 18 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 19 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 20 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 21 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 22 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 23 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 24 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 25 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 26 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 27 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 28 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 29 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 30 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 31 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 32 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 33 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 34 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 35 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 36 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 37 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 38 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 39 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 40 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 41 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 42 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 43 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 44 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 45 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 46 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 47 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 48 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 49 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 50 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 51 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 52 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 53 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 54 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 55 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 56 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 57 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 58 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 59 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| 60 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 | ATDGK2,DGK2 | | |
| | KOG1399 | 1.14.13.168 | K11816 | 0 AT4G13260.1 | YUC2 | | |

| | | | | | |
|----|---------|-------------------------|--------|-------------------------|------------------|
| 1 | | | | | |
| 2 | KOG1399 | 1.14.13.168 | K11816 | 0 | AT4G13260.1 YUC2 |
| 3 | KOG1399 | 1.14.13.168 | K11816 | 0 | AT4G13260.1 YUC2 |
| 4 | KOG1399 | 1.14.13.168 | K11816 | 0 | AT4G13260.1 YUC2 |
| 5 | KOG1399 | 1.14.13.168 | K11816 | 0 | AT4G13260.1 YUC2 |
| 6 | KOG1399 | 1.14.13.168 | K11816 | 0 | AT4G13260.1 YUC2 |
| 7 | KOG1399 | 1.14.13.168 | K11816 | 0 | AT4G13260.1 YUC2 |
| 8 | KOG1399 | 1.14.13.168 | K11816 | 0 | AT4G13260.1 YUC2 |
| 9 | KOG1399 | 1.14.13.168 | K11816 | 0 | AT4G13260.1 YUC2 |
| 10 | KOG1399 | 1.14.13.168 | K11816 | 0 | AT4G13260.1 YUC2 |
| 11 | KOG1399 | 1.14.13.168 | K11816 | 0 | AT4G13260.1 YUC2 |
| 12 | KOG1399 | 1.14.13.168 | K11816 | 0 | AT4G13260.1 YUC2 |
| 13 | | | | | |
| 14 | | 0 2.4.1.15,3.1.3 K16055 | | GO:0005992,(AT1G60140.1 | ATTPS10,TPS10 |
| 15 | | 0 2.4.1.15,3.1.3 K16055 | | GO:0005992,(AT1G60140.1 | ATTPS10,TPS10 |
| 16 | | 0 2.4.1.15,3.1.3 K16055 | | GO:0005992,(AT1G60140.1 | ATTPS10,TPS10 |
| 17 | | 0 2.4.1.15,3.1.3 K16055 | | GO:0005992,(AT1G60140.1 | ATTPS10,TPS10 |
| 18 | | 0 2.4.1.15,3.1.3 K16055 | | GO:0005992,(AT1G60140.1 | ATTPS10,TPS10 |
| 19 | | 0 2.4.1.15,3.1.3 K16055 | | GO:0005992,(AT1G60140.1 | ATTPS10,TPS10 |
| 20 | | 0 2.4.1.15,3.1.3 K16055 | | GO:0005992,(AT1G60140.1 | ATTPS10,TPS10 |
| 21 | | 0 2.4.1.15,3.1.3 K16055 | | GO:0005992,(AT1G60140.1 | ATTPS10,TPS10 |
| 22 | | 0 2.4.1.15,3.1.3 K16055 | | GO:0005992,(AT1G60140.1 | ATTPS10,TPS10 |
| 23 | | 0 2.4.1.15,3.1.3 K16055 | | GO:0005992,(AT1G60140.1 | ATTPS10,TPS10 |
| 24 | | 0 2.4.1.15,3.1.3 K16055 | | GO:0005992,(AT1G60140.1 | ATTPS10,TPS10 |
| 25 | | 0 2.4.1.15,3.1.3 K16055 | | GO:0005992,(AT1G60140.1 | ATTPS10,TPS10 |
| 26 | | 0 2.4.1.15,3.1.3 K16055 | | GO:0005992,(AT1G60140.1 | ATTPS10,TPS10 |
| 27 | | 0 2.4.1.15,3.1.3 K16055 | | GO:0005992,(AT1G60140.1 | ATTPS10,TPS10 |
| 28 | KOG1809 | 0 | 0 | 0 | AT1G48090.1 |
| 29 | KOG1809 | 0 | 0 | 0 | AT1G48090.1 |
| 30 | KOG1809 | 0 | 0 | 0 | AT1G48090.1 |
| 31 | KOG1809 | 0 | 0 | 0 | AT1G48090.1 |
| 32 | KOG1809 | 0 | 0 | 0 | AT1G48090.1 |
| 33 | KOG1809 | 0 | 0 | 0 | AT1G48090.1 |
| 34 | KOG1809 | 0 | 0 | 0 | AT1G48090.1 |
| 35 | KOG1809 | 0 | 0 | 0 | AT1G48090.1 |
| 36 | KOG1809 | 0 | 0 | 0 | AT1G48090.1 |
| 37 | KOG1809 | 0 | 0 | 0 | AT1G48090.1 |
| 38 | KOG1809 | 0 | 0 | 0 | AT1G48090.1 |
| 39 | KOG1809 | 0 | 0 | 0 | AT1G48090.1 |
| 40 | KOG1809 | 0 | 0 | 0 | AT1G48090.1 |
| 41 | KOG1809 | 0 | 0 | 0 | AT1G48090.1 |
| 42 | | | | | |
| 43 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT3G50000.1 | ATCKA2,CKA2 |
| 44 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT3G50000.1 | ATCKA2,CKA2 |
| 45 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT3G50000.1 | ATCKA2,CKA2 |
| 46 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT3G50000.1 | ATCKA2,CKA2 |
| 47 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT3G50000.1 | ATCKA2,CKA2 |
| 48 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT3G50000.1 | ATCKA2,CKA2 |
| 49 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT3G50000.1 | ATCKA2,CKA2 |
| 50 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT3G50000.1 | ATCKA2,CKA2 |
| 51 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT3G50000.1 | ATCKA2,CKA2 |
| 52 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT3G50000.1 | ATCKA2,CKA2 |
| 53 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT3G50000.1 | ATCKA2,CKA2 |
| 54 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT3G50000.1 | ATCKA2,CKA2 |
| 55 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT3G50000.1 | ATCKA2,CKA2 |
| 56 | KOG1558 | 0 | K14709 | GO:0055085,(AT1G31260.1 | ZIP10 |
| 57 | KOG1558 | 0 | K14709 | GO:0055085,(AT1G31260.1 | ZIP10 |
| 58 | KOG1558 | 0 | K14709 | GO:0055085,(AT1G31260.1 | ZIP10 |
| 59 | KOG1558 | 0 | K14709 | GO:0055085,(AT1G31260.1 | ZIP10 |
| 60 | KOG1558 | 0 | K14709 | GO:0055085,(AT1G31260.1 | ZIP10 |

| | | | | | | | |
|----|---------|-----------|----------|----------------------------------|-----------------------------|--|---|
| 1 | | | | | | | |
| 2 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | | |
| 3 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | | |
| 4 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | | |
| 5 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | | |
| 6 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | | |
| 7 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | | |
| 8 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | | |
| 9 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | | |
| 10 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | | |
| 11 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | | |
| 12 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | | |
| 13 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | | |
| 14 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | | |
| 15 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | | |
| 16 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | | |
| 17 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | | |
| 18 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | | |
| 19 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | | |
| 20 | KOG1558 | | 0 K14709 | GO:0055085,(AT1G31260.1 ZIP10 | | | |
| 21 | KOG0374 | 3.1.3.16 | 0 | GO:0005515,(AT2G27210.1 BSL3 | | | |
| 22 | KOG0374 | 3.1.3.16 | 0 | GO:0005515,(AT2G27210.1 BSL3 | | | |
| 23 | KOG0374 | 3.1.3.16 | 0 | GO:0005515,(AT2G27210.1 BSL3 | | | |
| 24 | KOG0374 | 3.1.3.16 | 0 | GO:0005515,(AT2G27210.1 BSL3 | | | |
| 25 | KOG0374 | 3.1.3.16 | 0 | GO:0005515,(AT2G27210.1 BSL3 | | | |
| 26 | KOG0374 | 3.1.3.16 | 0 | GO:0005515,(AT2G27210.1 BSL3 | | | |
| 27 | KOG0374 | 3.1.3.16 | 0 | GO:0005515,(AT2G27210.1 BSL3 | | | |
| 28 | KOG0374 | 3.1.3.16 | 0 | GO:0005515,(AT2G27210.1 BSL3 | | | |
| 29 | KOG0374 | 3.1.3.16 | 0 | GO:0005515,(AT2G27210.1 BSL3 | | | |
| 30 | KOG0374 | 3.1.3.16 | 0 | GO:0005515,(AT2G27210.1 BSL3 | | | |
| 31 | KOG0374 | 3.1.3.16 | 0 | GO:0005515,(AT2G27210.1 BSL3 | | | |
| 32 | KOG0374 | 3.1.3.16 | 0 | GO:0005515,(AT2G27210.1 BSL3 | | | |
| 33 | KOG0374 | 3.1.3.16 | 0 | GO:0005515,(AT2G27210.1 BSL3 | | | |
| 34 | KOG0374 | 3.1.3.16 | 0 | GO:0005515,(AT2G27210.1 BSL3 | | | |
| 35 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 | | 0 |
| 36 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 | | 0 |
| 37 | KOG1919 | 5.4.99.24 | | 0 | GO:0009982,(AT4G21770.1 | | 0 |
| 38 | KOG1919 | 5.4.99.24 | | 0 | GO:0009982,(AT4G21770.1 | | 0 |
| 39 | KOG1919 | 5.4.99.24 | | 0 | GO:0009982,(AT4G21770.1 | | 0 |
| 40 | KOG1919 | 5.4.99.24 | | 0 | GO:0009982,(AT4G21770.1 | | 0 |
| 41 | KOG1919 | 5.4.99.24 | | 0 | GO:0009982,(AT4G21770.1 | | 0 |
| 42 | KOG1919 | 5.4.99.24 | | 0 | GO:0009982,(AT4G21770.1 | | 0 |
| 43 | KOG1919 | 5.4.99.24 | | 0 | GO:0009982,(AT4G21770.1 | | 0 |
| 44 | KOG1919 | 5.4.99.24 | | 0 | GO:0009982,(AT4G21770.1 | | 0 |
| 45 | KOG1919 | 5.4.99.24 | | 0 | GO:0009982,(AT4G21770.1 | | 0 |
| 46 | KOG1919 | 5.4.99.24 | | 0 | GO:0009982,(AT4G21770.1 | | 0 |
| 47 | KOG1919 | 5.4.99.24 | | 0 | GO:0009982,(AT4G21770.1 | | 0 |
| 48 | KOG1919 | 5.4.99.24 | | 0 | GO:0009982,(AT4G21770.1 | | 0 |
| 49 | KOG1919 | 5.4.99.24 | | 0 | GO:0009982,(AT4G21770.1 | | 0 |
| 50 | | | | | | | |
| 51 | | 0 | 0 | 0 | 0 AT5G03170.1 ATFLA11,FLA11 | | |
| 52 | | 0 | 0 K14486 | GO:0003677,(AT2G33860.1 ARF3,ETT | | | |
| 53 | | 0 | 0 K14486 | GO:0003677,(AT2G33860.1 ARF3,ETT | | | |
| 54 | | 0 | 0 K14486 | GO:0003677,(AT2G33860.1 ARF3,ETT | | | |
| 55 | | 0 | 0 K14486 | GO:0003677,(AT2G33860.1 ARF3,ETT | | | |
| 56 | | 0 | 0 K14486 | GO:0003677,(AT2G33860.1 ARF3,ETT | | | |
| 57 | | 0 | 0 K14486 | GO:0003677,(AT2G33860.1 ARF3,ETT | | | |
| 58 | | 0 | 0 K14486 | GO:0003677,(AT2G33860.1 ARF3,ETT | | | |
| 59 | | 0 | 0 K14486 | GO:0003677,(AT2G33860.1 ARF3,ETT | | | |
| 60 | | 0 | 0 K14486 | GO:0003677,(AT2G33860.1 ARF3,ETT | | | |
| | | 0 | 0 K14486 | GO:0003677,(AT2G33860.1 ARF3,ETT | | | |

| | | | | | |
|----|---------|----------|----------|----------------------------------|---|
| 1 | | | | | |
| 2 | | 0 | 0 K14486 | GO:0003677,(AT2G33860.1 ARF3,ETT | |
| 3 | | 0 | 0 K14486 | GO:0003677,(AT2G33860.1 ARF3,ETT | |
| 4 | | 0 | 0 | 0 GO:0016020,(AT3G52060.2 | 0 |
| 5 | | 0 | 0 | 0 GO:0016020,(AT3G52060.2 | 0 |
| 6 | | 0 | 0 | 0 GO:0016020,(AT3G52060.2 | 0 |
| 7 | | 0 | 0 | 0 GO:0016020,(AT3G52060.2 | 0 |
| 8 | | 0 | 0 | 0 GO:0016020,(AT3G52060.2 | 0 |
| 9 | | 0 | 0 | 0 GO:0016020,(AT3G52060.2 | 0 |
| 10 | | 0 | 0 | 0 GO:0016020,(AT3G52060.2 | 0 |
| 11 | | 0 | 0 | 0 GO:0016020,(AT3G52060.2 | 0 |
| 12 | | 0 | 0 | 0 GO:0016020,(AT3G52060.2 | 0 |
| 13 | | 0 | 0 | 0 GO:0016020,(AT3G52060.2 | 0 |
| 14 | | 0 | 0 | 0 GO:0016020,(AT3G52060.2 | 0 |
| 15 | | 0 | 0 | 0 GO:0016020,(AT3G52060.2 | 0 |
| 16 | | 0 | 0 | 0 GO:0016020,(AT3G52060.2 | 0 |
| 17 | | 0 | 0 | 0 GO:0016020,(AT3G52060.2 | 0 |
| 18 | KOG0522 | | 0 | 0 AT1G04780.1 | 0 |
| 19 | KOG0522 | | 0 | 0 AT1G04780.1 | 0 |
| 20 | KOG0522 | | 0 | 0 AT1G04780.1 | 0 |
| 21 | KOG0522 | | 0 | 0 AT1G04780.1 | 0 |
| 22 | KOG0522 | | 0 | 0 AT1G04780.1 | 0 |
| 23 | KOG0522 | | 0 | 0 AT1G04780.1 | 0 |
| 24 | KOG0522 | | 0 | 0 AT1G04780.1 | 0 |
| 25 | KOG0522 | | 0 | 0 AT1G04780.1 | 0 |
| 26 | KOG0522 | | 0 | 0 AT1G04780.1 | 0 |
| 27 | KOG0522 | | 0 | 0 AT1G04780.1 | 0 |
| 28 | KOG0522 | | 0 | 0 AT1G04780.1 | 0 |
| 29 | KOG0522 | | 0 | 0 AT1G04780.1 | 0 |
| 30 | KOG0522 | | 0 | 0 AT1G04780.1 | 0 |
| 31 | KOG0522 | | 0 | 0 AT1G04780.1 | 0 |
| 32 | KOG0522 | | 0 | 0 AT1G04780.1 | 0 |
| 33 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 34 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 35 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 36 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 37 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 38 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 39 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 40 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 41 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 42 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 43 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 44 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 45 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 46 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 47 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 48 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 49 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 50 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 51 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 52 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 53 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 54 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 55 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 56 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 57 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 58 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 59 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| 60 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |
| | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT4G21410.1 CRK29 | |

| | | | | | | |
|----|---------|----------|----------|-------------------------|-------------------------|---|
| 1 | | | | | | |
| 2 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 3 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 4 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 5 | | | | | | |
| 6 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 7 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 8 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 9 | | | | | | |
| 10 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 11 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 12 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 13 | | | | | | |
| 14 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 15 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 16 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 17 | | | | | | |
| 18 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 19 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 20 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 21 | | | | | | |
| 22 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 23 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 24 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 25 | | | | | | |
| 26 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 27 | KOG4409 | 2.3.1.51 | 0 | 0 | AT4G24160.1 | 0 |
| 28 | | 0 | 0 | 0 | AT5G17690.1 LHP1,TFL2 | |
| 29 | | 0 | 0 | 0 | AT5G17690.1 LHP1,TFL2 | |
| 30 | | 0 | 0 | 0 | AT5G17690.1 LHP1,TFL2 | |
| 31 | | 0 | 0 | 0 | AT5G17690.1 LHP1,TFL2 | |
| 32 | | 0 | 0 | 0 | AT5G17690.1 LHP1,TFL2 | |
| 33 | | 0 | 0 | 0 | AT5G17690.1 LHP1,TFL2 | |
| 34 | | 0 | 0 | 0 | AT5G17690.1 LHP1,TFL2 | |
| 35 | | 0 | 0 | 0 | AT5G17690.1 LHP1,TFL2 | |
| 36 | | 0 | 0 | 0 | AT5G17690.1 LHP1,TFL2 | |
| 37 | | 0 | 0 | 0 | AT5G17690.1 LHP1,TFL2 | |
| 38 | | 0 | 0 | 0 | AT5G17690.1 LHP1,TFL2 | |
| 39 | | 0 | 0 | 0 | AT5G17690.1 LHP1,TFL2 | |
| 40 | | 0 | 0 | 0 | AT5G17690.1 LHP1,TFL2 | |
| 41 | | 0 | 0 | 0 | AT5G17690.1 LHP1,TFL2 | |
| 42 | | 0 | 0 | 0 | AT5G17690.1 LHP1,TFL2 | |
| 43 | | 0 | 0 K10523 | GO:0005515 | AT4G08455.1 | 0 |
| 44 | | 0 | 0 | 0 | AT3G50140.1 | 0 |
| 45 | | 0 | 0 | 0 | AT3G50140.1 | 0 |
| 46 | | 0 | 0 | 0 | AT3G50140.1 | 0 |
| 47 | | 0 | 0 | 0 | AT3G50140.1 | 0 |
| 48 | | 0 | 0 | 0 | AT3G50140.1 | 0 |
| 49 | | 0 | 0 | 0 | AT3G50140.1 | 0 |
| 50 | | 0 | 0 | 0 | AT3G50140.1 | 0 |
| 51 | | 0 | 0 | 0 | AT3G50140.1 | 0 |
| 52 | | 0 | 0 | 0 | AT3G50140.1 | 0 |
| 53 | | 0 | 0 | 0 | AT3G50140.1 | 0 |
| 54 | | 0 | 0 | 0 | AT3G50140.1 | 0 |
| 55 | | 0 | 0 | 0 | AT3G50140.1 | 0 |
| 56 | | 0 | 0 | 0 | AT3G50140.1 | 0 |
| 57 | | 0 | 0 | 0 | AT3G50140.1 | 0 |
| 58 | | 0 | 0 | 0 | AT3G50140.1 | 0 |
| 59 | | 0 | 0 | 0 | AT3G50140.1 | 0 |
| 60 | KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT3G14840.2 | 0 |
| | | 0 | 0 K09338 | GO:0003677,(AT5G60690.1 | IFL1,IFL1,REV | |

| | | | | | |
|----|---------|-----------|----------|--------------------------------------|---|
| 1 | | | | | |
| 2 | | 0 | 0 K09338 | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | |
| 3 | | 0 | 0 K09338 | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | |
| 4 | | 0 | 0 K09338 | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | |
| 5 | | 0 | 0 K09338 | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | |
| 6 | | 0 | 0 K09338 | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | |
| 7 | | 0 | 0 K09338 | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | |
| 8 | | 0 | 0 K09338 | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | |
| 9 | | 0 | 0 K09338 | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | |
| 10 | | 0 | 0 K09338 | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | |
| 11 | | 0 | 0 K09338 | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | |
| 12 | | 0 | 0 K09338 | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | |
| 13 | | 0 | 0 K09338 | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | |
| 14 | | 0 | 0 K09338 | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | |
| 15 | | 0 | 0 K09338 | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | |
| 16 | KOG1543 | 3.4.22.33 | 0 | GO:0008234,(AT5G45890.1 SAG12 | |
| 17 | KOG1543 | 3.4.22.33 | 0 | GO:0008234,(AT5G45890.1 SAG12 | |
| 18 | KOG1543 | 3.4.22.33 | 0 | GO:0008234,(AT5G45890.1 SAG12 | |
| 19 | KOG1543 | 3.4.22.33 | 0 | GO:0008234,(AT5G45890.1 SAG12 | |
| 20 | KOG1543 | 3.4.22.33 | 0 | GO:0008234,(AT5G45890.1 SAG12 | |
| 21 | KOG1543 | 3.4.22.33 | 0 | GO:0008234,(AT5G45890.1 SAG12 | |
| 22 | KOG1543 | 3.4.22.33 | 0 | GO:0008234,(AT5G45890.1 SAG12 | |
| 23 | KOG1543 | 3.4.22.33 | 0 | GO:0008234,(AT5G45890.1 SAG12 | |
| 24 | KOG1543 | 3.4.22.33 | 0 | GO:0008234,(AT5G45890.1 SAG12 | |
| 25 | KOG1543 | 3.4.22.33 | 0 | GO:0008234,(AT5G45890.1 SAG12 | |
| 26 | KOG1543 | 3.4.22.33 | 0 | GO:0008234,(AT5G45890.1 SAG12 | |
| 27 | KOG1543 | 3.4.22.33 | 0 | GO:0008234,(AT5G45890.1 SAG12 | |
| 28 | KOG1543 | 3.4.22.33 | 0 | GO:0008234,(AT5G45890.1 SAG12 | |
| 29 | KOG1543 | 3.4.22.33 | 0 | GO:0008234,(AT5G45890.1 SAG12 | |
| 30 | KOG1543 | 3.4.22.33 | 0 | GO:0008234,(AT5G45890.1 SAG12 | |
| 31 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 32 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 33 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 34 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 35 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 36 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 37 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 38 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 39 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 40 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 41 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 42 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 43 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 44 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 45 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 46 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 47 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 48 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 49 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 50 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 51 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 52 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 53 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 54 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 55 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 56 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 57 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 58 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(AT4G27290.1 | 0 |
| 59 | KOG1187 | 2.7.11.1 | 0 | GO:0004674,(AT4G27290.1 | 0 |
| 60 | KOG1187 | 2.7.11.1 | 0 | GO:0004674,(AT4G27290.1 | 0 |
| | | 0 3.1.1.3 | 0 | GO:0016788 AT5G33370.1 | 0 |

| | | | | | | |
|----|---------|-----------|----------|--------------|------------------|---|
| 1 | | | | | | |
| 2 | | 0 3.1.1.3 | | 0 GO:0016788 | AT5G33370.1 | 0 |
| 3 | | 0 3.1.1.3 | | 0 GO:0016788 | AT5G33370.1 | 0 |
| 4 | | 0 3.1.1.3 | | 0 GO:0016788 | AT5G33370.1 | 0 |
| 5 | | 0 3.1.1.3 | | 0 GO:0016788 | AT5G33370.1 | 0 |
| 6 | | 0 3.1.1.3 | | 0 GO:0016788 | AT5G33370.1 | 0 |
| 7 | | 0 3.1.1.3 | | 0 GO:0016788 | AT5G33370.1 | 0 |
| 8 | | 0 3.1.1.3 | | 0 GO:0016788 | AT5G33370.1 | 0 |
| 9 | | 0 3.1.1.3 | | 0 GO:0016788 | AT5G33370.1 | 0 |
| 10 | | 0 3.1.1.3 | | 0 GO:0016788 | AT5G33370.1 | 0 |
| 11 | | 0 3.1.1.3 | | 0 GO:0016788 | AT5G33370.1 | 0 |
| 12 | | 0 3.1.1.3 | | 0 GO:0016788 | AT5G33370.1 | 0 |
| 13 | | 0 3.1.1.3 | | 0 GO:0016788 | AT5G33370.1 | 0 |
| 14 | | 0 3.1.1.3 | | 0 GO:0016788 | AT5G33370.1 | 0 |
| 15 | KOG2275 | 3.5.1.14 | K14677 | GO:0016787,(| AT4G38220.1 | 0 |
| 16 | KOG2275 | 3.5.1.14 | K14677 | GO:0016787,(| AT4G38220.1 | 0 |
| 17 | KOG2275 | 3.5.1.14 | K14677 | GO:0016787,(| AT4G38220.1 | 0 |
| 18 | KOG2275 | 3.5.1.14 | K14677 | GO:0016787,(| AT4G38220.1 | 0 |
| 19 | KOG2275 | 3.5.1.14 | K14677 | GO:0016787,(| AT4G38220.1 | 0 |
| 20 | KOG2275 | 3.5.1.14 | K14677 | GO:0016787,(| AT4G38220.1 | 0 |
| 21 | KOG2275 | 3.5.1.14 | K14677 | GO:0016787,(| AT4G38220.1 | 0 |
| 22 | KOG2275 | 3.5.1.14 | K14677 | GO:0016787,(| AT4G38220.1 | 0 |
| 23 | KOG2275 | 3.5.1.14 | K14677 | GO:0016787,(| AT4G38220.1 | 0 |
| 24 | KOG2275 | 3.5.1.14 | K14677 | GO:0016787,(| AT4G38220.1 | 0 |
| 25 | KOG2275 | 3.5.1.14 | K14677 | GO:0016787,(| AT4G38220.1 | 0 |
| 26 | KOG2275 | 3.5.1.14 | K14677 | GO:0016787,(| AT4G38220.1 | 0 |
| 27 | KOG2275 | 3.5.1.14 | K14677 | GO:0016787,(| AT4G38220.1 | 0 |
| 28 | KOG2275 | 3.5.1.14 | K14677 | GO:0016787,(| AT4G38220.1 | 0 |
| 29 | KOG2275 | 3.5.1.14 | K14677 | GO:0016787,(| AT4G38220.1 | 0 |
| 30 | KOG2275 | 3.5.1.14 | K14677 | GO:0016787,(| AT4G38220.1 | 0 |
| 31 | | 0 | 0 | 0 | AT2G48070.1 RPH1 | |
| 32 | KOG3467 | | 0 K11254 | 0 | AT2G28740.1 HIS4 | |
| 33 | KOG3467 | | 0 K11254 | 0 | AT2G28740.1 HIS4 | |
| 34 | KOG3467 | | 0 K11254 | 0 | AT2G28740.1 HIS4 | |
| 35 | KOG3467 | | 0 K11254 | 0 | AT2G28740.1 HIS4 | |
| 36 | KOG3467 | | 0 K11254 | 0 | AT2G28740.1 HIS4 | |
| 37 | KOG3467 | | 0 K11254 | 0 | AT2G28740.1 HIS4 | |
| 38 | KOG3467 | | 0 K11254 | 0 | AT2G28740.1 HIS4 | |
| 39 | KOG3467 | | 0 K11254 | 0 | AT2G28740.1 HIS4 | |
| 40 | KOG3467 | | 0 K11254 | 0 | AT2G28740.1 HIS4 | |
| 41 | KOG3467 | | 0 K11254 | 0 | AT2G28740.1 HIS4 | |
| 42 | KOG3467 | | 0 K11254 | 0 | AT2G28740.1 HIS4 | |
| 43 | KOG3467 | | 0 K11254 | 0 | AT2G28740.1 HIS4 | |
| 44 | KOG3467 | | 0 K11254 | 0 | AT2G28740.1 HIS4 | |
| 45 | | 0 | 0 | 0 | AT3G53320.1 | 0 |
| 46 | | 0 | 0 | 0 | AT3G53320.1 | 0 |
| 47 | | 0 | 0 | 0 | AT3G53320.1 | 0 |
| 48 | | 0 | 0 | 0 | AT3G53320.1 | 0 |
| 49 | | 0 | 0 | 0 | AT3G53320.1 | 0 |
| 50 | | 0 | 0 | 0 | AT3G53320.1 | 0 |
| 51 | | 0 | 0 | 0 | AT3G53320.1 | 0 |
| 52 | | 0 | 0 | 0 | AT3G53320.1 | 0 |
| 53 | | 0 | 0 | 0 | AT3G53320.1 | 0 |
| 54 | | 0 | 0 | 0 | AT3G53320.1 | 0 |
| 55 | | 0 | 0 | 0 | AT3G53320.1 | 0 |
| 56 | | 0 | 0 | 0 | AT3G53320.1 | 0 |
| 57 | | 0 | 0 | 0 | AT3G53320.1 | 0 |
| 58 | | 0 | 0 | 0 | AT1G02610.1 | 0 |
| 59 | | 0 | 0 | 0 | AT1G02610.1 | 0 |
| 60 | | 0 | 0 | 0 | AT1G02610.1 | 0 |

| | | | | | |
|----|---------|-----------------|---|---|------------------------------------|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 3 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 4 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 5 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 6 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 7 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 8 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 9 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 10 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 11 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 12 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 13 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 14 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 15 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 16 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 17 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 18 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 19 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 20 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 21 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 22 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 23 | | 0 | 0 | 0 | 0 AT1G02610.1 |
| 24 | KOG2231 | | 0 | 0 | 0 AT3G62240.1 |
| 25 | KOG2231 | | 0 | 0 | 0 AT3G62240.1 |
| 26 | KOG2231 | | 0 | 0 | 0 AT3G62240.1 |
| 27 | KOG2231 | | 0 | 0 | 0 AT3G62240.1 |
| 28 | KOG2231 | | 0 | 0 | 0 AT3G62240.1 |
| 29 | KOG2231 | | 0 | 0 | 0 AT3G62240.1 |
| 30 | KOG2231 | | 0 | 0 | 0 AT3G62240.1 |
| 31 | KOG2231 | | 0 | 0 | 0 AT3G62240.1 |
| 32 | KOG2231 | | 0 | 0 | 0 AT3G62240.1 |
| 33 | KOG2231 | | 0 | 0 | 0 AT3G62240.1 |
| 34 | KOG2231 | | 0 | 0 | 0 AT3G62240.1 |
| 35 | KOG2231 | | 0 | 0 | 0 AT3G62240.1 |
| 36 | KOG2231 | | 0 | 0 | 0 AT3G62240.1 |
| 37 | KOG2231 | | 0 | 0 | 0 AT3G62240.1 |
| 38 | KOG2231 | | 0 | 0 | 0 AT3G62240.1 |
| 39 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 40 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 41 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 42 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 43 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 44 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 45 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 46 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 47 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 48 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 49 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 50 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 51 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 52 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 53 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 54 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 55 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 56 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 57 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 58 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 59 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| 60 | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |
| | KOG1187 | 2.7.11.1,2.7.11 | | 0 | GO:0006468,(AT2G28930.1 APK1B,PK1B |

| | | | | |
|----|---------|-----------------|--------------------------------------|---|
| 1 | | | | |
| 2 | KOG1187 | 2.7.11.1,2.7.11 | 0 GO:0006468,(AT2G28930.1 APK1B,PK1B | |
| 3 | KOG1187 | 2.7.11.1,2.7.11 | 0 GO:0006468,(AT2G28930.1 APK1B,PK1B | |
| 4 | KOG1187 | 2.7.11.1,2.7.11 | 0 GO:0006468,(AT2G28930.1 APK1B,PK1B | |
| 5 | | | | |
| 6 | KOG1187 | 2.7.11.1,2.7.11 | 0 GO:0006468,(AT2G28930.1 APK1B,PK1B | |
| 7 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 8 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 9 | | | | |
| 10 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 11 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 12 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 13 | | | | |
| 14 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 15 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 16 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 17 | | | | |
| 18 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 19 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 20 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 21 | | | | |
| 22 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 23 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 24 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 25 | | | | |
| 26 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 27 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 28 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 29 | | | | |
| 30 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 31 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 32 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 33 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 34 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 35 | | 0 1.10.3.3 | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 36 | | 0 2.3.1.45 | 0 AT2G34410.2 | 0 |
| 37 | | 0 2.3.1.45 | 0 AT2G34410.2 | 0 |
| 38 | | | | |
| 39 | | 0 2.3.1.45 | 0 AT2G34410.2 | 0 |
| 40 | | 0 2.3.1.45 | 0 AT2G34410.2 | 0 |
| 41 | | 0 2.3.1.45 | 0 AT2G34410.2 | 0 |
| 42 | | | | |
| 43 | | 0 2.3.1.45 | 0 AT2G34410.2 | 0 |
| 44 | | 0 2.3.1.45 | 0 AT2G34410.2 | 0 |
| 45 | | 0 2.3.1.45 | 0 AT2G34410.2 | 0 |
| 46 | | | | |
| 47 | | 0 2.3.1.45 | 0 AT2G34410.2 | 0 |
| 48 | | 0 2.3.1.45 | 0 AT2G34410.2 | 0 |
| 49 | | 0 4.4.1.19 | 0 GO:0019295 AT4G21320.1 HSA32 | |
| 50 | | | | |
| 51 | | 0 4.4.1.19 | 0 GO:0019295 AT4G21320.1 HSA32 | |
| 52 | | 0 4.4.1.19 | 0 GO:0019295 AT4G21320.1 HSA32 | |
| 53 | | 0 4.4.1.19 | 0 GO:0019295 AT4G21320.1 HSA32 | |
| 54 | | | | |
| 55 | | 0 4.4.1.19 | 0 GO:0019295 AT4G21320.1 HSA32 | |
| 56 | | 0 4.4.1.19 | 0 GO:0019295 AT4G21320.1 HSA32 | |
| 57 | | 0 4.4.1.19 | 0 GO:0019295 AT4G21320.1 HSA32 | |
| 58 | | | | |
| 59 | | 0 4.4.1.19 | 0 GO:0019295 AT4G21320.1 HSA32 | |
| 60 | | 0 4.4.1.19 | 0 GO:0019295 AT4G21320.1 HSA32 | |
| | | 0 4.4.1.19 | 0 GO:0019295 AT4G21320.1 HSA32 | |

| | | | | | |
|----|---------|------------|--------|--|---|
| 1 | | | | | |
| 2 | | 0 4.4.1.19 | | 0 GO:0019295 AT4G21320.1 HSA32 | |
| 3 | KOG1235 | 3.6.3.46 | | 0 AT5G64940.1 ATATH13,ATH13,, | |
| 4 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 5 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 6 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 7 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 8 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 9 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 10 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 11 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 12 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 13 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 14 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 15 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 16 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 17 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 18 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 19 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 20 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 21 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 22 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 23 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 24 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 25 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 26 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 27 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 28 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 29 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 30 | | 0 | 0 | 0 GO:0043047,(AT5G06310.1 AtPOT1b | |
| 31 | | 0 5.3.99.6 | K10525 | GO:0016853,(AT3G25780.1 AOC3 | |
| 32 | | 0 5.3.99.6 | K10525 | GO:0016853,(AT3G25780.1 AOC3 | |
| 33 | | 0 5.3.99.6 | K10525 | GO:0016853,(AT3G25780.1 AOC3 | |
| 34 | | 0 5.3.99.6 | K10525 | GO:0016853,(AT3G25780.1 AOC3 | |
| 35 | | 0 5.3.99.6 | K10525 | GO:0016853,(AT3G25780.1 AOC3 | |
| 36 | | 0 5.3.99.6 | K10525 | GO:0016853,(AT3G25780.1 AOC3 | |
| 37 | | 0 5.3.99.6 | K10525 | GO:0016853,(AT3G25780.1 AOC3 | |
| 38 | | 0 5.3.99.6 | K10525 | GO:0016853,(AT3G25780.1 AOC3 | |
| 39 | | 0 5.3.99.6 | K10525 | GO:0016853,(AT3G25780.1 AOC3 | |
| 40 | | 0 5.3.99.6 | K10525 | GO:0016853,(AT3G25780.1 AOC3 | |
| 41 | | 0 5.3.99.6 | K10525 | GO:0016853,(AT3G25780.1 AOC3 | |
| 42 | | 0 5.3.99.6 | K10525 | GO:0016853,(AT3G25780.1 AOC3 | |
| 43 | | 0 5.3.99.6 | K10525 | GO:0016853,(AT3G25780.1 AOC3 | |
| 44 | KOG1809 | | 0 | 0 AT1G48090.1 | 0 |
| 45 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT5G56040.2 | 0 |
| 46 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT5G56040.2 | 0 |
| 47 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT5G56040.2 | 0 |
| 48 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT5G56040.2 | 0 |
| 49 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT5G56040.2 | 0 |
| 50 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT5G56040.2 | 0 |
| 51 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT5G56040.2 | 0 |
| 52 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT5G56040.2 | 0 |
| 53 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT5G56040.2 | 0 |
| 54 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT5G56040.2 | 0 |
| 55 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT5G56040.2 | 0 |
| 56 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT5G56040.2 | 0 |
| 57 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT5G56040.2 | 0 |
| 58 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT5G56040.2 | 0 |
| 59 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT5G56040.2 | 0 |
| 60 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 | |
| | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 | |

| | | | | |
|----|---------|------------|--------|--|
| 1 | | | | |
| 2 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 3 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 4 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 5 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 6 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 7 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 8 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 9 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 10 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 11 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 12 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 13 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 14 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 15 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 16 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 17 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 18 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 19 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 20 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 21 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 22 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 23 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 24 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 25 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 26 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 27 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 |
| 28 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT2G23070.1 0 |
| 29 | | | | |
| 30 | KOG2182 | 3.4.14.2 | | 0 GO:0008236,(AT4G36195.1 0 |
| 31 | KOG2182 | 3.4.14.2 | | 0 GO:0008236,(AT4G36195.1 0 |
| 32 | KOG2182 | 3.4.14.2 | | 0 GO:0008236,(AT4G36195.1 0 |
| 33 | KOG2182 | 3.4.14.2 | | 0 GO:0008236,(AT4G36195.1 0 |
| 34 | KOG2182 | 3.4.14.2 | | 0 GO:0008236,(AT4G36195.1 0 |
| 35 | KOG2182 | 3.4.14.2 | | 0 GO:0008236,(AT4G36195.1 0 |
| 36 | KOG2182 | 3.4.14.2 | | 0 GO:0008236,(AT4G36195.1 0 |
| 37 | KOG2182 | 3.4.14.2 | | 0 GO:0008236,(AT4G36195.1 0 |
| 38 | KOG2182 | 3.4.14.2 | | 0 GO:0008236,(AT4G36195.1 0 |
| 39 | KOG2182 | 3.4.14.2 | | 0 GO:0008236,(AT4G36195.1 0 |
| 40 | KOG2182 | 3.4.14.2 | | 0 GO:0008236,(AT4G36195.1 0 |
| 41 | KOG2182 | 3.4.14.2 | | 0 GO:0008236,(AT4G36195.1 0 |
| 42 | KOG2182 | 3.4.14.2 | | 0 GO:0008236,(AT4G36195.1 0 |
| 43 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 0 |
| 44 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 0 |
| 45 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 0 |
| 46 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 0 |
| 47 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 0 |
| 48 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 0 |
| 49 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 0 |
| 50 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 0 |
| 51 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 0 |
| 52 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 0 |
| 53 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 0 |
| 54 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 0 |
| 55 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 0 |
| 56 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 0 |
| 57 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 0 |
| 58 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 0 |
| 59 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 0 |
| 60 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 0 |
| | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 0 |

| | | | | | |
|----|---------|-----------|--------|--|---|
| 1 | | | | | |
| 2 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 3 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 4 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 5 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 6 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 7 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 8 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 9 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 10 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 11 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 12 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 13 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 14 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 15 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 16 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 17 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 18 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 19 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 20 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 21 | KOG2182 | 3.4.21.26 | | 0 GO:0008236,(AT4G36195.1 | 0 |
| 22 | KOG4742 | 3.2.1.14 | K01183 | GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI | |
| 23 | KOG4742 | 3.2.1.14 | K01183 | GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI | |
| 24 | KOG4742 | 3.2.1.14 | K01183 | GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI | |
| 25 | KOG4742 | 3.2.1.14 | K01183 | GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI | |
| 26 | KOG4742 | 3.2.1.14 | K01183 | GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI | |
| 27 | KOG4742 | 3.2.1.14 | K01183 | GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI | |
| 28 | KOG4742 | 3.2.1.14 | K01183 | GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI | |
| 29 | KOG4742 | 3.2.1.14 | K01183 | GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI | |
| 30 | KOG4742 | 3.2.1.14 | K01183 | GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI | |
| 31 | KOG4742 | 3.2.1.14 | K01183 | GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI | |
| 32 | KOG4742 | 3.2.1.14 | K01183 | GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI | |
| 33 | KOG4742 | 3.2.1.14 | K01183 | GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI | |
| 34 | KOG4742 | 3.2.1.14 | K01183 | GO:0008061,(AT3G12500.1 ATHCHIB,B-CHI,CI | |
| 35 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 36 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 37 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 38 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 39 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 40 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 41 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 42 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 43 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 44 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 45 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 46 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 47 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 48 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 49 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 50 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 51 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 52 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 53 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 54 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 55 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 56 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 57 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 58 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 59 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| 60 | | 0 | 0 | 0 AT4G13750.1 NOV | |
| | | 0 | 0 | 0 GO:0016020 AT3G01100.1 ATHYP1,HYP1 | |

| | | | | |
|----|---------|----------|----------|--------------------------------------|
| 1 | | | | |
| 2 | | 0 | 0 | 0 GO:0016020 AT3G01100.1 ATHYP1,HYP1 |
| 3 | | 0 | 0 | 0 GO:0016020 AT3G01100.1 ATHYP1,HYP1 |
| 4 | | 0 | 0 | 0 GO:0016020 AT3G01100.1 ATHYP1,HYP1 |
| 5 | | 0 | 0 | 0 GO:0016020 AT3G01100.1 ATHYP1,HYP1 |
| 6 | | 0 | 0 | 0 GO:0016020 AT3G01100.1 ATHYP1,HYP1 |
| 7 | | 0 | 0 | 0 GO:0016020 AT3G01100.1 ATHYP1,HYP1 |
| 8 | | 0 | 0 | 0 GO:0016020 AT3G01100.1 ATHYP1,HYP1 |
| 9 | | 0 | 0 | 0 GO:0016020 AT3G01100.1 ATHYP1,HYP1 |
| 10 | | 0 | 0 | 0 GO:0016020 AT3G01100.1 ATHYP1,HYP1 |
| 11 | | 0 | 0 | 0 GO:0016020 AT3G01100.1 ATHYP1,HYP1 |
| 12 | | 0 | 0 | 0 GO:0016020 AT3G01100.1 ATHYP1,HYP1 |
| 13 | | 0 | 0 | 0 GO:0016020 AT3G01100.1 ATHYP1,HYP1 |
| 14 | | 0 | 0 | 0 GO:0016020 AT3G01100.1 ATHYP1,HYP1 |
| 15 | | 0 | 0 | 0 GO:0005515 AT5G22720.1 0 |
| 16 | | 0 | 0 | 0 GO:0005515 AT5G22720.1 0 |
| 17 | | | | |
| 18 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 19 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 20 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 21 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 22 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 23 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 24 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 25 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 26 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 27 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 28 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 29 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 30 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 31 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 32 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 33 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 34 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 35 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 36 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 37 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 38 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 39 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 40 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 41 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 42 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 43 | | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 0 |
| 44 | KOG1187 | 2.7.11.1 | | 0 GO:0004674,(AT4G21380.1 ARK3,RK3 |
| 45 | KOG1187 | 2.7.11.1 | | 0 GO:0004674,(AT4G21380.1 ARK3,RK3 |
| 46 | KOG1187 | 2.7.11.1 | | 0 GO:0004674,(AT4G21380.1 ARK3,RK3 |
| 47 | KOG1187 | 2.7.11.1 | | 0 GO:0004674,(AT4G21380.1 ARK3,RK3 |
| 48 | KOG1187 | 2.7.11.1 | | 0 GO:0004674,(AT4G21380.1 ARK3,RK3 |
| 49 | KOG1187 | 2.7.11.1 | | 0 GO:0004674,(AT4G21380.1 ARK3,RK3 |
| 50 | KOG1187 | 2.7.11.1 | | 0 GO:0004674,(AT4G21380.1 ARK3,RK3 |
| 51 | KOG1187 | 2.7.11.1 | | 0 GO:0004674,(AT4G21380.1 ARK3,RK3 |
| 52 | KOG1187 | 2.7.11.1 | | 0 GO:0004674,(AT4G21380.1 ARK3,RK3 |
| 53 | KOG1187 | 2.7.11.1 | | 0 GO:0004674,(AT4G21380.1 ARK3,RK3 |
| 54 | KOG1187 | 2.7.11.1 | | 0 GO:0004674,(AT4G21380.1 ARK3,RK3 |
| 55 | KOG1187 | 2.7.11.1 | | 0 GO:0004674,(AT4G21380.1 ARK3,RK3 |
| 56 | KOG1187 | 2.7.11.1 | | 0 GO:0004674,(AT4G21380.1 ARK3,RK3 |
| 57 | KOG1187 | 2.7.11.1 | | 0 GO:0004674,(AT4G21380.1 ARK3,RK3 |
| 58 | KOG0645 | | 0 | 0 GO:0005515 AT1G52360.1 0 |
| 59 | KOG0645 | | 0 | 0 GO:0005515 AT1G52360.1 0 |
| 60 | KOG0645 | | 0 | 0 GO:0005515 AT1G52360.1 0 |

| | | | | | |
|----|---------|-------------|----------------|-------------------------------|----------------------|
| 1 | | | | | |
| 2 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 3 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 4 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 5 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 6 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 7 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 8 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 9 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 10 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 11 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 12 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 13 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 14 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 15 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 16 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 17 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 18 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 19 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 20 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 21 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 22 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 23 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 24 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 25 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 26 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 27 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 28 | KOG0645 | 0 | 0 GO:0005515 | AT1G52360.1 | 0 |
| 29 | | 0 | 0 GO:0006886,(| AT2G38020.1 EMB258,MAN,VC | |
| 30 | | 0 | 0 K14404 | 0 AT1G30460.1 ATCPSF30,CPSF30 | |
| 31 | KOG1902 | 0 | 0 K14404 | 0 AT1G30460.1 ATCPSF30,CPSF30 | |
| 32 | KOG1902 | 0 | 0 K14404 | 0 AT1G30460.1 ATCPSF30,CPSF30 | |
| 33 | KOG1902 | 0 | 0 K14404 | 0 AT1G30460.1 ATCPSF30,CPSF30 | |
| 34 | KOG1902 | 0 | 0 K14404 | 0 AT1G30460.1 ATCPSF30,CPSF30 | |
| 35 | KOG1902 | 0 | 0 K14404 | 0 AT1G30460.1 ATCPSF30,CPSF30 | |
| 36 | KOG1902 | 0 | 0 K14404 | 0 AT1G30460.1 ATCPSF30,CPSF30 | |
| 37 | KOG1902 | 0 | 0 K14404 | 0 AT1G30460.1 ATCPSF30,CPSF30 | |
| 38 | KOG1902 | 0 | 0 K14404 | 0 AT1G30460.1 ATCPSF30,CPSF30 | |
| 39 | KOG1902 | 0 | 0 K14404 | 0 AT1G30460.1 ATCPSF30,CPSF30 | |
| 40 | KOG1902 | 0 | 0 K14404 | 0 AT1G30460.1 ATCPSF30,CPSF30 | |
| 41 | KOG1902 | 0 | 0 K14404 | 0 AT1G30460.1 ATCPSF30,CPSF30 | |
| 42 | KOG1902 | 0 | 0 K14404 | 0 AT1G30460.1 ATCPSF30,CPSF30 | |
| 43 | KOG1902 | 0 | 0 K14404 | 0 AT1G30460.1 ATCPSF30,CPSF30 | |
| 44 | KOG1902 | 0 | 0 K14404 | 0 AT1G30460.1 ATCPSF30,CPSF30 | |
| 45 | KOG1441 | 0 | 0 GO:0055085 | AT3G11320.1 | 0 |
| 46 | | 0 | 0 K14486 | GO:0003677,(| AT2G33860.1 ARF3,ETT |
| 47 | | 0 | 0 K14486 | GO:0003677,(| AT2G33860.1 ARF3,ETT |
| 48 | KOG1187 | 2.7.11.1 | 0 GO:0005515,(| AT1G68400.1 | 0 |
| 49 | KOG1187 | 2.7.11.1 | 0 GO:0005515,(| AT1G68400.1 | 0 |
| 50 | KOG1187 | 2.7.11.1 | 0 GO:0005515,(| AT1G68400.1 | 0 |
| 51 | KOG1187 | 2.7.11.1 | 0 GO:0005515,(| AT1G68400.1 | 0 |
| 52 | KOG1187 | 2.7.11.1 | 0 GO:0005515,(| AT1G68400.1 | 0 |
| 53 | KOG1187 | 2.7.11.1 | 0 GO:0005515,(| AT1G68400.1 | 0 |
| 54 | KOG1187 | 2.7.11.1 | 0 GO:0005515,(| AT1G68400.1 | 0 |
| 55 | KOG1187 | 2.7.11.1 | 0 GO:0005515,(| AT1G68400.1 | 0 |
| 56 | KOG1187 | 2.7.11.1 | 0 GO:0005515,(| AT1G68400.1 | 0 |
| 57 | KOG1187 | 2.7.11.1 | 0 GO:0005515,(| AT1G68400.1 | 0 |
| 58 | KOG1187 | 2.7.11.1 | 0 GO:0005515,(| AT1G68400.1 | 0 |
| 59 | KOG1187 | 2.7.11.1 | 0 GO:0005515,(| AT1G68400.1 | 0 |
| 60 | KOG1187 | 2.7.11.1 | 0 GO:0005515,(| AT1G68400.1 | 0 |
| | | 0 2.1.1.193 | 0 GO:0008168,(| AT1G50000.1 | 0 |

| | | | | | |
|----|---------|---------|---|---|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 GO:0006355,(AT4G09620.1 | 0 |
| 3 | | 0 | 0 | 0 GO:0006355,(AT4G09620.1 | 0 |
| 4 | | 0 | 0 | 0 GO:0006355,(AT4G09620.1 | 0 |
| 5 | | 0 | 0 | 0 GO:0006355,(AT4G09620.1 | 0 |
| 6 | | 0 | 0 | 0 GO:0006355,(AT4G09620.1 | 0 |
| 7 | | 0 | 0 | 0 GO:0006355,(AT4G09620.1 | 0 |
| 8 | | 0 | 0 | 0 GO:0006355,(AT4G09620.1 | 0 |
| 9 | | 0 | 0 | 0 GO:0006355,(AT4G09620.1 | 0 |
| 10 | | 0 | 0 | 0 GO:0006355,(AT4G09620.1 | 0 |
| 11 | | 0 | 0 | 0 GO:0006355,(AT4G09620.1 | 0 |
| 12 | | 0 | 0 | 0 GO:0006355,(AT4G09620.1 | 0 |
| 13 | | 0 | 0 | 0 GO:0006355,(AT4G09620.1 | 0 |
| 14 | | 0 | 0 | 0 GO:0006355,(AT4G09620.1 | 0 |
| 15 | | 0 | 0 | 0 GO:0006355,(AT4G09620.1 | 0 |
| 16 | | 0 | 0 | 0 GO:0006355,(AT4G09620.1 | 0 |
| 17 | | 0 | 0 | 0 GO:0006355,(AT4G09620.1 | 0 |
| 18 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 19 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 20 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 21 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 22 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 23 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 24 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 25 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 26 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 27 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 28 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 29 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 30 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 31 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 32 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 33 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 34 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 35 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 36 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 37 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 38 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 39 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 40 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 41 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 42 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 43 | KOG4793 | 2.7.7.7 | 0 | 0 AT5G26940.3 | 0 |
| 44 | | 0 | 0 | 0 AT2G38570.1 | 0 |
| 45 | | 0 | 0 | 0 AT2G38570.1 | 0 |
| 46 | | 0 | 0 | 0 AT2G38570.1 | 0 |
| 47 | | 0 | 0 | 0 AT2G38570.1 | 0 |
| 48 | | 0 | 0 | 0 AT2G38570.1 | 0 |
| 49 | | 0 | 0 | 0 AT2G38570.1 | 0 |
| 50 | | 0 | 0 | 0 AT2G38570.1 | 0 |
| 51 | | 0 | 0 | 0 AT2G38570.1 | 0 |
| 52 | | 0 | 0 | 0 AT2G38570.1 | 0 |
| 53 | | 0 | 0 | 0 AT2G38570.1 | 0 |
| 54 | | 0 | 0 | 0 AT2G38570.1 | 0 |
| 55 | | 0 | 0 | 0 AT2G38570.1 | 0 |
| 56 | | 0 | 0 | 0 AT2G38570.1 | 0 |
| 57 | | 0 | 0 | 0 AT2G38570.1 | 0 |
| 58 | | 0 | 0 | 0 AT2G38570.1 | 0 |
| 59 | KOG1586 | | 0 | 0 GO:0006886 AT3G56190.1 ALPHA-SNAP2,AS | |
| 60 | KOG1586 | | 0 | 0 GO:0006886 AT3G56190.1 ALPHA-SNAP2,AS | |
| | KOG1586 | | 0 | 0 GO:0006886 AT3G56190.1 ALPHA-SNAP2,AS | |

| | | | | | |
|----|---------|------------|--------|---|----------------------------|
| 1 | | | | | |
| 2 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 3 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 4 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 5 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 6 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 7 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 8 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 9 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 10 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 11 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 12 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 13 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 14 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 15 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 16 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 17 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 18 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 19 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 20 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 21 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 22 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 23 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 24 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 25 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 26 | KOG1586 | | 0 | 0 GO:0006886 | AT3G56190.1 ALPHA-SNAP2,AS |
| 27 | KOG0192 | 2.7.11.1 | | 0 GO:0005515,(AT3G24715.1 | 0 |
| 28 | KOG0192 | 2.7.11.1 | | 0 GO:0005515,(AT3G24715.1 | 0 |
| 29 | KOG0192 | 2.7.11.1 | | 0 GO:0005515,(AT3G24715.1 | 0 |
| 30 | KOG0192 | 2.7.11.1 | | 0 GO:0005515,(AT3G24715.1 | 0 |
| 31 | KOG0192 | 2.7.11.1 | | 0 GO:0005515,(AT3G24715.1 | 0 |
| 32 | KOG0192 | 2.7.11.1 | | 0 GO:0005515,(AT3G24715.1 | 0 |
| 33 | KOG0192 | 2.7.11.1 | | 0 GO:0005515,(AT3G24715.1 | 0 |
| 34 | KOG0192 | 2.7.11.1 | | 0 GO:0005515,(AT3G24715.1 | 0 |
| 35 | KOG0192 | 2.7.11.1 | | 0 GO:0005515,(AT3G24715.1 | 0 |
| 36 | KOG0192 | 2.7.11.1 | | 0 GO:0005515,(AT3G24715.1 | 0 |
| 37 | KOG0192 | 2.7.11.1 | | 0 GO:0005515,(AT3G24715.1 | 0 |
| 38 | KOG0192 | 2.7.11.1 | | 0 GO:0005515,(AT3G24715.1 | 0 |
| 39 | KOG0192 | 2.7.11.1 | | 0 GO:0005515,(AT3G24715.1 | 0 |
| 40 | KOG0192 | 2.7.11.1 | | 0 GO:0005515,(AT3G24715.1 | 0 |
| 41 | | 0 1.3.3.3 | K00228 | GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L | |
| 42 | | 0 1.3.3.3 | K00228 | GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L | |
| 43 | | 0 1.3.3.3 | K00228 | GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L | |
| 44 | | 0 1.3.3.3 | K00228 | GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L | |
| 45 | | 0 1.3.3.3 | K00228 | GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L | |
| 46 | | 0 1.3.3.3 | K00228 | GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L | |
| 47 | | 0 1.3.3.3 | K00228 | GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L | |
| 48 | | 0 1.3.3.3 | K00228 | GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L | |
| 49 | | 0 1.3.3.3 | K00228 | GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L | |
| 50 | | 0 1.3.3.3 | K00228 | GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L | |
| 51 | | 0 1.3.3.3 | K00228 | GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L | |
| 52 | | 0 1.3.3.3 | K00228 | GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L | |
| 53 | | 0 1.3.3.3 | K00228 | GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L | |
| 54 | | 0 1.3.3.3 | K00228 | GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L | |
| 55 | | 0 1.3.3.3 | K00228 | GO:0055114,(AT1G03475.1 ATCPO-I,HEMF1,L | |
| 56 | | 0 2.7.7.15 | | 0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1 | |
| 57 | | 0 2.7.7.15 | | 0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1 | |
| 58 | | 0 2.7.7.15 | | 0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1 | |
| 59 | | 0 2.7.7.15 | | 0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1 | |
| 60 | | 0 2.7.7.15 | | 0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1 | |

| | | | | | |
|----|---------|------------|----------|---------------------------------------|---|
| 1 | | | | | |
| 2 | | 0 2.7.7.15 | | 0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1 | |
| 3 | | 0 2.7.7.15 | | 0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1 | |
| 4 | | 0 2.7.7.15 | | 0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1 | |
| 5 | | 0 2.7.7.15 | | 0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1 | |
| 6 | | 0 2.7.7.15 | | 0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1 | |
| 7 | | 0 2.7.7.15 | | 0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1 | |
| 8 | | 0 2.7.7.15 | | 0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1 | |
| 9 | | 0 | | 0 AT5G17690.1 LHP1,TFL2 | |
| 10 | | 0 | 0 | 0 | |
| 11 | | 0 | 0 | 0 GO:0016788 AT1G53920.1 GLIP5 | |
| 12 | | 0 | 0 | 0 GO:0016788 AT1G53920.1 GLIP5 | |
| 13 | | 0 | 0 | 0 GO:0016788 AT1G53920.1 GLIP5 | |
| 14 | | 0 | 0 | 0 GO:0016788 AT1G53920.1 GLIP5 | |
| 15 | | 0 | 0 | 0 GO:0016788 AT1G53920.1 GLIP5 | |
| 16 | | 0 | 0 | 0 GO:0016788 AT1G53920.1 GLIP5 | |
| 17 | | 0 | 0 | 0 GO:0016788 AT1G53920.1 GLIP5 | |
| 18 | | 0 | 0 | 0 GO:0016788 AT1G53920.1 GLIP5 | |
| 19 | | 0 | 0 | 0 GO:0016788 AT1G53920.1 GLIP5 | |
| 20 | | 0 | 0 | 0 GO:0016788 AT1G53920.1 GLIP5 | |
| 21 | | 0 | 0 | 0 GO:0016788 AT1G53920.1 GLIP5 | |
| 22 | | 0 | 0 | 0 GO:0016788 AT1G53920.1 GLIP5 | |
| 23 | | 0 | 0 | 0 GO:0016788 AT1G53920.1 GLIP5 | |
| 24 | | 0 | 0 | 0 AT3G02645.1 | 0 |
| 25 | | | | | |
| 26 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G51990.1 | 0 |
| 27 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G51990.1 | 0 |
| 28 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G51990.1 | 0 |
| 29 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G51990.1 | 0 |
| 30 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G51990.1 | 0 |
| 31 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G51990.1 | 0 |
| 32 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G51990.1 | 0 |
| 33 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G51990.1 | 0 |
| 34 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G51990.1 | 0 |
| 35 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G51990.1 | 0 |
| 36 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G51990.1 | 0 |
| 37 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G51990.1 | 0 |
| 38 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G51990.1 | 0 |
| 39 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G51990.1 | 0 |
| 40 | | 0 | 0 K07399 | 0 AT1G49380.1 | 0 |
| 41 | | 0 | 0 K07399 | 0 AT1G49380.1 | 0 |
| 42 | | | | | |
| 43 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G14840.2 | 0 |
| 44 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G14840.2 | 0 |
| 45 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G14840.2 | 0 |
| 46 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G14840.2 | 0 |
| 47 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G14840.2 | 0 |
| 48 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G14840.2 | 0 |
| 49 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G14840.2 | 0 |
| 50 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G14840.2 | 0 |
| 51 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G14840.2 | 0 |
| 52 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G14840.2 | 0 |
| 53 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G14840.2 | 0 |
| 54 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G14840.2 | 0 |
| 55 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G14840.2 | 0 |
| 56 | KOG1543 | 3.4.22.33 | | 0 GO:0008234,(AT5G45890.1 SAG12 | |
| 57 | KOG1543 | 3.4.22.33 | | 0 GO:0008234,(AT5G45890.1 SAG12 | |
| 58 | KOG1543 | 3.4.22.33 | | 0 GO:0008234,(AT5G45890.1 SAG12 | |
| 59 | KOG1543 | 3.4.22.33 | | 0 GO:0008234,(AT5G45890.1 SAG12 | |
| 60 | KOG1543 | 3.4.22.33 | | 0 GO:0008234,(AT5G45890.1 SAG12 | |
| | KOG1543 | 3.4.22.33 | | 0 GO:0008234,(AT5G45890.1 SAG12 | |

| | | | | |
|----|---------|------------|---------------------------------|---|
| 1 | | | | |
| 2 | KOG1543 | 3.4.22.33 | 0 GO:0008234,(AT5G45890.1 SAG12 | |
| 3 | KOG1543 | 3.4.22.33 | 0 GO:0008234,(AT5G45890.1 SAG12 | |
| 4 | KOG1543 | 3.4.22.33 | 0 GO:0008234,(AT5G45890.1 SAG12 | |
| 5 | KOG1543 | 3.4.22.33 | 0 GO:0008234,(AT5G45890.1 SAG12 | |
| 6 | KOG1543 | 3.4.22.33 | 0 GO:0008234,(AT5G45890.1 SAG12 | |
| 7 | KOG1543 | 3.4.22.33 | 0 GO:0008234,(AT5G45890.1 SAG12 | |
| 8 | KOG1187 | 2.7.11.1 | 0 GO:0004674,(AT4G27290.1 | 0 |
| 9 | KOG1187 | 2.7.11.1 | 0 GO:0004674,(AT4G27290.1 | 0 |
| 10 | KOG1187 | 2.7.11.1 | 0 GO:0004674,(AT4G27290.1 | 0 |
| 11 | KOG1187 | 2.7.11.1 | 0 GO:0004674,(AT4G27290.1 | 0 |
| 12 | KOG1187 | 2.7.11.1 | 0 GO:0004674,(AT4G27290.1 | 0 |
| 13 | KOG1187 | 2.7.11.1 | 0 GO:0004674,(AT4G27290.1 | 0 |
| 14 | KOG1187 | 2.7.11.1 | 0 GO:0004674,(AT4G27290.1 | 0 |
| 15 | KOG1187 | 2.7.11.1 | 0 GO:0004674,(AT4G27290.1 | 0 |
| 16 | KOG1187 | 2.7.11.1 | 0 GO:0004674,(AT4G27290.1 | 0 |
| 17 | KOG1187 | 2.7.11.1 | 0 GO:0004674,(AT4G27290.1 | 0 |
| 18 | KOG1187 | 2.7.11.1 | 0 GO:0004674,(AT4G27290.1 | 0 |
| 19 | KOG1187 | 2.7.11.1 | 0 GO:0004674,(AT4G27290.1 | 0 |
| 20 | KOG1187 | 2.7.11.1 | 0 GO:0004674,(AT4G27290.1 | 0 |
| 21 | KOG1187 | 2.7.11.1 | 0 GO:0004674,(AT4G27290.1 | 0 |
| 22 | KOG1187 | 2.7.11.1 | 0 GO:0004674,(AT4G27290.1 | 0 |
| 23 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 24 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 25 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 26 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 27 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 28 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 29 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 30 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 31 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 32 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 33 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 34 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 35 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 36 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 37 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 38 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 39 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 40 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 41 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 42 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 43 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 44 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 45 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 46 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 47 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 48 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 49 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 50 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 51 | | 0 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 52 | KOG1187 | 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 53 | KOG1187 | 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 54 | KOG1187 | 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 55 | KOG1187 | 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 56 | KOG1187 | 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 57 | KOG1187 | 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 58 | KOG1187 | 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 59 | KOG1187 | 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| 60 | KOG1187 | 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |
| | KOG1187 | 2.7.11.1 | 0 GO:0048544,(AT4G27290.1 | 0 |

| | | | | | |
|----|---------|------------|----------|---------------------------------------|---|
| 1 | | | | | |
| 2 | KOG1187 | 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | 0 |
| 3 | KOG1187 | 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | 0 |
| 4 | KOG1187 | 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | 0 |
| 5 | KOG1187 | 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | 0 |
| 6 | KOG1187 | 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | 0 |
| 7 | KOG1187 | 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | 0 |
| 8 | KOG1187 | 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | 0 |
| 9 | KOG1187 | 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | 0 |
| 10 | KOG1187 | 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | 0 |
| 11 | KOG1187 | 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | 0 |
| 12 | KOG1187 | 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | 0 |
| 13 | KOG1187 | 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | 0 |
| 14 | KOG1187 | 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | 0 |
| 15 | KOG1187 | 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | 0 |
| 16 | KOG1187 | 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | 0 |
| 17 | KOG1187 | 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | 0 |
| 18 | KOG1187 | 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | 0 |
| 19 | | 0 | 0 K10268 | GO:0005515 AT4G02760.2 | 0 |
| 20 | | 0 | 0 K10268 | GO:0005515 AT4G02760.2 | 0 |
| 21 | | 0 | 0 K10268 | GO:0005515 AT4G02760.2 | 0 |
| 22 | | 0 | 0 K10268 | GO:0005515 AT4G02760.2 | 0 |
| 23 | | 0 | 0 K10268 | GO:0005515 AT4G02760.2 | 0 |
| 24 | | 0 | 0 K10268 | GO:0005515 AT4G02760.2 | 0 |
| 25 | | 0 | 0 K10268 | GO:0005515 AT4G02760.2 | 0 |
| 26 | | 0 | 0 K10268 | GO:0005515 AT4G02760.2 | 0 |
| 27 | | 0 | 0 K10268 | GO:0005515 AT4G02760.2 | 0 |
| 28 | | 0 | 0 K10268 | GO:0005515 AT4G02760.2 | 0 |
| 29 | | 0 | 0 K10268 | GO:0005515 AT4G02760.2 | 0 |
| 30 | | 0 | 0 K10268 | GO:0005515 AT4G02760.2 | 0 |
| 31 | | 0 | 0 K10268 | GO:0005515 AT4G02760.2 | 0 |
| 32 | | 0 | 0 K10268 | GO:0005515 AT4G02760.2 | 0 |
| 33 | | 0 | 0 | 0 AT5G03150.1 JKD | |
| 34 | | 0 | 0 | 0 AT5G03150.1 JKD | |
| 35 | | 0 | 0 | 0 AT5G03150.1 JKD | |
| 36 | | 0 | 0 | 0 AT5G03150.1 JKD | |
| 37 | | 0 | 0 | 0 AT5G03150.1 JKD | |
| 38 | | 0 | 0 | 0 AT5G03150.1 JKD | |
| 39 | | 0 | 0 | 0 AT5G03150.1 JKD | |
| 40 | | 0 | 0 | 0 AT5G03150.1 JKD | |
| 41 | | 0 | 0 | 0 AT5G03150.1 JKD | |
| 42 | | 0 | 0 | 0 AT5G03150.1 JKD | |
| 43 | | 0 | 0 | 0 AT5G03150.1 JKD | |
| 44 | | 0 | 0 | 0 AT5G03150.1 JKD | |
| 45 | | 0 | 0 | 0 AT5G03150.1 JKD | |
| 46 | | 0 | 0 | 0 AT5G03150.1 JKD | |
| 47 | | 0 | 0 | 0 AT5G03150.1 JKD | |
| 48 | | 0 1.10.3.3 | | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 49 | | 0 1.10.3.3 | | 0 GO:0055114,(AT1G55570.1 sks12 | |
| 50 | | 0 5.2.1.8 | K10598 | GO:0006457,(AT5G67530.1 ATPUB49,PUB49 | |
| 51 | | 0 5.2.1.8 | K10598 | GO:0006457,(AT5G67530.1 ATPUB49,PUB49 | |
| 52 | | 0 5.2.1.8 | K10598 | GO:0006457,(AT5G67530.1 ATPUB49,PUB49 | |
| 53 | | 0 5.2.1.8 | K10598 | GO:0006457,(AT5G67530.1 ATPUB49,PUB49 | |
| 54 | | 0 5.2.1.8 | K10598 | GO:0006457,(AT5G67530.1 ATPUB49,PUB49 | |
| 55 | | 0 5.2.1.8 | K10598 | GO:0006457,(AT5G67530.1 ATPUB49,PUB49 | |
| 56 | | 0 5.2.1.8 | K10598 | GO:0006457,(AT5G67530.1 ATPUB49,PUB49 | |
| 57 | | 0 5.2.1.8 | K10598 | GO:0006457,(AT5G67530.1 ATPUB49,PUB49 | |
| 58 | | 0 5.2.1.8 | K10598 | GO:0006457,(AT5G67530.1 ATPUB49,PUB49 | |
| 59 | | 0 5.2.1.8 | K10598 | GO:0006457,(AT5G67530.1 ATPUB49,PUB49 | |
| 60 | | 0 5.2.1.8 | K10598 | GO:0006457,(AT5G67530.1 ATPUB49,PUB49 | |
| | | 0 5.2.1.8 | K10598 | GO:0006457,(AT5G67530.1 ATPUB49,PUB49 | |

| | | | | |
|----|---------|-----------|--------|---------------------------------------|
| 1 | | | | |
| 2 | | 0 5.2.1.8 | K10598 | GO:0006457,(AT5G67530.1 ATPUB49,PUB49 |
| 3 | | 0 5.2.1.8 | K10598 | GO:0006457,(AT5G67530.1 ATPUB49,PUB49 |
| 4 | | 0 5.2.1.8 | K10598 | GO:0006457,(AT5G67530.1 ATPUB49,PUB49 |
| 5 | | | | |
| 6 | | 0 1.3.3.8 | | 0 GO:0055114,(AT2G34790.1 EDA28,MEE23 |
| 7 | | 0 1.3.3.8 | | 0 GO:0055114,(AT2G34790.1 EDA28,MEE23 |
| 8 | | 0 1.3.3.8 | | 0 GO:0055114,(AT2G34790.1 EDA28,MEE23 |
| 9 | | | | |
| 10 | | 0 1.3.3.8 | | 0 GO:0055114,(AT2G34790.1 EDA28,MEE23 |
| 11 | | 0 1.3.3.8 | | 0 GO:0055114,(AT2G34790.1 EDA28,MEE23 |
| 12 | | 0 1.3.3.8 | | 0 GO:0055114,(AT2G34790.1 EDA28,MEE23 |
| 13 | | | | |
| 14 | | 0 1.3.3.8 | | 0 GO:0055114,(AT2G34790.1 EDA28,MEE23 |
| 15 | | 0 1.3.3.8 | | 0 GO:0055114,(AT2G34790.1 EDA28,MEE23 |
| 16 | | 0 1.3.3.8 | | 0 GO:0055114,(AT2G34790.1 EDA28,MEE23 |
| 17 | | 0 1.3.3.8 | | 0 GO:0055114,(AT2G34790.1 EDA28,MEE23 |
| 18 | | 0 1.3.3.8 | | 0 GO:0055114,(AT2G34790.1 EDA28,MEE23 |
| 19 | | 0 1.3.3.8 | | 0 GO:0055114,(AT2G34790.1 EDA28,MEE23 |
| 20 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 21 | | | | |
| 22 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 23 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 24 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 25 | | | | |
| 26 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 27 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 28 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 29 | | | | |
| 30 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 31 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 32 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 33 | | | | |
| 34 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 35 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 36 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 37 | | | | |
| 38 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 39 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 40 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 41 | | | | |
| 42 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 43 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 44 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 45 | KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G10530.1 0 |
| 46 | | | | |
| 47 | KOG1235 | 3.6.3.46 | 0 | 0 AT5G64940.1 ATATH13,ATH13,, |
| 48 | KOG1235 | 3.6.3.46 | 0 | 0 AT5G64940.1 ATATH13,ATH13,, |
| 49 | KOG1235 | 3.6.3.46 | 0 | 0 AT5G64940.1 ATATH13,ATH13,, |
| 50 | | | | |
| 51 | KOG1235 | 3.6.3.46 | 0 | 0 AT5G64940.1 ATATH13,ATH13,, |
| 52 | KOG1235 | 3.6.3.46 | 0 | 0 AT5G64940.1 ATATH13,ATH13,, |
| 53 | KOG1235 | 3.6.3.46 | 0 | 0 AT5G64940.1 ATATH13,ATH13,, |
| 54 | | | | |
| 55 | KOG1235 | 3.6.3.46 | 0 | 0 AT5G64940.1 ATATH13,ATH13,, |
| 56 | KOG1235 | 3.6.3.46 | 0 | 0 AT5G64940.1 ATATH13,ATH13,, |
| 57 | KOG1235 | 3.6.3.46 | 0 | 0 AT5G64940.1 ATATH13,ATH13,, |
| 58 | | | | |
| 59 | KOG1235 | 3.6.3.46 | 0 | 0 AT5G64940.1 ATATH13,ATH13,, |
| 60 | KOG1235 | 3.6.3.46 | 0 | 0 AT5G64940.1 ATATH13,ATH13,, |
| | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 ATDGK2,DGK2 |

| | | | | |
|----|---------|-----------|----------|---------------------------------------|
| 1 | | | | |
| 2 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 ATDGK2,DGK2 |
| 3 | KOG1169 | 2.7.1.107 | | 0 GO:0035556,(AT5G63770.2 ATDGK2,DGK2 |
| 4 | | | | |
| 5 | | 0 | 0 | 0 GO:0004519 AT2G15820.1 OTP51 |
| 6 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 7 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 8 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 9 | | | | |
| 10 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 11 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 12 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 13 | | | | |
| 14 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 15 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 16 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 17 | | | | |
| 18 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 19 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 20 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 21 | | | | |
| 22 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 23 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 24 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 25 | | | | |
| 26 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 27 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 28 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 29 | | | | |
| 30 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 31 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 32 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 33 | | | | |
| 34 | KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EFE |
| 35 | KOG0748 | | 0 K07297 | GO:0016021 AT5G20270.1 HHP1 |
| 36 | KOG0748 | | 0 K07297 | GO:0016021 AT5G20270.1 HHP1 |
| 37 | KOG0748 | | 0 K07297 | GO:0016021 AT5G20270.1 HHP1 |
| 38 | | | | |
| 39 | KOG0748 | | 0 K07297 | GO:0016021 AT5G20270.1 HHP1 |
| 40 | KOG0748 | | 0 K07297 | GO:0016021 AT5G20270.1 HHP1 |
| 41 | KOG0748 | | 0 K07297 | GO:0016021 AT5G20270.1 HHP1 |
| 42 | | | | |
| 43 | KOG0748 | | 0 K07297 | GO:0016021 AT5G20270.1 HHP1 |
| 44 | KOG0748 | | 0 K07297 | GO:0016021 AT5G20270.1 HHP1 |
| 45 | KOG0748 | | 0 K07297 | GO:0016021 AT5G20270.1 HHP1 |
| 46 | | | | |
| 47 | KOG0748 | | 0 K07297 | GO:0016021 AT5G20270.1 HHP1 |
| 48 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 |
| 49 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 |
| 50 | | | | |
| 51 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 |
| 52 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 |
| 53 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 |
| 54 | | | | |
| 55 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 |
| 56 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 |
| 57 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 |
| 58 | | | | |
| 59 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 |
| 60 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 |
| | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 |

| | | | | | |
|----|---------|------------|--------|--|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 | |
| 3 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 | |
| 4 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 | |
| 5 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 | |
| 6 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 | |
| 7 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 | |
| 8 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 | |
| 9 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 | |
| 10 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 | |
| 11 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 | |
| 12 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 | |
| 13 | | 0 | 0 | 0 GO:0006355,(AT3G47500.1 CDF3 | |
| 14 | KOG0472 | 2.7.11.1 | | 0 GO:0005515 AT4G20140.1 GSO1 | |
| 15 | KOG0472 | 2.7.11.1 | | 0 GO:0005515 AT4G20140.1 GSO1 | |
| 16 | KOG0472 | 2.7.11.1 | | 0 GO:0005515 AT4G20140.1 GSO1 | |
| 17 | KOG0472 | 2.7.11.1 | | 0 GO:0005515 AT4G20140.1 GSO1 | |
| 18 | KOG0472 | 2.7.11.1 | | 0 GO:0005515 AT4G20140.1 GSO1 | |
| 19 | KOG0472 | 2.7.11.1 | | 0 GO:0005515 AT4G20140.1 GSO1 | |
| 20 | KOG0472 | 2.7.11.1 | | 0 GO:0005515 AT4G20140.1 GSO1 | |
| 21 | KOG0472 | 2.7.11.1 | | 0 GO:0005515 AT4G20140.1 GSO1 | |
| 22 | KOG0472 | 2.7.11.1 | | 0 GO:0005515 AT4G20140.1 GSO1 | |
| 23 | KOG0472 | 2.7.11.1 | | 0 GO:0005515 AT4G20140.1 GSO1 | |
| 24 | KOG0472 | 2.7.11.1 | | 0 GO:0005515 AT4G20140.1 GSO1 | |
| 25 | KOG0472 | 2.7.11.1 | | 0 GO:0005515 AT4G20140.1 GSO1 | |
| 26 | KOG0472 | 2.7.11.1 | | 0 GO:0005515 AT4G20140.1 GSO1 | |
| 27 | | 0 | 0 | 0 AT5G14410.1 | 0 |
| 28 | | 0 | 0 | 0 AT5G14410.1 | 0 |
| 29 | | 0 | 0 | 0 AT5G14410.1 | 0 |
| 30 | | 0 | 0 | 0 AT5G14410.1 | 0 |
| 31 | | 0 | 0 | 0 AT5G14410.1 | 0 |
| 32 | | 0 | 0 | 0 AT5G14410.1 | 0 |
| 33 | | 0 | 0 | 0 AT5G14410.1 | 0 |
| 34 | | 0 | 0 | 0 AT5G14410.1 | 0 |
| 35 | | 0 | 0 | 0 AT5G14410.1 | 0 |
| 36 | | 0 | 0 | 0 AT5G14410.1 | 0 |
| 37 | | 0 | 0 | 0 AT5G14410.1 | 0 |
| 38 | | 0 | 0 | 0 AT5G14410.1 | 0 |
| 39 | | 0 | 0 | 0 AT5G14410.1 | 0 |
| 40 | | 0 | 0 | 0 AT5G14410.1 | 0 |
| 41 | | 0 | 0 | 0 AT5G14410.1 | 0 |
| 42 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 | |
| 43 | | 0 | 0 | 0 GO:0006355,(AT5G46590.1 anac096,NAC096 | |
| 44 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT2G23070.1 | 0 |
| 45 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT2G23070.1 | 0 |
| 46 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT2G23070.1 | 0 |
| 47 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT2G23070.1 | 0 |
| 48 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT2G23070.1 | 0 |
| 49 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT2G23070.1 | 0 |
| 50 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT2G23070.1 | 0 |
| 51 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT2G23070.1 | 0 |
| 52 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT2G23070.1 | 0 |
| 53 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT2G23070.1 | 0 |
| 54 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT2G23070.1 | 0 |
| 55 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT2G23070.1 | 0 |
| 56 | | 0 2.7.11.1 | K03097 | GO:0006468,(AT2G23070.1 | 0 |
| 57 | | 0 | 0 | 0 GO:0007165,(AT5G17680.1 | 0 |
| 58 | | 0 | 0 | 0 GO:0007165,(AT5G17680.1 | 0 |
| 59 | | 0 | 0 | 0 GO:0007165,(AT5G17680.1 | 0 |
| 60 | | 0 | 0 | 0 GO:0007165,(AT5G17680.1 | 0 |
| | | 0 | 0 | 0 GO:0007165,(AT5G17680.1 | 0 |

| | | | | | |
|----|---------|-------------|--------|--|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 GO:0007165,(AT5G17680.1 | 0 |
| 3 | | 0 | 0 | 0 GO:0007165,(AT5G17680.1 | 0 |
| 4 | | 0 | 0 | 0 GO:0007165,(AT5G17680.1 | 0 |
| 5 | | 0 | 0 | 0 GO:0007165,(AT5G17680.1 | 0 |
| 6 | | 0 | 0 | 0 GO:0007165,(AT5G17680.1 | 0 |
| 7 | | 0 | 0 | 0 GO:0007165,(AT5G17680.1 | 0 |
| 8 | | 0 | 0 | 0 GO:0007165,(AT5G17680.1 | 0 |
| 9 | | 0 | 0 | 0 GO:0007165,(AT5G17680.1 | 0 |
| 10 | | 0 | 0 | 0 GO:0007165,(AT5G17680.1 | 0 |
| 11 | | 0 2.4.1.142 | K03842 | GO:0016757 AT1G16570.1 | 0 |
| 12 | | 0 2.4.1.142 | K03842 | GO:0016757 AT1G16570.1 | 0 |
| 13 | | 0 2.4.1.142 | K03842 | GO:0016757 AT1G16570.1 | 0 |
| 14 | | 0 2.4.1.142 | K03842 | GO:0016757 AT1G16570.1 | 0 |
| 15 | | 0 2.4.1.142 | K03842 | GO:0016757 AT1G16570.1 | 0 |
| 16 | | 0 2.4.1.142 | K03842 | GO:0016757 AT1G16570.1 | 0 |
| 17 | | 0 2.4.1.142 | K03842 | GO:0016757 AT1G16570.1 | 0 |
| 18 | | 0 2.4.1.142 | K03842 | GO:0016757 AT1G16570.1 | 0 |
| 19 | | 0 2.4.1.142 | K03842 | GO:0016757 AT1G16570.1 | 0 |
| 20 | | 0 2.4.1.142 | K03842 | GO:0016757 AT1G16570.1 | 0 |
| 21 | | 0 2.4.1.142 | K03842 | GO:0016757 AT1G16570.1 | 0 |
| 22 | | 0 2.4.1.142 | K03842 | GO:0016757 AT1G16570.1 | 0 |
| 23 | | 0 2.4.1.142 | K03842 | GO:0016757 AT1G16570.1 | 0 |
| 24 | | 0 | 0 | 0 GO:0005089 AT1G79860.1 ATROPGEF12,ME | |
| 25 | | | | | |
| 26 | KOG0519 | 2.7.11.1 | K14509 | GO:0005515,(AT3G04580.2 EIN4 | |
| 27 | KOG0519 | 2.7.11.1 | K14509 | GO:0005515,(AT3G04580.2 EIN4 | |
| 28 | KOG0519 | 2.7.11.1 | K14509 | GO:0005515,(AT3G04580.2 EIN4 | |
| 29 | KOG0519 | 2.7.11.1 | K14509 | GO:0005515,(AT3G04580.2 EIN4 | |
| 30 | KOG0519 | 2.7.11.1 | K14509 | GO:0005515,(AT3G04580.2 EIN4 | |
| 31 | KOG0519 | 2.7.11.1 | K14509 | GO:0005515,(AT3G04580.2 EIN4 | |
| 32 | KOG0519 | 2.7.11.1 | K14509 | GO:0005515,(AT3G04580.2 EIN4 | |
| 33 | KOG0519 | 2.7.11.1 | K14509 | GO:0005515,(AT3G04580.2 EIN4 | |
| 34 | KOG0519 | 2.7.11.1 | K14509 | GO:0005515,(AT3G04580.2 EIN4 | |
| 35 | KOG0519 | 2.7.11.1 | K14509 | GO:0005515,(AT3G04580.2 EIN4 | |
| 36 | KOG0519 | 2.7.11.1 | K14509 | GO:0005515,(AT3G04580.2 EIN4 | |
| 37 | KOG0519 | 2.7.11.1 | K14509 | GO:0005515,(AT3G04580.2 EIN4 | |
| 38 | KOG0519 | 2.7.11.1 | K14509 | GO:0005515,(AT3G04580.2 EIN4 | |
| 39 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 40 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 41 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 42 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 43 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 44 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 45 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 46 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 47 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 48 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 49 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 50 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 51 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 52 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 53 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 54 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 55 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 56 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 57 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 58 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 59 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 60 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |

| | | | | | |
|----|---------|-----------|---|---------------------------------------|--------------------|
| 1 | | | | | |
| 2 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 3 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 4 | | | | | |
| 5 | | 0 | 0 | 0 | 0 AT5G59320.1 LTP3 |
| 6 | KOG0039 | 1.16.1.7 | | 0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7 | |
| 7 | KOG0039 | 1.16.1.7 | | 0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7 | |
| 8 | KOG0039 | 1.16.1.7 | | 0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7 | |
| 9 | | | | | |
| 10 | KOG0039 | 1.16.1.7 | | 0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7 | |
| 11 | KOG0039 | 1.16.1.7 | | 0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7 | |
| 12 | KOG0039 | 1.16.1.7 | | 0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7 | |
| 13 | | | | | |
| 14 | KOG0039 | 1.16.1.7 | | 0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7 | |
| 15 | KOG0039 | 1.16.1.7 | | 0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7 | |
| 16 | KOG0039 | 1.16.1.7 | | 0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7 | |
| 17 | | | | | |
| 18 | KOG0039 | 1.16.1.7 | | 0 GO:0055114,(AT5G49740.1 ATFRO7,FRO7 | |
| 19 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 20 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 21 | | | | | |
| 22 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 23 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 24 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 25 | | | | | |
| 26 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 27 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 28 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 29 | | | | | |
| 30 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 31 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 32 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 33 | | | | | |
| 34 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 35 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 36 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 37 | | | | | |
| 38 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 39 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 40 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 41 | | | | | |
| 42 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 43 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 44 | KOG1471 | | 0 | 0 | 0 AT5G47730.1 |
| 45 | | | | | |
| 46 | | 0 | 0 | 0 | 0 AT2G45180.1 |
| 47 | | 0 | 0 | 0 | 0 AT2G45180.1 |
| 48 | | 0 | 0 | 0 | 0 AT2G45180.1 |
| 49 | | 0 | 0 | 0 | 0 AT2G45180.1 |
| 50 | | 0 | 0 | 0 | 0 AT2G45180.1 |
| 51 | | 0 | 0 | 0 | 0 AT2G45180.1 |
| 52 | | 0 | 0 | 0 | 0 AT2G45180.1 |
| 53 | | 0 | 0 | 0 | 0 AT2G45180.1 |
| 54 | | 0 | 0 | 0 | 0 AT2G45180.1 |
| 55 | | 0 | 0 | 0 | 0 AT2G45180.1 |
| 56 | | 0 | 0 | 0 | 0 AT2G45180.1 |
| 57 | | 0 | 0 | 0 | 0 AT2G45180.1 |
| 58 | | 0 | 0 | 0 | 0 AT2G45180.1 |
| 59 | | 0 | 0 | 0 | 0 AT2G45180.1 |
| 60 | KOG1919 | 5.4.99.24 | | 0 GO:0009982,(AT4G21770.1 | 0 |
| | KOG1919 | 5.4.99.24 | | 0 GO:0009982,(AT4G21770.1 | 0 |

| | | | | | | | |
|----|---------|-----------|---|---------------------------|-----------------------------|---|---|
| 1 | | | | | | | |
| 2 | KOG1919 | 5.4.99.24 | | 0 GO:0009982,(AT4G21770.1 | | | 0 |
| 3 | KOG1919 | 5.4.99.24 | | 0 GO:0009982,(AT4G21770.1 | | | 0 |
| 4 | KOG1919 | 5.4.99.24 | | 0 GO:0009982,(AT4G21770.1 | | | 0 |
| 5 | KOG1919 | 5.4.99.24 | | 0 GO:0009982,(AT4G21770.1 | | | 0 |
| 6 | KOG1919 | 5.4.99.24 | | 0 GO:0009982,(AT4G21770.1 | | | 0 |
| 7 | KOG1919 | 5.4.99.24 | | 0 GO:0009982,(AT4G21770.1 | | | 0 |
| 8 | KOG1919 | 5.4.99.24 | | 0 GO:0009982,(AT4G21770.1 | | | 0 |
| 9 | KOG1919 | 5.4.99.24 | | 0 GO:0009982,(AT4G21770.1 | | | 0 |
| 10 | KOG1919 | 5.4.99.24 | | 0 GO:0009982,(AT4G21770.1 | | | 0 |
| 11 | KOG1919 | 5.4.99.24 | | 0 GO:0009982,(AT4G21770.1 | | | 0 |
| 12 | | 0 | 0 | 0 | 0 AT5G03170.1 ATFLA11,FLA11 | | |
| 13 | | 0 | 0 | 0 | 0 AT5G03170.1 ATFLA11,FLA11 | | |
| 14 | | 0 | 0 | 0 | 0 AT5G03170.1 ATFLA11,FLA11 | | |
| 15 | | 0 | 0 | 0 | 0 AT5G03170.1 ATFLA11,FLA11 | | |
| 16 | | 0 | 0 | 0 | 0 AT5G03170.1 ATFLA11,FLA11 | | |
| 17 | | 0 | 0 | 0 | 0 AT5G03170.1 ATFLA11,FLA11 | | |
| 18 | | 0 | 0 | 0 | 0 AT5G03170.1 ATFLA11,FLA11 | | |
| 19 | | 0 | 0 | 0 | 0 AT5G03170.1 ATFLA11,FLA11 | | |
| 20 | | 0 | 0 | 0 | 0 AT5G03170.1 ATFLA11,FLA11 | | |
| 21 | | 0 | 0 | 0 | 0 AT5G03170.1 ATFLA11,FLA11 | | |
| 22 | | 0 | 0 | 0 | 0 AT5G03170.1 ATFLA11,FLA11 | | |
| 23 | | 0 | 0 | 0 | 0 AT5G03170.1 ATFLA11,FLA11 | | |
| 24 | | 0 | 0 | 0 | 0 AT5G03170.1 ATFLA11,FLA11 | | |
| 25 | | 0 | 0 | 0 | 0 AT5G03170.1 ATFLA11,FLA11 | | |
| 26 | KOG4793 | 2.7.7.7 | | 0 | 0 AT5G26940.3 | | 0 |
| 27 | KOG4793 | 2.7.7.7 | | 0 | 0 AT5G26940.3 | | 0 |
| 28 | | 0 | 0 | 0 | 0 AT3G01680.1 | | 0 |
| 29 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 30 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 31 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 32 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 33 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 34 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 35 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 36 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 37 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 38 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 39 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 40 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 41 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 42 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 43 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 44 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 45 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 46 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 47 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 48 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 49 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 50 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 51 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 52 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 53 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 54 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 55 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 56 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 57 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 58 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 59 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 60 | | 0 | 0 | 0 | 0 | 0 | 0 |
| | | 0 | 0 | 0 | 0 | 0 | 0 |

| | | | | | | |
|----|------------|----------|---------------------------|---------|---|---|
| 1 | | | | | | |
| 2 | 0 | 0 | 0 | 0 | 0 | 0 |
| 3 | 0 | 0 | 0 | 0 | 0 | 0 |
| 4 | 0 | 0 | 0 | 0 | 0 | 0 |
| 5 | 0 | 0 | 0 | 0 | 0 | 0 |
| 6 | 0 | 0 | 0 | 0 | 0 | 0 |
| 7 | 0 | 0 | 0 | 0 | 0 | 0 |
| 8 | 0 | 0 | 0 | 0 | 0 | 0 |
| 9 | 0 | 0 | 0 | 0 | 0 | 0 |
| 10 | 0 | 0 | 0 | 0 | 0 | 0 |
| 11 | 0 | 0 | 0 | 0 | 0 | 0 |
| 12 | 0 | 0 | 0 | 0 | 0 | 0 |
| 13 | 0 | 0 | 0 | 0 | 0 | 0 |
| 14 | 0 | 0 | 0 | 0 | 0 | 0 |
| 15 | 0 | 0 | 0 | 0 | 0 | 0 |
| 16 | 0 | 0 | 0 | 0 | 0 | 0 |
| 17 | 0 | 0 | 0 | 0 | 0 | 0 |
| 18 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | 0 | 0 | 0 | 0 | 0 |
| 22 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | 0 | 0 | 0 | 0 | 0 |
| 25 | 0 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | 0 | 0 | 0 | 0 | 0 |
| 27 | 0 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | 0 | 0 | 0 | 0 | 0 |
| 30 | 0 | 0 | 0 | 0 | 0 | 0 |
| 31 | 0 | 0 | 0 | 0 | 0 | 0 |
| 32 | 0 2.5.1.55 | K01627 | GO:0009058,(AT1G79500.4 | AtkdsA1 | | |
| 33 | 0 2.5.1.55 | K01627 | GO:0009058,(AT1G79500.4 | AtkdsA1 | | |
| 34 | 0 2.5.1.55 | K01627 | GO:0009058,(AT1G79500.4 | AtkdsA1 | | |
| 35 | 0 2.5.1.55 | K01627 | GO:0009058,(AT1G79500.4 | AtkdsA1 | | |
| 36 | 0 2.5.1.55 | K01627 | GO:0009058,(AT1G79500.4 | AtkdsA1 | | |
| 37 | 0 2.5.1.55 | K01627 | GO:0009058,(AT1G79500.4 | AtkdsA1 | | |
| 38 | 0 2.5.1.55 | K01627 | GO:0009058,(AT1G79500.4 | AtkdsA1 | | |
| 39 | 0 2.5.1.55 | K01627 | GO:0009058,(AT1G79500.4 | AtkdsA1 | | |
| 40 | 0 2.5.1.55 | K01627 | GO:0009058,(AT1G79500.4 | AtkdsA1 | | |
| 41 | 0 2.5.1.55 | K01627 | GO:0009058,(AT1G79500.4 | AtkdsA1 | | |
| 42 | 0 2.5.1.55 | K01627 | GO:0009058,(AT1G79500.4 | AtkdsA1 | | |
| 43 | 0 2.5.1.55 | K01627 | GO:0009058,(AT1G79500.4 | AtkdsA1 | | |
| 44 | 0 2.5.1.55 | K01627 | GO:0009058,(AT1G79500.4 | AtkdsA1 | | |
| 45 | 0 2.5.1.55 | K01627 | GO:0009058,(AT1G79500.4 | AtkdsA1 | | |
| 46 | 0 2.5.1.55 | K01627 | GO:0009058,(AT1G79500.4 | AtkdsA1 | | |
| 47 | 0 | 0 | 0 | 0 | 0 | 0 |
| 48 | 0 | 0 | 0 | 0 | 0 | 0 |
| 49 | 0 | 0 | 0 | 0 | 0 | 0 |
| 50 | 0 | 0 | 0 | 0 | 0 | 0 |
| 51 | 0 | 0 | 0 | 0 | 0 | 0 |
| 52 | 0 | 0 | 0 | 0 | 0 | 0 |
| 53 | 0 | 0 | 0 | 0 | 0 | 0 |
| 54 | 0 | 0 | 0 | 0 | 0 | 0 |
| 55 | 0 | 0 | 0 | 0 | 0 | 0 |
| 56 | 0 | 0 | 0 | 0 | 0 | 0 |
| 57 | 0 | 0 | 0 | 0 | 0 | 0 |
| 58 | 0 | 0 | 0 | 0 | 0 | 0 |
| 59 | 0 | 0 | 0 | 0 | 0 | 0 |
| 60 | KOG1187 | 2.7.11.1 | 0 GO:0005515,(AT3G47570.1 | | | 0 |
| | KOG1187 | 2.7.11.1 | 0 GO:0005515,(AT3G47570.1 | | | 0 |

| | | | | | |
|----|---------|------------|----------|--|---|
| 1 | | | | | |
| 2 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT3G47570.1 | 0 |
| 3 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT3G47570.1 | 0 |
| 4 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT3G47570.1 | 0 |
| 5 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT3G47570.1 | 0 |
| 6 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT3G47570.1 | 0 |
| 7 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT3G47570.1 | 0 |
| 8 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT3G47570.1 | 0 |
| 9 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT3G47570.1 | 0 |
| 10 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT3G47570.1 | 0 |
| 11 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT3G47570.1 | 0 |
| 12 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT3G47570.1 | 0 |
| 13 | | | | | |
| 14 | KOG2913 | | 0 K12386 | 0 AT5G40670.1 | 0 |
| 15 | KOG2913 | | 0 K12386 | 0 AT5G40670.1 | 0 |
| 16 | KOG2913 | | 0 K12386 | 0 AT5G40670.1 | 0 |
| 17 | KOG2913 | | 0 K12386 | 0 AT5G40670.1 | 0 |
| 18 | KOG2913 | | 0 K12386 | 0 AT5G40670.1 | 0 |
| 19 | KOG2913 | | 0 K12386 | 0 AT5G40670.1 | 0 |
| 20 | KOG2913 | | 0 K12386 | 0 AT5G40670.1 | 0 |
| 21 | KOG2913 | | 0 K12386 | 0 AT5G40670.1 | 0 |
| 22 | KOG2913 | | 0 K12386 | 0 AT5G40670.1 | 0 |
| 23 | KOG2913 | | 0 K12386 | 0 AT5G40670.1 | 0 |
| 24 | KOG2913 | | 0 K12386 | 0 AT5G40670.1 | 0 |
| 25 | KOG2913 | | 0 K12386 | 0 AT5G40670.1 | 0 |
| 26 | KOG2913 | | 0 K12386 | 0 AT5G40670.1 | 0 |
| 27 | KOG2913 | | 0 K12386 | 0 AT5G40670.1 | 0 |
| 28 | KOG2913 | | 0 K12386 | 0 AT5G40670.1 | 0 |
| 29 | | | | | |
| 30 | KOG0143 | 1.14.11.32 | | 0 GO:0055114,(AT5G58660.1 | 0 |
| 31 | KOG0143 | 1.14.11.32 | | 0 GO:0055114,(AT5G58660.1 | 0 |
| 32 | KOG0143 | 1.14.11.32 | | 0 GO:0055114,(AT5G58660.1 | 0 |
| 33 | KOG0143 | 1.14.11.32 | | 0 GO:0055114,(AT5G58660.1 | 0 |
| 34 | KOG0143 | 1.14.11.32 | | 0 GO:0055114,(AT5G58660.1 | 0 |
| 35 | KOG0143 | 1.14.11.32 | | 0 GO:0055114,(AT5G58660.1 | 0 |
| 36 | KOG0143 | 1.14.11.32 | | 0 GO:0055114,(AT5G58660.1 | 0 |
| 37 | KOG0143 | 1.14.11.32 | | 0 GO:0055114,(AT5G58660.1 | 0 |
| 38 | KOG0143 | 1.14.11.32 | | 0 GO:0055114,(AT5G58660.1 | 0 |
| 39 | KOG0143 | 1.14.11.32 | | 0 GO:0055114,(AT5G58660.1 | 0 |
| 40 | KOG0143 | 1.14.11.32 | | 0 GO:0055114,(AT5G58660.1 | 0 |
| 41 | KOG0143 | 1.14.11.32 | | 0 GO:0055114,(AT5G58660.1 | 0 |
| 42 | | | | | |
| 43 | | 0 2.7.7.15 | | 0 GO:0009058,(AT2G32260.1 ATCCT1,CCT1 | |
| 44 | KOG4409 | 2.3.1.51 | 0 | 0 AT4G24160.1 | 0 |
| 45 | KOG4409 | 2.3.1.51 | 0 | 0 AT4G24160.1 | 0 |
| 46 | | | | | |
| 47 | | 0 | 0 | 0 GO:0046983 AT4G00120.1 EDA33,GT140,IN[| |
| 48 | KOG1305 | | 0 K14207 | GO:0003333 AT3G30390.2 | 0 |
| 49 | KOG1305 | | 0 K14207 | GO:0003333 AT3G30390.2 | 0 |
| 50 | KOG1305 | | 0 K14207 | GO:0003333 AT3G30390.2 | 0 |
| 51 | KOG1305 | | 0 K14207 | GO:0003333 AT3G30390.2 | 0 |
| 52 | KOG1305 | | 0 K14207 | GO:0003333 AT3G30390.2 | 0 |
| 53 | KOG1305 | | 0 K14207 | GO:0003333 AT3G30390.2 | 0 |
| 54 | KOG1305 | | 0 K14207 | GO:0003333 AT3G30390.2 | 0 |
| 55 | KOG1305 | | 0 K14207 | GO:0003333 AT3G30390.2 | 0 |
| 56 | KOG1305 | | 0 K14207 | GO:0003333 AT3G30390.2 | 0 |
| 57 | KOG1305 | | 0 K14207 | GO:0003333 AT3G30390.2 | 0 |
| 58 | KOG1305 | | 0 K14207 | GO:0003333 AT3G30390.2 | 0 |
| 59 | KOG1305 | | 0 K14207 | GO:0003333 AT3G30390.2 | 0 |
| 60 | KOG1305 | | 0 K14207 | GO:0003333 AT3G30390.2 | 0 |
| | | 0 | 0 | 0 GO:0016788 AT1G53920.1 GLIP5 | |

| | | | | | |
|----|---------|------------|--------|---------------------------------------|---|
| 1 | | | | | |
| 2 | KOG1430 | 1.1.1.170 | K07748 | GO:0050662,(AT2G43420.1 | 0 |
| 3 | | 0 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | 0 |
| 4 | | 0 2.7.11.1 | | 0 GO:0048544,(AT4G27290.1 | 0 |
| 5 | | 0 3.1.1.3 | | 0 GO:0016788 AT5G33370.1 | 0 |
| 6 | | 0 | 0 | 0 AT4G36550.1 | 0 |
| 7 | | 0 3.1.1.3 | K14674 | GO:0006629,(AT5G04040.1 SDP1 | |
| 8 | | 0 3.1.1.3 | K14674 | GO:0006629,(AT5G04040.1 SDP1 | |
| 9 | | 0 3.1.1.3 | K14674 | GO:0006629,(AT5G04040.1 SDP1 | |
| 10 | | 0 3.1.1.3 | K14674 | GO:0006629,(AT5G04040.1 SDP1 | |
| 11 | | 0 3.1.1.3 | K14674 | GO:0006629,(AT5G04040.1 SDP1 | |
| 12 | | 0 3.1.1.3 | K14674 | GO:0006629,(AT5G04040.1 SDP1 | |
| 13 | | 0 3.1.1.3 | K14674 | GO:0006629,(AT5G04040.1 SDP1 | |
| 14 | | 0 3.1.1.3 | K14674 | GO:0006629,(AT5G04040.1 SDP1 | |
| 15 | | 0 3.1.1.3 | K14674 | GO:0006629,(AT5G04040.1 SDP1 | |
| 16 | | 0 3.1.1.3 | K14674 | GO:0006629,(AT5G04040.1 SDP1 | |
| 17 | | 0 3.1.1.3 | K14674 | GO:0006629,(AT5G04040.1 SDP1 | |
| 18 | | 0 3.1.1.3 | K14674 | GO:0006629,(AT5G04040.1 SDP1 | |
| 19 | | 0 3.1.1.3 | K14674 | GO:0006629,(AT5G04040.1 SDP1 | |
| 20 | | 0 3.1.1.3 | K14674 | GO:0006629,(AT5G04040.1 SDP1 | |
| 21 | | 0 | 0 | 0 GO:0007010,(AT2G41740.1 ATVLN2,VLN2 | |
| 22 | | 0 | 0 | 0 GO:0007010,(AT2G41740.1 ATVLN2,VLN2 | |
| 23 | | 0 | 0 | 0 GO:0007010,(AT2G41740.1 ATVLN2,VLN2 | |
| 24 | | 0 | 0 | 0 GO:0007010,(AT2G41740.1 ATVLN2,VLN2 | |
| 25 | KOG2231 | | | 0 AT3G62240.1 | 0 |
| 26 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 27 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 28 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 29 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 30 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 31 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 32 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 33 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 34 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 35 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 36 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 37 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 38 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 39 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 40 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 41 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 42 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 43 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 44 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 45 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 46 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 47 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 48 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 49 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 50 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 51 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 52 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 53 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 54 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 55 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 56 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 57 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 58 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 59 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 60 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |

| | | | | | |
|----|---------|-------------------------|----------|---------------------------------------|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 3 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 4 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 5 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 6 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 7 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 8 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 9 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 10 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 11 | KOG1471 | | 0 | 0 AT4G36490.1 ATSFH12,SFH12 | |
| 12 | KOG1471 | | 0 | 0 AT4G36490.1 ATSFH12,SFH12 | |
| 13 | KOG1471 | | 0 | 0 AT4G36490.1 ATSFH12,SFH12 | |
| 14 | KOG1471 | | 0 | 0 AT4G36490.1 ATSFH12,SFH12 | |
| 15 | KOG1138 | | 0 K13146 | GO:0032039,(AT3G07530.1 | 0 |
| 16 | KOG1138 | | 0 K13146 | GO:0032039,(AT3G07530.1 | 0 |
| 17 | KOG1138 | | 0 K13146 | GO:0032039,(AT3G07530.1 | 0 |
| 18 | KOG1138 | | 0 K13146 | GO:0032039,(AT3G07530.1 | 0 |
| 19 | KOG1138 | | 0 K13146 | GO:0032039,(AT3G07530.1 | 0 |
| 20 | KOG1138 | | 0 K13146 | GO:0032039,(AT3G07530.1 | 0 |
| 21 | KOG1138 | | 0 K13146 | GO:0032039,(AT3G07530.1 | 0 |
| 22 | KOG1138 | | 0 K13146 | GO:0032039,(AT3G07530.1 | 0 |
| 23 | KOG1138 | | 0 K13146 | GO:0032039,(AT3G07530.1 | 0 |
| 24 | KOG1138 | | 0 K13146 | GO:0032039,(AT3G07530.1 | 0 |
| 25 | KOG1138 | | 0 K13146 | GO:0032039,(AT3G07530.1 | 0 |
| 26 | KOG1138 | | 0 K13146 | GO:0032039,(AT3G07530.1 | 0 |
| 27 | KOG1138 | | 0 K13146 | GO:0032039,(AT3G07530.1 | 0 |
| 28 | KOG1138 | | 0 K13146 | GO:0032039,(AT3G07530.1 | 0 |
| 29 | | | | | |
| 30 | | 0 2.4.1.15,3.1.3 K16055 | | GO:0005992,(AT1G60140.1 ATTPS10,TPS10 | |
| 31 | KOG1028 | | 0 | 0 GO:0005515 AT1G74720.1 QKY | |
| 32 | KOG1028 | | 0 | 0 GO:0005515 AT1G74720.1 QKY | |
| 33 | KOG1028 | | 0 | 0 GO:0005515 AT1G74720.1 QKY | |
| 34 | KOG1028 | | 0 | 0 GO:0005515 AT1G74720.1 QKY | |
| 35 | KOG1028 | | 0 | 0 GO:0005515 AT1G74720.1 QKY | |
| 36 | KOG1028 | | 0 | 0 GO:0005515 AT1G74720.1 QKY | |
| 37 | KOG1028 | | 0 | 0 GO:0005515 AT1G74720.1 QKY | |
| 38 | KOG1028 | | 0 | 0 GO:0005515 AT1G74720.1 QKY | |
| 39 | KOG1028 | | 0 | 0 GO:0005515 AT1G74720.1 QKY | |
| 40 | KOG1028 | | 0 | 0 GO:0005515 AT1G74720.1 QKY | |
| 41 | KOG1028 | | 0 | 0 GO:0005515 AT1G74720.1 QKY | |
| 42 | KOG1028 | | 0 | 0 GO:0005515 AT1G74720.1 QKY | |
| 43 | KOG1028 | | 0 | 0 GO:0005515 AT1G74720.1 QKY | |
| 44 | KOG1973 | 2.3.1.48 | | 0 GO:0005515 AT4G14920.1 | 0 |
| 45 | KOG1973 | 2.3.1.48 | | 0 GO:0005515 AT4G14920.1 | 0 |
| 46 | KOG1973 | 2.3.1.48 | | 0 GO:0005515 AT4G14920.1 | 0 |
| 47 | KOG1973 | 2.3.1.48 | | 0 GO:0005515 AT4G14920.1 | 0 |
| 48 | KOG1973 | 2.3.1.48 | | 0 GO:0005515 AT4G14920.1 | 0 |
| 49 | KOG1973 | 2.3.1.48 | | 0 GO:0005515 AT4G14920.1 | 0 |
| 50 | KOG1973 | 2.3.1.48 | | 0 GO:0005515 AT4G14920.1 | 0 |
| 51 | KOG1973 | 2.3.1.48 | | 0 GO:0005515 AT4G14920.1 | 0 |
| 52 | KOG1973 | 2.3.1.48 | | 0 GO:0005515 AT4G14920.1 | 0 |
| 53 | KOG1973 | 2.3.1.48 | | 0 GO:0005515 AT4G14920.1 | 0 |
| 54 | KOG1973 | 2.3.1.48 | | 0 GO:0005515 AT4G14920.1 | 0 |
| 55 | KOG1973 | 2.3.1.48 | | 0 GO:0005515 AT4G14920.1 | 0 |
| 56 | KOG1973 | 2.3.1.48 | | 0 GO:0005515 AT4G14920.1 | 0 |
| 57 | KOG1973 | 2.3.1.48 | | 0 GO:0005515 AT4G14920.1 | 0 |
| 58 | KOG1973 | 2.3.1.48 | | 0 GO:0005515 AT4G14920.1 | 0 |
| 59 | KOG1973 | 2.3.1.48 | | 0 GO:0005515 AT4G14920.1 | 0 |
| 60 | KOG2826 | | 0 K05758 | GO:0034314,(AT1G30825.1 ARPC2A,DIS2 | |
| | KOG2826 | | 0 K05758 | GO:0034314,(AT1G30825.1 ARPC2A,DIS2 | |

| | | | | | |
|----|-------------|----------|-------------------------------------|--|---|
| 1 | | | | | |
| 2 | KOG2826 | 0 K05758 | GO:0034314,(AT1G30825.1 ARPC2A,DIS2 | | |
| 3 | KOG2826 | 0 K05758 | GO:0034314,(AT1G30825.1 ARPC2A,DIS2 | | |
| 4 | KOG2826 | 0 K05758 | GO:0034314,(AT1G30825.1 ARPC2A,DIS2 | | |
| 5 | KOG2826 | 0 K05758 | GO:0034314,(AT1G30825.1 ARPC2A,DIS2 | | |
| 6 | KOG2826 | 0 K05758 | GO:0034314,(AT1G30825.1 ARPC2A,DIS2 | | |
| 7 | KOG2826 | 0 K05758 | GO:0034314,(AT1G30825.1 ARPC2A,DIS2 | | |
| 8 | KOG2826 | 0 K05758 | GO:0034314,(AT1G30825.1 ARPC2A,DIS2 | | |
| 9 | KOG2826 | 0 K05758 | GO:0034314,(AT1G30825.1 ARPC2A,DIS2 | | |
| 10 | KOG2826 | 0 K05758 | GO:0034314,(AT1G30825.1 ARPC2A,DIS2 | | |
| 11 | KOG2826 | 0 K05758 | GO:0034314,(AT1G30825.1 ARPC2A,DIS2 | | |
| 12 | KOG2826 | 0 K05758 | GO:0034314,(AT1G30825.1 ARPC2A,DIS2 | | |
| 13 | | | | | |
| 14 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 15 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 16 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 17 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 18 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 19 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 20 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 21 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 22 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 23 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 24 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 25 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 26 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 27 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 28 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 29 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 30 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 31 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 32 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 33 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 34 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 35 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 36 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 37 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 38 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 39 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 40 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 41 | 0 | 0 | 0 GO:0005515 AT5G22720.1 | | 0 |
| 42 | | | | | |
| 43 | KOG2547 | 0 | 0 GO:0016757 AT2G19880.2 | | 0 |
| 44 | KOG2547 | 0 | 0 GO:0016757 AT2G19880.2 | | 0 |
| 45 | KOG2547 | 0 | 0 GO:0016757 AT2G19880.2 | | 0 |
| 46 | KOG2547 | 0 | 0 GO:0016757 AT2G19880.2 | | 0 |
| 47 | KOG2547 | 0 | 0 GO:0016757 AT2G19880.2 | | 0 |
| 48 | KOG2547 | 0 | 0 GO:0016757 AT2G19880.2 | | 0 |
| 49 | KOG2547 | 0 | 0 GO:0016757 AT2G19880.2 | | 0 |
| 50 | KOG2547 | 0 | 0 GO:0016757 AT2G19880.2 | | 0 |
| 51 | KOG2547 | 0 | 0 GO:0016757 AT2G19880.2 | | 0 |
| 52 | KOG2547 | 0 | 0 GO:0016757 AT2G19880.2 | | 0 |
| 53 | KOG2547 | 0 | 0 GO:0016757 AT2G19880.2 | | 0 |
| 54 | KOG2547 | 0 | 0 GO:0016757 AT2G19880.2 | | 0 |
| 55 | KOG2547 | 0 | 0 GO:0016757 AT2G19880.2 | | 0 |
| 56 | KOG2547 | 0 | 0 GO:0016757 AT2G19880.2 | | 0 |
| 57 | KOG2547 | 0 | 0 GO:0016757 AT2G19880.2 | | 0 |
| 58 | | | | | |
| 59 | 0 2.4.1.142 | K03842 | GO:0016757 AT1G16570.1 | | 0 |
| 60 | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 | | 0 |
| | 0 | 0 K19041 | GO:0008270,(AT1G53190.1 | | 0 |

| | | | | | |
|----|---------|------------|----------|---|---|
| 1 | | | | | |
| 2 | KOG1698 | | 0 K02884 | GO:0006412,(AT4G11630.1 | 0 |
| 3 | KOG1698 | | 0 K02884 | GO:0006412,(AT4G11630.1 | 0 |
| 4 | KOG1698 | | 0 K02884 | GO:0006412,(AT4G11630.1 | 0 |
| 5 | KOG1698 | | 0 K02884 | GO:0006412,(AT4G11630.1 | 0 |
| 6 | KOG1698 | | 0 K02884 | GO:0006412,(AT4G11630.1 | 0 |
| 7 | KOG1698 | | 0 K02884 | GO:0006412,(AT4G11630.1 | 0 |
| 8 | KOG1698 | | 0 K02884 | GO:0006412,(AT4G11630.1 | 0 |
| 9 | KOG1698 | | 0 K02884 | GO:0006412,(AT4G11630.1 | 0 |
| 10 | KOG1698 | | 0 K02884 | GO:0006412,(AT4G11630.1 | 0 |
| 11 | KOG1698 | | 0 K02884 | GO:0006412,(AT4G11630.1 | 0 |
| 12 | KOG1698 | | 0 K02884 | GO:0006412,(AT4G11630.1 | 0 |
| 13 | KOG1698 | | 0 K02884 | GO:0006412,(AT4G11630.1 | 0 |
| 14 | KOG1698 | | 0 K02884 | GO:0006412,(AT4G11630.1 | 0 |
| 15 | KOG0519 | 2.7.11.1 | K14509 | GO:0005515,(AT3G04580.2 EIN4 | |
| 16 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 17 | KOG0519 | 2.7.11.1 | | 0 GO:0007165,(AT3G04580.1 EIN4 | |
| 18 | | | | | |
| 19 | | 0 | 0 | 0 AT5G59320.1 LTP3 | |
| 20 | | 0 | 0 | 0 AT5G59320.1 LTP3 | |
| 21 | | 0 | 0 | 0 AT5G59320.1 LTP3 | |
| 22 | | 0 | 0 | 0 AT5G59320.1 LTP3 | |
| 23 | | 0 | 0 | 0 AT5G59320.1 LTP3 | |
| 24 | | 0 | 0 | 0 AT5G59320.1 LTP3 | |
| 25 | | 0 | 0 | 0 AT5G59320.1 LTP3 | |
| 26 | | 0 | 0 | 0 AT5G59320.1 LTP3 | |
| 27 | | 0 | 0 | 0 AT5G59320.1 LTP3 | |
| 28 | | 0 | 0 | 0 AT5G59320.1 LTP3 | |
| 29 | | 0 | 0 | 0 AT5G59320.1 LTP3 | |
| 30 | | 0 | 0 | 0 AT5G59320.1 LTP3 | |
| 31 | | 0 | 0 | 0 AT5G59320.1 LTP3 | |
| 32 | | 0 | 0 | 0 AT5G59320.1 LTP3 | |
| 33 | | 0 | 0 | 0 AT1G32583.1 | 0 |
| 34 | | 0 | 0 | 0 AT1G32583.1 | 0 |
| 35 | | 0 | 0 | 0 AT1G32583.1 | 0 |
| 36 | | 0 | 0 | 0 AT1G32583.1 | 0 |
| 37 | | 0 | 0 | 0 AT1G32583.1 | 0 |
| 38 | | 0 | 0 | 0 AT1G32583.1 | 0 |
| 39 | | 0 | 0 | 0 AT1G32583.1 | 0 |
| 40 | | 0 | 0 | 0 AT1G32583.1 | 0 |
| 41 | | 0 | 0 | 0 AT1G32583.1 | 0 |
| 42 | | 0 | 0 | 0 AT1G32583.1 | 0 |
| 43 | | 0 | 0 | 0 AT1G32583.1 | 0 |
| 44 | | 0 | 0 | 0 AT1G32583.1 | 0 |
| 45 | | 0 | 0 | 0 AT1G32583.1 | 0 |
| 46 | | 0 | 0 | 0 AT1G32583.1 | 0 |
| 47 | | 0 | 0 | 0 AT2G45180.1 | 0 |
| 48 | KOG0809 | | 0 | 0 GO:0005515 AT3G05710.2 ATSYP43,SYP43 | |
| 49 | KOG0809 | | 0 | 0 GO:0005515 AT3G05710.2 ATSYP43,SYP43 | |
| 50 | KOG0809 | | 0 | 0 GO:0005515 AT3G05710.2 ATSYP43,SYP43 | |
| 51 | KOG0809 | | 0 | 0 GO:0005515 AT3G05710.2 ATSYP43,SYP43 | |
| 52 | KOG0809 | | 0 | 0 GO:0005515 AT3G05710.2 ATSYP43,SYP43 | |
| 53 | KOG0809 | | 0 | 0 GO:0005515 AT3G05710.2 ATSYP43,SYP43 | |
| 54 | KOG0809 | | 0 | 0 GO:0005515 AT3G05710.2 ATSYP43,SYP43 | |
| 55 | KOG0809 | | 0 | 0 GO:0005515 AT3G05710.2 ATSYP43,SYP43 | |
| 56 | KOG0809 | | 0 | 0 GO:0005515 AT3G05710.2 ATSYP43,SYP43 | |
| 57 | KOG0809 | | 0 | 0 GO:0005515 AT3G05710.2 ATSYP43,SYP43 | |
| 58 | KOG0809 | | 0 | 0 GO:0005515 AT3G05710.2 ATSYP43,SYP43 | |
| 59 | KOG0809 | | 0 | 0 GO:0005515 AT3G05710.2 ATSYP43,SYP43 | |
| 60 | KOG0809 | | 0 | 0 GO:0005515 AT3G05710.2 ATSYP43,SYP43 | |
| | | 0 2.5.1.36 | K09833 | GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1 | |

| | | | | | |
|----|---------|------------|--------|---|---|
| 1 | | | | | |
| 2 | | 0 2.5.1.36 | K09833 | GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1 | |
| 3 | | 0 2.5.1.36 | K09833 | GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1 | |
| 4 | | 0 2.5.1.36 | K09833 | GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1 | |
| 5 | | 0 2.5.1.36 | K09833 | GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1 | |
| 6 | | 0 2.5.1.36 | K09833 | GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1 | |
| 7 | | 0 2.5.1.36 | K09833 | GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1 | |
| 8 | | 0 2.5.1.36 | K09833 | GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1 | |
| 9 | | 0 2.5.1.36 | K09833 | GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1 | |
| 10 | | 0 2.5.1.36 | K09833 | GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1 | |
| 11 | | 0 2.5.1.36 | K09833 | GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1 | |
| 12 | | 0 2.5.1.36 | K09833 | GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1 | |
| 13 | | 0 2.5.1.36 | K09833 | GO:0016021,(AT2G18950.1 ATHPT,HPT1,TPT1 | |
| 14 | | 0 6.6.1.1 | K03403 | GO:0016851,(AT5G13630.1 ABAR,CCH,CCH1,(| |
| 15 | | 0 | 0 | 0 AT5G13390.1 NEF1 | |
| 16 | | 0 | 0 | 0 AT5G13390.1 NEF1 | |
| 17 | | 0 | 0 | 0 GO:0006412,(AT5G39785.1 | 0 |
| 18 | | 0 | 0 | 0 GO:0006412,(AT5G39785.1 | 0 |
| 19 | | 0 | 0 | 0 GO:0006412,(AT5G39785.1 | 0 |
| 20 | | 0 | 0 | 0 GO:0006412,(AT5G39785.1 | 0 |
| 21 | | 0 | 0 | 0 GO:0006412,(AT5G39785.1 | 0 |
| 22 | | 0 | 0 | 0 GO:0006412,(AT5G39785.1 | 0 |
| 23 | | 0 | 0 | 0 GO:0006412,(AT5G39785.1 | 0 |
| 24 | | 0 | 0 | 0 GO:0006412,(AT5G39785.1 | 0 |
| 25 | | 0 | 0 | 0 GO:0006412,(AT5G39785.1 | 0 |
| 26 | | 0 | 0 | 0 GO:0006412,(AT5G39785.1 | 0 |
| 27 | | 0 | 0 | 0 GO:0006412,(AT5G39785.1 | 0 |
| 28 | | 0 | 0 | 0 GO:0006412,(AT5G39785.1 | 0 |
| 29 | | 0 | 0 | 0 GO:0006412,(AT5G39785.1 | 0 |
| 30 | | 0 | 0 | 0 GO:0006412,(AT5G39785.1 | 0 |
| 31 | | 0 | 0 | 0 GO:0006412,(AT5G39785.1 | 0 |
| 32 | | 0 | 0 | 0 AT2G38570.1 | 0 |
| 33 | | | | | |
| 34 | KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT3G47570.1 | 0 |
| 35 | | 0 2.5.1.54 | K01626 | GO:0009073,(AT1G22410.1 | 0 |
| 36 | | 0 2.5.1.54 | K01626 | GO:0009073,(AT1G22410.1 | 0 |
| 37 | | 0 2.5.1.54 | K01626 | GO:0009073,(AT1G22410.1 | 0 |
| 38 | | 0 2.5.1.54 | K01626 | GO:0009073,(AT1G22410.1 | 0 |
| 39 | | 0 2.5.1.54 | K01626 | GO:0009073,(AT1G22410.1 | 0 |
| 40 | | 0 2.5.1.54 | K01626 | GO:0009073,(AT1G22410.1 | 0 |
| 41 | | 0 2.5.1.54 | K01626 | GO:0009073,(AT1G22410.1 | 0 |
| 42 | | 0 2.5.1.54 | K01626 | GO:0009073,(AT1G22410.1 | 0 |
| 43 | | 0 2.5.1.54 | K01626 | GO:0009073,(AT1G22410.1 | 0 |
| 44 | | 0 2.5.1.54 | K01626 | GO:0009073,(AT1G22410.1 | 0 |
| 45 | | 0 2.5.1.54 | K01626 | GO:0009073,(AT1G22410.1 | 0 |
| 46 | | 0 2.5.1.54 | K01626 | GO:0009073,(AT1G22410.1 | 0 |
| 47 | | 0 2.5.1.54 | K01626 | GO:0009073,(AT1G22410.1 | 0 |
| 48 | | 0 | 0 | 0 AT3G59300.1 | 0 |
| 49 | | 0 | 0 | 0 AT3G59300.1 | 0 |
| 50 | | 0 | 0 | 0 AT2G30130.1 ASL5,LBD12,PCK1 | |
| 51 | | | | | |
| 52 | KOG0251 | | 0 | 0 GO:0005543 AT2G25430.1 | 0 |
| 53 | KOG0251 | | 0 | 0 GO:0005543 AT2G25430.1 | 0 |
| 54 | KOG0251 | | 0 | 0 GO:0005543 AT2G25430.1 | 0 |
| 55 | KOG0251 | | 0 | 0 GO:0005543 AT2G25430.1 | 0 |
| 56 | KOG0251 | | 0 | 0 GO:0005543 AT2G25430.1 | 0 |
| 57 | KOG0251 | | 0 | 0 GO:0005543 AT2G25430.1 | 0 |
| 58 | KOG0251 | | 0 | 0 GO:0005543 AT2G25430.1 | 0 |
| 59 | KOG0251 | | 0 | 0 GO:0005543 AT2G25430.1 | 0 |
| 60 | KOG0251 | | 0 | 0 GO:0005543 AT2G25430.1 | 0 |
| | KOG0251 | | 0 | 0 GO:0005543 AT2G25430.1 | 0 |

| | | | | | | | |
|----|---------|------------|---|--------------|-------------|--------|---|
| 1 | | | | | | | |
| 2 | KOG0251 | 0 | 0 | GO:0005543 | AT2G25430.1 | | 0 |
| 3 | KOG0251 | 0 | 0 | GO:0005543 | AT2G25430.1 | | 0 |
| 4 | KOG0251 | 0 | 0 | GO:0005543 | AT2G25430.1 | | 0 |
| 5 | | | | | | | |
| 6 | KOG2063 | 0 | 0 | GO:0016192,(| AT1G22860.1 | | 0 |
| 7 | | 0 | 0 | GO:0043565,(| AT2G16770.1 | bZIP23 | |
| 8 | | 0 | 0 | GO:0043565,(| AT2G16770.1 | bZIP23 | |
| 9 | | 0 | 0 | GO:0043565,(| AT2G16770.1 | bZIP23 | |
| 10 | | 0 | 0 | GO:0043565,(| AT2G16770.1 | bZIP23 | |
| 11 | | 0 | 0 | GO:0043565,(| AT2G16770.1 | bZIP23 | |
| 12 | | 0 | 0 | GO:0043565,(| AT2G16770.1 | bZIP23 | |
| 13 | | 0 | 0 | GO:0043565,(| AT2G16770.1 | bZIP23 | |
| 14 | | 0 | 0 | GO:0043565,(| AT2G16770.1 | bZIP23 | |
| 15 | | 0 | 0 | GO:0043565,(| AT2G16770.1 | bZIP23 | |
| 16 | | 0 | 0 | GO:0043565,(| AT2G16770.1 | bZIP23 | |
| 17 | | 0 | 0 | GO:0043565,(| AT2G16770.1 | bZIP23 | |
| 18 | | 0 | 0 | GO:0043565,(| AT2G16770.1 | bZIP23 | |
| 19 | | 0 | 0 | GO:0043565,(| AT2G16770.1 | bZIP23 | |
| 20 | | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | | | | | | | |
| 22 | KOG1187 | 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 23 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 24 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 25 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 26 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 27 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 28 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 29 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 30 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 31 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 32 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 33 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 34 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 35 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 36 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 37 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 38 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 39 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 40 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 41 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 42 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 43 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 44 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 45 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 46 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 47 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 48 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 49 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 50 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 51 | | 0 2.7.11.1 | 0 | GO:0048544,(| AT4G27290.1 | | 0 |
| 52 | | | | | | | |
| 53 | | | | | | | |
| 54 | | | | | | | |
| 55 | | | | | | | |
| 56 | | | | | | | |
| 57 | | | | | | | |
| 58 | | | | | | | |
| 59 | | | | | | | |
| 60 | | | | | | | |

| | arabi-defline | ID | Annot_defline |
|----|--|---------------------------|---------------|
| 1 | | | |
| 2 | arabi-defline | | |
| 3 | related to AP2.7 | Phvul.001G17K09284 - AP2- | |
| 4 | related to AP2.7 | Phvul.001G17K09284 - AP2- | |
| 5 | related to AP2.7 | Phvul.001G17K09284 - AP2- | |
| 6 | related to AP2.7 | Phvul.001G17K09284 - AP2- | |
| 7 | related to AP2.7 | Phvul.001G17K09284 - AP2- | |
| 8 | related to AP2.7 | Phvul.001G17K09284 - AP2- | |
| 9 | related to AP2.7 | Phvul.001G17K09284 - AP2- | |
| 10 | related to AP2.7 | Phvul.001G17K09284 - AP2- | |
| 11 | related to AP2.7 | Phvul.001G17K09284 - AP2- | |
| 12 | related to AP2.7 | Phvul.001G17K09284 - AP2- | |
| 13 | related to AP2.7 | Phvul.001G17K09284 - AP2- | |
| 14 | related to AP2.7 | Phvul.001G17K09284 - AP2- | |
| 15 | related to AP2.7 | Phvul.001G17K09284 - AP2- | |
| 16 | related to AP2.7 | Phvul.001G17K09284 - AP2- | |
| 17 | | | |
| 18 | Integrase-type DNA-binding superfamily protein | Phvul.002G01PTHR32467:SF | |
| 19 | Integrase-type DNA-binding superfamily protein | Phvul.002G01PTHR32467:SF | |
| 20 | Integrase-type DNA-binding superfamily protein | Phvul.002G01PTHR32467:SF | |
| 21 | Integrase-type DNA-binding superfamily protein | Phvul.002G01PTHR32467:SF | |
| 22 | Integrase-type DNA-binding superfamily protein | Phvul.002G01PTHR32467:SF | |
| 23 | Integrase-type DNA-binding superfamily protein | Phvul.002G01PTHR32467:SF | |
| 24 | Integrase-type DNA-binding superfamily protein | Phvul.002G01PTHR32467:SF | |
| 25 | Integrase-type DNA-binding superfamily protein | Phvul.002G01PTHR32467:SF | |
| 26 | Integrase-type DNA-binding superfamily protein | Phvul.002G01PTHR32467:SF | |
| 27 | Integrase-type DNA-binding superfamily protein | Phvul.002G01PTHR32467:SF | |
| 28 | Integrase-type DNA-binding superfamily protein | Phvul.002G01PTHR32467:SF | |
| 29 | Integrase-type DNA-binding superfamily protein | Phvul.002G01PTHR32467:SF | |
| 30 | Integrase-type DNA-binding superfamily protein | Phvul.002G01PTHR32467:SF | |
| 31 | Integrase-type DNA-binding superfamily protein | Phvul.002G01PTHR32467:SF | |
| 32 | Integrase-type DNA-binding superfamily protein | Phvul.003G24PTHR32467:SF | |
| 33 | Integrase-type DNA-binding superfamily protein | Phvul.003G24PTHR32467:SF | |
| 34 | Integrase-type DNA-binding superfamily protein | Phvul.003G24PTHR32467:SF | |
| 35 | Integrase-type DNA-binding superfamily protein | Phvul.003G24PTHR32467:SF | |
| 36 | Integrase-type DNA-binding superfamily protein | Phvul.003G24PTHR32467:SF | |
| 37 | Integrase-type DNA-binding superfamily protein | Phvul.003G24PTHR32467:SF | |
| 38 | Integrase-type DNA-binding superfamily protein | Phvul.003G24PTHR32467:SF | |
| 39 | Integrase-type DNA-binding superfamily protein | Phvul.003G24PTHR32467:SF | |
| 40 | Integrase-type DNA-binding superfamily protein | Phvul.003G24PTHR32467:SF | |
| 41 | Integrase-type DNA-binding superfamily protein | Phvul.003G24PTHR32467:SF | |
| 42 | Integrase-type DNA-binding superfamily protein | Phvul.003G24PTHR32467:SF | |
| 43 | Integrase-type DNA-binding superfamily protein | Phvul.003G24PTHR32467:SF | |
| 44 | Integrase-type DNA-binding superfamily protein | Phvul.003G24PTHR32467:SF | |
| 45 | Integrase-type DNA-binding superfamily protein | Phvul.003G24PTHR32467:SF | |
| 46 | Integrase-type DNA-binding superfamily protein | Phvul.003G24PTHR32467:SF | |
| 47 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 48 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 49 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 50 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 51 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 52 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 53 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 54 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 55 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 56 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 57 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 58 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 59 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 60 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| | related to AP2.7 | Phvul.011G07PTHR32467:SF | |

| | | | |
|----|--|---------------------------|---|
| 1 | | | |
| 2 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 3 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 4 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 5 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 6 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 7 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 8 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 9 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 10 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 11 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 12 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 13 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 14 | related to AP2.7 | Phvul.011G07PTHR32467:SF | |
| 15 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 16 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 17 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 18 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 19 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 20 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 21 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 22 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 23 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 24 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 25 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 26 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 27 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 28 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 29 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 30 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 31 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 32 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 33 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 34 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 35 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 36 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 37 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 38 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 39 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 40 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 41 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 42 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 43 | related to AP2.7 | Phvul.L00030PTHR32467:SF | |
| 44 | related to AP2.7 | Phvul.001G17K09284 - AP2- | |
| 45 | Integrase-type DNA-binding superfamily protein | Phvul.002G01PTHR32467:SF | |
| 46 | Integrase-type DNA-binding superfamily protein | Phvul.003G24PTHR32467:SF | |
| 47 | | | |
| 48 | | 0 | 0 |
| 49 | | 0 | 0 |
| 50 | | 0 | 0 |
| 51 | | 0 | 0 |
| 52 | | 0 | 0 |
| 53 | | 0 | 0 |
| 54 | | 0 | 0 |
| 55 | | 0 | 0 |
| 56 | | 0 | 0 |
| 57 | | 0 | 0 |
| 58 | | 0 | 0 |
| 59 | | 0 | 0 |
| 60 | | 0 | 0 |

| | | | | |
|----|------------------|---|--------------------------|---|
| 1 | | | | |
| 2 | | 0 | 0 | 0 |
| 3 | | 0 | 0 | 0 |
| 4 | | 0 | 0 | 0 |
| 5 | | 0 | 0 | 0 |
| 6 | | 0 | 0 | 0 |
| 7 | | 0 | 0 | 0 |
| 8 | | 0 | 0 | 0 |
| 9 | | 0 | 0 | 0 |
| 10 | | 0 | 0 | 0 |
| 11 | | 0 | 0 | 0 |
| 12 | | 0 | 0 | 0 |
| 13 | | 0 | 0 | 0 |
| 14 | | 0 | 0 | 0 |
| 15 | | 0 | 0 | 0 |
| 16 | related to AP2.7 | | Phvul.007G24PTHR32467:SF | |
| 17 | related to AP2.7 | | Phvul.007G24PTHR32467:SF | |
| 18 | related to AP2.7 | | Phvul.007G24PTHR32467:SF | |
| 19 | related to AP2.7 | | Phvul.007G24PTHR32467:SF | |
| 20 | related to AP2.7 | | Phvul.007G24PTHR32467:SF | |
| 21 | related to AP2.7 | | Phvul.007G24PTHR32467:SF | |
| 22 | related to AP2.7 | | Phvul.007G24PTHR32467:SF | |
| 23 | related to AP2.7 | | Phvul.007G24PTHR32467:SF | |
| 24 | related to AP2.7 | | Phvul.007G24PTHR32467:SF | |
| 25 | related to AP2.7 | | Phvul.007G24PTHR32467:SF | |
| 26 | related to AP2.7 | | Phvul.007G24PTHR32467:SF | |
| 27 | related to AP2.7 | | Phvul.007G24PTHR32467:SF | |
| 28 | related to AP2.7 | | Phvul.007G24PTHR32467:SF | |
| 29 | related to AP2.7 | | Phvul.007G24PTHR32467:SF | |
| 30 | related to AP2.7 | | Phvul.007G24PTHR32467:SF | |
| 31 | | 0 | 0 | 0 |
| 32 | | 0 | 0 | 0 |
| 33 | | 0 | 0 | 0 |
| 34 | | 0 | 0 | 0 |
| 35 | | 0 | 0 | 0 |
| 36 | | 0 | 0 | 0 |
| 37 | | 0 | 0 | 0 |
| 38 | | 0 | 0 | 0 |
| 39 | | 0 | 0 | 0 |
| 40 | | 0 | 0 | 0 |
| 41 | | 0 | 0 | 0 |
| 42 | | 0 | 0 | 0 |
| 43 | | 0 | 0 | 0 |
| 44 | | 0 | 0 | 0 |
| 45 | | 0 | 0 | 0 |
| 46 | | 0 | 0 | 0 |
| 47 | | 0 | 0 | 0 |
| 48 | | 0 | 0 | 0 |
| 49 | | 0 | 0 | 0 |
| 50 | | 0 | 0 | 0 |
| 51 | | 0 | 0 | 0 |
| 52 | | 0 | 0 | 0 |
| 53 | | 0 | 0 | 0 |
| 54 | | 0 | 0 | 0 |
| 55 | | 0 | 0 | 0 |
| 56 | | 0 | 0 | 0 |
| 57 | | 0 | 0 | 0 |
| 58 | | 0 | 0 | 0 |
| 59 | | 0 | 0 | 0 |
| 60 | | 0 | 0 | 0 |

| | | | | |
|----|---|---|----------------------------|---|
| 1 | | | | |
| 2 | | 0 | 0 | 0 |
| 3 | | 0 | 0 | 0 |
| 4 | | 0 | 0 | 0 |
| 5 | | 0 | 0 | 0 |
| 6 | | 0 | 0 | 0 |
| 7 | | 0 | 0 | 0 |
| 8 | | 0 | 0 | 0 |
| 9 | | 0 | 0 | 0 |
| 10 | | 0 | 0 | 0 |
| 11 | | 0 | 0 | 0 |
| 12 | | 0 | 0 | 0 |
| 13 | | | | |
| 14 | related to AP2.7 | | Phvul.011G07PTHR32467:SF | |
| 15 | related to AP2.7 | | Phvul.011G07PTHR32467:SF | |
| 16 | related to AP2.7 | | Phvul.L00030{PTHR32467:SF | |
| 17 | related to AP2.7 | | Phvul.L00030{PTHR32467:SF | |
| 18 | allene oxide cyclase 3 | | Phvul.003G11K10525 - allen | |
| 19 | BRI1 suppressor 1 (BSU1)-like 3 | | Phvul.005G11PTHR11668//I | |
| 20 | cysteine-rich RLK (RECEPTOR-like protein kinase) 29 | | Phvul.008G05PTHR27002:SF | |
| 21 | cysteine-rich RLK (RECEPTOR-like protein kinase) 29 | | Phvul.008G05PTHR27002:SF | |
| 22 | S-locus lectin protein kinase family protein | | Phvul.011G15PTHR27002:SF | |
| 23 | | 0 | Phvul.001G03PTHR13135 - C | |
| 24 | | 0 | Phvul.001G03PTHR13135 - C | |
| 25 | | 0 | Phvul.001G03PTHR13135 - C | |
| 26 | | 0 | Phvul.001G03PTHR13135 - C | |
| 27 | | 0 | Phvul.001G03PTHR13135 - C | |
| 28 | | 0 | Phvul.001G03PTHR13135 - C | |
| 29 | | 0 | Phvul.001G03PTHR13135 - C | |
| 30 | | 0 | Phvul.001G03PTHR13135 - C | |
| 31 | | 0 | Phvul.001G03PTHR13135 - C | |
| 32 | | 0 | Phvul.001G03PTHR13135 - C | |
| 33 | | 0 | Phvul.001G03PTHR13135 - C | |
| 34 | | 0 | Phvul.001G03PTHR13135 - C | |
| 35 | | 0 | Phvul.001G03PTHR13135 - C | |
| 36 | | 0 | Phvul.001G03PTHR13135 - C | |
| 37 | | 0 | Phvul.001G03PTHR13135 - C | |
| 38 | | 0 | Phvul.001G03PTHR13135 - C | |
| 39 | | 0 | Phvul.001G03PTHR13135 - C | |
| 40 | | 0 | Phvul.001G03PTHR13135 - C | |
| 41 | | 0 | Phvul.001G03PTHR13135 - C | |
| 42 | | 0 | Phvul.001G03PTHR13135 - C | |
| 43 | | 0 | Phvul.001G03PTHR13135 - C | |
| 44 | | 0 | Phvul.001G03PTHR13135 - C | |
| 45 | | 0 | Phvul.001G03PTHR13135 - C | |
| 46 | | 0 | Phvul.001G03PTHR13135 - C | |
| 47 | | 0 | Phvul.001G03PTHR13135 - C | |
| 48 | | 0 | Phvul.001G03PTHR13135 - C | |
| 49 | | 0 | Phvul.001G03PTHR13135 - C | |
| 50 | | 0 | Phvul.001G03PTHR13135 - C | |
| 51 | | 0 | Phvul.001G03PTHR13135 - C | |
| 52 | | 0 | Phvul.001G03PTHR13135 - C | |
| 53 | | 0 | Phvul.001G03PTHR13135 - C | |
| 54 | | 0 | Phvul.001G03PTHR13135 - C | |
| 55 | | 0 | 0 | 0 |
| 56 | | 0 | 0 | 0 |
| 57 | | 0 | 0 | 0 |
| 58 | | 0 | 0 | 0 |
| 59 | | 0 | 0 | 0 |
| 60 | | 0 | 0 | 0 |

| | | | |
|----|---|---|----------------------------|
| 1 | | | |
| 2 | | 0 | 0 |
| 3 | | 0 | 0 |
| 4 | | 0 | 0 |
| 5 | | 0 | 0 |
| 6 | | 0 | 0 |
| 7 | | 0 | 0 |
| 8 | | 0 | 0 |
| 9 | | 0 | 0 |
| 10 | RING/FYVE/PHD zinc finger superfamily protein | | Phvul.001G21PTHR23012:SF |
| 11 | RING/FYVE/PHD zinc finger superfamily protein | | Phvul.001G21PTHR23012:SF |
| 12 | casein kinase alpha 1 | | Phvul.002G01K03097 - case |
| 13 | casein kinase alpha 1 | | Phvul.002G01K03097 - case |
| 14 | casein kinase alpha 1 | | Phvul.002G01K03097 - case |
| 15 | casein kinase alpha 1 | | Phvul.002G01K03097 - case |
| 16 | casein kinase alpha 1 | | Phvul.002G01K03097 - case |
| 17 | casein kinase alpha 1 | | Phvul.002G01K03097 - case |
| 18 | casein kinase alpha 1 | | Phvul.002G01K03097 - case |
| 19 | casein kinase alpha 1 | | Phvul.002G01K03097 - case |
| 20 | casein kinase alpha 1 | | Phvul.002G01K03097 - case |
| 21 | casein kinase alpha 1 | | Phvul.002G01K03097 - case |
| 22 | casein kinase alpha 1 | | Phvul.002G01K03097 - case |
| 23 | casein kinase alpha 1 | | Phvul.002G01K03097 - case |
| 24 | casein kinase alpha 1 | | Phvul.002G01K03097 - case |
| 25 | O-acetyltransferase family protein | | Phvul.002G19PTHR13533:SF |
| 26 | Aldolase-type TIM barrel family protein | | Phvul.002G214.4.1.19 - Pho |
| 27 | Nucleic acid-binding, OB-fold-like protein | | Phvul.002G33PTHR14513 - I |
| 28 | Nucleic acid-binding, OB-fold-like protein | | Phvul.002G33PTHR14513 - I |
| 29 | zinc transporter 10 precursor | | Phvul.003G26PTHR11040:SF |
| 30 | zinc transporter 10 precursor | | Phvul.003G26PTHR11040:SF |
| 31 | S-locus lectin protein kinase family protein | | Phvul.005G03PF00954//PFC |
| 32 | S-locus lectin protein kinase family protein | | Phvul.005G03PF00954//PFC |
| 33 | S-locus lectin protein kinase family protein | | Phvul.005G03PF00954//PFC |
| 34 | S-locus lectin protein kinase family protein | | Phvul.005G03PF00954//PFC |
| 35 | S-locus lectin protein kinase family protein | | Phvul.005G03PF00954//PFC |
| 36 | S-locus lectin protein kinase family protein | | Phvul.005G03PF00954//PFC |
| 37 | S-locus lectin protein kinase family protein | | Phvul.005G03PF00954//PFC |
| 38 | S-locus lectin protein kinase family protein | | Phvul.005G03PF00954//PFC |
| 39 | S-locus lectin protein kinase family protein | | Phvul.005G03PF00954//PFC |
| 40 | S-locus lectin protein kinase family protein | | Phvul.005G03PF00954//PFC |
| 41 | S-locus lectin protein kinase family protein | | Phvul.005G03PF00954//PFC |
| 42 | S-locus lectin protein kinase family protein | | Phvul.005G03PF00954//PFC |
| 43 | S-locus lectin protein kinase family protein | | Phvul.005G03PF00954//PFC |
| 44 | S-locus lectin protein kinase family protein | | Phvul.005G03PF00954//PFC |
| 45 | S-locus lectin protein kinase family protein | | Phvul.005G03PF00954//PFC |
| 46 | S-locus lectin protein kinase family protein | | Phvul.005G03PF00954//PFC |
| 47 | S-locus lectin protein kinase family protein | | Phvul.005G03PF00954//PFC |
| 48 | S-locus lectin protein kinase family protein | | Phvul.005G03PF00954//PFC |
| 49 | S-locus lectin protein kinase family protein | | Phvul.005G08PF00954//PFC |
| 50 | S-locus lectin protein kinase family protein | | Phvul.005G08PF00954//PFC |
| 51 | S-locus lectin protein kinase family protein | | Phvul.005G08PF00954//PFC |
| 52 | S-locus lectin protein kinase family protein | | Phvul.005G08PF00954//PFC |
| 53 | receptor kinase 3 | | Phvul.005G08PF00954//PFC |
| 54 | serine carboxypeptidase-like 48 | | Phvul.005G13K16298 - serin |
| 55 | serine carboxypeptidase-like 48 | | Phvul.005G13K16298 - serin |
| 56 | serine carboxypeptidase-like 48 | | Phvul.005G13K16298 - serin |
| 57 | serine carboxypeptidase-like 48 | | Phvul.005G13K16298 - serin |
| 58 | serine carboxypeptidase-like 48 | | Phvul.005G13K16298 - serin |
| 59 | serine carboxypeptidase-like 48 | | Phvul.005G13K16298 - serin |
| 60 | serine carboxypeptidase-like 48 | | Phvul.005G13K16298 - serin |

| | | | |
|----|---|----------------------------|---|
| 1 | | | |
| 2 | serine carboxypeptidase-like 48 | Phvul.005G13K16298 - serin | |
| 3 | serine carboxypeptidase-like 48 | Phvul.005G13K16298 - serin | |
| 4 | serine carboxypeptidase-like 48 | Phvul.005G13K16298 - serin | |
| 5 | serine carboxypeptidase-like 48 | Phvul.005G13K16298 - serin | |
| 6 | serine carboxypeptidase-like 48 | Phvul.005G13K16298 - serin | |
| 7 | serine carboxypeptidase-like 48 | Phvul.005G13K16298 - serin | |
| 8 | serine carboxypeptidase-like 48 | Phvul.005G13K16298 - serin | |
| 9 | | | |
| 10 | | 0 | 0 |
| 11 | | 0 | 0 |
| 12 | Nucleotide-sugar transporter family protein | Phvul.006G13PTHR11132//I | |
| 13 | Nucleotide-sugar transporter family protein | Phvul.006G13PTHR11132//I | |
| 14 | Nucleotide-sugar transporter family protein | Phvul.006G13PTHR11132//I | |
| 15 | Nucleotide-sugar transporter family protein | Phvul.006G13PTHR11132//I | |
| 16 | Nucleotide-sugar transporter family protein | Phvul.006G13PTHR11132//I | |
| 17 | Nucleotide-sugar transporter family protein | Phvul.006G13PTHR11132//I | |
| 18 | Nucleotide-sugar transporter family protein | Phvul.006G13PTHR11132//I | |
| 19 | Nucleotide-sugar transporter family protein | Phvul.006G13PTHR11132//I | |
| 20 | Nucleotide-sugar transporter family protein | Phvul.006G13PTHR11132//I | |
| 21 | Nucleotide-sugar transporter family protein | Phvul.006G13PTHR11132//I | |
| 22 | Nucleotide-sugar transporter family protein | Phvul.006G13PTHR11132//I | |
| 23 | Nucleotide-sugar transporter family protein | Phvul.006G13PTHR11132//I | |
| 24 | Nucleotide-sugar transporter family protein | Phvul.006G13PTHR11132//I | |
| 25 | Nucleotide-sugar transporter family protein | Phvul.006G13PTHR11132//I | |
| 26 | Nucleotide-sugar transporter family protein | Phvul.006G13PTHR11132//I | |
| 27 | related to AP2.7 | Phvul.007G24PTHR32467:SF | |
| 28 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 29 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 30 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 31 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 32 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 33 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 34 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 35 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 36 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 37 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 38 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 39 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 40 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 41 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 42 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 43 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 44 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 45 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 46 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 47 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 48 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 49 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 50 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 51 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 52 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 53 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 54 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 55 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 56 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 57 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 58 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 59 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |
| 60 | magnesium transporter 4 | Phvul.008G03PTHR13890:SF | |

| | | | |
|----|---|-----------------------------|---|
| 1 | | | |
| 2 | magnesium transporter 4 | Phvul.008G03 PTHR13890:SF | |
| 3 | magnesium transporter 4 | Phvul.008G03 PTHR13890:SF | |
| 4 | magnesium transporter 4 | Phvul.008G03 PTHR13890:SF | |
| 5 | magnesium transporter 4 | Phvul.008G03 PTHR13890:SF | |
| 6 | magnesium transporter 4 | Phvul.008G03 PTHR13890:SF | |
| 7 | magnesium transporter 4 | Phvul.008G03 PTHR13890:SF | |
| 8 | magnesium transporter 4 | Phvul.008G03 PTHR13890:SF | |
| 9 | magnesium transporter 4 | Phvul.008G03 PTHR13890:SF | |
| 10 | magnesium transporter 4 | Phvul.008G03 PTHR13890:SF | |
| 11 | magnesium transporter 4 | Phvul.008G03 PTHR13890:SF | |
| 12 | magnesium transporter 4 | Phvul.008G03 PTHR13890:SF | |
| 13 | magnesium transporter 4 | Phvul.008G03 PTHR13890:SF | |
| 14 | magnesium transporter 4 | Phvul.008G03 PTHR13890:SF | |
| 15 | BTB/POZ domain-containing protein | Phvul.009G13 K10523 - spec | |
| 16 | BTB/POZ domain-containing protein | Phvul.009G13 K10523 - spec | |
| 17 | BTB/POZ domain-containing protein | Phvul.009G13 K10523 - spec | |
| 18 | BTB/POZ domain-containing protein | Phvul.009G13 K10523 - spec | |
| 19 | BTB/POZ domain-containing protein | Phvul.009G13 K10523 - spec | |
| 20 | BTB/POZ domain-containing protein | Phvul.009G13 K10523 - spec | |
| 21 | BTB/POZ domain-containing protein | Phvul.009G13 K10523 - spec | |
| 22 | BTB/POZ domain-containing protein | Phvul.009G13 K10523 - spec | |
| 23 | BTB/POZ domain-containing protein | Phvul.009G13 K10523 - spec | |
| 24 | BTB/POZ domain-containing protein | Phvul.009G13 K10523 - spec | |
| 25 | BTB/POZ domain-containing protein | Phvul.009G13 K10523 - spec | |
| 26 | BTB/POZ domain-containing protein | Phvul.009G13 K10523 - spec | |
| 27 | BTB/POZ domain-containing protein | Phvul.009G13 K10523 - spec | |
| 28 | BTB/POZ domain-containing protein | Phvul.009G13 K10523 - spec | |
| 29 | Tetratricopeptide repeat (TPR)-like superfamily protein | Phvul.009G24 PF01535//PF1 | |
| 30 | | | |
| 31 | | 0 | 0 |
| 32 | S-locus lectin protein kinase family protein | Phvul.011G15 PF00954//PFC | |
| 33 | S-locus lectin protein kinase family protein | Phvul.011G15 PTHR27002:SF | |
| 34 | S-locus lectin protein kinase family protein | Phvul.011G15 PTHR27002:SF | |
| 35 | S-locus lectin protein kinase family protein | Phvul.011G15 PTHR27002:SF | |
| 36 | S-locus lectin protein kinase family protein | Phvul.011G15 PTHR27002:SF | |
| 37 | S-locus lectin protein kinase family protein | Phvul.011G15 PTHR27002:SF | |
| 38 | S-locus lectin protein kinase family protein | Phvul.011G15 PTHR27002:SF | |
| 39 | S-locus lectin protein kinase family protein | Phvul.011G15 PTHR27002:SF | |
| 40 | S-locus lectin protein kinase family protein | Phvul.011G15 PF00954//PFC | |
| 41 | S-locus lectin protein kinase family protein | Phvul.011G16 PTHR27002:SF | |
| 42 | | | |
| 43 | | 0 | 0 |
| 44 | | 0 | 0 |
| 45 | Plant protein of unknown function (DUF247) | Phvul.001G18 PF03140 - Plai | |
| 46 | Plant protein of unknown function (DUF247) | Phvul.001G18 PF03140 - Plai | |
| 47 | Plant protein of unknown function (DUF247) | Phvul.001G18 PF03140 - Plai | |
| 48 | Plant protein of unknown function (DUF247) | Phvul.001G18 PF03140 - Plai | |
| 49 | Plant protein of unknown function (DUF247) | Phvul.001G18 PF03140 - Plai | |
| 50 | Plant protein of unknown function (DUF247) | Phvul.001G18 PF03140 - Plai | |
| 51 | Plant protein of unknown function (DUF247) | Phvul.001G18 PF03140 - Plai | |
| 52 | Plant protein of unknown function (DUF247) | Phvul.001G18 PF03140 - Plai | |
| 53 | Plant protein of unknown function (DUF247) | Phvul.001G18 PF03140 - Plai | |
| 54 | Plant protein of unknown function (DUF247) | Phvul.001G18 PF03140 - Plai | |
| 55 | Plant protein of unknown function (DUF247) | Phvul.001G18 PF03140 - Plai | |
| 56 | Plant protein of unknown function (DUF247) | Phvul.001G18 PF03140 - Plai | |
| 57 | Plant protein of unknown function (DUF247) | Phvul.001G18 PF03140 - Plai | |
| 58 | Plant protein of unknown function (DUF247) | Phvul.001G18 PF03140 - Plai | |
| 59 | Plant protein of unknown function (DUF247) | Phvul.001G18 PF03140 - Plai | |
| 60 | Plant protein of unknown function (DUF247) | Phvul.001G18 PF03140 - Plai | |
| | | 0 | 0 |

| | | | | |
|----|--|---|---|---------------------------|
| 1 | | | | |
| 2 | | 0 | 0 | 0 |
| 3 | casein kinase alpha 1 | | | Phvul.002G01K03097 - case |
| 4 | Mitochondrial transcription termination factor family protei | | | Phvul.002G08PTHR13068//I |
| 5 | Mitochondrial transcription termination factor family protei | | | Phvul.002G08PTHR13068//I |
| 6 | Mitochondrial transcription termination factor family protei | | | Phvul.002G08PTHR13068//I |
| 7 | Mitochondrial transcription termination factor family protei | | | Phvul.002G08PTHR13068//I |
| 8 | Mitochondrial transcription termination factor family protei | | | Phvul.002G08PTHR13068//I |
| 9 | Mitochondrial transcription termination factor family protei | | | Phvul.002G08PTHR13068//I |
| 10 | Mitochondrial transcription termination factor family protei | | | Phvul.002G08PTHR13068//I |
| 11 | Mitochondrial transcription termination factor family protei | | | Phvul.002G08PTHR13068//I |
| 12 | Mitochondrial transcription termination factor family protei | | | Phvul.002G08PTHR13068//I |
| 13 | Mitochondrial transcription termination factor family protei | | | Phvul.002G08PTHR13068//I |
| 14 | Mitochondrial transcription termination factor family protei | | | Phvul.002G08PTHR13068//I |
| 15 | Mitochondrial transcription termination factor family protei | | | Phvul.002G08PTHR13068//I |
| 16 | Mitochondrial transcription termination factor family protei | | | Phvul.002G08PTHR13068//I |
| 17 | Mitochondrial transcription termination factor family protei | | | Phvul.002G08PTHR13068//I |
| 18 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 19 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 20 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 21 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 22 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 23 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 24 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 25 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 26 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 27 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 28 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 29 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 30 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 31 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 32 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 33 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 34 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 35 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 36 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 37 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 38 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 39 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 40 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 41 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 42 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 43 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 44 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 45 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 46 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 47 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 48 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 49 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 50 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 51 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 52 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 53 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 54 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 55 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 56 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 57 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 58 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 59 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| 60 | diacylglycerol kinase 2 | | | Phvul.002G27PTHR11255:SF |
| | Flavin-binding monooxygenase family protein | | | Phvul.002G31PTHR23023//I |

| | | |
|----|--|----------------------------|
| 1 | | |
| 2 | Flavin-binding monooxygenase family protein | Phvul.002G31PTHR23023//I |
| 3 | Flavin-binding monooxygenase family protein | Phvul.002G31PTHR23023//I |
| 4 | Flavin-binding monooxygenase family protein | Phvul.002G31PTHR23023//I |
| 5 | Flavin-binding monooxygenase family protein | Phvul.002G31PTHR23023//I |
| 6 | Flavin-binding monooxygenase family protein | Phvul.002G31PTHR23023//I |
| 7 | Flavin-binding monooxygenase family protein | Phvul.002G31PTHR23023//I |
| 8 | Flavin-binding monooxygenase family protein | Phvul.002G31PTHR23023//I |
| 9 | Flavin-binding monooxygenase family protein | Phvul.002G31PTHR23023//I |
| 10 | Flavin-binding monooxygenase family protein | Phvul.002G31PTHR23023//I |
| 11 | Flavin-binding monooxygenase family protein | Phvul.002G31PTHR23023//I |
| 12 | Flavin-binding monooxygenase family protein | Phvul.002G31PTHR23023//I |
| 13 | Flavin-binding monooxygenase family protein | Phvul.002G31PTHR23023//I |
| 14 | trehalose phosphate synthase | Phvul.003G052.4.1.15//3.1. |
| 15 | trehalose phosphate synthase | Phvul.003G052.4.1.15//3.1. |
| 16 | trehalose phosphate synthase | Phvul.003G052.4.1.15//3.1. |
| 17 | trehalose phosphate synthase | Phvul.003G052.4.1.15//3.1. |
| 18 | trehalose phosphate synthase | Phvul.003G052.4.1.15//3.1. |
| 19 | trehalose phosphate synthase | Phvul.003G052.4.1.15//3.1. |
| 20 | trehalose phosphate synthase | Phvul.003G052.4.1.15//3.1. |
| 21 | trehalose phosphate synthase | Phvul.003G052.4.1.15//3.1. |
| 22 | trehalose phosphate synthase | Phvul.003G052.4.1.15//3.1. |
| 23 | trehalose phosphate synthase | Phvul.003G052.4.1.15//3.1. |
| 24 | trehalose phosphate synthase | Phvul.003G052.4.1.15//3.1. |
| 25 | trehalose phosphate synthase | Phvul.003G052.4.1.15//3.1. |
| 26 | trehalose phosphate synthase | Phvul.003G052.4.1.15//3.1. |
| 27 | trehalose phosphate synthase | Phvul.003G052.4.1.15//3.1. |
| 28 | calcium-dependent lipid-binding family protein | Phvul.003G11PTHR16166:SF |
| 29 | calcium-dependent lipid-binding family protein | Phvul.003G11PTHR16166:SF |
| 30 | calcium-dependent lipid-binding family protein | Phvul.003G11PTHR16166:SF |
| 31 | calcium-dependent lipid-binding family protein | Phvul.003G11PTHR16166:SF |
| 32 | calcium-dependent lipid-binding family protein | Phvul.003G11PTHR16166:SF |
| 33 | calcium-dependent lipid-binding family protein | Phvul.003G11PTHR16166:SF |
| 34 | calcium-dependent lipid-binding family protein | Phvul.003G11PTHR16166:SF |
| 35 | calcium-dependent lipid-binding family protein | Phvul.003G11PTHR16166:SF |
| 36 | calcium-dependent lipid-binding family protein | Phvul.003G11PTHR16166:SF |
| 37 | calcium-dependent lipid-binding family protein | Phvul.003G11PTHR16166:SF |
| 38 | calcium-dependent lipid-binding family protein | Phvul.003G11PTHR16166:SF |
| 39 | calcium-dependent lipid-binding family protein | Phvul.003G11PTHR16166:SF |
| 40 | calcium-dependent lipid-binding family protein | Phvul.003G11PTHR16166:SF |
| 41 | calcium-dependent lipid-binding family protein | Phvul.003G11PTHR16166:SF |
| 42 | calcium-dependent lipid-binding family protein | Phvul.003G11PTHR16166:SF |
| 43 | casein kinase II, alpha chain 2 | Phvul.003G23K03097 - case |
| 44 | casein kinase II, alpha chain 2 | Phvul.003G23K03097 - case |
| 45 | casein kinase II, alpha chain 2 | Phvul.003G23K03097 - case |
| 46 | casein kinase II, alpha chain 2 | Phvul.003G23K03097 - case |
| 47 | casein kinase II, alpha chain 2 | Phvul.003G23K03097 - case |
| 48 | casein kinase II, alpha chain 2 | Phvul.003G23K03097 - case |
| 49 | casein kinase II, alpha chain 2 | Phvul.003G23K03097 - case |
| 50 | casein kinase II, alpha chain 2 | Phvul.003G23K03097 - case |
| 51 | casein kinase II, alpha chain 2 | Phvul.003G23K03097 - case |
| 52 | casein kinase II, alpha chain 2 | Phvul.003G23K03097 - case |
| 53 | casein kinase II, alpha chain 2 | Phvul.003G23K03097 - case |
| 54 | casein kinase II, alpha chain 2 | Phvul.003G23K03097 - case |
| 55 | casein kinase II, alpha chain 2 | Phvul.003G23K03097 - case |
| 56 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 57 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 58 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 59 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 60 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |

| | | |
|----|--|--------------------------|
| 1 | | |
| 2 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 3 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 4 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 5 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 6 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 7 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 8 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 9 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 10 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 11 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 12 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 13 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 14 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 15 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 16 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 17 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 18 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 19 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 20 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 21 | zinc transporter 10 precursor | Phvul.003G26PTHR11040:SF |
| 22 | BRI1 suppressor 1 (BSU1)-like 3 | Phvul.005G11PTHR11668//I |
| 23 | BRI1 suppressor 1 (BSU1)-like 3 | Phvul.005G11PTHR11668//I |
| 24 | BRI1 suppressor 1 (BSU1)-like 3 | Phvul.005G11PTHR11668//I |
| 25 | BRI1 suppressor 1 (BSU1)-like 3 | Phvul.005G11PTHR11668//I |
| 26 | BRI1 suppressor 1 (BSU1)-like 3 | Phvul.005G11PTHR11668//I |
| 27 | BRI1 suppressor 1 (BSU1)-like 3 | Phvul.005G11PTHR11668//I |
| 28 | BRI1 suppressor 1 (BSU1)-like 3 | Phvul.005G11PTHR11668//I |
| 29 | BRI1 suppressor 1 (BSU1)-like 3 | Phvul.005G11PTHR11668//I |
| 30 | BRI1 suppressor 1 (BSU1)-like 3 | Phvul.005G11PTHR11668//I |
| 31 | BRI1 suppressor 1 (BSU1)-like 3 | Phvul.005G11PTHR11668//I |
| 32 | BRI1 suppressor 1 (BSU1)-like 3 | Phvul.005G11PTHR11668//I |
| 33 | BRI1 suppressor 1 (BSU1)-like 3 | Phvul.005G11PTHR11668//I |
| 34 | BRI1 suppressor 1 (BSU1)-like 3 | Phvul.005G11PTHR11668//I |
| 35 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 36 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 37 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF |
| 38 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF |
| 39 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF |
| 40 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF |
| 41 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF |
| 42 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF |
| 43 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF |
| 44 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF |
| 45 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF |
| 46 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF |
| 47 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF |
| 48 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF |
| 49 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF |
| 50 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF |
| 51 | FASCICLIN-like arabinogalactan-protein 11 | Phvul.006G17PTHR32077:SF |
| 52 | Transcriptional factor B3 family protein / auxin-responsive fa | Phvul.006G18PTHR31384:SF |
| 53 | Transcriptional factor B3 family protein / auxin-responsive fa | Phvul.006G18PTHR31384:SF |
| 54 | Transcriptional factor B3 family protein / auxin-responsive fa | Phvul.006G18PTHR31384:SF |
| 55 | Transcriptional factor B3 family protein / auxin-responsive fa | Phvul.006G18PTHR31384:SF |
| 56 | Transcriptional factor B3 family protein / auxin-responsive fa | Phvul.006G18PTHR31384:SF |
| 57 | Transcriptional factor B3 family protein / auxin-responsive fa | Phvul.006G18PTHR31384:SF |
| 58 | Transcriptional factor B3 family protein / auxin-responsive fa | Phvul.006G18PTHR31384:SF |
| 59 | Transcriptional factor B3 family protein / auxin-responsive fa | Phvul.006G18PTHR31384:SF |
| 60 | Transcriptional factor B3 family protein / auxin-responsive fa | Phvul.006G18PTHR31384:SF |

| | | |
|----|---|-----------------------------|
| 1 | | |
| 2 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 3 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 4 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 5 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 6 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 7 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 8 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 9 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 10 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 11 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 12 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 13 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 14 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 15 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 16 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 17 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 18 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 19 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 20 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 21 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 22 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 23 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 24 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 25 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 26 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 27 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01 PTHR10992//I |
| 28 | like heterochromatin protein (LHP1) | Phvul.009G11 PTHR22812 - (|
| 29 | like heterochromatin protein (LHP1) | Phvul.009G11 PTHR22812 - (|
| 30 | like heterochromatin protein (LHP1) | Phvul.009G11 PTHR22812 - (|
| 31 | like heterochromatin protein (LHP1) | Phvul.009G11 PTHR22812 - (|
| 32 | like heterochromatin protein (LHP1) | Phvul.009G11 PTHR22812 - (|
| 33 | like heterochromatin protein (LHP1) | Phvul.009G11 PTHR22812 - (|
| 34 | like heterochromatin protein (LHP1) | Phvul.009G11 PTHR22812 - (|
| 35 | like heterochromatin protein (LHP1) | Phvul.009G11 PTHR22812 - (|
| 36 | like heterochromatin protein (LHP1) | Phvul.009G11 PTHR22812 - (|
| 37 | like heterochromatin protein (LHP1) | Phvul.009G11 PTHR22812 - (|
| 38 | like heterochromatin protein (LHP1) | Phvul.009G11 PTHR22812 - (|
| 39 | like heterochromatin protein (LHP1) | Phvul.009G11 PTHR22812 - (|
| 40 | like heterochromatin protein (LHP1) | Phvul.009G11 PTHR22812 - (|
| 41 | like heterochromatin protein (LHP1) | Phvul.009G11 PTHR22812 - (|
| 42 | like heterochromatin protein (LHP1) | Phvul.009G11 PTHR22812 - (|
| 43 | BTB/POZ domain-containing protein | Phvul.009G13 K10523 - spec |
| 44 | Plant protein of unknown function (DUF247) | Phvul.010G00 PF03140 - Plai |
| 45 | Plant protein of unknown function (DUF247) | Phvul.010G00 PF03140 - Plai |
| 46 | Plant protein of unknown function (DUF247) | Phvul.010G00 PF03140 - Plai |
| 47 | Plant protein of unknown function (DUF247) | Phvul.010G00 PF03140 - Plai |
| 48 | Plant protein of unknown function (DUF247) | Phvul.010G00 PF03140 - Plai |
| 49 | Plant protein of unknown function (DUF247) | Phvul.010G00 PF03140 - Plai |
| 50 | Plant protein of unknown function (DUF247) | Phvul.010G00 PF03140 - Plai |
| 51 | Plant protein of unknown function (DUF247) | Phvul.010G00 PF03140 - Plai |
| 52 | Plant protein of unknown function (DUF247) | Phvul.010G00 PF03140 - Plai |
| 53 | Plant protein of unknown function (DUF247) | Phvul.010G00 PF03140 - Plai |
| 54 | Plant protein of unknown function (DUF247) | Phvul.010G00 PF03140 - Plai |
| 55 | Plant protein of unknown function (DUF247) | Phvul.010G00 PF03140 - Plai |
| 56 | Plant protein of unknown function (DUF247) | Phvul.010G00 PF03140 - Plai |
| 57 | Plant protein of unknown function (DUF247) | Phvul.010G00 PF03140 - Plai |
| 58 | Plant protein of unknown function (DUF247) | Phvul.010G00 PF03140 - Plai |
| 59 | Plant protein of unknown function (DUF247) | Phvul.010G00 PF03140 - Plai |
| 60 | Leucine-rich repeat transmembrane protein kinase | Phvul.011G06 PF00069//PF1 |
| | Homeobox-leucine zipper family protein / lipid-binding STAR | Phvul.011G07 PF08670 - ME |

| | | |
|----|---|---------------------------|
| 1 | | |
| 2 | Homeobox-leucine zipper family protein / lipid-binding STAR | Phvul.011G07PF08670 - ME |
| 3 | Homeobox-leucine zipper family protein / lipid-binding STAR | Phvul.011G07PF08670 - ME |
| 4 | Homeobox-leucine zipper family protein / lipid-binding STAR | Phvul.011G07PF08670 - ME |
| 5 | Homeobox-leucine zipper family protein / lipid-binding STAR | Phvul.011G07PF08670 - ME |
| 6 | Homeobox-leucine zipper family protein / lipid-binding STAR | Phvul.011G07PF08670 - ME |
| 7 | Homeobox-leucine zipper family protein / lipid-binding STAR | Phvul.011G07PF08670 - ME |
| 8 | Homeobox-leucine zipper family protein / lipid-binding STAR | Phvul.011G07PF08670 - ME |
| 9 | Homeobox-leucine zipper family protein / lipid-binding STAR | Phvul.011G07PF08670 - ME |
| 10 | Homeobox-leucine zipper family protein / lipid-binding STAR | Phvul.011G07PF08670 - ME |
| 11 | Homeobox-leucine zipper family protein / lipid-binding STAR | Phvul.011G07PF08670 - ME |
| 12 | Homeobox-leucine zipper family protein / lipid-binding STAR | Phvul.011G07PF08670 - ME |
| 13 | Homeobox-leucine zipper family protein / lipid-binding STAR | Phvul.011G07PF08670 - ME |
| 14 | Homeobox-leucine zipper family protein / lipid-binding STAR | Phvul.011G07PF08670 - ME |
| 15 | Homeobox-leucine zipper family protein / lipid-binding STAR | Phvul.011G07PF08670 - ME |
| 16 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 17 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 18 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 19 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 20 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 21 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 22 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 23 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 24 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 25 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 26 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 27 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 28 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 29 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 30 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 31 | S-locus lectin protein kinase family protein | Phvul.011G14PF00954//PFC |
| 32 | S-locus lectin protein kinase family protein | Phvul.011G14PF00954//PFC |
| 33 | S-locus lectin protein kinase family protein | Phvul.011G14PF00954//PFC |
| 34 | S-locus lectin protein kinase family protein | Phvul.011G14PF00954//PFC |
| 35 | S-locus lectin protein kinase family protein | Phvul.011G14PF00954//PFC |
| 36 | S-locus lectin protein kinase family protein | Phvul.011G14PF00954//PFC |
| 37 | S-locus lectin protein kinase family protein | Phvul.011G14PF00954//PFC |
| 38 | S-locus lectin protein kinase family protein | Phvul.011G14PF00954//PFC |
| 39 | S-locus lectin protein kinase family protein | Phvul.011G14PF00954//PFC |
| 40 | S-locus lectin protein kinase family protein | Phvul.011G14PF00954//PFC |
| 41 | S-locus lectin protein kinase family protein | Phvul.011G14PF00954//PFC |
| 42 | S-locus lectin protein kinase family protein | Phvul.011G14PF00954//PFC |
| 43 | S-locus lectin protein kinase family protein | Phvul.011G14PF00954//PFC |
| 44 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF |
| 45 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF |
| 46 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF |
| 47 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF |
| 48 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF |
| 49 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF |
| 50 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF |
| 51 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF |
| 52 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF |
| 53 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF |
| 54 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF |
| 55 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF |
| 56 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF |
| 57 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF |
| 58 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF |
| 59 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF |
| 60 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF |
| | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.L00233;PTHR22835//I |

| | | | |
|----|--|-----------------------------|---|
| 1 | | | |
| 2 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.L00233;PTHR22835//I | |
| 3 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.L00233;PTHR22835//I | |
| 4 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.L00233;PTHR22835//I | |
| 5 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.L00233;PTHR22835//I | |
| 6 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.L00233;PTHR22835//I | |
| 7 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.L00233;PTHR22835//I | |
| 8 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.L00233;PTHR22835//I | |
| 9 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.L00233;PTHR22835//I | |
| 10 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.L00233;PTHR22835//I | |
| 11 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.L00233;PTHR22835//I | |
| 12 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.L00233;PTHR22835//I | |
| 13 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.L00233;PTHR22835//I | |
| 14 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.L00233;PTHR22835//I | |
| 15 | Peptidase M20/M25/M40 family protein | Phvul.003G003.5.1.14 - N-ac | |
| 16 | Peptidase M20/M25/M40 family protein | Phvul.003G003.5.1.14 - N-ac | |
| 17 | Peptidase M20/M25/M40 family protein | Phvul.003G003.5.1.14 - N-ac | |
| 18 | Peptidase M20/M25/M40 family protein | Phvul.003G003.5.1.14 - N-ac | |
| 19 | Peptidase M20/M25/M40 family protein | Phvul.003G003.5.1.14 - N-ac | |
| 20 | Peptidase M20/M25/M40 family protein | Phvul.003G003.5.1.14 - N-ac | |
| 21 | Peptidase M20/M25/M40 family protein | Phvul.003G003.5.1.14 - N-ac | |
| 22 | Peptidase M20/M25/M40 family protein | Phvul.003G003.5.1.14 - N-ac | |
| 23 | Peptidase M20/M25/M40 family protein | Phvul.003G003.5.1.14 - N-ac | |
| 24 | Peptidase M20/M25/M40 family protein | Phvul.003G003.5.1.14 - N-ac | |
| 25 | Peptidase M20/M25/M40 family protein | Phvul.003G003.5.1.14 - N-ac | |
| 26 | Peptidase M20/M25/M40 family protein | Phvul.003G003.5.1.14 - N-ac | |
| 27 | Peptidase M20/M25/M40 family protein | Phvul.003G003.5.1.14 - N-ac | |
| 28 | Peptidase M20/M25/M40 family protein | Phvul.003G003.5.1.14 - N-ac | |
| 29 | Peptidase M20/M25/M40 family protein | Phvul.003G003.5.1.14 - N-ac | |
| 30 | Peptidase M20/M25/M40 family protein | Phvul.003G003.5.1.14 - N-ac | |
| 31 | resistance to phytophthora 1 | Phvul.001G14PTHR36359:SF | |
| 32 | histone H4 | Phvul.001G16K11254 - histc | |
| 33 | histone H4 | Phvul.001G16K11254 - histc | |
| 34 | histone H4 | Phvul.001G16K11254 - histc | |
| 35 | histone H4 | Phvul.001G16K11254 - histc | |
| 36 | histone H4 | Phvul.001G16K11254 - histc | |
| 37 | histone H4 | Phvul.001G16K11254 - histc | |
| 38 | histone H4 | Phvul.001G16K11254 - histc | |
| 39 | histone H4 | Phvul.001G16K11254 - histc | |
| 40 | histone H4 | Phvul.001G16K11254 - histc | |
| 41 | histone H4 | Phvul.001G16K11254 - histc | |
| 42 | histone H4 | Phvul.001G16K11254 - histc | |
| 43 | histone H4 | Phvul.001G16K11254 - histc | |
| 44 | histone H4 | Phvul.001G16K11254 - histc | |
| 45 | | 0 | 0 |
| 46 | | 0 | 0 |
| 47 | | 0 | 0 |
| 48 | | 0 | 0 |
| 49 | | 0 | 0 |
| 50 | | 0 | 0 |
| 51 | | 0 | 0 |
| 52 | | 0 | 0 |
| 53 | | 0 | 0 |
| 54 | | 0 | 0 |
| 55 | | 0 | 0 |
| 56 | | 0 | 0 |
| 57 | | 0 | 0 |
| 58 | | | |
| 59 | RING/FYVE/PHD zinc finger superfamily protein | Phvul.001G21PTHR23012:SF | |
| 60 | RING/FYVE/PHD zinc finger superfamily protein | Phvul.001G21PTHR23012:SF | |
| | RING/FYVE/PHD zinc finger superfamily protein | Phvul.001G21PTHR23012:SF | |

| | | |
|----|---|----------------------------|
| 1 | | |
| 2 | protein kinase 1B | Phvul.001G232.7.10.2//2.7. |
| 3 | protein kinase 1B | Phvul.001G232.7.10.2//2.7. |
| 4 | protein kinase 1B | Phvul.001G232.7.10.2//2.7. |
| 5 | protein kinase 1B | Phvul.001G232.7.10.2//2.7. |
| 6 | protein kinase 1B | Phvul.001G232.7.10.2//2.7. |
| 7 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 8 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 9 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 10 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 11 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 12 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 13 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 14 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 15 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 16 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 17 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 18 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 19 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 20 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 21 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 22 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 23 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 24 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 25 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 26 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 27 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 28 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 29 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 30 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 31 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 32 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 33 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 34 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 35 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 36 | O-acetyltransferase family protein | Phvul.002G19PTHR13533:SF |
| 37 | O-acetyltransferase family protein | Phvul.002G19PTHR13533:SF |
| 38 | O-acetyltransferase family protein | Phvul.002G19PTHR13533:SF |
| 39 | O-acetyltransferase family protein | Phvul.002G19PTHR13533:SF |
| 40 | O-acetyltransferase family protein | Phvul.002G19PTHR13533:SF |
| 41 | O-acetyltransferase family protein | Phvul.002G19PTHR13533:SF |
| 42 | O-acetyltransferase family protein | Phvul.002G19PTHR13533:SF |
| 43 | O-acetyltransferase family protein | Phvul.002G19PTHR13533:SF |
| 44 | O-acetyltransferase family protein | Phvul.002G19PTHR13533:SF |
| 45 | O-acetyltransferase family protein | Phvul.002G19PTHR13533:SF |
| 46 | O-acetyltransferase family protein | Phvul.002G19PTHR13533:SF |
| 47 | O-acetyltransferase family protein | Phvul.002G19PTHR13533:SF |
| 48 | O-acetyltransferase family protein | Phvul.002G19PTHR13533:SF |
| 49 | Aldolase-type TIM barrel family protein | Phvul.002G214.4.1.19 - Pho |
| 50 | Aldolase-type TIM barrel family protein | Phvul.002G214.4.1.19 - Pho |
| 51 | Aldolase-type TIM barrel family protein | Phvul.002G214.4.1.19 - Pho |
| 52 | Aldolase-type TIM barrel family protein | Phvul.002G214.4.1.19 - Pho |
| 53 | Aldolase-type TIM barrel family protein | Phvul.002G214.4.1.19 - Pho |
| 54 | Aldolase-type TIM barrel family protein | Phvul.002G214.4.1.19 - Pho |
| 55 | Aldolase-type TIM barrel family protein | Phvul.002G214.4.1.19 - Pho |
| 56 | Aldolase-type TIM barrel family protein | Phvul.002G214.4.1.19 - Pho |
| 57 | Aldolase-type TIM barrel family protein | Phvul.002G214.4.1.19 - Pho |
| 58 | Aldolase-type TIM barrel family protein | Phvul.002G214.4.1.19 - Pho |
| 59 | Aldolase-type TIM barrel family protein | Phvul.002G214.4.1.19 - Pho |
| 60 | Aldolase-type TIM barrel family protein | Phvul.002G214.4.1.19 - Pho |

| | | |
|----|--|----------------------------|
| 1 | | |
| 2 | Aldolase-type TIM barrel family protein | Phvul.002G214.4.1.19 - Pho |
| 3 | ABC2 homolog 13 | Phvul.002G26PTHR10566:SF |
| 4 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 5 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 6 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 7 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 8 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 9 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 10 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 11 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 12 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 13 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 14 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 15 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 16 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 17 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 18 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 19 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 20 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 21 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 22 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 23 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 24 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 25 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 26 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 27 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 28 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 29 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 30 | Nucleic acid-binding, OB-fold-like protein | Phvul.002G33PTHR14513 - I |
| 31 | allene oxide cyclase 3 | Phvul.003G11K10525 - allen |
| 32 | allene oxide cyclase 3 | Phvul.003G11K10525 - allen |
| 33 | allene oxide cyclase 3 | Phvul.003G11K10525 - allen |
| 34 | allene oxide cyclase 3 | Phvul.003G11K10525 - allen |
| 35 | allene oxide cyclase 3 | Phvul.003G11K10525 - allen |
| 36 | allene oxide cyclase 3 | Phvul.003G11K10525 - allen |
| 37 | allene oxide cyclase 3 | Phvul.003G11K10525 - allen |
| 38 | allene oxide cyclase 3 | Phvul.003G11K10525 - allen |
| 39 | allene oxide cyclase 3 | Phvul.003G11K10525 - allen |
| 40 | allene oxide cyclase 3 | Phvul.003G11K10525 - allen |
| 41 | allene oxide cyclase 3 | Phvul.003G11K10525 - allen |
| 42 | allene oxide cyclase 3 | Phvul.003G11K10525 - allen |
| 43 | allene oxide cyclase 3 | Phvul.003G11K10525 - allen |
| 44 | calcium-dependent lipid-binding family protein | Phvul.003G11PTHR16166:SF |
| 45 | Leucine-rich receptor-like protein kinase family protein | Phvul.003G20PF00069//PFC |
| 46 | Leucine-rich receptor-like protein kinase family protein | Phvul.003G20PF00069//PFC |
| 47 | Leucine-rich receptor-like protein kinase family protein | Phvul.003G20PF00069//PFC |
| 48 | Leucine-rich receptor-like protein kinase family protein | Phvul.003G20PF00069//PFC |
| 49 | Leucine-rich receptor-like protein kinase family protein | Phvul.003G20PF00069//PFC |
| 50 | Leucine-rich receptor-like protein kinase family protein | Phvul.003G20PF00069//PFC |
| 51 | Leucine-rich receptor-like protein kinase family protein | Phvul.003G20PF00069//PFC |
| 52 | Leucine-rich receptor-like protein kinase family protein | Phvul.003G20PF00069//PFC |
| 53 | Leucine-rich receptor-like protein kinase family protein | Phvul.003G20PF00069//PFC |
| 54 | Leucine-rich receptor-like protein kinase family protein | Phvul.003G20PF00069//PFC |
| 55 | Leucine-rich receptor-like protein kinase family protein | Phvul.003G20PF00069//PFC |
| 56 | Leucine-rich receptor-like protein kinase family protein | Phvul.003G20PF00069//PFC |
| 57 | Leucine-rich receptor-like protein kinase family protein | Phvul.003G20PF00069//PFC |
| 58 | Leucine-rich receptor-like protein kinase family protein | Phvul.003G20PF00069//PFC |
| 59 | Leucine-rich receptor-like protein kinase family protein | Phvul.003G20PF00069//PFC |
| 60 | NAC domain containing protein 96 | Phvul.003G22PTHR31989:SF |
| | NAC domain containing protein 96 | Phvul.003G22PTHR31989:SF |

| | | |
|----|------------------------------------|----------------------------|
| 1 | | |
| 2 | hypothetical protein 1 | Phvul.004G03PTHR13018//I |
| 3 | hypothetical protein 1 | Phvul.004G03PTHR13018//I |
| 4 | hypothetical protein 1 | Phvul.004G03PTHR13018//I |
| 5 | hypothetical protein 1 | Phvul.004G03PTHR13018//I |
| 6 | hypothetical protein 1 | Phvul.004G03PTHR13018//I |
| 7 | hypothetical protein 1 | Phvul.004G03PTHR13018//I |
| 8 | hypothetical protein 1 | Phvul.004G03PTHR13018//I |
| 9 | hypothetical protein 1 | Phvul.004G03PTHR13018//I |
| 10 | hypothetical protein 1 | Phvul.004G03PTHR13018//I |
| 11 | hypothetical protein 1 | Phvul.004G03PTHR13018//I |
| 12 | hypothetical protein 1 | Phvul.004G03PTHR13018//I |
| 13 | hypothetical protein 1 | Phvul.004G03PTHR13018//I |
| 14 | hypothetical protein 1 | Phvul.004G03PTHR13018//I |
| 15 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-b |
| 16 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-b |
| 17 | | |
| 18 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 19 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 20 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 21 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 22 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 23 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 24 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 25 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 26 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 27 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 28 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 29 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 30 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 31 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 32 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 33 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 34 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 35 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 36 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 37 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 38 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 39 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 40 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 41 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 42 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 43 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| 44 | receptor kinase 3 | Phvul.005G08PF00954//PFC |
| 45 | receptor kinase 3 | Phvul.005G08PF00954//PFC |
| 46 | receptor kinase 3 | Phvul.005G08PF00954//PFC |
| 47 | receptor kinase 3 | Phvul.005G08PF00954//PFC |
| 48 | receptor kinase 3 | Phvul.005G08PF00954//PFC |
| 49 | receptor kinase 3 | Phvul.005G08PF00954//PFC |
| 50 | receptor kinase 3 | Phvul.005G08PF00954//PFC |
| 51 | receptor kinase 3 | Phvul.005G08PF00954//PFC |
| 52 | receptor kinase 3 | Phvul.005G08PF00954//PFC |
| 53 | receptor kinase 3 | Phvul.005G08PF00954//PFC |
| 54 | receptor kinase 3 | Phvul.005G08PF00954//PFC |
| 55 | receptor kinase 3 | Phvul.005G08PF00954//PFC |
| 56 | receptor kinase 3 | Phvul.005G08PF00954//PFC |
| 57 | receptor kinase 3 | Phvul.005G08PF00954//PFC |
| 58 | Coatomer, beta\` subunit | Phvul.005G17KOG0265//KC |
| 59 | Coatomer, beta\` subunit | Phvul.005G17KOG0265//KC |
| 60 | Coatomer, beta\` subunit | Phvul.005G17KOG0265//KC |

| | | |
|----|--|-----------------------------|
| 1 | | |
| 2 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 3 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 4 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 5 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 6 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 7 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 8 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 9 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 10 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 11 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 12 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 13 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 14 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 15 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 16 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 17 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 18 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 19 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 20 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 21 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 22 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 23 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 24 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 25 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 26 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 27 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 28 | Coatomer, beta\' subunit | Phvul.005G17KOG0265//KC |
| 29 | vacuoleless1 (VCL1) | Phvul.006G02PTHR12811 - \ |
| 30 | | |
| 31 | cleavage and polyadenylation specificity factor 30 | Phvul.006G13PTHR12357:SF |
| 32 | cleavage and polyadenylation specificity factor 30 | Phvul.006G13PTHR12357:SF |
| 33 | cleavage and polyadenylation specificity factor 30 | Phvul.006G13PTHR12357:SF |
| 34 | cleavage and polyadenylation specificity factor 30 | Phvul.006G13PTHR12357:SF |
| 35 | cleavage and polyadenylation specificity factor 30 | Phvul.006G13PTHR12357:SF |
| 36 | cleavage and polyadenylation specificity factor 30 | Phvul.006G13PTHR12357:SF |
| 37 | cleavage and polyadenylation specificity factor 30 | Phvul.006G13PTHR12357:SF |
| 38 | cleavage and polyadenylation specificity factor 30 | Phvul.006G13PTHR12357:SF |
| 39 | cleavage and polyadenylation specificity factor 30 | Phvul.006G13PTHR12357:SF |
| 40 | cleavage and polyadenylation specificity factor 30 | Phvul.006G13PTHR12357:SF |
| 41 | cleavage and polyadenylation specificity factor 30 | Phvul.006G13PTHR12357:SF |
| 42 | cleavage and polyadenylation specificity factor 30 | Phvul.006G13PTHR12357:SF |
| 43 | cleavage and polyadenylation specificity factor 30 | Phvul.006G13PTHR12357:SF |
| 44 | cleavage and polyadenylation specificity factor 30 | Phvul.006G13PTHR12357:SF |
| 45 | Nucleotide-sugar transporter family protein | Phvul.006G13PTHR11132//I |
| 46 | | |
| 47 | Transcriptional factor B3 family protein / auxin-responsive fa | Phvul.006G18PTHR31384:SF |
| 48 | leucine-rich repeat transmembrane protein kinase family prc | Phvul.007G02PF00560//PFC |
| 49 | leucine-rich repeat transmembrane protein kinase family prc | Phvul.007G02PF00560//PFC |
| 50 | leucine-rich repeat transmembrane protein kinase family prc | Phvul.007G02PF00560//PFC |
| 51 | leucine-rich repeat transmembrane protein kinase family prc | Phvul.007G02PF00560//PFC |
| 52 | leucine-rich repeat transmembrane protein kinase family prc | Phvul.007G02PF00560//PFC |
| 53 | leucine-rich repeat transmembrane protein kinase family prc | Phvul.007G02PF00560//PFC |
| 54 | leucine-rich repeat transmembrane protein kinase family prc | Phvul.007G02PF00560//PFC |
| 55 | leucine-rich repeat transmembrane protein kinase family prc | Phvul.007G02PF00560//PFC |
| 56 | leucine-rich repeat transmembrane protein kinase family prc | Phvul.007G02PF00560//PFC |
| 57 | leucine-rich repeat transmembrane protein kinase family prc | Phvul.007G02PF00560//PFC |
| 58 | leucine-rich repeat transmembrane protein kinase family prc | Phvul.007G02PF00560//PFC |
| 59 | leucine-rich repeat transmembrane protein kinase family prc | Phvul.007G02PF00560//PFC |
| 60 | leucine-rich repeat transmembrane protein kinase family prc | Phvul.007G02PF00560//PFC |
| | methyltransferases | Phvul.007G042.1.1.193 - 16: |

| | | | |
|----|--|---------------------------|---|
| 1 | | | |
| 2 | Mitochondrial transcription termination factor family protei | Phvul.007G08PTHR13068:SF | |
| 3 | Mitochondrial transcription termination factor family protei | Phvul.007G08PTHR13068:SF | |
| 4 | Mitochondrial transcription termination factor family protei | Phvul.007G08PTHR13068:SF | |
| 5 | Mitochondrial transcription termination factor family protei | Phvul.007G08PTHR13068:SF | |
| 6 | Mitochondrial transcription termination factor family protei | Phvul.007G08PTHR13068:SF | |
| 7 | Mitochondrial transcription termination factor family protei | Phvul.007G08PTHR13068:SF | |
| 8 | Mitochondrial transcription termination factor family protei | Phvul.007G08PTHR13068:SF | |
| 9 | Mitochondrial transcription termination factor family protei | Phvul.007G08PTHR13068:SF | |
| 10 | Mitochondrial transcription termination factor family protei | Phvul.007G08PTHR13068:SF | |
| 11 | Mitochondrial transcription termination factor family protei | Phvul.007G08PTHR13068:SF | |
| 12 | Mitochondrial transcription termination factor family protei | Phvul.007G08PTHR13068:SF | |
| 13 | Mitochondrial transcription termination factor family protei | Phvul.007G08PTHR13068:SF | |
| 14 | Mitochondrial transcription termination factor family protei | Phvul.007G08PTHR13068:SF | |
| 15 | Mitochondrial transcription termination factor family protei | Phvul.007G08PTHR13068:SF | |
| 16 | Mitochondrial transcription termination factor family protei | Phvul.007G08PTHR13068:SF | |
| 17 | Mitochondrial transcription termination factor family protei | Phvul.007G08PTHR13068:SF | |
| 18 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 19 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 20 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 21 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 22 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 23 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 24 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 25 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 26 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 27 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 28 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 29 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 30 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 31 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 32 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 33 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 34 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 35 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 36 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 37 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 38 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 39 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 40 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 41 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 42 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 43 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | |
| 44 | | 0 | 0 |
| 45 | | 0 | 0 |
| 46 | | 0 | 0 |
| 47 | | 0 | 0 |
| 48 | | 0 | 0 |
| 49 | | 0 | 0 |
| 50 | | 0 | 0 |
| 51 | | 0 | 0 |
| 52 | | 0 | 0 |
| 53 | | 0 | 0 |
| 54 | | 0 | 0 |
| 55 | | 0 | 0 |
| 56 | | 0 | 0 |
| 57 | | 0 | 0 |
| 58 | | 0 | 0 |
| 59 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alph | |
| 60 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alph | |
| | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alph | |

| | | |
|----|---|-----------------------------|
| 1 | | |
| 2 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 3 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 4 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 5 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 6 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 7 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 8 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 9 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 10 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 11 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 12 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 13 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 14 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 15 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 16 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 17 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 18 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 19 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 20 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 21 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 22 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 23 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 24 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 25 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 26 | alpha-soluble NSF attachment protein 2 | Phvul.008G08K15296 - alpha |
| 27 | Protein kinase superfamily protein with octicosapeptide/Phc | Phvul.008G12 PTHR23257//I |
| 28 | Protein kinase superfamily protein with octicosapeptide/Phc | Phvul.008G12 PTHR23257//I |
| 29 | Protein kinase superfamily protein with octicosapeptide/Phc | Phvul.008G12 PTHR23257//I |
| 30 | Protein kinase superfamily protein with octicosapeptide/Phc | Phvul.008G12 PTHR23257//I |
| 31 | Protein kinase superfamily protein with octicosapeptide/Phc | Phvul.008G12 PTHR23257//I |
| 32 | Protein kinase superfamily protein with octicosapeptide/Phc | Phvul.008G12 PTHR23257//I |
| 33 | Protein kinase superfamily protein with octicosapeptide/Phc | Phvul.008G12 PTHR23257//I |
| 34 | Protein kinase superfamily protein with octicosapeptide/Phc | Phvul.008G12 PTHR23257//I |
| 35 | Protein kinase superfamily protein with octicosapeptide/Phc | Phvul.008G12 PTHR23257//I |
| 36 | Protein kinase superfamily protein with octicosapeptide/Phc | Phvul.008G12 PTHR23257//I |
| 37 | Protein kinase superfamily protein with octicosapeptide/Phc | Phvul.008G12 PTHR23257//I |
| 38 | Protein kinase superfamily protein with octicosapeptide/Phc | Phvul.008G12 PTHR23257//I |
| 39 | Protein kinase superfamily protein with octicosapeptide/Phc | Phvul.008G12 PTHR23257//I |
| 40 | Protein kinase superfamily protein with octicosapeptide/Phc | Phvul.008G12 PTHR23257//I |
| 41 | Coproporphyrinogen III oxidase | Phvul.008G281.3.3.3 - Copro |
| 42 | Coproporphyrinogen III oxidase | Phvul.008G281.3.3.3 - Copro |
| 43 | Coproporphyrinogen III oxidase | Phvul.008G281.3.3.3 - Copro |
| 44 | Coproporphyrinogen III oxidase | Phvul.008G281.3.3.3 - Copro |
| 45 | Coproporphyrinogen III oxidase | Phvul.008G281.3.3.3 - Copro |
| 46 | Coproporphyrinogen III oxidase | Phvul.008G281.3.3.3 - Copro |
| 47 | Coproporphyrinogen III oxidase | Phvul.008G281.3.3.3 - Copro |
| 48 | Coproporphyrinogen III oxidase | Phvul.008G281.3.3.3 - Copro |
| 49 | Coproporphyrinogen III oxidase | Phvul.008G281.3.3.3 - Copro |
| 50 | Coproporphyrinogen III oxidase | Phvul.008G281.3.3.3 - Copro |
| 51 | Coproporphyrinogen III oxidase | Phvul.008G281.3.3.3 - Copro |
| 52 | Coproporphyrinogen III oxidase | Phvul.008G281.3.3.3 - Copro |
| 53 | Coproporphyrinogen III oxidase | Phvul.008G281.3.3.3 - Copro |
| 54 | Coproporphyrinogen III oxidase | Phvul.008G281.3.3.3 - Copro |
| 55 | Coproporphyrinogen III oxidase | Phvul.008G281.3.3.3 - Copro |
| 56 | phosphorylcholine cytidylyltransferase | Phvul.008G292.7.7.15 - Cho |
| 57 | phosphorylcholine cytidylyltransferase | Phvul.008G292.7.7.15 - Cho |
| 58 | phosphorylcholine cytidylyltransferase | Phvul.008G292.7.7.15 - Cho |
| 59 | phosphorylcholine cytidylyltransferase | Phvul.008G292.7.7.15 - Cho |
| 60 | phosphorylcholine cytidylyltransferase | Phvul.008G292.7.7.15 - Cho |

| | | |
|----|--|----------------------------|
| 1 | | |
| 2 | phosphorylcholine cytidylyltransferase | Phvul.008G292.7.7.15 - Cho |
| 3 | phosphorylcholine cytidylyltransferase | Phvul.008G292.7.7.15 - Cho |
| 4 | phosphorylcholine cytidylyltransferase | Phvul.008G292.7.7.15 - Cho |
| 5 | phosphorylcholine cytidylyltransferase | Phvul.008G292.7.7.15 - Cho |
| 6 | phosphorylcholine cytidylyltransferase | Phvul.008G292.7.7.15 - Cho |
| 7 | phosphorylcholine cytidylyltransferase | Phvul.008G292.7.7.15 - Cho |
| 8 | phosphorylcholine cytidylyltransferase | Phvul.008G292.7.7.15 - Cho |
| 9 | like heterochromatin protein (LHP1) | Phvul.009G11PTHR22812 - (|
| 10 | GDSL-motif lipase 5 | Phvul.010G12PTHR22835:SF |
| 11 | GDSL-motif lipase 5 | Phvul.010G12PTHR22835:SF |
| 12 | GDSL-motif lipase 5 | Phvul.010G12PTHR22835:SF |
| 13 | GDSL-motif lipase 5 | Phvul.010G12PTHR22835:SF |
| 14 | GDSL-motif lipase 5 | Phvul.010G12PTHR22835:SF |
| 15 | GDSL-motif lipase 5 | Phvul.010G12PTHR22835:SF |
| 16 | GDSL-motif lipase 5 | Phvul.010G12PTHR22835:SF |
| 17 | GDSL-motif lipase 5 | Phvul.010G12PTHR22835:SF |
| 18 | GDSL-motif lipase 5 | Phvul.010G12PTHR22835:SF |
| 19 | GDSL-motif lipase 5 | Phvul.010G12PTHR22835:SF |
| 20 | GDSL-motif lipase 5 | Phvul.010G12PTHR22835:SF |
| 21 | GDSL-motif lipase 5 | Phvul.010G12PTHR22835:SF |
| 22 | GDSL-motif lipase 5 | Phvul.010G12PTHR22835:SF |
| 23 | GDSL-motif lipase 5 | Phvul.010G12PTHR22835:SF |
| 24 | Plant protein of unknown function (DUF247) | Phvul.010G15PF03140 - Plai |
| 25 | Protein kinase superfamily protein | Phvul.011G012.7.11.1 - Non |
| 26 | Protein kinase superfamily protein | Phvul.011G012.7.11.1 - Non |
| 27 | Protein kinase superfamily protein | Phvul.011G012.7.11.1 - Non |
| 28 | Protein kinase superfamily protein | Phvul.011G012.7.11.1 - Non |
| 29 | Protein kinase superfamily protein | Phvul.011G012.7.11.1 - Non |
| 30 | Protein kinase superfamily protein | Phvul.011G012.7.11.1 - Non |
| 31 | Protein kinase superfamily protein | Phvul.011G012.7.11.1 - Non |
| 32 | Protein kinase superfamily protein | Phvul.011G012.7.11.1 - Non |
| 33 | Protein kinase superfamily protein | Phvul.011G012.7.11.1 - Non |
| 34 | Protein kinase superfamily protein | Phvul.011G012.7.11.1 - Non |
| 35 | Protein kinase superfamily protein | Phvul.011G012.7.11.1 - Non |
| 36 | Protein kinase superfamily protein | Phvul.011G012.7.11.1 - Non |
| 37 | Protein kinase superfamily protein | Phvul.011G012.7.11.1 - Non |
| 38 | Protein kinase superfamily protein | Phvul.011G012.7.11.1 - Non |
| 39 | cytochrome c biogenesis protein family | Phvul.011G04K07399 - cyto |
| 40 | cytochrome c biogenesis protein family | Phvul.011G04K07399 - cyto |
| 41 | Leucine-rich repeat transmembrane protein kinase | Phvul.011G06PF00069//PF1 |
| 42 | Leucine-rich repeat transmembrane protein kinase | Phvul.011G06PF00069//PF1 |
| 43 | Leucine-rich repeat transmembrane protein kinase | Phvul.011G06PF00069//PF1 |
| 44 | Leucine-rich repeat transmembrane protein kinase | Phvul.011G06PF00069//PF1 |
| 45 | Leucine-rich repeat transmembrane protein kinase | Phvul.011G06PF00069//PF1 |
| 46 | Leucine-rich repeat transmembrane protein kinase | Phvul.011G06PF00069//PF1 |
| 47 | Leucine-rich repeat transmembrane protein kinase | Phvul.011G06PF00069//PF1 |
| 48 | Leucine-rich repeat transmembrane protein kinase | Phvul.011G06PF00069//PF1 |
| 49 | Leucine-rich repeat transmembrane protein kinase | Phvul.011G06PF00069//PF1 |
| 50 | Leucine-rich repeat transmembrane protein kinase | Phvul.011G06PF00069//PF1 |
| 51 | Leucine-rich repeat transmembrane protein kinase | Phvul.011G06PF00069//PF1 |
| 52 | Leucine-rich repeat transmembrane protein kinase | Phvul.011G06PF00069//PF1 |
| 53 | Leucine-rich repeat transmembrane protein kinase | Phvul.011G06PF00069//PF1 |
| 54 | Leucine-rich repeat transmembrane protein kinase | Phvul.011G06PF00069//PF1 |
| 55 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 56 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 57 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 58 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 59 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |
| 60 | senescence-associated gene 12 | Phvul.011G12PTHR12411//I |

| | | |
|----|--|---------------------------|
| 1 | | |
| 2 | S-locus lectin protein kinase family protein | Phvul.011G16PTHR27002:SF |
| 3 | S-locus lectin protein kinase family protein | Phvul.011G16PTHR27002:SF |
| 4 | S-locus lectin protein kinase family protein | Phvul.011G20PF00954//PFC |
| 5 | S-locus lectin protein kinase family protein | Phvul.011G20PF00954//PFC |
| 6 | S-locus lectin protein kinase family protein | Phvul.011G20PF00954//PFC |
| 7 | S-locus lectin protein kinase family protein | Phvul.011G20PF00954//PFC |
| 8 | S-locus lectin protein kinase family protein | Phvul.011G20PF00954//PFC |
| 9 | S-locus lectin protein kinase family protein | Phvul.011G20PF00954//PFC |
| 10 | S-locus lectin protein kinase family protein | Phvul.011G20PF00954//PFC |
| 11 | S-locus lectin protein kinase family protein | Phvul.011G20PF00954//PFC |
| 12 | S-locus lectin protein kinase family protein | Phvul.011G20PF00954//PFC |
| 13 | S-locus lectin protein kinase family protein | Phvul.011G20PF00954//PFC |
| 14 | S-locus lectin protein kinase family protein | Phvul.011G20PF00954//PFC |
| 15 | S-locus lectin protein kinase family protein | Phvul.011G20PF00954//PFC |
| 16 | S-locus lectin protein kinase family protein | Phvul.011G20PF00954//PFC |
| 17 | S-locus lectin protein kinase family protein | Phvul.011G20PF00954//PFC |
| 18 | S-locus lectin protein kinase family protein | Phvul.011G20PF00954//PFC |
| 19 | RNI-like superfamily protein | Phvul.001G15K10268 - F-bo |
| 20 | RNI-like superfamily protein | Phvul.001G15K10268 - F-bo |
| 21 | RNI-like superfamily protein | Phvul.001G15K10268 - F-bo |
| 22 | RNI-like superfamily protein | Phvul.001G15K10268 - F-bo |
| 23 | RNI-like superfamily protein | Phvul.001G15K10268 - F-bo |
| 24 | RNI-like superfamily protein | Phvul.001G15K10268 - F-bo |
| 25 | RNI-like superfamily protein | Phvul.001G15K10268 - F-bo |
| 26 | RNI-like superfamily protein | Phvul.001G15K10268 - F-bo |
| 27 | RNI-like superfamily protein | Phvul.001G15K10268 - F-bo |
| 28 | RNI-like superfamily protein | Phvul.001G15K10268 - F-bo |
| 29 | RNI-like superfamily protein | Phvul.001G15K10268 - F-bo |
| 30 | RNI-like superfamily protein | Phvul.001G15K10268 - F-bo |
| 31 | RNI-like superfamily protein | Phvul.001G15K10268 - F-bo |
| 32 | RNI-like superfamily protein | Phvul.001G15K10268 - F-bo |
| 33 | C2H2-like zinc finger protein | Phvul.001G17PTHR10593:SF |
| 34 | C2H2-like zinc finger protein | Phvul.001G17PTHR10593:SF |
| 35 | C2H2-like zinc finger protein | Phvul.001G17PTHR10593:SF |
| 36 | C2H2-like zinc finger protein | Phvul.001G17PTHR10593:SF |
| 37 | C2H2-like zinc finger protein | Phvul.001G17PTHR10593:SF |
| 38 | C2H2-like zinc finger protein | Phvul.001G17PTHR10593:SF |
| 39 | C2H2-like zinc finger protein | Phvul.001G17PTHR10593:SF |
| 40 | C2H2-like zinc finger protein | Phvul.001G17PTHR10593:SF |
| 41 | C2H2-like zinc finger protein | Phvul.001G17PTHR10593:SF |
| 42 | C2H2-like zinc finger protein | Phvul.001G17PTHR10593:SF |
| 43 | C2H2-like zinc finger protein | Phvul.001G17PTHR10593:SF |
| 44 | C2H2-like zinc finger protein | Phvul.001G17PTHR10593:SF |
| 45 | C2H2-like zinc finger protein | Phvul.001G17PTHR10593:SF |
| 46 | C2H2-like zinc finger protein | Phvul.001G17PTHR10593:SF |
| 47 | C2H2-like zinc finger protein | Phvul.001G17PTHR10593:SF |
| 48 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 49 | SKU5 similar 12 | Phvul.001G26PTHR11709:SF |
| 50 | plant U-box 49 | Phvul.002G01K10598 - pept |
| 51 | plant U-box 49 | Phvul.002G01K10598 - pept |
| 52 | plant U-box 49 | Phvul.002G01K10598 - pept |
| 53 | plant U-box 49 | Phvul.002G01K10598 - pept |
| 54 | plant U-box 49 | Phvul.002G01K10598 - pept |
| 55 | plant U-box 49 | Phvul.002G01K10598 - pept |
| 56 | plant U-box 49 | Phvul.002G01K10598 - pept |
| 57 | plant U-box 49 | Phvul.002G01K10598 - pept |
| 58 | plant U-box 49 | Phvul.002G01K10598 - pept |
| 59 | plant U-box 49 | Phvul.002G01K10598 - pept |
| 60 | plant U-box 49 | Phvul.002G01K10598 - pept |

| | | |
|----|--|-----------------------------|
| 1 | | |
| 2 | plant U-box 49 | Phvul.002G01K10598 - pept |
| 3 | plant U-box 49 | Phvul.002G01K10598 - pept |
| 4 | plant U-box 49 | Phvul.002G01K10598 - pept |
| 5 | | |
| 6 | FAD-binding Berberine family protein | Phvul.002G191.3.3.8 - Tetra |
| 7 | FAD-binding Berberine family protein | Phvul.002G191.3.3.8 - Tetra |
| 8 | FAD-binding Berberine family protein | Phvul.002G191.3.3.8 - Tetra |
| 9 | | |
| 10 | FAD-binding Berberine family protein | Phvul.002G191.3.3.8 - Tetra |
| 11 | FAD-binding Berberine family protein | Phvul.002G191.3.3.8 - Tetra |
| 12 | FAD-binding Berberine family protein | Phvul.002G191.3.3.8 - Tetra |
| 13 | FAD-binding Berberine family protein | Phvul.002G191.3.3.8 - Tetra |
| 14 | FAD-binding Berberine family protein | Phvul.002G191.3.3.8 - Tetra |
| 15 | FAD-binding Berberine family protein | Phvul.002G191.3.3.8 - Tetra |
| 16 | FAD-binding Berberine family protein | Phvul.002G191.3.3.8 - Tetra |
| 17 | FAD-binding Berberine family protein | Phvul.002G191.3.3.8 - Tetra |
| 18 | FAD-binding Berberine family protein | Phvul.002G191.3.3.8 - Tetra |
| 19 | FAD-binding Berberine family protein | Phvul.002G191.3.3.8 - Tetra |
| 20 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PTHR27007:SF |
| 21 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PTHR27007:SF |
| 22 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PTHR27007:SF |
| 23 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PTHR27007:SF |
| 24 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PTHR27007:SF |
| 25 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PTHR27007:SF |
| 26 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PTHR27007:SF |
| 27 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PTHR27007:SF |
| 28 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PTHR27007:SF |
| 29 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PTHR27007:SF |
| 30 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PTHR27007:SF |
| 31 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PTHR27007:SF |
| 32 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PTHR27007:SF |
| 33 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PF00139//PFC |
| 34 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PF00139//PFC |
| 35 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PF00139//PFC |
| 36 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PF00139//PFC |
| 37 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PF00139//PFC |
| 38 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PF00139//PFC |
| 39 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PF00139//PFC |
| 40 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PF00139//PFC |
| 41 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PF00139//PFC |
| 42 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PF00139//PFC |
| 43 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PF00139//PFC |
| 44 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PF00139//PFC |
| 45 | Concanavalin A-like lectin protein kinase family protein | Phvul.002G21PF00139//PFC |
| 46 | | |
| 47 | ABC2 homolog 13 | Phvul.002G26PTHR10566:SF |
| 48 | ABC2 homolog 13 | Phvul.002G26PTHR10566:SF |
| 49 | ABC2 homolog 13 | Phvul.002G26PTHR10566:SF |
| 50 | | |
| 51 | ABC2 homolog 13 | Phvul.002G26PTHR10566:SF |
| 52 | ABC2 homolog 13 | Phvul.002G26PTHR10566:SF |
| 53 | ABC2 homolog 13 | Phvul.002G26PTHR10566:SF |
| 54 | ABC2 homolog 13 | Phvul.002G26PTHR10566:SF |
| 55 | ABC2 homolog 13 | Phvul.002G26PTHR10566:SF |
| 56 | ABC2 homolog 13 | Phvul.002G26PTHR10566:SF |
| 57 | ABC2 homolog 13 | Phvul.002G26PTHR10566:SF |
| 58 | ABC2 homolog 13 | Phvul.002G26PTHR10566:SF |
| 59 | ABC2 homolog 13 | Phvul.002G26PTHR10566:SF |
| 60 | ABC2 homolog 13 | Phvul.002G26PTHR10566:SF |
| | diacylglycerol kinase 2 | Phvul.002G27PTHR11255:SF |

| | | |
|----|-------------------------------------|---------------------------|
| 1 | | |
| 2 | diacylglycerol kinase 2 | Phvul.002G27PTHR11255:SI |
| 3 | diacylglycerol kinase 2 | Phvul.002G27PTHR11255:SI |
| 4 | endonucleases | Phvul.002G30PF03161 - LAC |
| 5 | | |
| 6 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 7 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 8 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 9 | | |
| 10 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 11 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 12 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 13 | | |
| 14 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 15 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 16 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 17 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 18 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 19 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 20 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 21 | | |
| 22 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 23 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 24 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 25 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 26 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 27 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 28 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 29 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 30 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 31 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 32 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 33 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 34 | ethylene-forming enzyme | Phvul.002G32K05933 - amir |
| 35 | heptahelical transmembrane protein1 | Phvul.003G17PTHR20855//I |
| 36 | heptahelical transmembrane protein1 | Phvul.003G17PTHR20855//I |
| 37 | heptahelical transmembrane protein1 | Phvul.003G17PTHR20855//I |
| 38 | heptahelical transmembrane protein1 | Phvul.003G17PTHR20855//I |
| 39 | heptahelical transmembrane protein1 | Phvul.003G17PTHR20855//I |
| 40 | heptahelical transmembrane protein1 | Phvul.003G17PTHR20855//I |
| 41 | heptahelical transmembrane protein1 | Phvul.003G17PTHR20855//I |
| 42 | heptahelical transmembrane protein1 | Phvul.003G17PTHR20855//I |
| 43 | heptahelical transmembrane protein1 | Phvul.003G17PTHR20855//I |
| 44 | heptahelical transmembrane protein1 | Phvul.003G17PTHR20855//I |
| 45 | heptahelical transmembrane protein1 | Phvul.003G17PTHR20855//I |
| 46 | heptahelical transmembrane protein1 | Phvul.003G17PTHR20855//I |
| 47 | heptahelical transmembrane protein1 | Phvul.003G17PTHR20855//I |
| 48 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SI |
| 49 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SI |
| 50 | | |
| 51 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SI |
| 52 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SI |
| 53 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SI |
| 54 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SI |
| 55 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SI |
| 56 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SI |
| 57 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SI |
| 58 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SI |
| 59 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SI |
| 60 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SI |
| | cycling DOF factor 3 | Phvul.003G18PTHR31089:SI |

| | | | |
|----|--|--------------------------|---|
| 1 | | | |
| 2 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SF | |
| 3 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SF | |
| 4 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SF | |
| 5 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SF | |
| 6 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SF | |
| 7 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SF | |
| 8 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SF | |
| 9 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SF | |
| 10 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SF | |
| 11 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SF | |
| 12 | cycling DOF factor 3 | Phvul.003G18PTHR31089:SF | |
| 13 | | | |
| 14 | Leucine-rich repeat transmembrane protein kinase | Phvul.003G20PF00560//PFC | |
| 15 | Leucine-rich repeat transmembrane protein kinase | Phvul.003G20PF00560//PFC | |
| 16 | Leucine-rich repeat transmembrane protein kinase | Phvul.003G20PF00560//PFC | |
| 17 | Leucine-rich repeat transmembrane protein kinase | Phvul.003G20PF00560//PFC | |
| 18 | Leucine-rich repeat transmembrane protein kinase | Phvul.003G20PF00560//PFC | |
| 19 | Leucine-rich repeat transmembrane protein kinase | Phvul.003G20PF00560//PFC | |
| 20 | Leucine-rich repeat transmembrane protein kinase | Phvul.003G20PF00560//PFC | |
| 21 | Leucine-rich repeat transmembrane protein kinase | Phvul.003G20PF00560//PFC | |
| 22 | Leucine-rich repeat transmembrane protein kinase | Phvul.003G20PF00560//PFC | |
| 23 | Leucine-rich repeat transmembrane protein kinase | Phvul.003G20PF00560//PFC | |
| 24 | Leucine-rich repeat transmembrane protein kinase | Phvul.003G20PF00560//PFC | |
| 25 | Leucine-rich repeat transmembrane protein kinase | Phvul.003G20PF00560//PFC | |
| 26 | | | |
| 27 | | 0 | 0 |
| 28 | | 0 | 0 |
| 29 | | 0 | 0 |
| 30 | | 0 | 0 |
| 31 | | 0 | 0 |
| 32 | | 0 | 0 |
| 33 | | 0 | 0 |
| 34 | | 0 | 0 |
| 35 | | 0 | 0 |
| 36 | | 0 | 0 |
| 37 | | 0 | 0 |
| 38 | | 0 | 0 |
| 39 | | 0 | 0 |
| 40 | | 0 | 0 |
| 41 | NAC domain containing protein 96 | Phvul.003G22PTHR31989:SF | |
| 42 | NAC domain containing protein 96 | Phvul.003G22PTHR31989:SF | |
| 43 | Protein kinase superfamily protein | Phvul.003G23PTHR24054:SF | |
| 44 | Protein kinase superfamily protein | Phvul.003G23PTHR24054:SF | |
| 45 | Protein kinase superfamily protein | Phvul.003G23PTHR24054:SF | |
| 46 | Protein kinase superfamily protein | Phvul.003G23PTHR24054:SF | |
| 47 | Protein kinase superfamily protein | Phvul.003G23PTHR24054:SF | |
| 48 | Protein kinase superfamily protein | Phvul.003G23PTHR24054:SF | |
| 49 | Protein kinase superfamily protein | Phvul.003G23PTHR24054:SF | |
| 50 | Protein kinase superfamily protein | Phvul.003G23PTHR24054:SF | |
| 51 | Protein kinase superfamily protein | Phvul.003G23PTHR24054:SF | |
| 52 | Protein kinase superfamily protein | Phvul.003G23PTHR24054:SF | |
| 53 | Protein kinase superfamily protein | Phvul.003G23PTHR24054:SF | |
| 54 | Protein kinase superfamily protein | Phvul.003G23PTHR24054:SF | |
| 55 | Protein kinase superfamily protein | Phvul.003G23PTHR24054:SF | |
| 56 | Protein kinase superfamily protein | Phvul.003G23PTHR24054:SF | |
| 57 | disease resistance protein (TIR-NBS-LRR class), putative | Phvul.004G04PTHR11017//I | |
| 58 | disease resistance protein (TIR-NBS-LRR class), putative | Phvul.004G04PTHR11017//I | |
| 59 | disease resistance protein (TIR-NBS-LRR class), putative | Phvul.004G04PTHR11017//I | |
| 60 | disease resistance protein (TIR-NBS-LRR class), putative | Phvul.004G04PTHR11017//I | |

| | | |
|----|--|-----------------------------|
| 1 | | |
| 2 | Signal transduction histidine kinase, hybrid-type, ethylene se | Phvul.006G10K14509 - ethy |
| 3 | Signal transduction histidine kinase, hybrid-type, ethylene se | Phvul.006G10K14509 - ethy |
| 4 | lipid transfer protein 3 | Phvul.006G11PF00234 - Pro |
| 5 | | |
| 6 | ferric reduction oxidase 7 | Phvul.006G131.16.1.7 - Ferr |
| 7 | ferric reduction oxidase 7 | Phvul.006G131.16.1.7 - Ferr |
| 8 | ferric reduction oxidase 7 | Phvul.006G131.16.1.7 - Ferr |
| 9 | | |
| 10 | ferric reduction oxidase 7 | Phvul.006G131.16.1.7 - Ferr |
| 11 | ferric reduction oxidase 7 | Phvul.006G131.16.1.7 - Ferr |
| 12 | ferric reduction oxidase 7 | Phvul.006G131.16.1.7 - Ferr |
| 13 | ferric reduction oxidase 7 | Phvul.006G131.16.1.7 - Ferr |
| 14 | ferric reduction oxidase 7 | Phvul.006G131.16.1.7 - Ferr |
| 15 | ferric reduction oxidase 7 | Phvul.006G131.16.1.7 - Ferr |
| 16 | ferric reduction oxidase 7 | Phvul.006G131.16.1.7 - Ferr |
| 17 | ferric reduction oxidase 7 | Phvul.006G131.16.1.7 - Ferr |
| 18 | | |
| 19 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 20 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 21 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 22 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 23 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 24 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 25 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 26 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 27 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 28 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 29 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 30 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 31 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 32 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 33 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 34 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 35 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 36 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 37 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 38 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 39 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 40 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 41 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 42 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 43 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 44 | Sec14p-like phosphatidylinositol transfer family protein | Phvul.006G13PTHR23324//I |
| 45 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S | Phvul.006G13PTHR31731:SF |
| 46 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S | Phvul.006G13PTHR31731:SF |
| 47 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S | Phvul.006G13PTHR31731:SF |
| 48 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S | Phvul.006G13PTHR31731:SF |
| 49 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S | Phvul.006G13PTHR31731:SF |
| 50 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S | Phvul.006G13PTHR31731:SF |
| 51 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S | Phvul.006G13PTHR31731:SF |
| 52 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S | Phvul.006G13PTHR31731:SF |
| 53 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S | Phvul.006G13PTHR31731:SF |
| 54 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S | Phvul.006G13PTHR31731:SF |
| 55 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S | Phvul.006G13PTHR31731:SF |
| 56 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S | Phvul.006G13PTHR31731:SF |
| 57 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S | Phvul.006G13PTHR31731:SF |
| 58 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S | Phvul.006G13PTHR31731:SF |
| 59 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S | Phvul.006G13PTHR31731:SF |
| 60 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF |
| | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF |

| | | | | |
|----|--|-----------------------------|---|---|
| 1 | | | | |
| 2 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF | | |
| 3 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF | | |
| 4 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF | | |
| 5 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF | | |
| 6 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF | | |
| 7 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF | | |
| 8 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF | | |
| 9 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF | | |
| 10 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF | | |
| 11 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SF | | |
| 12 | FASCICLIN-like arabinogalactan-protein 11 | Phvul.006G17PTHR32077:SF | | |
| 13 | FASCICLIN-like arabinogalactan-protein 11 | Phvul.006G17PTHR32077:SF | | |
| 14 | FASCICLIN-like arabinogalactan-protein 11 | Phvul.006G17PTHR32077:SF | | |
| 15 | FASCICLIN-like arabinogalactan-protein 11 | Phvul.006G17PTHR32077:SF | | |
| 16 | FASCICLIN-like arabinogalactan-protein 11 | Phvul.006G17PTHR32077:SF | | |
| 17 | FASCICLIN-like arabinogalactan-protein 11 | Phvul.006G17PTHR32077:SF | | |
| 18 | FASCICLIN-like arabinogalactan-protein 11 | Phvul.006G17PTHR32077:SF | | |
| 19 | FASCICLIN-like arabinogalactan-protein 11 | Phvul.006G17PTHR32077:SF | | |
| 20 | FASCICLIN-like arabinogalactan-protein 11 | Phvul.006G17PTHR32077:SF | | |
| 21 | FASCICLIN-like arabinogalactan-protein 11 | Phvul.006G17PTHR32077:SF | | |
| 22 | FASCICLIN-like arabinogalactan-protein 11 | Phvul.006G17PTHR32077:SF | | |
| 23 | FASCICLIN-like arabinogalactan-protein 11 | Phvul.006G17PTHR32077:SF | | |
| 24 | FASCICLIN-like arabinogalactan-protein 11 | Phvul.006G17PTHR32077:SF | | |
| 25 | | | | |
| 26 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | | |
| 27 | Polynucleotidyl transferase, ribonuclease H-like superfamily | Phvul.007G19KOG4793 - Th | | |
| 28 | | 0 Phvul.007G28PF14577 - Sie | | |
| 29 | | 0 | 0 | 0 |
| 30 | | 0 | 0 | 0 |
| 31 | | 0 | 0 | 0 |
| 32 | | 0 | 0 | 0 |
| 33 | | 0 | 0 | 0 |
| 34 | | 0 | 0 | 0 |
| 35 | | 0 | 0 | 0 |
| 36 | | 0 | 0 | 0 |
| 37 | | 0 | 0 | 0 |
| 38 | | 0 | 0 | 0 |
| 39 | | 0 | 0 | 0 |
| 40 | | 0 | 0 | 0 |
| 41 | | 0 | 0 | 0 |
| 42 | | 0 | 0 | 0 |
| 43 | | 0 | 0 | 0 |
| 44 | | 0 | 0 | 0 |
| 45 | | 0 | 0 | 0 |
| 46 | | 0 | 0 | 0 |
| 47 | | 0 | 0 | 0 |
| 48 | | 0 | 0 | 0 |
| 49 | | 0 | 0 | 0 |
| 50 | | 0 | 0 | 0 |
| 51 | | 0 | 0 | 0 |
| 52 | | 0 | 0 | 0 |
| 53 | | 0 | 0 | 0 |
| 54 | | 0 | 0 | 0 |
| 55 | | 0 | 0 | 0 |
| 56 | | 0 | 0 | 0 |
| 57 | | 0 | 0 | 0 |
| 58 | | 0 | 0 | 0 |
| 59 | | 0 | 0 | 0 |
| 60 | | 0 | 0 | 0 |

| | | | |
|----|---|-----------------------------|---|
| 1 | | | |
| 2 | | 0 | 0 |
| 3 | | 0 | 0 |
| 4 | | 0 | 0 |
| 5 | | 0 | 0 |
| 6 | | 0 | 0 |
| 7 | | 0 | 0 |
| 8 | | 0 | 0 |
| 9 | | 0 | 0 |
| 10 | | 0 | 0 |
| 11 | | 0 | 0 |
| 12 | | 0 | 0 |
| 13 | | 0 | 0 |
| 14 | | 0 | 0 |
| 15 | | 0 | 0 |
| 16 | | 0 | 0 |
| 17 | | 0 | 0 |
| 18 | | 0 | 0 |
| 19 | | 0 | 0 |
| 20 | | 0 | 0 |
| 21 | | 0 | 0 |
| 22 | | 0 | 0 |
| 23 | | 0 | 0 |
| 24 | | 0 | 0 |
| 25 | | 0 | 0 |
| 26 | | 0 | 0 |
| 27 | | 0 | 0 |
| 28 | | 0 | 0 |
| 29 | | 0 | 0 |
| 30 | | 0 | 0 |
| 31 | | 0 | 0 |
| 32 | Aldolase-type TIM barrel family protein | Phvul.008G042.5.1.55 - 3-de | |
| 33 | Aldolase-type TIM barrel family protein | Phvul.008G042.5.1.55 - 3-de | |
| 34 | Aldolase-type TIM barrel family protein | Phvul.008G042.5.1.55 - 3-de | |
| 35 | Aldolase-type TIM barrel family protein | Phvul.008G042.5.1.55 - 3-de | |
| 36 | Aldolase-type TIM barrel family protein | Phvul.008G042.5.1.55 - 3-de | |
| 37 | Aldolase-type TIM barrel family protein | Phvul.008G042.5.1.55 - 3-de | |
| 38 | Aldolase-type TIM barrel family protein | Phvul.008G042.5.1.55 - 3-de | |
| 39 | Aldolase-type TIM barrel family protein | Phvul.008G042.5.1.55 - 3-de | |
| 40 | Aldolase-type TIM barrel family protein | Phvul.008G042.5.1.55 - 3-de | |
| 41 | Aldolase-type TIM barrel family protein | Phvul.008G042.5.1.55 - 3-de | |
| 42 | Aldolase-type TIM barrel family protein | Phvul.008G042.5.1.55 - 3-de | |
| 43 | Aldolase-type TIM barrel family protein | Phvul.008G042.5.1.55 - 3-de | |
| 44 | Aldolase-type TIM barrel family protein | Phvul.008G042.5.1.55 - 3-de | |
| 45 | Aldolase-type TIM barrel family protein | Phvul.008G042.5.1.55 - 3-de | |
| 46 | | | |
| 47 | | 0 | 0 |
| 48 | | 0 | 0 |
| 49 | | 0 | 0 |
| 50 | | 0 | 0 |
| 51 | | 0 | 0 |
| 52 | | 0 | 0 |
| 53 | | 0 | 0 |
| 54 | | 0 | 0 |
| 55 | | 0 | 0 |
| 56 | | 0 | 0 |
| 57 | | 0 | 0 |
| 58 | | 0 | 0 |
| 59 | | 0 | 0 |
| 60 | Leucine-rich repeat protein kinase family protein | Phvul.008G09PF00069//PFC | |
| | Leucine-rich repeat protein kinase family protein | Phvul.008G09PF00069//PFC | |

| | | |
|----|--|---------------------------------|
| 1 | | |
| 2 | Leucine-rich repeat protein kinase family protein | Phvul.008G09PF00069//PFC |
| 3 | Leucine-rich repeat protein kinase family protein | Phvul.008G09PF00069//PFC |
| 4 | Leucine-rich repeat protein kinase family protein | Phvul.008G09PF00069//PFC |
| 5 | Leucine-rich repeat protein kinase family protein | Phvul.008G09PF00069//PFC |
| 6 | Leucine-rich repeat protein kinase family protein | Phvul.008G09PF00069//PFC |
| 7 | Leucine-rich repeat protein kinase family protein | Phvul.008G09PF00069//PFC |
| 8 | Leucine-rich repeat protein kinase family protein | Phvul.008G09PF00069//PFC |
| 9 | Leucine-rich repeat protein kinase family protein | Phvul.008G09PF00069//PFC |
| 10 | Leucine-rich repeat protein kinase family protein | Phvul.008G09PF00069//PFC |
| 11 | Leucine-rich repeat protein kinase family protein | Phvul.008G09PF00069//PFC |
| 12 | Leucine-rich repeat protein kinase family protein | Phvul.008G09PF00069//PFC |
| 13 | Leucine-rich repeat protein kinase family protein | Phvul.008G09PF00069//PFC |
| 14 | PQ-loop repeat family protein / transmembrane family prote | Phvul.008G14K12386 - cysti |
| 15 | PQ-loop repeat family protein / transmembrane family prote | Phvul.008G14K12386 - cysti |
| 16 | PQ-loop repeat family protein / transmembrane family prote | Phvul.008G14K12386 - cysti |
| 17 | PQ-loop repeat family protein / transmembrane family prote | Phvul.008G14K12386 - cysti |
| 18 | PQ-loop repeat family protein / transmembrane family prote | Phvul.008G14K12386 - cysti |
| 19 | PQ-loop repeat family protein / transmembrane family prote | Phvul.008G14K12386 - cysti |
| 20 | PQ-loop repeat family protein / transmembrane family prote | Phvul.008G14K12386 - cysti |
| 21 | PQ-loop repeat family protein / transmembrane family prote | Phvul.008G14K12386 - cysti |
| 22 | PQ-loop repeat family protein / transmembrane family prote | Phvul.008G14K12386 - cysti |
| 23 | PQ-loop repeat family protein / transmembrane family prote | Phvul.008G14K12386 - cysti |
| 24 | PQ-loop repeat family protein / transmembrane family prote | Phvul.008G14K12386 - cysti |
| 25 | PQ-loop repeat family protein / transmembrane family prote | Phvul.008G14K12386 - cysti |
| 26 | PQ-loop repeat family protein / transmembrane family prote | Phvul.008G14K12386 - cysti |
| 27 | PQ-loop repeat family protein / transmembrane family prote | Phvul.008G14K12386 - cysti |
| 28 | PQ-loop repeat family protein / transmembrane family prote | Phvul.008G14K12386 - cysti |
| 29 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super | Phvul.008G26PTHR10209:SF |
| 30 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super | Phvul.008G26PTHR10209:SF |
| 31 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super | Phvul.008G26PTHR10209:SF |
| 32 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super | Phvul.008G26PTHR10209:SF |
| 33 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super | Phvul.008G26PTHR10209:SF |
| 34 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super | Phvul.008G26PTHR10209:SF |
| 35 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super | Phvul.008G26PTHR10209:SF |
| 36 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super | Phvul.008G26PTHR10209:SF |
| 37 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super | Phvul.008G26PTHR10209:SF |
| 38 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super | Phvul.008G26PTHR10209:SF |
| 39 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super | Phvul.008G26PTHR10209:SF |
| 40 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super | Phvul.008G26PTHR10209:SF |
| 41 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super | Phvul.008G26PTHR10209:SF |
| 42 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super | Phvul.008G26PTHR10209:SF |
| 43 | phosphorylcholine cytidyltransferase | Phvul.008G292.7.7.15 - Cho |
| 44 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01PTHR10992//I |
| 45 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01PTHR10992//I |
| 46 | alpha/beta-Hydrolases superfamily protein | Phvul.009G01PTHR10992//I |
| 47 | basic helix-loop-helix (bHLH) DNA-binding superfamily protei | Phvul.009G14PTHR12565:SF |
| 48 | Transmembrane amino acid transporter family protein | Phvul.009G19PTHR22950:SF |
| 49 | Transmembrane amino acid transporter family protein | Phvul.009G19PTHR22950:SF |
| 50 | Transmembrane amino acid transporter family protein | Phvul.009G19PTHR22950:SF |
| 51 | Transmembrane amino acid transporter family protein | Phvul.009G19PTHR22950:SF |
| 52 | Transmembrane amino acid transporter family protein | Phvul.009G19PTHR22950:SF |
| 53 | Transmembrane amino acid transporter family protein | Phvul.009G19PTHR22950:SF |
| 54 | Transmembrane amino acid transporter family protein | Phvul.009G19PTHR22950:SF |
| 55 | Transmembrane amino acid transporter family protein | Phvul.009G19PTHR22950:SF |
| 56 | Transmembrane amino acid transporter family protein | Phvul.009G19PTHR22950:SF |
| 57 | Transmembrane amino acid transporter family protein | Phvul.009G19PTHR22950:SF |
| 58 | Transmembrane amino acid transporter family protein | Phvul.009G19PTHR22950:SF |
| 59 | Transmembrane amino acid transporter family protein | Phvul.009G19PTHR22950:SF |
| 60 | Transmembrane amino acid transporter family protein | Phvul.009G19PTHR22950:SF |
| | GDSL-motif lipase 5 | Phvul.010G12PTHR22835:SF |

| | | |
|----|---|----------------------------|
| 1 | | |
| 2 | 3-beta hydroxysteroid dehydrogenase/isomerase family prot | Phvul.011G05 PTHR10366:SF |
| 3 | S-locus lectin protein kinase family protein | Phvul.011G15 PTHR27002:SF |
| 4 | S-locus lectin protein kinase family protein | Phvul.011G15 PTHR27002:SF |
| 5 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.L00233;PTHR22835//I |
| 6 | ARM repeat superfamily protein | Phvul.001G01 PTHR22849:SF |
| 7 | Patatin-like phospholipase family protein | Phvul.001G12 K14674 - TAG |
| 8 | Patatin-like phospholipase family protein | Phvul.001G12 K14674 - TAG |
| 9 | Patatin-like phospholipase family protein | Phvul.001G12 K14674 - TAG |
| 10 | Patatin-like phospholipase family protein | Phvul.001G12 K14674 - TAG |
| 11 | Patatin-like phospholipase family protein | Phvul.001G12 K14674 - TAG |
| 12 | Patatin-like phospholipase family protein | Phvul.001G12 K14674 - TAG |
| 13 | Patatin-like phospholipase family protein | Phvul.001G12 K14674 - TAG |
| 14 | Patatin-like phospholipase family protein | Phvul.001G12 K14674 - TAG |
| 15 | Patatin-like phospholipase family protein | Phvul.001G12 K14674 - TAG |
| 16 | Patatin-like phospholipase family protein | Phvul.001G12 K14674 - TAG |
| 17 | Patatin-like phospholipase family protein | Phvul.001G12 K14674 - TAG |
| 18 | Patatin-like phospholipase family protein | Phvul.001G12 K14674 - TAG |
| 19 | Patatin-like phospholipase family protein | Phvul.001G12 K14674 - TAG |
| 20 | Patatin-like phospholipase family protein | Phvul.001G12 K14674 - TAG |
| 21 | villin 2 | Phvul.001G13 PTHR11977:SF |
| 22 | villin 2 | Phvul.001G13 PTHR11977:SF |
| 23 | villin 2 | Phvul.001G13 PTHR11977:SF |
| 24 | RING/U-box superfamily protein | Phvul.001G21 PTHR22938 - ; |
| 25 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 26 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 27 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 28 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 29 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 30 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 31 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 32 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 33 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 34 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 35 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 36 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 37 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 38 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 39 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 40 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 41 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 42 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 43 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 44 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 45 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 46 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 47 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 48 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 49 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 50 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 51 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 52 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 53 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 54 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 55 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 56 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 57 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 58 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 59 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |
| 60 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13 PTHR21493//I |

| | | |
|----|--|-----------------------------------|
| 1 | | |
| 2 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13PTHR21493//I |
| 3 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13PTHR21493//I |
| 4 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13PTHR21493//I |
| 5 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13PTHR21493//I |
| 6 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13PTHR21493//I |
| 7 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13PTHR21493//I |
| 8 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13PTHR21493//I |
| 9 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13PTHR21493//I |
| 10 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.002G13PTHR21493//I |
| 11 | SEC14-like 12 | Phvul.002G16PTHR23324:SF |
| 12 | SEC14-like 12 | Phvul.002G16PTHR23324:SF |
| 13 | SEC14-like 12 | Phvul.002G16PTHR23324:SF |
| 14 | | Phvul.002G16PTHR23324:SF |
| 15 | | 0 Phvul.002G28K13146 - integ |
| 16 | | 0 Phvul.002G28K13146 - integ |
| 17 | | 0 Phvul.002G28K13146 - integ |
| 18 | | 0 Phvul.002G28K13146 - integ |
| 19 | | 0 Phvul.002G28K13146 - integ |
| 20 | | 0 Phvul.002G28K13146 - integ |
| 21 | | 0 Phvul.002G28K13146 - integ |
| 22 | | 0 Phvul.002G28K13146 - integ |
| 23 | | 0 Phvul.002G28K13146 - integ |
| 24 | | 0 Phvul.002G28K13146 - integ |
| 25 | | 0 Phvul.002G28K13146 - integ |
| 26 | | 0 Phvul.002G28K13146 - integ |
| 27 | | 0 Phvul.002G28K13146 - integ |
| 28 | | 0 Phvul.002G28K13146 - integ |
| 29 | | 0 Phvul.002G28K13146 - integ |
| 30 | trehalose phosphate synthase | Phvul.003G052.4.1.15//3.1. |
| 31 | C2 calcium/lipid-binding plant phosphoribosyltransferase far | Phvul.003G19PTHR10024:SF |
| 32 | C2 calcium/lipid-binding plant phosphoribosyltransferase far | Phvul.003G19PTHR10024:SF |
| 33 | C2 calcium/lipid-binding plant phosphoribosyltransferase far | Phvul.003G19PTHR10024:SF |
| 34 | C2 calcium/lipid-binding plant phosphoribosyltransferase far | Phvul.003G19PTHR10024:SF |
| 35 | C2 calcium/lipid-binding plant phosphoribosyltransferase far | Phvul.003G19PTHR10024:SF |
| 36 | C2 calcium/lipid-binding plant phosphoribosyltransferase far | Phvul.003G19PTHR10024:SF |
| 37 | C2 calcium/lipid-binding plant phosphoribosyltransferase far | Phvul.003G19PTHR10024:SF |
| 38 | C2 calcium/lipid-binding plant phosphoribosyltransferase far | Phvul.003G19PTHR10024:SF |
| 39 | C2 calcium/lipid-binding plant phosphoribosyltransferase far | Phvul.003G19PTHR10024:SF |
| 40 | C2 calcium/lipid-binding plant phosphoribosyltransferase far | Phvul.003G19PTHR10024:SF |
| 41 | C2 calcium/lipid-binding plant phosphoribosyltransferase far | Phvul.003G19PTHR10024:SF |
| 42 | C2 calcium/lipid-binding plant phosphoribosyltransferase far | Phvul.003G19PTHR10024:SF |
| 43 | C2 calcium/lipid-binding plant phosphoribosyltransferase far | Phvul.003G19PTHR10024:SF |
| 44 | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi | Phvul.003G22PTHR24098:SF |
| 45 | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi | Phvul.003G22PTHR24098:SF |
| 46 | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi | Phvul.003G22PTHR24098:SF |
| 47 | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi | Phvul.003G22PTHR24098:SF |
| 48 | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi | Phvul.003G22PTHR24098:SF |
| 49 | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi | Phvul.003G22PTHR24098:SF |
| 50 | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi | Phvul.003G22PTHR24098:SF |
| 51 | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi | Phvul.003G22PTHR24098:SF |
| 52 | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi | Phvul.003G22PTHR24098:SF |
| 53 | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi | Phvul.003G22PTHR24098:SF |
| 54 | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi | Phvul.003G22PTHR24098:SF |
| 55 | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi | Phvul.003G22PTHR24098:SF |
| 56 | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi | Phvul.003G22PTHR24098:SF |
| 57 | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi | Phvul.003G22PTHR24098:SF |
| 58 | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi | Phvul.003G22PTHR24098:SF |
| 59 | Arp2/3 complex, 34 kD subunit p34-Arc | Phvul.003G27K05758 - actin |
| 60 | Arp2/3 complex, 34 kD subunit p34-Arc | Phvul.003G27K05758 - actin |

| | | |
|----|--|-----------------------------|
| 1 | | |
| 2 | Arp2/3 complex, 34 kD subunit p34-Arc | Phvul.003G27K05758 - actin |
| 3 | Arp2/3 complex, 34 kD subunit p34-Arc | Phvul.003G27K05758 - actin |
| 4 | Arp2/3 complex, 34 kD subunit p34-Arc | Phvul.003G27K05758 - actin |
| 5 | Arp2/3 complex, 34 kD subunit p34-Arc | Phvul.003G27K05758 - actin |
| 6 | Arp2/3 complex, 34 kD subunit p34-Arc | Phvul.003G27K05758 - actin |
| 7 | Arp2/3 complex, 34 kD subunit p34-Arc | Phvul.003G27K05758 - actin |
| 8 | Arp2/3 complex, 34 kD subunit p34-Arc | Phvul.003G27K05758 - actin |
| 9 | Arp2/3 complex, 34 kD subunit p34-Arc | Phvul.003G27K05758 - actin |
| 10 | Arp2/3 complex, 34 kD subunit p34-Arc | Phvul.003G27K05758 - actin |
| 11 | Arp2/3 complex, 34 kD subunit p34-Arc | Phvul.003G27K05758 - actin |
| 12 | Arp2/3 complex, 34 kD subunit p34-Arc | Phvul.003G27K05758 - actin |
| 13 | Arp2/3 complex, 34 kD subunit p34-Arc | Phvul.003G27K05758 - actin |
| 14 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 15 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 16 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 17 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 18 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 19 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 20 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 21 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 22 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 23 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 24 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 25 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 26 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 27 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 28 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 29 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 30 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 31 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 32 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 33 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 34 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 35 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 36 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 37 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 38 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 39 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 40 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 41 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 42 | F-box/RNI-like superfamily protein | Phvul.004G11PF00646 - F-box |
| 43 | Nucleotide-diphospho-sugar transferases superfamily protei | Phvul.004G17PTHR12726 - C |
| 44 | Nucleotide-diphospho-sugar transferases superfamily protei | Phvul.004G17PTHR12726 - C |
| 45 | Nucleotide-diphospho-sugar transferases superfamily protei | Phvul.004G17PTHR12726 - C |
| 46 | Nucleotide-diphospho-sugar transferases superfamily protei | Phvul.004G17PTHR12726 - C |
| 47 | Nucleotide-diphospho-sugar transferases superfamily protei | Phvul.004G17PTHR12726 - C |
| 48 | Nucleotide-diphospho-sugar transferases superfamily protei | Phvul.004G17PTHR12726 - C |
| 49 | Nucleotide-diphospho-sugar transferases superfamily protei | Phvul.004G17PTHR12726 - C |
| 50 | Nucleotide-diphospho-sugar transferases superfamily protei | Phvul.004G17PTHR12726 - C |
| 51 | Nucleotide-diphospho-sugar transferases superfamily protei | Phvul.004G17PTHR12726 - C |
| 52 | Nucleotide-diphospho-sugar transferases superfamily protei | Phvul.004G17PTHR12726 - C |
| 53 | Nucleotide-diphospho-sugar transferases superfamily protei | Phvul.004G17PTHR12726 - C |
| 54 | Nucleotide-diphospho-sugar transferases superfamily protei | Phvul.004G17PTHR12726 - C |
| 55 | Nucleotide-diphospho-sugar transferases superfamily protei | Phvul.004G17PTHR12726 - C |
| 56 | Nucleotide-diphospho-sugar transferases superfamily protei | Phvul.004G17PTHR12726 - C |
| 57 | Nucleotide-diphospho-sugar transferases superfamily protei | Phvul.004G17PTHR12726 - C |
| 58 | Nucleotide-diphospho-sugar transferases superfamily protei | Phvul.004G17PTHR12726 - C |
| 59 | UDP-Glycosyltransferase superfamily protein | Phvul.005G052.4.1.142 - Ch |
| 60 | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |
| | RING/U-box superfamily protein | Phvul.005G06K19041 - E3 ul |

| | | | |
|----|--|-----------------------------|---|
| 1 | | | |
| 2 | Ribosomal protein L19 family protein | Phvul.006G05 PTHR15680:SF | |
| 3 | Ribosomal protein L19 family protein | Phvul.006G05 PTHR15680:SF | |
| 4 | Ribosomal protein L19 family protein | Phvul.006G05 PTHR15680:SF | |
| 5 | Ribosomal protein L19 family protein | Phvul.006G05 PTHR15680:SF | |
| 6 | Ribosomal protein L19 family protein | Phvul.006G05 PTHR15680:SF | |
| 7 | Ribosomal protein L19 family protein | Phvul.006G05 PTHR15680:SF | |
| 8 | Ribosomal protein L19 family protein | Phvul.006G05 PTHR15680:SF | |
| 9 | Ribosomal protein L19 family protein | Phvul.006G05 PTHR15680:SF | |
| 10 | Ribosomal protein L19 family protein | Phvul.006G05 PTHR15680:SF | |
| 11 | Ribosomal protein L19 family protein | Phvul.006G05 PTHR15680:SF | |
| 12 | Ribosomal protein L19 family protein | Phvul.006G05 PTHR15680:SF | |
| 13 | Ribosomal protein L19 family protein | Phvul.006G05 PTHR15680:SF | |
| 14 | Ribosomal protein L19 family protein | Phvul.006G05 PTHR15680:SF | |
| 15 | Signal transduction histidine kinase, hybrid-type, ethylene se | Phvul.006G10K14509 - ethy | |
| 16 | Signal transduction histidine kinase, hybrid-type, ethylene se | Phvul.006G10K14509 - ethy | |
| 17 | Signal transduction histidine kinase, hybrid-type, ethylene se | Phvul.006G10K14509 - ethy | |
| 18 | Signal transduction histidine kinase, hybrid-type, ethylene se | Phvul.006G10K14509 - ethy | |
| 19 | lipid transfer protein 3 | Phvul.006G11 PF00234 - Pro | |
| 20 | lipid transfer protein 3 | Phvul.006G11 PF00234 - Pro | |
| 21 | lipid transfer protein 3 | Phvul.006G11 PF00234 - Pro | |
| 22 | lipid transfer protein 3 | Phvul.006G11 PF00234 - Pro | |
| 23 | lipid transfer protein 3 | Phvul.006G11 PF00234 - Pro | |
| 24 | lipid transfer protein 3 | Phvul.006G11 PF00234 - Pro | |
| 25 | lipid transfer protein 3 | Phvul.006G11 PF00234 - Pro | |
| 26 | lipid transfer protein 3 | Phvul.006G11 PF00234 - Pro | |
| 27 | lipid transfer protein 3 | Phvul.006G11 PF00234 - Pro | |
| 28 | lipid transfer protein 3 | Phvul.006G11 PF00234 - Pro | |
| 29 | lipid transfer protein 3 | Phvul.006G11 PF00234 - Pro | |
| 30 | lipid transfer protein 3 | Phvul.006G11 PF00234 - Pro | |
| 31 | lipid transfer protein 3 | Phvul.006G11 PF00234 - Pro | |
| 32 | lipid transfer protein 3 | Phvul.006G11 PF00234 - Pro | |
| 33 | | 0 | 0 |
| 34 | | 0 | 0 |
| 35 | | 0 | 0 |
| 36 | | 0 | 0 |
| 37 | | 0 | 0 |
| 38 | | 0 | 0 |
| 39 | | 0 | 0 |
| 40 | | 0 | 0 |
| 41 | | 0 | 0 |
| 42 | | 0 | 0 |
| 43 | | 0 | 0 |
| 44 | | 0 | 0 |
| 45 | | 0 | 0 |
| 46 | | 0 | 0 |
| 47 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S | Phvul.006G13 PTHR31731:SF | |
| 48 | syntaxin of plants 43 | Phvul.007G19K08489 - synt | |
| 49 | syntaxin of plants 43 | Phvul.007G19K08489 - synt | |
| 50 | syntaxin of plants 43 | Phvul.007G19K08489 - synt | |
| 51 | syntaxin of plants 43 | Phvul.007G19K08489 - synt | |
| 52 | syntaxin of plants 43 | Phvul.007G19K08489 - synt | |
| 53 | syntaxin of plants 43 | Phvul.007G19K08489 - synt | |
| 54 | syntaxin of plants 43 | Phvul.007G19K08489 - synt | |
| 55 | syntaxin of plants 43 | Phvul.007G19K08489 - synt | |
| 56 | syntaxin of plants 43 | Phvul.007G19K08489 - synt | |
| 57 | syntaxin of plants 43 | Phvul.007G19K08489 - synt | |
| 58 | syntaxin of plants 43 | Phvul.007G19K08489 - synt | |
| 59 | syntaxin of plants 43 | Phvul.007G19K08489 - synt | |
| 60 | syntaxin of plants 43 | Phvul.007G19K08489 - synt | |
| | homogentisate phytyltransferase 1 | Phvul.007G222.5.1.36 - Trih | |

| | | |
|----|---|-----------------------------|
| 1 | | |
| 2 | homogentisate phytyltransferase 1 | Phvul.007G222.5.1.36 - Trih |
| 3 | homogentisate phytyltransferase 1 | Phvul.007G222.5.1.36 - Trih |
| 4 | homogentisate phytyltransferase 1 | Phvul.007G222.5.1.36 - Trih |
| 5 | homogentisate phytyltransferase 1 | Phvul.007G222.5.1.36 - Trih |
| 6 | homogentisate phytyltransferase 1 | Phvul.007G222.5.1.36 - Trih |
| 7 | homogentisate phytyltransferase 1 | Phvul.007G222.5.1.36 - Trih |
| 8 | homogentisate phytyltransferase 1 | Phvul.007G222.5.1.36 - Trih |
| 9 | homogentisate phytyltransferase 1 | Phvul.007G222.5.1.36 - Trih |
| 10 | homogentisate phytyltransferase 1 | Phvul.007G222.5.1.36 - Trih |
| 11 | homogentisate phytyltransferase 1 | Phvul.007G222.5.1.36 - Trih |
| 12 | homogentisate phytyltransferase 1 | Phvul.007G222.5.1.36 - Trih |
| 13 | homogentisate phytyltransferase 1 | Phvul.007G222.5.1.36 - Trih |
| 14 | magnesium-chelatase subunit chlH, chloroplast, putative / M | Phvul.007G25K03403 - mag |
| 15 | no exine formation 1 | Phvul.008G00PTHR35313:SF |
| 16 | no exine formation 1 | Phvul.008G00PTHR35313:SF |
| 17 | Protein of unknown function (DUF1666) | Phvul.008G04PTHR10759//I |
| 18 | Protein of unknown function (DUF1666) | Phvul.008G04PTHR10759//I |
| 19 | Protein of unknown function (DUF1666) | Phvul.008G04PTHR10759//I |
| 20 | Protein of unknown function (DUF1666) | Phvul.008G04PTHR10759//I |
| 21 | Protein of unknown function (DUF1666) | Phvul.008G04PTHR10759//I |
| 22 | Protein of unknown function (DUF1666) | Phvul.008G04PTHR10759//I |
| 23 | Protein of unknown function (DUF1666) | Phvul.008G04PTHR10759//I |
| 24 | Protein of unknown function (DUF1666) | Phvul.008G04PTHR10759//I |
| 25 | Protein of unknown function (DUF1666) | Phvul.008G04PTHR10759//I |
| 26 | Protein of unknown function (DUF1666) | Phvul.008G04PTHR10759//I |
| 27 | Protein of unknown function (DUF1666) | Phvul.008G04PTHR10759//I |
| 28 | Protein of unknown function (DUF1666) | Phvul.008G04PTHR10759//I |
| 29 | Protein of unknown function (DUF1666) | Phvul.008G04PTHR10759//I |
| 30 | Protein of unknown function (DUF1666) | Phvul.008G04PTHR10759//I |
| 31 | Protein of unknown function (DUF1666) | Phvul.008G04PTHR10759//I |
| 32 | | 0 0 0 |
| 33 | Leucine-rich repeat protein kinase family protein | Phvul.008G09PF00069//PFC |
| 34 | Class-II DAHP synthetase family protein | Phvul.008G172.5.1.54 - 3-de |
| 35 | Class-II DAHP synthetase family protein | Phvul.008G172.5.1.54 - 3-de |
| 36 | Class-II DAHP synthetase family protein | Phvul.008G172.5.1.54 - 3-de |
| 37 | Class-II DAHP synthetase family protein | Phvul.008G172.5.1.54 - 3-de |
| 38 | Class-II DAHP synthetase family protein | Phvul.008G172.5.1.54 - 3-de |
| 39 | Class-II DAHP synthetase family protein | Phvul.008G172.5.1.54 - 3-de |
| 40 | Class-II DAHP synthetase family protein | Phvul.008G172.5.1.54 - 3-de |
| 41 | Class-II DAHP synthetase family protein | Phvul.008G172.5.1.54 - 3-de |
| 42 | Class-II DAHP synthetase family protein | Phvul.008G172.5.1.54 - 3-de |
| 43 | Class-II DAHP synthetase family protein | Phvul.008G172.5.1.54 - 3-de |
| 44 | Class-II DAHP synthetase family protein | Phvul.008G172.5.1.54 - 3-de |
| 45 | Class-II DAHP synthetase family protein | Phvul.008G172.5.1.54 - 3-de |
| 46 | Class-II DAHP synthetase family protein | Phvul.008G172.5.1.54 - 3-de |
| 47 | Class-II DAHP synthetase family protein | Phvul.008G172.5.1.54 - 3-de |
| 48 | Pentatricopeptide repeat (PPR) superfamily protein | Phvul.008G19PTHR13343:SF |
| 49 | Pentatricopeptide repeat (PPR) superfamily protein | Phvul.008G19PTHR13343:SF |
| 50 | Lateral organ boundaries (LOB) domain family protein | Phvul.008G25PTHR31301:SF |
| 51 | epsin N-terminal homology (ENTH) domain-containing prote | Phvul.009G09PTHR22951//I |
| 52 | epsin N-terminal homology (ENTH) domain-containing prote | Phvul.009G09PTHR22951//I |
| 53 | epsin N-terminal homology (ENTH) domain-containing prote | Phvul.009G09PTHR22951//I |
| 54 | epsin N-terminal homology (ENTH) domain-containing prote | Phvul.009G09PTHR22951//I |
| 55 | epsin N-terminal homology (ENTH) domain-containing prote | Phvul.009G09PTHR22951//I |
| 56 | epsin N-terminal homology (ENTH) domain-containing prote | Phvul.009G09PTHR22951//I |
| 57 | epsin N-terminal homology (ENTH) domain-containing prote | Phvul.009G09PTHR22951//I |
| 58 | epsin N-terminal homology (ENTH) domain-containing prote | Phvul.009G09PTHR22951//I |
| 59 | epsin N-terminal homology (ENTH) domain-containing prote | Phvul.009G09PTHR22951//I |
| 60 | epsin N-terminal homology (ENTH) domain-containing prote | Phvul.009G09PTHR22951//I |

| | | | |
|----|---|---------------------------|---|
| 1 | | | |
| 2 | epsin N-terminal homology (ENTH) domain-containing prote | Phvul.009G09PTHR22951//I | |
| 3 | epsin N-terminal homology (ENTH) domain-containing prote | Phvul.009G09PTHR22951//I | |
| 4 | epsin N-terminal homology (ENTH) domain-containing prote | Phvul.009G09PTHR22951//I | |
| 5 | | | |
| 6 | Vacuolar sorting protein 39 | Phvul.010G05PTHR12894:SF | |
| 7 | Basic-leucine zipper (bZIP) transcription factor family protein | Phvul.011G03PTHR23334 - (| |
| 8 | Basic-leucine zipper (bZIP) transcription factor family protein | Phvul.011G03PTHR23334 - (| |
| 9 | | | |
| 10 | Basic-leucine zipper (bZIP) transcription factor family protein | Phvul.011G03PTHR23334 - (| |
| 11 | Basic-leucine zipper (bZIP) transcription factor family protein | Phvul.011G03PTHR23334 - (| |
| 12 | Basic-leucine zipper (bZIP) transcription factor family protein | Phvul.011G03PTHR23334 - (| |
| 13 | Basic-leucine zipper (bZIP) transcription factor family protein | Phvul.011G03PTHR23334 - (| |
| 14 | Basic-leucine zipper (bZIP) transcription factor family protein | Phvul.011G03PTHR23334 - (| |
| 15 | Basic-leucine zipper (bZIP) transcription factor family protein | Phvul.011G03PTHR23334 - (| |
| 16 | Basic-leucine zipper (bZIP) transcription factor family protein | Phvul.011G03PTHR23334 - (| |
| 17 | Basic-leucine zipper (bZIP) transcription factor family protein | Phvul.011G03PTHR23334 - (| |
| 18 | Basic-leucine zipper (bZIP) transcription factor family protein | Phvul.011G03PTHR23334 - (| |
| 19 | Basic-leucine zipper (bZIP) transcription factor family protein | Phvul.011G03PTHR23334 - (| |
| 20 | | 0 | 0 |
| 21 | | | |
| 22 | S-locus lectin protein kinase family protein | Phvul.011G14PF00954//PFC | |
| 23 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 24 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 25 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 26 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 27 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 28 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 29 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 30 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 31 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 32 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 33 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 34 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 35 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 36 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 37 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 38 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 39 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 40 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 41 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 42 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 43 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 44 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 45 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 46 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 47 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 48 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 49 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 50 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 51 | S-locus lectin protein kinase family protein | Phvul.011G15PTHR27002:SF | |
| 52 | | | |
| 53 | | | |
| 54 | | | |
| 55 | | | |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

1 Phvul.001G17 not assigned.ε (original description: pacid=37169336 transcript=Phvul.001G172501.1
2 Phvul.001G17 not assigned.ε (original description: pacid=37169336 transcript=Phvul.001G172501.1
3 Phvul.001G17 not assigned.ε (original description: pacid=37169336 transcript=Phvul.001G172501.1
4 Phvul.001G17 not assigned.ε (original description: pacid=37169336 transcript=Phvul.001G172501.1
5 Phvul.001G17 not assigned.ε (original description: pacid=37169336 transcript=Phvul.001G172501.1
6 Phvul.001G17 not assigned.ε (original description: pacid=37169336 transcript=Phvul.001G172501.1
7 Phvul.001G17 not assigned.ε (original description: pacid=37169336 transcript=Phvul.001G172501.1
8 Phvul.001G17 not assigned.ε (original description: pacid=37169336 transcript=Phvul.001G172501.1
9 Phvul.001G17 not assigned.ε (original description: pacid=37169336 transcript=Phvul.001G172501.1
10 **Phvul.001G21 Protein home RING-v-class E3 ligase (original description: pacid=37167834 transcript**
11 **Phvul.001G21 Protein home RING-v-class E3 ligase (original description: pacid=37167834 transcript**
12 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac
13 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac
14 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac
15 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac
16 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac
17 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac
18 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac
19 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac
20 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac
21 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac
22 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac
23 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac
24 Phvul.002G01 Protein modif catalytic subunit alpha of CK-II protein kinase (original description: pac
25 Phvul.002G19 Cell wall organ O-acetyltransferase (RWA) (original description: pacid=37175788 trans
26 Phvul.002G21 not assigned.ε (original description: pacid=37176061 transcript=Phvul.002G218300.1
27 Phvul.002G33 Cell cycle organ associated component POT of telomerase ribonucleoprotein complex (
28 Phvul.002G33 Cell cycle organ associated component POT of telomerase ribonucleoprotein complex (
29 Phvul.003G26 Solute transport metal cation transporter (ZIP) (original description: pacid=37145610 tr
30 Phvul.003G26 Solute transport metal cation transporter (ZIP) (original description: pacid=37146252 tr
31 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=
32 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=
33 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=
34 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=
35 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=
36 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=
37 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=
38 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=
39 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=
40 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=
41 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=
42 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=
43 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=
44 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=
45 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=
46 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=
47 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=
48 Phvul.005G03 Protein modif protein kinase (SD-1) (original description: pacid=37154114 transcript=
49 Phvul.005G08 Protein modif protein kinase (SD-1) (original description: pacid=37153153 transcript=
50 Phvul.005G08 Protein modif protein kinase (SD-1) (original description: pacid=37153153 transcript=
51 Phvul.005G08 Protein modif protein kinase (SD-1) (original description: pacid=37153153 transcript=
52 Phvul.005G08 Protein modif protein kinase (SD-1) (original description: pacid=37153153 transcript=
53 Phvul.005G08 Protein modif protein kinase (SD-1) (original description: pacid=37153816 transcript=
54 Phvul.005G13 Protein home serine carboxypeptidase (original description: pacid=37152353 transcr
55 Phvul.005G13 Protein home serine carboxypeptidase (original description: pacid=37152353 transcr
56 Phvul.005G13 Protein home serine carboxypeptidase (original description: pacid=37152353 transcr
57 Phvul.005G13 Protein home serine carboxypeptidase (original description: pacid=37152353 transcr
58 Phvul.005G13 Protein home serine carboxypeptidase (original description: pacid=37152353 transcr
59 Phvul.005G13 Protein home serine carboxypeptidase (original description: pacid=37152353 transcr
60 Phvul.005G13 Protein home serine carboxypeptidase (original description: pacid=37152353 transcr

1 Phvul.008G29Lipid metabolite CTP:phosphorylcholine cytidyltransferase (original description: pacid:
2 Phvul.008G29Lipid metabolite CTP:phosphorylcholine cytidyltransferase (original description: pacid:
3 Phvul.008G29Lipid metabolite CTP:phosphorylcholine cytidyltransferase (original description: pacid:
4 Phvul.008G29Lipid metabolite CTP:phosphorylcholine cytidyltransferase (original description: pacid:
5 Phvul.008G29Lipid metabolite CTP:phosphorylcholine cytidyltransferase (original description: pacid:
6 Phvul.008G29Lipid metabolite CTP:phosphorylcholine cytidyltransferase (original description: pacid:
7 Phvul.008G29Lipid metabolite CTP:phosphorylcholine cytidyltransferase (original description: pacid:
8 Phvul.008G29Lipid metabolite CTP:phosphorylcholine cytidyltransferase (original description: pacid:
9 Phvul.009G11Chromatin organization modification reader component Pc of PRC1 histone mono-ubiquitinatio
10 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1
11 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1
12 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1
13 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1
14 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1
15 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1
16 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1
17 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1
18 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1
19 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1
20 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1
21 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1
22 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1
23 Phvul.010G12not assigned.α (original description: pacid=37142336 transcript=Phvul.010G124800.1
24 Phvul.010G15not assigned.α (original description: pacid=37143692 transcript=Phvul.010G158100.1
25 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi
26 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi
27 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi
28 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi
29 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi
30 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi
31 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi
32 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi
33 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi
34 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi
35 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi
36 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi
37 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi
38 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi
39 Phvul.011G01Enzyme class:Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidopsi
40 Phvul.011G04Photosynthesis assembly factor CcsB of CCS cytochrome f/c6 maturation system (syste
41 Phvul.011G04Photosynthesis assembly factor CcsB of CCS cytochrome f/c6 maturation system (syste
42 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans
43 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans
44 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans
45 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans
46 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans
47 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans
48 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans
49 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans
50 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans
51 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans
52 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans
53 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans
54 Phvul.011G06Protein modification protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans
55 Phvul.011G12Protein homeostasis protease (Papain) (original description: pacid=37155382 transcript=Ph
56 Phvul.011G12Protein homeostasis protease (Papain) (original description: pacid=37155382 transcript=Ph
57 Phvul.011G12Protein homeostasis protease (Papain) (original description: pacid=37155382 transcript=Ph
58 Phvul.011G12Protein homeostasis protease (Papain) (original description: pacid=37155382 transcript=Ph
59 Phvul.011G12Protein homeostasis protease (Papain) (original description: pacid=37155382 transcript=Ph
60 Phvul.011G12Protein homeostasis protease (Papain) (original description: pacid=37155382 transcript=Ph

1 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac
2 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac
3 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac
4 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac
5 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac
6 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac
7 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac
8 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac
9 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac
10 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac
11 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac
12 Phvul.007G22Redox homeo homogentisate phytyltransferase (VTE2/HPT) (original description: pac
13 Phvul.007G25Phytohormon ABAR chloroplast envelope-localized abscisic acid receptor (original de
14 Phvul.008G00Cell wall orgar exine patterning factor (NEF1) (original description: pacid=37158156 tr
15 Phvul.008G00Cell wall orgar exine patterning factor (NEF1) (original description: pacid=37158156 tr
16 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G
17 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G
18 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G
19 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G
20 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G
21 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G
22 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G
23 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G
24 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G
25 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G
26 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G
27 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G
28 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G
29 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G
30 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G
31 Phvul.008G04not assigned.r no hits & (original description: pacid=37159608 transcript=Phvul.008G
32 Phvul.008G08not assigned.r no hits & (original description: pacid=37157729 transcript=Phvul.008G
33 Phvul.008G09Protein modif protein kinase (LRR-XII) (original description: pacid=37157650 transcrip
34 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
35 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
36 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
37 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
38 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
39 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
40 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
41 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
42 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
43 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
44 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
45 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
46 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
47 Phvul.008G17Amino acid m 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
48 Phvul.008G19not assigned.ã (original description: pacid=37158415 transcript=Phvul.008G199500.1
49 Phvul.008G19not assigned.ã (original description: pacid=37158415 transcript=Phvul.008G199500.1
50 Phvul.008G25RNA biosynthetranscription factor (AS2/LOB) (original description: pacid=37161314 tr
51 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d
52 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d
53 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d
54 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d
55 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d
56 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d
57 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d
58 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d
59 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d
60 Phvul.009G09Vesicle trafficlcomponent CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d

- 1
- 2
- 3 2.1) &
- 4 2.1) &
- 5 2.1) &
- 6 2.1) &
- 7 2.1) &
- 8 2.1) &
- 9 2.1) &
- 10 2.1) &
- 11 2.1) &
- 12 2.1) &
- 13 2.1) &
- 14 2.1) &
- 15 2.1) &
- 16 2.1) &
- 17 2.1) &
- 18 2.1) &
- 19 2.1) &
- 20 2.1) &
- 21 2.1) &
- 22 2.1) &
- 23 2.1) &
- 24 2.1) &
- 25 2.1) &
- 26 2.1) &
- 27 2.1) &
- 28 2.1) &
- 29 2.1) &
- 30 2.1) &
- 31 2.1) &
- 32 2.1) &
- 33 2.1) &
- 34 2.1) &
- 35 2.1) &
- 36 2.1) &
- 37 2.1) &
- 38 2.1) &
- 39 2.1) &
- 40 2.1) &
- 41 2.1) &
- 42 2.1) &
- 43 2.1) &
- 44 2.1) &
- 45 2.1) &
- 46 2.1) &
- 47 2.1) &
- 48 2.1) &
- 49 2.1) &
- 50 2.1) &
- 51 2.1) &
- 52 2.1) &
- 53 2.1) &
- 54 2.1) &
- 55 2.1) &
- 56 2.1) &
- 57 2.1) &
- 58 2.1) &
- 59 2.1) &
- 60 2.1) &

Do not distribute

1
2 2.1) &
3 2.1) &
4 2.1) &
5 2.1) &
6 2.1) &
7 2.1) &
8 2.1) &
9 2.1) &
10 2.1) &
11 2.1) &
12 2.1) &
13 2.1) &
14 2.1) &

Do not distribute

15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44 2.1) &
45 2.1) &
46 2.1) &
47 2.1) &
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

2.1) &
2.1) &
2.1) &
2.1) &
2.1) &
2.1) &
2.1) &
2.1) &
2.1) &
2.1) &
2.1) &
2.1) &
2.1) &
2.1) &

Do not distribute

1
2 rg complex subunit 5 OS=Arabidopsis thaliana (sp|q8h1u4|apc5_arath : 98.6)
3 rg complex subunit 5 OS=Arabidopsis thaliana (sp|q8h1u4|apc5_arath : 98.6)
4 rg complex subunit 5 OS=Arabidopsis thaliana (sp|q8h1u4|apc5_arath : 98.6)
5 rg complex subunit 5 OS=Arabidopsis thaliana (sp|q8h1u4|apc5_arath : 98.6)
6 rg complex subunit 5 OS=Arabidopsis thaliana (sp|q8h1u4|apc5_arath : 98.6)
7 rg complex subunit 5 OS=Arabidopsis thaliana (sp|q8h1u4|apc5_arath : 98.6)
8 rg complex subunit 5 OS=Arabidopsis thaliana (sp|q8h1u4|apc5_arath : 98.6)
9
10 &
11 &
12 !.1 annot-version=v2.1) &
13 !.1 annot-version=v2.1) &
14 !.1 annot-version=v2.1) &
15 !.1 annot-version=v2.1) &
16 !.1 annot-version=v2.1) &
17 !.1 annot-version=v2.1) &
18 !.1 annot-version=v2.1) &
19 !.1 annot-version=v2.1) &
20 !.1 annot-version=v2.1) &
21 !.1 annot-version=v2.1) &
22 !.1 annot-version=v2.1) &
23 !.1 annot-version=v2.1) &
24 !.1 annot-version=v2.1) &
25 v2.1) &
26
27 SS-ASSOCIATED 32 OS=Arabidopsis thaliana (sp|q8gwl1|hsa32_arath : 383.0)
28 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
29 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
30 n=v2.1) &
31 n=v2.1) &
32
33 &
34 &
35 &
36 &
37 &
38 &
39 &
40 &
41 &
42 &
43 &
44 &
45 &
46 &
47 &
48 &
49 &
50 &
51 &
52 &
53 &
54
55 .1) &
56 .1) &
57 .1) &
58 .1) &
59 .1) &
60 .1) &

1
2 .1) &
3 .1) &
4 .1) &
5 .1) &
6 .1) &
7 .1) &
8 .1) &
9
10
11
12 sphate/phosphate translocator At3g11320 OS=Arabidopsis thaliana (sp|q5xf09|pt311_arath : 446.0
13 sphate/phosphate translocator At3g11320 OS=Arabidopsis thaliana (sp|q5xf09|pt311_arath : 446.0
14 sphate/phosphate translocator At3g11320 OS=Arabidopsis thaliana (sp|q5xf09|pt311_arath : 446.0
15 sphate/phosphate translocator At3g11320 OS=Arabidopsis thaliana (sp|q5xf09|pt311_arath : 446.0
16 sphate/phosphate translocator At3g11320 OS=Arabidopsis thaliana (sp|q5xf09|pt311_arath : 446.0
17 sphate/phosphate translocator At3g11320 OS=Arabidopsis thaliana (sp|q5xf09|pt311_arath : 446.0
18 sphate/phosphate translocator At3g11320 OS=Arabidopsis thaliana (sp|q5xf09|pt311_arath : 446.0
19 sphate/phosphate translocator At3g11320 OS=Arabidopsis thaliana (sp|q5xf09|pt311_arath : 446.0
20 sphate/phosphate translocator At3g11320 OS=Arabidopsis thaliana (sp|q5xf09|pt311_arath : 446.0
21 sphate/phosphate translocator At3g11320 OS=Arabidopsis thaliana (sp|q5xf09|pt311_arath : 446.0
22 sphate/phosphate translocator At3g11320 OS=Arabidopsis thaliana (sp|q5xf09|pt311_arath : 446.0
23 sphate/phosphate translocator At3g11320 OS=Arabidopsis thaliana (sp|q5xf09|pt311_arath : 446.0
24 sphate/phosphate translocator At3g11320 OS=Arabidopsis thaliana (sp|q5xf09|pt311_arath : 446.0
25 sphate/phosphate translocator At3g11320 OS=Arabidopsis thaliana (sp|q5xf09|pt311_arath : 446.0
26 sphate/phosphate translocator At3g11320 OS=Arabidopsis thaliana (sp|q5xf09|pt311_arath : 446.0
27 2.1) &
28 t-version=v2.1) &
29 t-version=v2.1) &
30 t-version=v2.1) &
31 t-version=v2.1) &
32 t-version=v2.1) &
33 t-version=v2.1) &
34 t-version=v2.1) &
35 t-version=v2.1) &
36 t-version=v2.1) &
37 t-version=v2.1) &
38 t-version=v2.1) &
39 t-version=v2.1) &
40 t-version=v2.1) &
41 t-version=v2.1) &
42 t-version=v2.1) &
43 t-version=v2.1) &
44 t-version=v2.1) &
45 t-version=v2.1) &
46 t-version=v2.1) &
47 t-version=v2.1) &
48 t-version=v2.1) &
49 t-version=v2.1) &
50 t-version=v2.1) &
51 t-version=v2.1) &
52 t-version=v2.1) &
53 t-version=v2.1) &
54 t-version=v2.1) &
55 t-version=v2.1) &
56 t-version=v2.1) &
57 t-version=v2.1) &
58 t-version=v2.1) &
59 t-version=v2.1) &
60 t-version=v2.1) &

1 t-version=v2.1) &
2 t-version=v2.1) &
3 t-version=v2.1) &
4 t-version=v2.1) &
5 t-version=v2.1) &
6 t-version=v2.1) &
7 t-version=v2.1) &
8 t-version=v2.1) &
9 t-version=v2.1) &
10 t-version=v2.1) &
11 t-version=v2.1) &
12 t-version=v2.1) &
13 t-version=v2.1) &
14 t-version=v2.1) &
15 ontaining protein At4g08455 OS=Arabidopsis thaliana (sp|q6dbn1|y4845_arath : 243.0)
16 ontaining protein At4g08455 OS=Arabidopsis thaliana (sp|q6dbn1|y4845_arath : 243.0)
17 ontaining protein At4g08455 OS=Arabidopsis thaliana (sp|q6dbn1|y4845_arath : 243.0)
18 ontaining protein At4g08455 OS=Arabidopsis thaliana (sp|q6dbn1|y4845_arath : 243.0)
19 ontaining protein At4g08455 OS=Arabidopsis thaliana (sp|q6dbn1|y4845_arath : 243.0)
20 ontaining protein At4g08455 OS=Arabidopsis thaliana (sp|q6dbn1|y4845_arath : 243.0)
21 ontaining protein At4g08455 OS=Arabidopsis thaliana (sp|q6dbn1|y4845_arath : 243.0)
22 ontaining protein At4g08455 OS=Arabidopsis thaliana (sp|q6dbn1|y4845_arath : 243.0)
23 ontaining protein At4g08455 OS=Arabidopsis thaliana (sp|q6dbn1|y4845_arath : 243.0)
24 ontaining protein At4g08455 OS=Arabidopsis thaliana (sp|q6dbn1|y4845_arath : 243.0)
25 ontaining protein At4g08455 OS=Arabidopsis thaliana (sp|q6dbn1|y4845_arath : 243.0)
26 ontaining protein At4g08455 OS=Arabidopsis thaliana (sp|q6dbn1|y4845_arath : 243.0)
27 ontaining protein At4g08455 OS=Arabidopsis thaliana (sp|q6dbn1|y4845_arath : 243.0)
28 ontaining protein At4g08455 OS=Arabidopsis thaliana (sp|q6dbn1|y4845_arath : 243.0)
29 ontaining protein At4g08455 OS=Arabidopsis thaliana (sp|q6dbn1|y4845_arath : 243.0)
30 epeat-containing protein At5g50990 OS=Arabidopsis thaliana (sp|q9fi49|pp428_arath : 614.0)
31
32 &
33 &
34 &
35 &
36 &
37 &
38 &
39 &
40 &
41 &
42 &
43
44
45 t3g47200 OS=Arabidopsis thaliana (sp|q9sd53|y3720_arath : 274.0)
46 t3g47200 OS=Arabidopsis thaliana (sp|q9sd53|y3720_arath : 274.0)
47 t3g47200 OS=Arabidopsis thaliana (sp|q9sd53|y3720_arath : 274.0)
48 t3g47200 OS=Arabidopsis thaliana (sp|q9sd53|y3720_arath : 274.0)
49 t3g47200 OS=Arabidopsis thaliana (sp|q9sd53|y3720_arath : 274.0)
50 t3g47200 OS=Arabidopsis thaliana (sp|q9sd53|y3720_arath : 274.0)
51 t3g47200 OS=Arabidopsis thaliana (sp|q9sd53|y3720_arath : 274.0)
52 t3g47200 OS=Arabidopsis thaliana (sp|q9sd53|y3720_arath : 274.0)
53 t3g47200 OS=Arabidopsis thaliana (sp|q9sd53|y3720_arath : 274.0)
54 t3g47200 OS=Arabidopsis thaliana (sp|q9sd53|y3720_arath : 274.0)
55 t3g47200 OS=Arabidopsis thaliana (sp|q9sd53|y3720_arath : 274.0)
56 t3g47200 OS=Arabidopsis thaliana (sp|q9sd53|y3720_arath : 274.0)
57 t3g47200 OS=Arabidopsis thaliana (sp|q9sd53|y3720_arath : 274.0)
58 t3g47200 OS=Arabidopsis thaliana (sp|q9sd53|y3720_arath : 274.0)
59 t3g47200 OS=Arabidopsis thaliana (sp|q9sd53|y3720_arath : 274.0)
60 t3g47200 OS=Arabidopsis thaliana (sp|q9sd53|y3720_arath : 274.0)

1
2
3 !.1 annot-version=v2.1) &
4 =v2.1) &
5 =v2.1) &
6 =v2.1) &
7 =v2.1) &
8 =v2.1) &
9 =v2.1) &
10 =v2.1) &
11 =v2.1) &
12 =v2.1) &
13 =v2.1) &
14 =v2.1) &
15 =v2.1) &
16 =v2.1) &
17
18 `k
19 `k
20 `k
21 `k
22 `k
23 `k
24 `k
25 `k
26 `k
27 `k
28 `k
29 `k
30 `k
31 `k
32 `k
33 `k
34 `k
35 `k
36 `k
37 `k
38 `k
39 `k
40 `k
41 `k
42 `k
43 `k
44 `k
45 `k
46 `k
47 `k
48 `k
49 `k
50 `k
51 `k
52 `k
53 `k
54 `k
55 `k
56 `k
57 `k
58 `k
59 `k
60 `k
ion=v2.1) &

Do not distribute

1
2 ion=v2.1) &
3 ion=v2.1) &
4 ion=v2.1) &
5 ion=v2.1) &
6 ion=v2.1) &
7 ion=v2.1) &
8 ion=v2.1) &
9 ion=v2.1) &
10 ion=v2.1) &
11 ion=v2.1) &
12 ion=v2.1) &
13 ion=v2.1) &

14 ses.EC_2.4 glycosyltransferase(50.2.4 : 568.2) (original description: pacid=37146124 transcript=Phv
15 ses.EC_2.4 glycosyltransferase(50.2.4 : 568.2) (original description: pacid=37146124 transcript=Phv
16 ses.EC_2.4 glycosyltransferase(50.2.4 : 568.2) (original description: pacid=37146124 transcript=Phv
17 ses.EC_2.4 glycosyltransferase(50.2.4 : 568.2) (original description: pacid=37146124 transcript=Phv
18 ses.EC_2.4 glycosyltransferase(50.2.4 : 568.2) (original description: pacid=37146124 transcript=Phv
19 ses.EC_2.4 glycosyltransferase(50.2.4 : 568.2) (original description: pacid=37146124 transcript=Phv
20 ses.EC_2.4 glycosyltransferase(50.2.4 : 568.2) (original description: pacid=37146124 transcript=Phv
21 ses.EC_2.4 glycosyltransferase(50.2.4 : 568.2) (original description: pacid=37146124 transcript=Phv
22 ses.EC_2.4 glycosyltransferase(50.2.4 : 568.2) (original description: pacid=37146124 transcript=Phv
23 ses.EC_2.4 glycosyltransferase(50.2.4 : 568.2) (original description: pacid=37146124 transcript=Phv
24 ses.EC_2.4 glycosyltransferase(50.2.4 : 568.2) (original description: pacid=37146124 transcript=Phv
25 ses.EC_2.4 glycosyltransferase(50.2.4 : 568.2) (original description: pacid=37146124 transcript=Phv
26 ses.EC_2.4 glycosyltransferase(50.2.4 : 568.2) (original description: pacid=37146124 transcript=Phv
27 ses.EC_2.4 glycosyltransferase(50.2.4 : 568.2) (original description: pacid=37146124 transcript=Phv
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42

43 !.1 annot-version=v2.1) &
44 !.1 annot-version=v2.1) &
45 !.1 annot-version=v2.1) &
46 !.1 annot-version=v2.1) &
47 !.1 annot-version=v2.1) &
48 !.1 annot-version=v2.1) &
49 !.1 annot-version=v2.1) &
50 !.1 annot-version=v2.1) &
51 !.1 annot-version=v2.1) &
52 !.1 annot-version=v2.1) &
53 !.1 annot-version=v2.1) &
54 !.1 annot-version=v2.1) &
55 !.1 annot-version=v2.1) &
56 n=v2.1) &
57 n=v2.1) &
58 n=v2.1) &
59 n=v2.1) &
60 n=v2.1) &

1
2 n=v2.1) &
3 n=v2.1) &
4 n=v2.1) &
5 n=v2.1) &
6 n=v2.1) &
7 n=v2.1) &
8 n=v2.1) &
9 n=v2.1) &
10 n=v2.1) &
11 n=v2.1) &
12 n=v2.1) &
13 n=v2.1) &
14 n=v2.1) &
15 n=v2.1) &
16 n=v2.1) &
17 n=v2.1) &
18 n=v2.1) &
19 n=v2.1) &
20 n=v2.1) &
21
22
23
24
25
26
27
28
29
30
31
32
33
34

35 ol/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
36 ol/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
37 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
38 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
39 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
40 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
41 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
42 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
43 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
44 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
45 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
46 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
47 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
48 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
49 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
50
51 ot-version=v2.1) &
52 2.1) &
53 2.1) &
54 2.1) &
55 2.1) &
56 2.1) &
57 2.1) &
58 2.1) &
59 2.1) &
60 2.1) &
2.1) &

1
2 2.1) &
3 2.1) &
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32

33 &
34 &
35 &
36 &
37 &
38 &
39 &
40 &
41 &
42 &
43 &
44 &
45 &
46 &
47 &
48 &
49 &
50 &
51 &
52 &
53 &
54 &
55 &
56 &
57 &
58 &
59 &
60 &

Do not distribute

1
2 on=v2.1) &
3 on=v2.1) &
4 on=v2.1) &
5 on=v2.1) &
6 on=v2.1) &
7 on=v2.1) &
8 on=v2.1) &
9 on=v2.1) &
10 on=v2.1) &
11 on=v2.1) &
12 on=v2.1) &
13 on=v2.1) &
14 on=v2.1) &
15 on=v2.1) &

16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31 &
32 &
33 &
34 &
35 &
36 &
37 &
38 &
39 &
40 &
41 &
42 &
43 &
44 &
45 &
46 &
47 &
48 &
49 &
50 &
51 &
52 &
53 &
54 &
55 &
56 &
57 &
58 &
59 &
60 &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15 ranscript=Phvul.003G001200.1 locus=Phvul.003G001200 ID=Phvul.003G001200.1.v2.1 annot-versic
16 ranscript=Phvul.003G001200.1 locus=Phvul.003G001200 ID=Phvul.003G001200.1.v2.1 annot-versic
17 ranscript=Phvul.003G001200.1 locus=Phvul.003G001200 ID=Phvul.003G001200.1.v2.1 annot-versic
18 ranscript=Phvul.003G001200.1 locus=Phvul.003G001200 ID=Phvul.003G001200.1.v2.1 annot-versic
19 ranscript=Phvul.003G001200.1 locus=Phvul.003G001200 ID=Phvul.003G001200.1.v2.1 annot-versic
20 ranscript=Phvul.003G001200.1 locus=Phvul.003G001200 ID=Phvul.003G001200.1.v2.1 annot-versic
21 ranscript=Phvul.003G001200.1 locus=Phvul.003G001200 ID=Phvul.003G001200.1.v2.1 annot-versic
22 ranscript=Phvul.003G001200.1 locus=Phvul.003G001200 ID=Phvul.003G001200.1.v2.1 annot-versic
23 ranscript=Phvul.003G001200.1 locus=Phvul.003G001200 ID=Phvul.003G001200.1.v2.1 annot-versic
24 ranscript=Phvul.003G001200.1 locus=Phvul.003G001200 ID=Phvul.003G001200.1.v2.1 annot-versic
25 ranscript=Phvul.003G001200.1 locus=Phvul.003G001200 ID=Phvul.003G001200.1.v2.1 annot-versic
26 ranscript=Phvul.003G001200.1 locus=Phvul.003G001200 ID=Phvul.003G001200.1.v2.1 annot-versic
27 ranscript=Phvul.003G001200.1 locus=Phvul.003G001200 ID=Phvul.003G001200.1.v2.1 annot-versic
28 ranscript=Phvul.003G001200.1 locus=Phvul.003G001200 ID=Phvul.003G001200.1.v2.1 annot-versic
29 ranscript=Phvul.003G001200.1 locus=Phvul.003G001200 ID=Phvul.003G001200.1.v2.1 annot-versic
30 ranscript=Phvul.003G001200.1 locus=Phvul.003G001200 ID=Phvul.003G001200.1.v2.1 annot-versic
31 lable(sp|m1c5m7|rph1_soltu : 239.0)
32
33
34
35
36
37
38
39
40
41
42
43
44

45 version=v2.1) &
46 version=v2.1) &
47 version=v2.1) &
48 version=v2.1) &
49 version=v2.1) &
50 version=v2.1) &
51 version=v2.1) &
52 version=v2.1) &
53 version=v2.1) &
54 version=v2.1) &
55 version=v2.1) &
56 version=v2.1) &
57 version=v2.1) &
58 &
59 &
60 &

1
2 &
3 &
4 &
5 &
6 &
7 &
8 &
9 &
10 &
11 &
12 &
13 &
14 &
15 &
16 &
17 &
18 &
19 &
20 &
21 &
22 &
23 &
24 -version=v2.1) &
25 -version=v2.1) &
26 -version=v2.1) &
27 -version=v2.1) &
28 -version=v2.1) &
29 -version=v2.1) &
30 -version=v2.1) &
31 -version=v2.1) &
32 -version=v2.1) &
33 -version=v2.1) &
34 -version=v2.1) &
35 -version=v2.1) &
36 -version=v2.1) &
37 -version=v2.1) &
38
39 ǔ
40 ǔ
41 ǔ
42 ǔ
43 ǔ
44 ǔ
45 ǔ
46 ǔ
47 ǔ
48 ǔ
49 ǔ
50 ǔ
51 ǔ
52 ǔ
53 ǔ
54 ǔ
55 ǔ
56 ǔ
57 ǔ
58 ǔ
59 ǔ
60 ǔ

Do not distribute

1 SS-ASSOCIATED 32 OS=Arabidopsis thaliana (sp|q8gwl1|hsa32_arath : 383.0)
2 &
3
4 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
5 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
6 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
7 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
8 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
9 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
10 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
11 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
12 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
13 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
14 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
15 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
16 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
17 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
18 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
19 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
20 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
21 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
22 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
23 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
24 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
25 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
26 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
27 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
28 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
29 =Phvul.002G330500.5.v2.1 annot-version=v2.1) &
30 =v2.1) &
31 =v2.1) &
32 =v2.1) &
33 =v2.1) &
34 =v2.1) &
35 =v2.1) &
36 =v2.1) &
37 =v2.1) &
38 =v2.1) &
39 =v2.1) &
40 =v2.1) &
41 =v2.1) &
42 =v2.1) &
43 =v2.1) &
44
45) &
46) &
47) &
48) &
49) &
50) &
51) &
52) &
53) &
54) &
55) &
56) &
57) &
58) &
59) &
60 2.1) &
2.1) &

1
2 2.1) &
3 2.1) &
4 2.1) &
5 2.1) &
6 2.1) &
7 2.1) &
8 2.1) &
9 2.1) &
10 2.1) &
11 2.1) &
12 2.1) &
13 2.1) &
14 2.1) &
15 2.1) &
16 2.1) &
17 2.1) &
18 2.1) &
19 2.1) &
20 2.1) &
21 2.1) &
22 2.1) &
23 2.1) &
24 2.1) &
25 2.1) &
26 2.1) &
27 2.1) &
28 !.1 annot-version=v2.1) &
29 ersion=v2.1) &
30 ersion=v2.1) &
31 ersion=v2.1) &
32 ersion=v2.1) &
33 ersion=v2.1) &
34 ersion=v2.1) &
35 ersion=v2.1) &
36 ersion=v2.1) &
37 ersion=v2.1) &
38 ersion=v2.1) &
39 ersion=v2.1) &
40 ersion=v2.1) &
41 ersion=v2.1) &
42 ersion=v2.1) &
43 ersion=v2.1) &
44 ersion=v2.1) &
45 ersion=v2.1) &
46 ersion=v2.1) &
47 ersion=v2.1) &
48 ersion=v2.1) &
49 ersion=v2.1) &
50 ersion=v2.1) &
51 ersion=v2.1) &
52 ersion=v2.1) &
53 ersion=v2.1) &
54 ersion=v2.1) &
55 ersion=v2.1) &
56 ersion=v2.1) &
57 ersion=v2.1) &
58 ersion=v2.1) &
59 ersion=v2.1) &
60 ersion=v2.1) &

Do not distribute

1
2 ersion=v2.1) &
3 ersion=v2.1) &
4 ersion=v2.1) &
5 ersion=v2.1) &
6 ersion=v2.1) &
7 ersion=v2.1) &
8 ersion=v2.1) &
9 ersion=v2.1) &
10 ersion=v2.1) &
11 ersion=v2.1) &
12 ersion=v2.1) &
13 ersion=v2.1) &
14 ersion=v2.1) &
15 ersion=v2.1) &
16 ersion=v2.1) &
17 ersion=v2.1) &
18 ersion=v2.1) &
19 ersion=v2.1) &
20 ersion=v2.1) &
21 isum sativum (sp|p36907|chix_pea : 377.0)
22 isum sativum (sp|p36907|chix_pea : 377.0)
23 isum sativum (sp|p36907|chix_pea : 377.0)
24 isum sativum (sp|p36907|chix_pea : 377.0)
25 isum sativum (sp|p36907|chix_pea : 377.0)
26 isum sativum (sp|p36907|chix_pea : 377.0)
27 isum sativum (sp|p36907|chix_pea : 377.0)
28 isum sativum (sp|p36907|chix_pea : 377.0)
29 isum sativum (sp|p36907|chix_pea : 377.0)
30 isum sativum (sp|p36907|chix_pea : 377.0)
31 isum sativum (sp|p36907|chix_pea : 377.0)
32 isum sativum (sp|p36907|chix_pea : 377.0)
33 isum sativum (sp|p36907|chix_pea : 377.0)
34 isum sativum (sp|p36907|chix_pea : 377.0)
35 lable(sp|f4jts8|nov_arath : 2070.0)
36 lable(sp|f4jts8|nov_arath : 2070.0)
37 lable(sp|f4jts8|nov_arath : 2070.0)
38 lable(sp|f4jts8|nov_arath : 2070.0)
39 lable(sp|f4jts8|nov_arath : 2070.0)
40 lable(sp|f4jts8|nov_arath : 2070.0)
41 lable(sp|f4jts8|nov_arath : 2070.0)
42 lable(sp|f4jts8|nov_arath : 2070.0)
43 lable(sp|f4jts8|nov_arath : 2070.0)
44 lable(sp|f4jts8|nov_arath : 2070.0)
45 lable(sp|f4jts8|nov_arath : 2070.0)
46 lable(sp|f4jts8|nov_arath : 2070.0)
47 lable(sp|f4jts8|nov_arath : 2070.0)
48 lable(sp|f4jts8|nov_arath : 2070.0)
49 lable(sp|f4jts8|nov_arath : 2070.0)
50 lable(sp|f4jts8|nov_arath : 2070.0)
51 lable(sp|f4jts8|nov_arath : 2070.0)
52 lable(sp|f4jts8|nov_arath : 2070.0)
53 lable(sp|f4jts8|nov_arath : 2070.0)
54 lable(sp|f4jts8|nov_arath : 2070.0)
55 lable(sp|f4jts8|nov_arath : 2070.0)
56 lable(sp|f4jts8|nov_arath : 2070.0)
57 lable(sp|f4jts8|nov_arath : 2070.0)
58 lable(sp|f4jts8|nov_arath : 2070.0)
59 lable(sp|f4jts8|nov_arath : 2070.0)
60 lable(sp|f4jts8|nov_arath : 2070.0)
 ersion=v2.1) &

1
2 version=v2.1) &
3 version=v2.1) &
4 version=v2.1) &
5 version=v2.1) &
6 version=v2.1) &
7 version=v2.1) &
8 version=v2.1) &
9 version=v2.1) &
10 version=v2.1) &
11 version=v2.1) &
12 version=v2.1) &
13 version=v2.1) &
14 version=v2.1) &

15 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)

16 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)

17 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

18 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

19 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

20 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

21 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

22 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

23 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

24 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

25 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

26 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

27 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

28 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

29 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

30 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

31 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

32 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

33 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

34 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

35 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

36 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

37 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

38 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

39 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

40 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

41 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

42 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

43 tin-protein ligase ZFP1 OS=Oryza sativa subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

44 &

45 &

46 &

47 &

48 &

49 &

50 &

51 &

52 &

53 &

54 &

55 &

56 &

57 &

58 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)

59 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)

60 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)

1 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
2 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
3 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
4 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
5 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
6 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
7 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
8 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
9 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
10 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
11 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
12 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
13 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
14 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
15 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
16 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
17 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
18 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
19 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
20 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
21 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
22 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
23 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
24 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
25 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
26 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
27 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
28 eta-2 OS=Arabidopsis thaliana (sp|q9c827|cob22_arath : 307.0)
29 00 ID=Phvul.006G022400.1.v2.1 annot-version=v2.1) &
30 :Phvul.006G130200 ID=Phvul.006G130200.1.v2.1 annot-version=v2.1) &
31 :Phvul.006G130200 ID=Phvul.006G130200.1.v2.1 annot-version=v2.1) &
32 :Phvul.006G130200 ID=Phvul.006G130200.1.v2.1 annot-version=v2.1) &
33 :Phvul.006G130200 ID=Phvul.006G130200.1.v2.1 annot-version=v2.1) &
34 :Phvul.006G130200 ID=Phvul.006G130200.1.v2.1 annot-version=v2.1) &
35 :Phvul.006G130200 ID=Phvul.006G130200.1.v2.1 annot-version=v2.1) &
36 :Phvul.006G130200 ID=Phvul.006G130200.1.v2.1 annot-version=v2.1) &
37 :Phvul.006G130200 ID=Phvul.006G130200.1.v2.1 annot-version=v2.1) &
38 :Phvul.006G130200 ID=Phvul.006G130200.1.v2.1 annot-version=v2.1) &
39 :Phvul.006G130200 ID=Phvul.006G130200.1.v2.1 annot-version=v2.1) &
40 :Phvul.006G130200 ID=Phvul.006G130200.1.v2.1 annot-version=v2.1) &
41 :Phvul.006G130200 ID=Phvul.006G130200.1.v2.1 annot-version=v2.1) &
42 :Phvul.006G130200 ID=Phvul.006G130200.1.v2.1 annot-version=v2.1) &
43 :Phvul.006G130200 ID=Phvul.006G130200.1.v2.1 annot-version=v2.1) &
44 :Phvul.006G130200 ID=Phvul.006G130200.1.v2.1 annot-version=v2.1) &
45 osphate/phosphate translocator At3g11320 OS=Arabidopsis thaliana (sp|q5xf09|pt311_arath : 446.1
46 .1) &
47) &
48) &
49) &
50) &
51) &
52) &
53) &
54) &
55) &
56) &
57) &
58) &
59) &
60) &

1
2 =v2.1) &
3 =v2.1) &
4 =v2.1) &
5 =v2.1) &
6 =v2.1) &
7 =v2.1) &
8 =v2.1) &
9 =v2.1) &
10 =v2.1) &
11 =v2.1) &
12 =v2.1) &
13 =v2.1) &
14 =v2.1) &
15 =v2.1) &
16 =v2.1) &
17 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
18 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
19 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
20 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
21 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
22 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
23 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
24 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
25 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
26 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
27 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
28 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
29 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
30 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
31 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
32 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
33 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
34 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
35 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
36 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
37 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
38 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
39 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
40 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
41 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
42 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
43 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
59 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
60 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)

1 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
2 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
3 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
4 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
5 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
6 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
7 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
8 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
9 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
10 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
11 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
12 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
13 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
14 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
15 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
16 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
17 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
18 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
19 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
20 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
21 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
22 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
23 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
24 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
25 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
26 attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
27 =v2.1) &
28 =v2.1) &
29 =v2.1) &
30 =v2.1) &
31 =v2.1) &
32 =v2.1) &
33 =v2.1) &
34 =v2.1) &
35 =v2.1) &
36 =v2.1) &
37 =v2.1) &
38 =v2.1) &
39 =v2.1) &
40 =v2.1) &
41 G289900.1.v2.1 annot-version=v2.1) &
42 G289900.1.v2.1 annot-version=v2.1) &
43 G289900.1.v2.1 annot-version=v2.1) &
44 G289900.1.v2.1 annot-version=v2.1) &
45 G289900.1.v2.1 annot-version=v2.1) &
46 G289900.1.v2.1 annot-version=v2.1) &
47 G289900.1.v2.1 annot-version=v2.1) &
48 G289900.1.v2.1 annot-version=v2.1) &
49 G289900.1.v2.1 annot-version=v2.1) &
50 G289900.1.v2.1 annot-version=v2.1) &
51 G289900.1.v2.1 annot-version=v2.1) &
52 G289900.1.v2.1 annot-version=v2.1) &
53 G289900.1.v2.1 annot-version=v2.1) &
54 G289900.1.v2.1 annot-version=v2.1) &
55 G289900.1.v2.1 annot-version=v2.1) &
56 . annot-version=v2.1) &
57 . annot-version=v2.1) &
58 . annot-version=v2.1) &
59 . annot-version=v2.1) &
60 . annot-version=v2.1) &

1
2 . annot-version=v2.1) &
3 . annot-version=v2.1) &
4 . annot-version=v2.1) &
5 . annot-version=v2.1) &
6 . annot-version=v2.1) &
7 . annot-version=v2.1) &
8 . annot-version=v2.1) &
9
10 G117500 ID=Phvul.009G117500.1.v2.1 annot-version=v2.1) &
11 se 5 OS=Arabidopsis thaliana (sp|q9ssa7|glip5_arath : 192.0)
12 se 5 OS=Arabidopsis thaliana (sp|q9ssa7|glip5_arath : 192.0)
13 se 5 OS=Arabidopsis thaliana (sp|q9ssa7|glip5_arath : 192.0)
14 se 5 OS=Arabidopsis thaliana (sp|q9ssa7|glip5_arath : 192.0)
15 se 5 OS=Arabidopsis thaliana (sp|q9ssa7|glip5_arath : 192.0)
16 se 5 OS=Arabidopsis thaliana (sp|q9ssa7|glip5_arath : 192.0)
17 se 5 OS=Arabidopsis thaliana (sp|q9ssa7|glip5_arath : 192.0)
18 se 5 OS=Arabidopsis thaliana (sp|q9ssa7|glip5_arath : 192.0)
19 se 5 OS=Arabidopsis thaliana (sp|q9ssa7|glip5_arath : 192.0)
20 se 5 OS=Arabidopsis thaliana (sp|q9ssa7|glip5_arath : 192.0)
21 se 5 OS=Arabidopsis thaliana (sp|q9ssa7|glip5_arath : 192.0)
22 se 5 OS=Arabidopsis thaliana (sp|q9ssa7|glip5_arath : 192.0)
23 se 5 OS=Arabidopsis thaliana (sp|q9ssa7|glip5_arath : 192.0)
24 yrotein At3g02645 OS=Arabidopsis thaliana (sp|p0c897|y3264_arath : 278.0)
25 ferase transferring phosphorus-containing group(50.2.7 : 73.1) (original description: pacid=371568:
26 ferase transferring phosphorus-containing group(50.2.7 : 73.1) (original description: pacid=371568:
27 ferase transferring phosphorus-containing group(50.2.7 : 73.1) (original description: pacid=371568:
28 ferase transferring phosphorus-containing group(50.2.7 : 73.1) (original description: pacid=371568:
29 ferase transferring phosphorus-containing group(50.2.7 : 73.1) (original description: pacid=371568:
30 ferase transferring phosphorus-containing group(50.2.7 : 73.1) (original description: pacid=371568:
31 ferase transferring phosphorus-containing group(50.2.7 : 73.1) (original description: pacid=371568:
32 ferase transferring phosphorus-containing group(50.2.7 : 73.1) (original description: pacid=371568:
33 ferase transferring phosphorus-containing group(50.2.7 : 73.1) (original description: pacid=371568:
34 ferase transferring phosphorus-containing group(50.2.7 : 73.1) (original description: pacid=371568:
35 ferase transferring phosphorus-containing group(50.2.7 : 73.1) (original description: pacid=371568:
36 ferase transferring phosphorus-containing group(50.2.7 : 73.1) (original description: pacid=371568:
37 ferase transferring phosphorus-containing group(50.2.7 : 73.1) (original description: pacid=371568:
38 ferase transferring phosphorus-containing group(50.2.7 : 73.1) (original description: pacid=371568:
39 ferase transferring phosphorus-containing group(50.2.7 : 73.1) (original description: pacid=371568:
40 300 ID=Phvul.011G047800.2.v2.1 annot-version=v2.1) &
41 300 ID=Phvul.011G047800.2.v2.1 annot-version=v2.1) &
42 .2.1) &
43 .2.1) &
44 .2.1) &
45 .2.1) &
46 .2.1) &
47 .2.1) &
48 .2.1) &
49 .2.1) &
50 .2.1) &
51 .2.1) &
52 .2.1) &
53 .2.1) &
54 .2.1) &
55 .2.1) &
56
57
58
59
60

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8 &
- 9 &
- 10 &
- 11 &
- 12 &
- 13 &
- 14 &
- 15 &
- 16 &
- 17 &
- 18 &
- 19 &
- 20 &
- 21 &
- 22 &
- 23 &
- 24 &
- 25 &
- 26 &
- 27 &
- 28 &
- 29 &
- 30 &
- 31 &
- 32 &
- 33 &
- 34 &
- 35 &
- 36 &
- 37 &
- 38 &
- 39 &
- 40 &
- 41 &
- 42 &
- 43 &
- 44 &
- 45 &
- 46 &
- 47 &
- 48 &
- 49 &
- 50 &
- 51 &
- 52 &
- 53 &
- 54 &
- 55 &
- 56 &
- 57 &
- 58 &
- 59 &
- 60 &

Do not distribute

1
2 &
3 &
4 &
5 &
6 &
7 &
8 &
9 &
10 &
11 &
12 &
13 &
14 &
15 &
16 &
17 &
18 &
19 &
20 &
21 &
22 &
23 &
24 &
25 &
26 &
27 &
28 &
29 &
30 &
31 &
32 &
33 &
34 &
35 &
36 &
37 &
38 &
39 &
40 &
41 &
42 &
43 &
44 &
45 &
46 &
47 &
48 &
49 &
50 &
51 &
52 &
53 &
54 &
55 &
56 &
57 &
58 &
59 &
60 &

Do not distribute

1 &
2 &
3 &
4 &
5 &
6 &
7 &
8 &
9 &
10 &
11 &
12 &
13 &
14 &
15 &
16 &
17 &
18 &
19 .7 OS=Arabidopsis thaliana (sp|q0wrc9|ski17_arath : 270.0)
20 .7 OS=Arabidopsis thaliana (sp|q0wrc9|ski17_arath : 270.0)
21 .7 OS=Arabidopsis thaliana (sp|q0wrc9|ski17_arath : 270.0)
22 .7 OS=Arabidopsis thaliana (sp|q0wrc9|ski17_arath : 270.0)
23 .7 OS=Arabidopsis thaliana (sp|q0wrc9|ski17_arath : 270.0)
24 .7 OS=Arabidopsis thaliana (sp|q0wrc9|ski17_arath : 270.0)
25 .7 OS=Arabidopsis thaliana (sp|q0wrc9|ski17_arath : 270.0)
26 .7 OS=Arabidopsis thaliana (sp|q0wrc9|ski17_arath : 270.0)
27 .7 OS=Arabidopsis thaliana (sp|q0wrc9|ski17_arath : 270.0)
28 .7 OS=Arabidopsis thaliana (sp|q0wrc9|ski17_arath : 270.0)
29 .7 OS=Arabidopsis thaliana (sp|q0wrc9|ski17_arath : 270.0)
30 .7 OS=Arabidopsis thaliana (sp|q0wrc9|ski17_arath : 270.0)
31 .7 OS=Arabidopsis thaliana (sp|q0wrc9|ski17_arath : 270.0)
32 .7 OS=Arabidopsis thaliana (sp|q0wrc9|ski17_arath : 270.0)
33 -version=v2.1) &
34 -version=v2.1) &
35 -version=v2.1) &
36 -version=v2.1) &
37 -version=v2.1) &
38 -version=v2.1) &
39 -version=v2.1) &
40 -version=v2.1) &
41 -version=v2.1) &
42 -version=v2.1) &
43 -version=v2.1) &
44 -version=v2.1) &
45 -version=v2.1) &
46 -version=v2.1) &
47 -version=v2.1) &
48 101 or related substance as donor(50.1.10 : 138.7) (original description: pacid=37170741 transcript=
49 101 or related substance as donor(50.1.10 : 138.7) (original description: pacid=37168554 transcript=
50) &
51) &
52) &
53) &
54) &
55) &
56) &
57) &
58) &
59) &
60) &

1
2 .) &
3 .) &
4 .) &
5
6 va (sp|a6p6w0|casl1_cansa : 505.0) (original description: pacid=37175030 transcript=Phvul.002G1!
7 va (sp|a6p6w0|casl1_cansa : 505.0) (original description: pacid=37175030 transcript=Phvul.002G1!
8 va (sp|a6p6w0|casl1_cansa : 505.0) (original description: pacid=37175030 transcript=Phvul.002G1!
9
10 va (sp|a6p6w0|casl1_cansa : 505.0) (original description: pacid=37175030 transcript=Phvul.002G1!
11 va (sp|a6p6w0|casl1_cansa : 505.0) (original description: pacid=37175030 transcript=Phvul.002G1!
12 va (sp|a6p6w0|casl1_cansa : 505.0) (original description: pacid=37175030 transcript=Phvul.002G1!
13 va (sp|a6p6w0|casl1_cansa : 505.0) (original description: pacid=37175030 transcript=Phvul.002G1!
14 va (sp|a6p6w0|casl1_cansa : 505.0) (original description: pacid=37175030 transcript=Phvul.002G1!
15 va (sp|a6p6w0|casl1_cansa : 505.0) (original description: pacid=37175030 transcript=Phvul.002G1!
16 va (sp|a6p6w0|casl1_cansa : 505.0) (original description: pacid=37175030 transcript=Phvul.002G1!
17 va (sp|a6p6w0|casl1_cansa : 505.0) (original description: pacid=37175030 transcript=Phvul.002G1!
18 va (sp|a6p6w0|casl1_cansa : 505.0) (original description: pacid=37175030 transcript=Phvul.002G1!
19 va (sp|a6p6w0|casl1_cansa : 505.0) (original description: pacid=37175030 transcript=Phvul.002G1!
20 1) &
21 1) &
22 1) &
23 1) &
24 1) &
25 1) &
26 1) &
27 1) &
28 1) &
29 1) &
30 1) &
31 1) &
32 1) &
33 1) &
34 1) &
35 1) &
36 1) &
37 1) &
38 1) &
39 1) &
40 1) &
41 1) &
42 1) &
43 1) &
44 1) &
45 1) &
46 &
47 &
48 &
49 &
50 &
51 &
52 &
53 &
54 &
55 &
56 &
57 &
58 &
59 &
60 &
k



1
2 k
3 k
4 version=v2.1) &
5 0.2.v2.1 annot-version=v2.1) &
6 0.2.v2.1 annot-version=v2.1) &
7 0.2.v2.1 annot-version=v2.1) &
8 0.2.v2.1 annot-version=v2.1) &
9 0.2.v2.1 annot-version=v2.1) &
10 0.2.v2.1 annot-version=v2.1) &
11 0.2.v2.1 annot-version=v2.1) &
12 0.2.v2.1 annot-version=v2.1) &
13 0.2.v2.1 annot-version=v2.1) &
14 0.2.v2.1 annot-version=v2.1) &
15 0.2.v2.1 annot-version=v2.1) &
16 0.2.v2.1 annot-version=v2.1) &
17 0.2.v2.1 annot-version=v2.1) &
18 0.2.v2.1 annot-version=v2.1) &
19 0.2.v2.1 annot-version=v2.1) &
20 0.2.v2.1 annot-version=v2.1) &
21 0.2.v2.1 annot-version=v2.1) &
22 0.2.v2.1 annot-version=v2.1) &
23 0.2.v2.1 annot-version=v2.1) &
24 0.2.v2.1 annot-version=v2.1) &
25 0.2.v2.1 annot-version=v2.1) &
26 0.2.v2.1 annot-version=v2.1) &
27 0.2.v2.1 annot-version=v2.1) &
28 0.2.v2.1 annot-version=v2.1) &
29 0.2.v2.1 annot-version=v2.1) &
30 0.2.v2.1 annot-version=v2.1) &
31 0.2.v2.1 annot-version=v2.1) &
32 0.2.v2.1 annot-version=v2.1) &
33 0.2.v2.1 annot-version=v2.1) &
34 0.2.v2.1 annot-version=v2.1) &
35 membrane protein 1 OS=Arabidopsis thaliana (sp|q93zh9|hhp1_arath : 364.0)
36 membrane protein 1 OS=Arabidopsis thaliana (sp|q93zh9|hhp1_arath : 364.0)
37 membrane protein 1 OS=Arabidopsis thaliana (sp|q93zh9|hhp1_arath : 364.0)
38 membrane protein 1 OS=Arabidopsis thaliana (sp|q93zh9|hhp1_arath : 364.0)
39 membrane protein 1 OS=Arabidopsis thaliana (sp|q93zh9|hhp1_arath : 364.0)
40 membrane protein 1 OS=Arabidopsis thaliana (sp|q93zh9|hhp1_arath : 364.0)
41 membrane protein 1 OS=Arabidopsis thaliana (sp|q93zh9|hhp1_arath : 364.0)
42 membrane protein 1 OS=Arabidopsis thaliana (sp|q93zh9|hhp1_arath : 364.0)
43 membrane protein 1 OS=Arabidopsis thaliana (sp|q93zh9|hhp1_arath : 364.0)
44 membrane protein 1 OS=Arabidopsis thaliana (sp|q93zh9|hhp1_arath : 364.0)
45 membrane protein 1 OS=Arabidopsis thaliana (sp|q93zh9|hhp1_arath : 364.0)
46 membrane protein 1 OS=Arabidopsis thaliana (sp|q93zh9|hhp1_arath : 364.0)
47 membrane protein 1 OS=Arabidopsis thaliana (sp|q93zh9|hhp1_arath : 364.0)
48 2.1) &
49 2.1) &
50 2.1) &
51 2.1) &
52 2.1) &
53 2.1) &
54 2.1) &
55 2.1) &
56 2.1) &
57 2.1) &
58 2.1) &
59 2.1) &
60 2.1) &

1
2 2.1) &
3 2.1) &
4 2.1) &
5 2.1) &
6 2.1) &
7 2.1) &
8 2.1) &
9 2.1) &
10 2.1) &
11 2.1) &
12 2.1) &
13
14 v2.1) &
15 v2.1) &
16 v2.1) &
17 v2.1) &
18 v2.1) &
19 v2.1) &
20 v2.1) &
21 v2.1) &
22 v2.1) &
23 v2.1) &
24 v2.1) &
25 v2.1) &
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41 2.1) &
42 2.1) &
43 2.1) &
44 !.1 annot-version=v2.1) &
45 !.1 annot-version=v2.1) &
46 !.1 annot-version=v2.1) &
47 !.1 annot-version=v2.1) &
48 !.1 annot-version=v2.1) &
49 !.1 annot-version=v2.1) &
50 !.1 annot-version=v2.1) &
51 !.1 annot-version=v2.1) &
52 !.1 annot-version=v2.1) &
53 !.1 annot-version=v2.1) &
54 !.1 annot-version=v2.1) &
55 !.1 annot-version=v2.1) &
56 !.1 annot-version=v2.1) &
57 .) &
58 .) &
59 .) &
60 .) &

Do not distribute

1
2 .) &
3 .) &
4 .) &
5 .) &
6 .) &
7 .) &
8 .) &
9 .) &
10 .) &
11 ot-version=v2.1) &
12 ot-version=v2.1) &
13 ot-version=v2.1) &
14 ot-version=v2.1) &
15 ot-version=v2.1) &
16 ot-version=v2.1) &
17 ot-version=v2.1) &
18 ot-version=v2.1) &
19 ot-version=v2.1) &
20 ot-version=v2.1) &
21 ot-version=v2.1) &
22 ot-version=v2.1) &
23 ot-version=v2.1) &
24 168700.1.v2.1 annot-version=v2.1) &
25 inot-version=v2.1) &
26 inot-version=v2.1) &
27 inot-version=v2.1) &
28 inot-version=v2.1) &
29 inot-version=v2.1) &
30 inot-version=v2.1) &
31 inot-version=v2.1) &
32 inot-version=v2.1) &
33 inot-version=v2.1) &
34 inot-version=v2.1) &
35 inot-version=v2.1) &
36 inot-version=v2.1) &
37 inot-version=v2.1) &
38 inot-version=v2.1) &
39 inot-version=v2.1) &
40 inot-version=v2.1) &
41 inot-version=v2.1) &
42 inot-version=v2.1) &
43 inot-version=v2.1) &
44 inot-version=v2.1) &
45 inot-version=v2.1) &
46 inot-version=v2.1) &
47 inot-version=v2.1) &
48 inot-version=v2.1) &
49 inot-version=v2.1) &
50 inot-version=v2.1) &
51 inot-version=v2.1) &
52 inot-version=v2.1) &
53 inot-version=v2.1) &
54 inot-version=v2.1) &
55 inot-version=v2.1) &
56 inot-version=v2.1) &
57 inot-version=v2.1) &
58 inot-version=v2.1) &
59 inot-version=v2.1) &
60 inot-version=v2.1) &
inot-version=v2.1) &

Do not distribute

1
2 inot-version=v2.1) &
3 inot-version=v2.1) &
4

5
6 ersion=v2.1) &
7 ersion=v2.1) &
8 ersion=v2.1) &
9 ersion=v2.1) &
10 ersion=v2.1) &
11 ersion=v2.1) &
12 ersion=v2.1) &
13 ersion=v2.1) &
14 ersion=v2.1) &
15 ersion=v2.1) &
16 ersion=v2.1) &
17 ersion=v2.1) &
18 ersion=v2.1) &

19)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
20)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
21)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
22)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
23)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
24)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
25)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
26)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
27)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
28)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
29)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
30)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
31)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
32)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
33)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
34)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
35)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
36)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
37)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
38)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
39)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
40)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
41)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
42)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
43)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
44)l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
45 protein DC2.15 OS=Daucus carota (sp|p14009|14kd_dauca : 82.8)
46 protein DC2.15 OS=Daucus carota (sp|p14009|14kd_dauca : 82.8)
47 protein DC2.15 OS=Daucus carota (sp|p14009|14kd_dauca : 82.8)
48 protein DC2.15 OS=Daucus carota (sp|p14009|14kd_dauca : 82.8)
49 protein DC2.15 OS=Daucus carota (sp|p14009|14kd_dauca : 82.8)
50 protein DC2.15 OS=Daucus carota (sp|p14009|14kd_dauca : 82.8)
51 protein DC2.15 OS=Daucus carota (sp|p14009|14kd_dauca : 82.8)
52 protein DC2.15 OS=Daucus carota (sp|p14009|14kd_dauca : 82.8)
53 protein DC2.15 OS=Daucus carota (sp|p14009|14kd_dauca : 82.8)
54 protein DC2.15 OS=Daucus carota (sp|p14009|14kd_dauca : 82.8)
55 protein DC2.15 OS=Daucus carota (sp|p14009|14kd_dauca : 82.8)
56 protein DC2.15 OS=Daucus carota (sp|p14009|14kd_dauca : 82.8)
57 protein DC2.15 OS=Daucus carota (sp|p14009|14kd_dauca : 82.8)
58 protein DC2.15 OS=Daucus carota (sp|p14009|14kd_dauca : 82.8)
59 protein DC2.15 OS=Daucus carota (sp|p14009|14kd_dauca : 82.8)
60 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)

1
2 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
3 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
4 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
5 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
6 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
7 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
8 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
9 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
10 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
11 synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
12 ot-version=v2.1) &
13 ot-version=v2.1) &
14 ot-version=v2.1) &
15 ot-version=v2.1) &
16 ot-version=v2.1) &
17 ot-version=v2.1) &
18 ot-version=v2.1) &
19 ot-version=v2.1) &
20 ot-version=v2.1) &
21 ot-version=v2.1) &
22 ot-version=v2.1) &
23 ot-version=v2.1) &
24 ot-version=v2.1) &
25 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
26 chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
27 IENT OCCLUSION B OS=Arabidopsis thaliana (sp|q9ss87|seob_arath : 168.0)
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

v2.1) &
v2.1) &
v2.1) &
v2.1) &
v2.1) &
v2.1) &
v2.1) &
v2.1) &
v2.1) &
v2.1) &
v2.1) &
v2.1) &
v2.1) &
v2.1) &
v2.1) &

l) &
l) &

Do not distribute

1
2 l) &
3 l) &
4 l) &
5 l) &
6 l) &
7 l) &
8 l) &
9 l) &
10 l) &
11 l) &
12 l) &
13
14 ; OS=Arabidopsis thaliana (sp|p57758|ctns_arath : 363.0)
15 ; OS=Arabidopsis thaliana (sp|p57758|ctns_arath : 363.0)
16 ; OS=Arabidopsis thaliana (sp|p57758|ctns_arath : 363.0)
17 ; OS=Arabidopsis thaliana (sp|p57758|ctns_arath : 363.0)
18 ; OS=Arabidopsis thaliana (sp|p57758|ctns_arath : 363.0)
19 ; OS=Arabidopsis thaliana (sp|p57758|ctns_arath : 363.0)
20 ; OS=Arabidopsis thaliana (sp|p57758|ctns_arath : 363.0)
21 ; OS=Arabidopsis thaliana (sp|p57758|ctns_arath : 363.0)
22 ; OS=Arabidopsis thaliana (sp|p57758|ctns_arath : 363.0)
23 ; OS=Arabidopsis thaliana (sp|p57758|ctns_arath : 363.0)
24 ; OS=Arabidopsis thaliana (sp|p57758|ctns_arath : 363.0)
25 ; OS=Arabidopsis thaliana (sp|p57758|ctns_arath : 363.0)
26 ; OS=Arabidopsis thaliana (sp|p57758|ctns_arath : 363.0)
27 ; OS=Arabidopsis thaliana (sp|p57758|ctns_arath : 363.0)
28 ; OS=Arabidopsis thaliana (sp|p57758|ctns_arath : 363.0)
29
30 in or reduction of molecular oxygen(50.1.13 : 88.1) (original description: pacid=37160400 transcript
31 in or reduction of molecular oxygen(50.1.13 : 88.1) (original description: pacid=37160400 transcript
32 in or reduction of molecular oxygen(50.1.13 : 88.1) (original description: pacid=37160400 transcript
33 in or reduction of molecular oxygen(50.1.13 : 88.1) (original description: pacid=37160400 transcript
34 in or reduction of molecular oxygen(50.1.13 : 88.1) (original description: pacid=37160400 transcript
35 in or reduction of molecular oxygen(50.1.13 : 88.1) (original description: pacid=37160400 transcript
36 in or reduction of molecular oxygen(50.1.13 : 88.1) (original description: pacid=37160400 transcript
37 in or reduction of molecular oxygen(50.1.13 : 88.1) (original description: pacid=37160400 transcript
38 in or reduction of molecular oxygen(50.1.13 : 88.1) (original description: pacid=37160400 transcript
39 in or reduction of molecular oxygen(50.1.13 : 88.1) (original description: pacid=37160400 transcript
40 in or reduction of molecular oxygen(50.1.13 : 88.1) (original description: pacid=37160400 transcript
41 in or reduction of molecular oxygen(50.1.13 : 88.1) (original description: pacid=37160400 transcript
42 in or reduction of molecular oxygen(50.1.13 : 88.1) (original description: pacid=37160400 transcript
43 . annot-version=v2.1) &
44 &
45 &
46 v2.1) &
47 2.1) &
48 2.1) &
49 2.1) &
50 2.1) &
51 2.1) &
52 2.1) &
53 2.1) &
54 2.1) &
55 2.1) &
56 2.1) &
57 2.1) &
58 2.1) &
59 2.1) &
60 2.1) &
se 5 OS=Arabidopsis thaliana (sp|q9ssa7|glip5_arath : 192.0)

1
2 ot-version=v2.1) &
3 &
4 &
5

6
7 aining protein 5 OS=Arabidopsis thaliana (sp|o23225|pub5_arath : 122.0)
8
9

10
11
12
13
14
15
16
17
18
19
20
21
22 r=v2.1) &
23 r=v2.1) &
24 r=v2.1) &
25 -version=v2.1) &
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11 ul/phosphatidylcholine transfer protein SFH10 OS=Arabidopsis thaliana (sp|q9si13|sfh10_arath : 53
12 ul/phosphatidylcholine transfer protein SFH10 OS=Arabidopsis thaliana (sp|q9si13|sfh10_arath : 53
13 ul/phosphatidylcholine transfer protein SFH10 OS=Arabidopsis thaliana (sp|q9si13|sfh10_arath : 53
14 ul/phosphatidylcholine transfer protein SFH10 OS=Arabidopsis thaliana (sp|q9si13|sfh10_arath : 53
15 00.1.v2.1 annot-version=v2.1) &
16 00.1.v2.1 annot-version=v2.1) &
17 00.1.v2.1 annot-version=v2.1) &
18 00.1.v2.1 annot-version=v2.1) &
19 00.1.v2.1 annot-version=v2.1) &
20 00.1.v2.1 annot-version=v2.1) &
21 00.1.v2.1 annot-version=v2.1) &
22 00.1.v2.1 annot-version=v2.1) &
23 00.1.v2.1 annot-version=v2.1) &
24 00.1.v2.1 annot-version=v2.1) &
25 00.1.v2.1 annot-version=v2.1) &
26 00.1.v2.1 annot-version=v2.1) &
27 00.1.v2.1 annot-version=v2.1) &
28 00.1.v2.1 annot-version=v2.1) &
29 **ases.EC_2.4 glycosyltransferase(50.2.4 : 568.2) (original description: pacid=37146124 transcript=Phv**
30 **=Arabidopsis thaliana (sp|b8xch5|qky_arath : 1272.0)**
31 **=Arabidopsis thaliana (sp|b8xch5|qky_arath : 1272.0)**
32 **=Arabidopsis thaliana (sp|b8xch5|qky_arath : 1272.0)**
33 **=Arabidopsis thaliana (sp|b8xch5|qky_arath : 1272.0)**
34 **=Arabidopsis thaliana (sp|b8xch5|qky_arath : 1272.0)**
35 **=Arabidopsis thaliana (sp|b8xch5|qky_arath : 1272.0)**
36 **=Arabidopsis thaliana (sp|b8xch5|qky_arath : 1272.0)**
37 **=Arabidopsis thaliana (sp|b8xch5|qky_arath : 1272.0)**
38 **=Arabidopsis thaliana (sp|b8xch5|qky_arath : 1272.0)**
39 **=Arabidopsis thaliana (sp|b8xch5|qky_arath : 1272.0)**
40 **=Arabidopsis thaliana (sp|b8xch5|qky_arath : 1272.0)**
41 **=Arabidopsis thaliana (sp|b8xch5|qky_arath : 1272.0)**
42 **=Arabidopsis thaliana (sp|b8xch5|qky_arath : 1272.0)**
43 **=Arabidopsis thaliana (sp|b8xch5|qky_arath : 1272.0)**
44 on=v2.1) &
45 on=v2.1) &
46 on=v2.1) &
47 on=v2.1) &
48 on=v2.1) &
49 on=v2.1) &
50 on=v2.1) &
51 on=v2.1) &
52 on=v2.1) &
53 on=v2.1) &
54 on=v2.1) &
55 on=v2.1) &
56 on=v2.1) &
57 on=v2.1) &
58 on=v2.1) &
59 on=v2.1) &
60 Phvul.003G274500.1.v2.1 annot-version=v2.1) &
Phvul.003G274500.1.v2.1 annot-version=v2.1) &

1 Phvul.003G274500.1.v2.1 annot-version=v2.1) &
2 Phvul.003G274500.1.v2.1 annot-version=v2.1) &
3 Phvul.003G274500.1.v2.1 annot-version=v2.1) &
4 Phvul.003G274500.1.v2.1 annot-version=v2.1) &
5 Phvul.003G274500.1.v2.1 annot-version=v2.1) &
6 Phvul.003G274500.1.v2.1 annot-version=v2.1) &
7 Phvul.003G274500.1.v2.1 annot-version=v2.1) &
8 Phvul.003G274500.1.v2.1 annot-version=v2.1) &
9 Phvul.003G274500.1.v2.1 annot-version=v2.1) &
10 Phvul.003G274500.1.v2.1 annot-version=v2.1) &
11 Phvul.003G274500.1.v2.1 annot-version=v2.1) &
12 Phvul.003G274500.1.v2.1 annot-version=v2.1) &
13
14 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
15 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
16 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
17 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
18 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
19 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
20 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
21 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
22 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
23 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
24 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
25 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
26 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
27 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
28 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
29 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
30 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
31 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
32 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
33 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
34 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
35 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
36 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
37 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
38 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
39 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
40 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
41 iated F-box protein At5g22720 OS=Arabidopsis thaliana (sp|q9fni9|fbd14_arath : 87.4)
42
43 n=v2.1) &
44 n=v2.1) &
45 n=v2.1) &
46 n=v2.1) &
47 n=v2.1) &
48 n=v2.1) &
49 n=v2.1) &
50 n=v2.1) &
51 n=v2.1) &
52 n=v2.1) &
53 n=v2.1) &
54 n=v2.1) &
55 n=v2.1) &
56 n=v2.1) &
57 n=v2.1) &
58
59 ot-version=v2.1) &
60 **tin-protein ligase ZFP1 OS=*Oryza sativa* subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)**
tin-protein ligase ZFP1 OS=*Oryza sativa* subsp. japonica (sp|q5qlr5|zfp1_orysj : 161.0)

1 G055700.1.v2.1 annot-version=v2.1) &
2 G055700.1.v2.1 annot-version=v2.1) &
3 G055700.1.v2.1 annot-version=v2.1) &
4 G055700.1.v2.1 annot-version=v2.1) &
5 G055700.1.v2.1 annot-version=v2.1) &
6 G055700.1.v2.1 annot-version=v2.1) &
7 G055700.1.v2.1 annot-version=v2.1) &
8 G055700.1.v2.1 annot-version=v2.1) &
9 G055700.1.v2.1 annot-version=v2.1) &
10 G055700.1.v2.1 annot-version=v2.1) &
11 G055700.1.v2.1 annot-version=v2.1) &
12 G055700.1.v2.1 annot-version=v2.1) &
13 G055700.1.v2.1 annot-version=v2.1) &
14 G055700.1.v2.1 annot-version=v2.1) &
15 not-version=v2.1) &
16 not-version=v2.1) &
17 not-version=v2.1) &
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33 /2.1) &
34 /2.1) &
35 /2.1) &
36 /2.1) &
37 /2.1) &
38 /2.1) &
39 /2.1) &
40 /2.1) &
41 /2.1) &
42 /2.1) &
43 /2.1) &
44 /2.1) &
45 /2.1) &
46 protein DC2.15 OS=Daucus carota (sp|p14009|14kd_dauca : 82.8)
47 not-version=v2.1) &
48 not-version=v2.1) &
49 not-version=v2.1) &
50 not-version=v2.1) &
51 not-version=v2.1) &
52 not-version=v2.1) &
53 not-version=v2.1) &
54 not-version=v2.1) &
55 not-version=v2.1) &
56 not-version=v2.1) &
57 not-version=v2.1) &
58 not-version=v2.1) &
59 not-version=v2.1) &
60 not-version=v2.1) &
2.1 annot-version=v2.1) &

1
2 2.1 annot-version=v2.1) &
3 2.1 annot-version=v2.1) &
4 2.1 annot-version=v2.1) &
5 2.1 annot-version=v2.1) &
6 2.1 annot-version=v2.1) &
7 2.1 annot-version=v2.1) &
8 2.1 annot-version=v2.1) &
9 2.1 annot-version=v2.1) &
10 2.1 annot-version=v2.1) &
11 2.1 annot-version=v2.1) &
12 2.1 annot-version=v2.1) &
13 G252700.1.v2.1 annot-version=v2.1) &
14 n=v2.1) &
15 n=v2.1) &
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33 l) &
34
35 ul.008G176200.1.v2.1 annot-version=v2.1) &
36 ul.008G176200.1.v2.1 annot-version=v2.1) &
37 ul.008G176200.1.v2.1 annot-version=v2.1) &
38 ul.008G176200.1.v2.1 annot-version=v2.1) &
39 ul.008G176200.1.v2.1 annot-version=v2.1) &
40 ul.008G176200.1.v2.1 annot-version=v2.1) &
41 ul.008G176200.1.v2.1 annot-version=v2.1) &
42 ul.008G176200.1.v2.1 annot-version=v2.1) &
43 ul.008G176200.1.v2.1 annot-version=v2.1) &
44 ul.008G176200.1.v2.1 annot-version=v2.1) &
45 ul.008G176200.1.v2.1 annot-version=v2.1) &
46 ul.008G176200.1.v2.1 annot-version=v2.1) &
47 ul.008G176200.1.v2.1 annot-version=v2.1) &
48 otein At3g49140 OS=Arabidopsis thaliana (sp|q0wmn5|y3913_arath : 104.0)
49 otein At3g49140 OS=Arabidopsis thaliana (sp|q0wmn5|y3913_arath : 104.0)
50 n=v2.1) &
51
52 9G092600.1.v2.1 annot-version=v2.1) &
53 9G092600.1.v2.1 annot-version=v2.1) &
54 9G092600.1.v2.1 annot-version=v2.1) &
55 9G092600.1.v2.1 annot-version=v2.1) &
56 9G092600.1.v2.1 annot-version=v2.1) &
57 9G092600.1.v2.1 annot-version=v2.1) &
58 9G092600.1.v2.1 annot-version=v2.1) &
59 9G092600.1.v2.1 annot-version=v2.1) &
60 9G092600.1.v2.1 annot-version=v2.1) &
9G092600.1.v2.1 annot-version=v2.1) &

1 9G092600.1.v2.1 annot-version=v2.1) &
2 9G092600.1.v2.1 annot-version=v2.1) &
3 9G092600.1.v2.1 annot-version=v2.1) &
4 9G092600.1.v2.1 annot-version=v2.1) &
5)10G053600 ID=Phvul.010G053600.2.v2.1 annot-version=v2.1) &
6 version=v2.1) &
7 version=v2.1) &
8 version=v2.1) &
9 version=v2.1) &
10 version=v2.1) &
11 version=v2.1) &
12 version=v2.1) &
13 version=v2.1) &
14 version=v2.1) &
15 version=v2.1) &
16 version=v2.1) &
17 version=v2.1) &
18 version=v2.1) &
19 version=v2.1) &

20
21 &
22 &
23 &
24 &
25 &
26 &
27 &
28 &
29 &
30 &
31 &
32 &
33 &
34 &
35 &
36 &
37 &
38 &
39 &
40 &
41 &
42 &
43 &
44 &
45 &
46 &
47 &
48 &
49 &
50 &
51 &

Do not distribute

52
53
54
55
56
57
58
59
60

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

0)
0)
0)
0)
0)
0)
0)
0)
0)
0)
0)
0)
0)
0)
0)
0)
0)
0)
0)
0)
0)

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

/ul.003G053000.1 locus=Phvul.003G053000 ID=Phvul.003G053000.1.v2.1 annot-version=v2.1) &
/ul.003G053000.1 locus=Phvul.003G053000 ID=Phvul.003G053000.1.v2.1 annot-version=v2.1) &
/ul.003G053000.1 locus=Phvul.003G053000 ID=Phvul.003G053000.1.v2.1 annot-version=v2.1) &
/ul.003G053000.1 locus=Phvul.003G053000 ID=Phvul.003G053000.1.v2.1 annot-version=v2.1) &
/ul.003G053000.1 locus=Phvul.003G053000 ID=Phvul.003G053000.1.v2.1 annot-version=v2.1) &
/ul.003G053000.1 locus=Phvul.003G053000 ID=Phvul.003G053000.1.v2.1 annot-version=v2.1) &
/ul.003G053000.1 locus=Phvul.003G053000 ID=Phvul.003G053000.1.v2.1 annot-version=v2.1) &
/ul.003G053000.1 locus=Phvul.003G053000 ID=Phvul.003G053000.1.v2.1 annot-version=v2.1) &
/ul.003G053000.1 locus=Phvul.003G053000 ID=Phvul.003G053000.1.v2.1 annot-version=v2.1) &
/ul.003G053000.1 locus=Phvul.003G053000 ID=Phvul.003G053000.1.v2.1 annot-version=v2.1) &
/ul.003G053000.1 locus=Phvul.003G053000 ID=Phvul.003G053000.1.v2.1 annot-version=v2.1) &
/ul.003G053000.1 locus=Phvul.003G053000 ID=Phvul.003G053000.1.v2.1 annot-version=v2.1) &
/ul.003G053000.1 locus=Phvul.003G053000 ID=Phvul.003G053000.1.v2.1 annot-version=v2.1) &
/ul.003G053000.1 locus=Phvul.003G053000 ID=Phvul.003G053000.1.v2.1 annot-version=v2.1) &
/ul.003G053000.1 locus=Phvul.003G053000 ID=Phvul.003G053000.1.v2.1 annot-version=v2.1) &
/ul.003G053000.1 locus=Phvul.003G053000 ID=Phvul.003G053000.1.v2.1 annot-version=v2.1) &
/ul.003G053000.1 locus=Phvul.003G053000 ID=Phvul.003G053000.1.v2.1 annot-version=v2.1) &
/ul.003G053000.1 locus=Phvul.003G053000 ID=Phvul.003G053000.1.v2.1 annot-version=v2.1) &

Not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

n=v2.1) &
n=v2.1) &
n=v2.1) &
n=v2.1) &
n=v2.1) &
n=v2.1) &
n=v2.1) &
n=v2.1) &
n=v2.1) &
n=v2.1) &
n=v2.1) &
n=v2.1) &
n=v2.1) &
n=v2.1) &
n=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

0)

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26 15 transcript=Phvul.011G013100.1 locus=Phvul.011G013100 ID=Phvul.011G013100.1.v2.1 annot-ve
27 15 transcript=Phvul.011G013100.1 locus=Phvul.011G013100 ID=Phvul.011G013100.1.v2.1 annot-ve
28 15 transcript=Phvul.011G013100.1 locus=Phvul.011G013100 ID=Phvul.011G013100.1.v2.1 annot-ve
29 15 transcript=Phvul.011G013100.1 locus=Phvul.011G013100 ID=Phvul.011G013100.1.v2.1 annot-ve
30 15 transcript=Phvul.011G013100.1 locus=Phvul.011G013100 ID=Phvul.011G013100.1.v2.1 annot-ve
31 15 transcript=Phvul.011G013100.1 locus=Phvul.011G013100 ID=Phvul.011G013100.1.v2.1 annot-ve
32 15 transcript=Phvul.011G013100.1 locus=Phvul.011G013100 ID=Phvul.011G013100.1.v2.1 annot-ve
33 15 transcript=Phvul.011G013100.1 locus=Phvul.011G013100 ID=Phvul.011G013100.1.v2.1 annot-ve
34 15 transcript=Phvul.011G013100.1 locus=Phvul.011G013100 ID=Phvul.011G013100.1.v2.1 annot-ve
35 15 transcript=Phvul.011G013100.1 locus=Phvul.011G013100 ID=Phvul.011G013100.1.v2.1 annot-ve
36 15 transcript=Phvul.011G013100.1 locus=Phvul.011G013100 ID=Phvul.011G013100.1.v2.1 annot-ve
37 15 transcript=Phvul.011G013100.1 locus=Phvul.011G013100 ID=Phvul.011G013100.1.v2.1 annot-ve
38 15 transcript=Phvul.011G013100.1 locus=Phvul.011G013100 ID=Phvul.011G013100.1.v2.1 annot-ve
39 15 transcript=Phvul.011G013100.1 locus=Phvul.011G013100 ID=Phvul.011G013100.1.v2.1 annot-ve
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

:Phvul.001G269200.1 locus=Phvul.001G269200 ID=Phvul.001G269200.1.v2.1 annot-version=v2.1) &
:Phvul.001G269301.1 locus=Phvul.001G269301 ID=Phvul.001G269301.1.v2.1 annot-version=v2.1) &

1
2
3
4
5
6 99800.1 locus=Phvul.002G199800 ID=Phvul.002G199800.1.v2.1 annot-version=v2.1) &
7 99800.1 locus=Phvul.002G199800 ID=Phvul.002G199800.1.v2.1 annot-version=v2.1) &
8 99800.1 locus=Phvul.002G199800 ID=Phvul.002G199800.1.v2.1 annot-version=v2.1) &
9 99800.1 locus=Phvul.002G199800 ID=Phvul.002G199800.1.v2.1 annot-version=v2.1) &
10 99800.1 locus=Phvul.002G199800 ID=Phvul.002G199800.1.v2.1 annot-version=v2.1) &
11 99800.1 locus=Phvul.002G199800 ID=Phvul.002G199800.1.v2.1 annot-version=v2.1) &
12 99800.1 locus=Phvul.002G199800 ID=Phvul.002G199800.1.v2.1 annot-version=v2.1) &
13 99800.1 locus=Phvul.002G199800 ID=Phvul.002G199800.1.v2.1 annot-version=v2.1) &
14 99800.1 locus=Phvul.002G199800 ID=Phvul.002G199800.1.v2.1 annot-version=v2.1) &
15 99800.1 locus=Phvul.002G199800 ID=Phvul.002G199800.1.v2.1 annot-version=v2.1) &
16 99800.1 locus=Phvul.002G199800 ID=Phvul.002G199800.1.v2.1 annot-version=v2.1) &
17 99800.1 locus=Phvul.002G199800 ID=Phvul.002G199800.1.v2.1 annot-version=v2.1) &
18 99800.1 locus=Phvul.002G199800 ID=Phvul.002G199800.1.v2.1 annot-version=v2.1) &
19 99800.1 locus=Phvul.002G199800 ID=Phvul.002G199800.1.v2.1 annot-version=v2.1) &
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

3.0)
3.0)
3.0)

Do not distribute

[/ul.003G053000.1 locus=Phvul.003G053000 ID=Phvul.003G053000.1.v2.1 annot-version=v2.1\) &](#)

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

ersion=v2.1) &
ersion=v2.1) &
ersion=v2.1) &
ersion=v2.1) &
ersion=v2.1) &
ersion=v2.1) &
ersion=v2.1) &
ersion=v2.1) &
ersion=v2.1) &
ersion=v2.1) &
ersion=v2.1) &
ersion=v2.1) &
ersion=v2.1) &
ersion=v2.1) &
ersion=v2.1) &
ersion=v2.1) &
ersion=v2.1) &
ersion=v2.1) &
ersion=v2.1) &
ersion=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
1

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

&
&
&
&
&
&
&
&
&
&
&

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

| 1 | miRNA_Acc. | Target_Acc. | Expectation | UPE\$ | miRNA_start | miRNA_end |
|----|--------------|--------------------|-------------|-------|-------------|-----------|
| 2 | uuccacagcuuu | Phvul.003G168301.2 | 1.5 | -1 | 1 | 21 |
| 3 | uuccacagcuuu | Phvul.003G168301.1 | 1.5 | -1 | 1 | 21 |
| 4 | uuccacagcuuu | Phvul.003G168301.2 | 1.5 | -1 | 1 | 21 |
| 5 | uuccacagcuuu | Phvul.003G168301.1 | 1.5 | -1 | 1 | 21 |
| 6 | uuccacagcuuu | Phvul.003G168301.2 | 1.5 | -1 | 1 | 21 |
| 7 | uuccacagcuuu | Phvul.003G168301.1 | 1.5 | -1 | 1 | 21 |
| 8 | uuccacagcuuu | Phvul.003G168301.2 | 1.5 | -1 | 1 | 21 |
| 9 | uuccacagcuuu | Phvul.003G168301.1 | 1.5 | -1 | 1 | 21 |
| 10 | uuccacagcuuu | Phvul.003G168301.2 | 1.5 | -1 | 1 | 21 |
| 11 | uuccacagcuuu | Phvul.003G168301.1 | 1.5 | -1 | 1 | 21 |
| 12 | uuccacagcuuu | Phvul.003G168301.2 | 1.5 | -1 | 1 | 21 |
| 13 | uuccacagcuuu | Phvul.003G168301.1 | 1.5 | -1 | 1 | 21 |
| 14 | uuccacagcuuu | Phvul.003G168301.2 | 1.5 | -1 | 1 | 21 |
| 15 | uuccacagcuuu | Phvul.003G168301.1 | 1.5 | -1 | 1 | 21 |
| 16 | uuccacagcuuu | Phvul.003G168301.2 | 1.5 | -1 | 1 | 21 |
| 17 | uuccacagcuuu | Phvul.003G168301.1 | 1.5 | -1 | 1 | 21 |
| 18 | uuccacagcuuu | Phvul.003G168301.2 | 1.5 | -1 | 1 | 21 |
| 19 | uuccacagcuuu | Phvul.003G168301.1 | 1.5 | -1 | 1 | 21 |
| 20 | uuccacagcuuu | Phvul.003G168301.2 | 1.5 | -1 | 1 | 21 |
| 21 | uuccacagcuuu | Phvul.003G168301.1 | 1.5 | -1 | 1 | 21 |
| 22 | uuccacagcuuu | Phvul.003G168301.2 | 1.5 | -1 | 1 | 21 |
| 23 | uuccacagcuuu | Phvul.003G168301.1 | 1.5 | -1 | 1 | 21 |
| 24 | uuccacagcuuu | Phvul.003G168301.2 | 1.5 | -1 | 1 | 21 |
| 25 | uuccacagcuuu | Phvul.003G168301.1 | 1.5 | -1 | 1 | 21 |
| 26 | uuccacagcuuu | Phvul.003G168301.2 | 1.5 | -1 | 1 | 21 |
| 27 | uuccacagcuuu | Phvul.003G168301.1 | 1.5 | -1 | 1 | 21 |
| 28 | uuccacagcuuu | Phvul.003G168301.2 | 1.5 | -1 | 1 | 21 |
| 29 | uuccacagcuuu | Phvul.003G168301.1 | 1.5 | -1 | 1 | 21 |
| 30 | uuccacagcuuu | Phvul.003G168301.2 | 1.5 | -1 | 1 | 21 |
| 31 | uuccacagcuuu | Phvul.003G168301.1 | 1.5 | -1 | 1 | 21 |
| 32 | uuccacagcuuu | Phvul.003G168301.2 | 1.5 | -1 | 1 | 22 |
| 33 | uuccacagcuuu | Phvul.003G168301.1 | 1.5 | -1 | 1 | 22 |
| 34 | uuccacagcuuu | Phvul.008G204300.1 | 1.5 | -1 | 1 | 21 |
| 35 | uuccacagcuuu | Phvul.008G204300.1 | 1.5 | -1 | 1 | 21 |
| 36 | uuccacagcuuu | Phvul.008G204300.1 | 1.5 | -1 | 1 | 21 |
| 37 | uuccacagcuuu | Phvul.008G204300.1 | 1.5 | -1 | 1 | 21 |
| 38 | uuccacagcuuu | Phvul.008G204300.1 | 1.5 | -1 | 1 | 21 |
| 39 | uuccacagcuuu | Phvul.008G204300.1 | 1.5 | -1 | 1 | 21 |
| 40 | uuccacagcuuu | Phvul.008G204300.1 | 1.5 | -1 | 1 | 21 |
| 41 | uuccacagcuuu | Phvul.008G204300.1 | 1.5 | -1 | 1 | 21 |
| 42 | uuccacagcuuu | Phvul.008G204300.1 | 1.5 | -1 | 1 | 21 |
| 43 | uuccacagcuuu | Phvul.008G204300.1 | 1.5 | -1 | 1 | 21 |
| 44 | uuccacagcuuu | Phvul.008G204300.1 | 1.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuu | Phvul.008G204300.1 | 1.5 | -1 | 1 | 21 |
| 46 | uuccacagcuuu | Phvul.008G204300.1 | 1.5 | -1 | 1 | 21 |
| 47 | uuccacagcuuu | Phvul.008G204300.1 | 1.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuu | Phvul.008G204300.1 | 1.5 | -1 | 1 | 21 |
| 49 | uuccacagcuuu | Phvul.008G204300.1 | 1.5 | -1 | 1 | 22 |
| 50 | uuccacagcuuu | Phvul.003G168400.1 | 2 | -1 | 1 | 21 |
| 51 | uuccacagcuuu | Phvul.003G168400.1 | 2 | -1 | 1 | 21 |
| 52 | uuccacagcuuu | Phvul.003G168400.1 | 2 | -1 | 1 | 21 |
| 53 | uuccacagcuuu | Phvul.003G168400.1 | 2 | -1 | 1 | 21 |
| 54 | uuccacagcuuu | Phvul.003G168400.1 | 2 | -1 | 1 | 21 |
| 55 | uuccacagcuuu | Phvul.003G168400.1 | 2 | -1 | 1 | 21 |
| 56 | uuccacagcuuu | Phvul.003G168400.1 | 2 | -1 | 1 | 21 |
| 57 | uuccacagcuuu | Phvul.003G168400.1 | 2 | -1 | 1 | 21 |
| 58 | uuccacagcuuu | Phvul.003G168400.1 | 2 | -1 | 1 | 21 |
| 59 | uuccacagcuuu | Phvul.003G168400.1 | 2 | -1 | 1 | 21 |
| 60 | uuccacagcuuu | Phvul.003G168400.1 | 2 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.003G168400.1 | 2 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.003G168400.1 | 2 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.003G168400.1 | 2 | -1 | 1 | 22 |
| 5 | | | | | |
| 6 | uuccacagcuuu Phvul.007G253900.1 | 2 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.007G253900.1 | 2 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.007G253900.1 | 2 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uuccacagcuuu Phvul.007G253900.1 | 2 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.007G253900.1 | 2 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.007G253900.1 | 2 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.007G253900.1 | 2 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.007G253900.1 | 2 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.007G253900.1 | 2 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.007G253900.1 | 2 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.007G253900.1 | 2 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.007G253900.1 | 2 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.007G253900.1 | 2 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.007G253900.1 | 2 | -1 | 1 | 22 |
| 21 | | | | | |
| 22 | uuccacagcuuu Phvul.001G155150.1 | 2.5 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.001G155150.1 | 2.5 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.001G155150.1 | 2.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uuccacagcuuu Phvul.001G155150.1 | 2.5 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.001G155150.1 | 2.5 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.001G155150.1 | 2.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uuccacagcuuu Phvul.001G155150.1 | 2.5 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.001G155150.1 | 2.5 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.001G155150.1 | 2.5 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.001G155150.1 | 2.5 | -1 | 1 | 21 |
| 34 | uuccacagcuuu Phvul.001G155150.1 | 2.5 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.001G155150.1 | 2.5 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.001G155150.1 | 2.5 | -1 | 1 | 22 |
| 37 | uuccacagcuuu Phvul.002G254800.1 | 2.5 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | uuccacagcuuu Phvul.002G254800.1 | 2.5 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.002G254800.1 | 2.5 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.002G254800.1 | 2.5 | -1 | 1 | 21 |
| 42 | uuccacagcuuu Phvul.002G254800.1 | 2.5 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.002G254800.1 | 2.5 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.002G254800.1 | 2.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.002G254800.1 | 2.5 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.002G254800.1 | 2.5 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.002G254800.1 | 2.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.002G254800.1 | 2.5 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.002G254800.1 | 2.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uuccacagcuuu Phvul.002G254800.1 | 2.5 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.002G254800.1 | 2.5 | -1 | 1 | 22 |
| 53 | uuccacagcuuu Phvul.004G046200.1 | 2.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uuccacagcuuu Phvul.004G046200.1 | 2.5 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.004G046200.1 | 2.5 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.004G046200.1 | 2.5 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.004G046200.1 | 2.5 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.004G046200.1 | 2.5 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.004G046200.1 | 2.5 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.004G046200.1 | 2.5 | -1 | 1 | 21 |

| | | | | | |
|----|--------------|--------------------|-----|----|------|
| 1 | | | | | |
| 2 | uuccacagcuuu | Phvul.004G046200.1 | 2.5 | -1 | 1 21 |
| 3 | uuccacagcuuu | Phvul.004G046200.1 | 2.5 | -1 | 1 21 |
| 4 | uuccacagcuuu | Phvul.004G046200.1 | 2.5 | -1 | 1 21 |
| 5 | uuccacagcuuu | Phvul.004G046200.1 | 2.5 | -1 | 1 21 |
| 6 | uuccacagcuuu | Phvul.004G046200.1 | 2.5 | -1 | 1 21 |
| 7 | uuccacagcuuu | Phvul.004G046200.1 | 2.5 | -1 | 1 22 |
| 8 | uuccacagcuuu | Phvul.008G188400.1 | 2.5 | -1 | 1 21 |
| 9 | uuccacagcuuu | Phvul.008G188400.1 | 2.5 | -1 | 1 21 |
| 10 | uuccacagcuuu | Phvul.008G188400.1 | 2.5 | -1 | 1 21 |
| 11 | uuccacagcuuu | Phvul.008G188400.1 | 2.5 | -1 | 1 21 |
| 12 | uuccacagcuuu | Phvul.008G188400.1 | 2.5 | -1 | 1 21 |
| 13 | uuccacagcuuu | Phvul.008G188400.1 | 2.5 | -1 | 1 21 |
| 14 | uuccacagcuuu | Phvul.008G188400.1 | 2.5 | -1 | 1 21 |
| 15 | uuccacagcuuu | Phvul.008G188400.1 | 2.5 | -1 | 1 21 |
| 16 | uuccacagcuuu | Phvul.008G188400.1 | 2.5 | -1 | 1 21 |
| 17 | uuccacagcuuu | Phvul.008G188400.1 | 2.5 | -1 | 1 21 |
| 18 | uuccacagcuuu | Phvul.008G188400.1 | 2.5 | -1 | 1 21 |
| 19 | uuccacagcuuu | Phvul.008G188400.1 | 2.5 | -1 | 1 21 |
| 20 | uuccacagcuuu | Phvul.008G188400.1 | 2.5 | -1 | 1 21 |
| 21 | uuccacagcuuu | Phvul.008G188400.1 | 2.5 | -1 | 1 21 |
| 22 | uuccacagcuuu | Phvul.008G188400.1 | 2.5 | -1 | 1 21 |
| 23 | uuccacagcuuu | Phvul.008G188400.1 | 2.5 | -1 | 1 22 |
| 24 | uuccacagcuuu | Phvul.011G215800.1 | 2.5 | -1 | 1 21 |
| 25 | uuccacagcuuu | Phvul.011G215800.1 | 2.5 | -1 | 1 21 |
| 26 | uuccacagcuuu | Phvul.011G215800.1 | 2.5 | -1 | 1 21 |
| 27 | uuccacagcuuu | Phvul.011G215800.1 | 2.5 | -1 | 1 21 |
| 28 | uuccacagcuuu | Phvul.011G215800.1 | 2.5 | -1 | 1 21 |
| 29 | uuccacagcuuu | Phvul.011G215800.1 | 2.5 | -1 | 1 21 |
| 30 | uuccacagcuuu | Phvul.011G215800.1 | 2.5 | -1 | 1 21 |
| 31 | uuccacagcuuu | Phvul.011G215800.1 | 2.5 | -1 | 1 21 |
| 32 | uuccacagcuuu | Phvul.011G215800.1 | 2.5 | -1 | 1 21 |
| 33 | uuccacagcuuu | Phvul.011G215800.1 | 2.5 | -1 | 1 21 |
| 34 | uuccacagcuuu | Phvul.011G215800.1 | 2.5 | -1 | 1 21 |
| 35 | uuccacagcuuu | Phvul.011G215800.1 | 2.5 | -1 | 1 21 |
| 36 | uuccacagcuuu | Phvul.011G215800.1 | 2.5 | -1 | 1 21 |
| 37 | uuccacagcuuu | Phvul.011G215800.1 | 2.5 | -1 | 1 21 |
| 38 | uuccacagcuuu | Phvul.011G215800.1 | 2.5 | -1 | 1 21 |
| 39 | uuccacagcuuu | Phvul.011G215800.1 | 2.5 | -1 | 1 22 |
| 40 | uuccacagcuuu | Phvul.001G031000.1 | 3 | -1 | 1 21 |
| 41 | uuccacagcuuu | Phvul.001G031000.1 | 3 | -1 | 1 21 |
| 42 | uuccacagcuuu | Phvul.001G031000.1 | 3 | -1 | 1 21 |
| 43 | uuccacagcuuu | Phvul.001G031000.1 | 3 | -1 | 1 21 |
| 44 | uuccacagcuuu | Phvul.001G031000.1 | 3 | -1 | 1 21 |
| 45 | uuccacagcuuu | Phvul.001G031000.1 | 3 | -1 | 1 21 |
| 46 | uuccacagcuuu | Phvul.001G031000.1 | 3 | -1 | 1 21 |
| 47 | uuccacagcuuu | Phvul.001G031000.1 | 3 | -1 | 1 21 |
| 48 | uuccacagcuuu | Phvul.001G031000.1 | 3 | -1 | 1 21 |
| 49 | uuccacagcuuu | Phvul.001G031000.1 | 3 | -1 | 1 21 |
| 50 | uuccacagcuuu | Phvul.001G031000.1 | 3 | -1 | 1 21 |
| 51 | uuccacagcuuu | Phvul.001G031000.1 | 3 | -1 | 1 21 |
| 52 | uuccacagcuuu | Phvul.001G031000.1 | 3 | -1 | 1 21 |
| 53 | uuccacagcuuu | Phvul.001G031000.1 | 3 | -1 | 1 21 |
| 54 | uuccacagcuuu | Phvul.001G031000.1 | 3 | -1 | 1 21 |
| 55 | uuccacagcuuu | Phvul.001G031000.1 | 3 | -1 | 1 22 |
| 56 | uuccacagcuuu | Phvul.001G147700.1 | 3 | -1 | 1 21 |
| 57 | uuccacagcuuu | Phvul.001G147700.1 | 3 | -1 | 1 21 |
| 58 | uuccacagcuuu | Phvul.001G147700.1 | 3 | -1 | 1 21 |
| 59 | uuccacagcuuu | Phvul.001G147700.1 | 3 | -1 | 1 21 |
| 60 | uuccacagcuuu | Phvul.001G147700.1 | 3 | -1 | 1 21 |
| | uuccacagcuuu | Phvul.001G147700.1 | 3 | -1 | 1 21 |

| | | | | | | |
|----|--------------|--------------------|---|----|---|----|
| 1 | | | | | | |
| 2 | uuccacagcuuu | Phvul.001G147700.1 | 3 | -1 | 1 | 21 |
| 3 | uuccacagcuuu | Phvul.001G147700.1 | 3 | -1 | 1 | 21 |
| 4 | uuccacagcuuu | Phvul.001G147700.1 | 3 | -1 | 1 | 21 |
| 5 | uuccacagcuuu | Phvul.001G147700.1 | 3 | -1 | 1 | 21 |
| 6 | uuccacagcuuu | Phvul.001G147700.1 | 3 | -1 | 1 | 21 |
| 7 | uuccacagcuuu | Phvul.001G147700.1 | 3 | -1 | 1 | 21 |
| 8 | uuccacagcuuu | Phvul.001G147700.1 | 3 | -1 | 1 | 21 |
| 9 | uuccacagcuuu | Phvul.001G147700.1 | 3 | -1 | 1 | 21 |
| 10 | uuccacagcuuu | Phvul.001G147700.1 | 3 | -1 | 1 | 22 |
| 11 | uuccacagcuuu | Phvul.001G162000.1 | 3 | -1 | 1 | 21 |
| 12 | uuccacagcuuu | Phvul.001G162000.1 | 3 | -1 | 1 | 21 |
| 13 | uuccacagcuuu | Phvul.001G162000.1 | 3 | -1 | 1 | 21 |
| 14 | uuccacagcuuu | Phvul.001G162000.1 | 3 | -1 | 1 | 21 |
| 15 | uuccacagcuuu | Phvul.001G162000.1 | 3 | -1 | 1 | 21 |
| 16 | uuccacagcuuu | Phvul.001G162000.1 | 3 | -1 | 1 | 21 |
| 17 | uuccacagcuuu | Phvul.001G162000.1 | 3 | -1 | 1 | 21 |
| 18 | uuccacagcuuu | Phvul.001G162000.1 | 3 | -1 | 1 | 21 |
| 19 | uuccacagcuuu | Phvul.001G162000.1 | 3 | -1 | 1 | 21 |
| 20 | uuccacagcuuu | Phvul.001G162000.1 | 3 | -1 | 1 | 21 |
| 21 | uuccacagcuuu | Phvul.001G162000.1 | 3 | -1 | 1 | 21 |
| 22 | uuccacagcuuu | Phvul.001G162000.1 | 3 | -1 | 1 | 21 |
| 23 | uuccacagcuuu | Phvul.001G162000.1 | 3 | -1 | 1 | 21 |
| 24 | uuccacagcuuu | Phvul.001G162000.1 | 3 | -1 | 1 | 21 |
| 25 | uuccacagcuuu | Phvul.001G162000.1 | 3 | -1 | 1 | 21 |
| 26 | uuccacagcuuu | Phvul.001G187500.1 | 3 | -1 | 1 | 21 |
| 27 | uuccacagcuuu | Phvul.001G187500.1 | 3 | -1 | 1 | 21 |
| 28 | uuccacagcuuu | Phvul.001G187500.1 | 3 | -1 | 1 | 21 |
| 29 | uuccacagcuuu | Phvul.001G187500.1 | 3 | -1 | 1 | 21 |
| 30 | uuccacagcuuu | Phvul.001G187500.1 | 3 | -1 | 1 | 21 |
| 31 | uuccacagcuuu | Phvul.001G187500.1 | 3 | -1 | 1 | 21 |
| 32 | uuccacagcuuu | Phvul.001G187500.1 | 3 | -1 | 1 | 21 |
| 33 | uuccacagcuuu | Phvul.001G187500.1 | 3 | -1 | 1 | 21 |
| 34 | uuccacagcuuu | Phvul.001G187500.1 | 3 | -1 | 1 | 21 |
| 35 | uuccacagcuuu | Phvul.001G187500.1 | 3 | -1 | 1 | 21 |
| 36 | uuccacagcuuu | Phvul.001G187500.1 | 3 | -1 | 1 | 21 |
| 37 | uuccacagcuuu | Phvul.001G187500.1 | 3 | -1 | 1 | 21 |
| 38 | uuccacagcuuu | Phvul.001G187500.1 | 3 | -1 | 1 | 21 |
| 39 | uuccacagcuuu | Phvul.001G187500.1 | 3 | -1 | 1 | 21 |
| 40 | uuccacagcuuu | Phvul.001G187500.1 | 3 | -1 | 1 | 22 |
| 41 | uuccacagcuuu | Phvul.002G041800.2 | 3 | -1 | 1 | 21 |
| 42 | uuccacagcuuu | Phvul.002G041800.1 | 3 | -1 | 1 | 21 |
| 43 | uuccacagcuuu | Phvul.002G041800.1 | 3 | -1 | 1 | 21 |
| 44 | uuccacagcuuu | Phvul.002G041800.2 | 3 | -1 | 1 | 21 |
| 45 | uuccacagcuuu | Phvul.002G041800.1 | 3 | -1 | 1 | 21 |
| 46 | uuccacagcuuu | Phvul.002G041800.2 | 3 | -1 | 1 | 21 |
| 47 | uuccacagcuuu | Phvul.002G041800.2 | 3 | -1 | 1 | 21 |
| 48 | uuccacagcuuu | Phvul.002G041800.1 | 3 | -1 | 1 | 21 |
| 49 | uuccacagcuuu | Phvul.002G041800.2 | 3 | -1 | 1 | 21 |
| 50 | uuccacagcuuu | Phvul.002G041800.2 | 3 | -1 | 1 | 21 |
| 51 | uuccacagcuuu | Phvul.002G041800.1 | 3 | -1 | 1 | 21 |
| 52 | uuccacagcuuu | Phvul.002G041800.2 | 3 | -1 | 1 | 21 |
| 53 | uuccacagcuuu | Phvul.002G041800.1 | 3 | -1 | 1 | 21 |
| 54 | uuccacagcuuu | Phvul.002G041800.1 | 3 | -1 | 1 | 21 |
| 55 | uuccacagcuuu | Phvul.002G041800.2 | 3 | -1 | 1 | 21 |
| 56 | uuccacagcuuu | Phvul.002G041800.1 | 3 | -1 | 1 | 21 |
| 57 | uuccacagcuuu | Phvul.002G041800.2 | 3 | -1 | 1 | 21 |
| 58 | uuccacagcuuu | Phvul.002G041800.2 | 3 | -1 | 1 | 21 |
| 59 | uuccacagcuuu | Phvul.002G041800.1 | 3 | -1 | 1 | 21 |
| 60 | uuccacagcuuu | Phvul.002G041800.2 | 3 | -1 | 1 | 21 |
| | uuccacagcuuu | Phvul.002G041800.1 | 3 | -1 | 1 | 21 |

| | | | | | |
|----|--------------|--------------------|---|----|------|
| 1 | | | | | |
| 2 | uuccacagcuuu | Phvul.002G041800.2 | 3 | -1 | 1 21 |
| 3 | uuccacagcuuu | Phvul.002G041800.1 | 3 | -1 | 1 21 |
| 4 | uuccacagcuuu | Phvul.002G041800.2 | 3 | -1 | 1 21 |
| 5 | uuccacagcuuu | Phvul.002G041800.2 | 3 | -1 | 1 21 |
| 6 | uuccacagcuuu | Phvul.002G041800.1 | 3 | -1 | 1 21 |
| 7 | uuccacagcuuu | Phvul.002G041800.2 | 3 | -1 | 1 21 |
| 8 | uuccacagcuuu | Phvul.002G041800.1 | 3 | -1 | 1 21 |
| 9 | uuccacagcuuu | Phvul.002G041800.1 | 3 | -1 | 1 21 |
| 10 | uuccacagcuuu | Phvul.002G041800.2 | 3 | -1 | 1 22 |
| 11 | uuccacagcuuu | Phvul.002G041800.1 | 3 | -1 | 1 22 |
| 12 | uuccacagcuuu | Phvul.002G061900.1 | 3 | -1 | 1 21 |
| 13 | uuccacagcuuu | Phvul.002G061900.1 | 3 | -1 | 1 21 |
| 14 | uuccacagcuuu | Phvul.002G061900.1 | 3 | -1 | 1 21 |
| 15 | uuccacagcuuu | Phvul.002G061900.1 | 3 | -1 | 1 21 |
| 16 | uuccacagcuuu | Phvul.002G061900.1 | 3 | -1 | 1 21 |
| 17 | uuccacagcuuu | Phvul.002G061900.1 | 3 | -1 | 1 21 |
| 18 | uuccacagcuuu | Phvul.002G061900.1 | 3 | -1 | 1 21 |
| 19 | uuccacagcuuu | Phvul.002G061900.1 | 3 | -1 | 1 21 |
| 20 | uuccacagcuuu | Phvul.002G061900.1 | 3 | -1 | 1 21 |
| 21 | uuccacagcuuu | Phvul.002G061900.1 | 3 | -1 | 1 21 |
| 22 | uuccacagcuuu | Phvul.002G061900.1 | 3 | -1 | 1 21 |
| 23 | uuccacagcuuu | Phvul.002G061900.1 | 3 | -1 | 1 21 |
| 24 | uuccacagcuuu | Phvul.002G061900.1 | 3 | -1 | 1 21 |
| 25 | uuccacagcuuu | Phvul.002G061900.1 | 3 | -1 | 1 21 |
| 26 | uuccacagcuuu | Phvul.002G061900.1 | 3 | -1 | 1 21 |
| 27 | uuccacagcuuu | Phvul.002G061900.1 | 3 | -1 | 1 22 |
| 28 | uuccacagcuuu | Phvul.002G131700.1 | 3 | -1 | 1 21 |
| 29 | uuccacagcuuu | Phvul.002G131700.1 | 3 | -1 | 1 21 |
| 30 | uuccacagcuuu | Phvul.002G131700.1 | 3 | -1 | 1 21 |
| 31 | uuccacagcuuu | Phvul.002G131700.1 | 3 | -1 | 1 21 |
| 32 | uuccacagcuuu | Phvul.002G131700.1 | 3 | -1 | 1 21 |
| 33 | uuccacagcuuu | Phvul.002G131700.1 | 3 | -1 | 1 21 |
| 34 | uuccacagcuuu | Phvul.002G131700.1 | 3 | -1 | 1 21 |
| 35 | uuccacagcuuu | Phvul.002G131700.1 | 3 | -1 | 1 21 |
| 36 | uuccacagcuuu | Phvul.002G131700.1 | 3 | -1 | 1 21 |
| 37 | uuccacagcuuu | Phvul.002G131700.1 | 3 | -1 | 1 21 |
| 38 | uuccacagcuuu | Phvul.002G131700.1 | 3 | -1 | 1 21 |
| 39 | uuccacagcuuu | Phvul.002G131700.1 | 3 | -1 | 1 21 |
| 40 | uuccacagcuuu | Phvul.002G131700.1 | 3 | -1 | 1 21 |
| 41 | uuccacagcuuu | Phvul.002G131700.1 | 3 | -1 | 1 21 |
| 42 | uuccacagcuuu | Phvul.002G131700.1 | 3 | -1 | 1 21 |
| 43 | uuccacagcuuu | Phvul.002G131700.1 | 3 | -1 | 1 22 |
| 44 | uuccacagcuuu | Phvul.002G147600.1 | 3 | -1 | 1 21 |
| 45 | uuccacagcuuu | Phvul.002G147600.1 | 3 | -1 | 1 21 |
| 46 | uuccacagcuuu | Phvul.002G147600.1 | 3 | -1 | 1 21 |
| 47 | uuccacagcuuu | Phvul.002G147600.1 | 3 | -1 | 1 21 |
| 48 | uuccacagcuuu | Phvul.002G147600.1 | 3 | -1 | 1 21 |
| 49 | uuccacagcuuu | Phvul.002G147600.1 | 3 | -1 | 1 21 |
| 50 | uuccacagcuuu | Phvul.002G147600.1 | 3 | -1 | 1 21 |
| 51 | uuccacagcuuu | Phvul.002G147600.1 | 3 | -1 | 1 21 |
| 52 | uuccacagcuuu | Phvul.002G147600.1 | 3 | -1 | 1 21 |
| 53 | uuccacagcuuu | Phvul.002G147600.1 | 3 | -1 | 1 21 |
| 54 | uuccacagcuuu | Phvul.002G147600.1 | 3 | -1 | 1 21 |
| 55 | uuccacagcuuu | Phvul.002G147600.1 | 3 | -1 | 1 21 |
| 56 | uuccacagcuuu | Phvul.002G147600.1 | 3 | -1 | 1 21 |
| 57 | uuccacagcuuu | Phvul.002G147600.1 | 3 | -1 | 1 21 |
| 58 | uuccacagcuuu | Phvul.002G147600.1 | 3 | -1 | 1 21 |
| 59 | uuccacagcuuu | Phvul.002G147600.1 | 3 | -1 | 1 22 |
| 60 | uuccacagcuuu | Phvul.002G162900.1 | 3 | -1 | 1 21 |
| | uuccacagcuuu | Phvul.002G162900.1 | 3 | -1 | 1 21 |

| | | | | | |
|----|--------------|--------------------|---|----|------|
| 1 | | | | | |
| 2 | uuccacagcuuu | Phvul.002G162900.1 | 3 | -1 | 1 21 |
| 3 | uuccacagcuuu | Phvul.002G162900.1 | 3 | -1 | 1 21 |
| 4 | uuccacagcuuu | Phvul.002G162900.1 | 3 | -1 | 1 21 |
| 5 | uuccacagcuuu | Phvul.002G162900.1 | 3 | -1 | 1 21 |
| 6 | uuccacagcuuu | Phvul.002G162900.1 | 3 | -1 | 1 21 |
| 7 | uuccacagcuuu | Phvul.002G162900.1 | 3 | -1 | 1 21 |
| 8 | uuccacagcuuu | Phvul.002G162900.1 | 3 | -1 | 1 21 |
| 9 | uuccacagcuuu | Phvul.002G162900.1 | 3 | -1 | 1 21 |
| 10 | uuccacagcuuu | Phvul.002G162900.1 | 3 | -1 | 1 21 |
| 11 | uuccacagcuuu | Phvul.002G162900.1 | 3 | -1 | 1 21 |
| 12 | uuccacagcuuu | Phvul.002G162900.1 | 3 | -1 | 1 21 |
| 13 | uuccacagcuuu | Phvul.002G162900.1 | 3 | -1 | 1 21 |
| 14 | uuccacagcuuu | Phvul.002G162900.1 | 3 | -1 | 1 22 |
| 15 | uuccacagcuuu | Phvul.002G250000.1 | 3 | -1 | 1 21 |
| 16 | uuccacagcuuu | Phvul.002G250000.1 | 3 | -1 | 1 21 |
| 17 | uuccacagcuuu | Phvul.002G250000.1 | 3 | -1 | 1 21 |
| 18 | uuccacagcuuu | Phvul.002G250000.1 | 3 | -1 | 1 21 |
| 19 | uuccacagcuuu | Phvul.002G250000.1 | 3 | -1 | 1 21 |
| 20 | uuccacagcuuu | Phvul.002G250000.1 | 3 | -1 | 1 21 |
| 21 | uuccacagcuuu | Phvul.002G250000.1 | 3 | -1 | 1 21 |
| 22 | uuccacagcuuu | Phvul.002G250000.1 | 3 | -1 | 1 21 |
| 23 | uuccacagcuuu | Phvul.002G250000.1 | 3 | -1 | 1 21 |
| 24 | uuccacagcuuu | Phvul.002G250000.1 | 3 | -1 | 1 21 |
| 25 | uuccacagcuuu | Phvul.002G250000.1 | 3 | -1 | 1 21 |
| 26 | uuccacagcuuu | Phvul.002G250000.1 | 3 | -1 | 1 21 |
| 27 | uuccacagcuuu | Phvul.002G250000.1 | 3 | -1 | 1 21 |
| 28 | uuccacagcuuu | Phvul.002G250000.1 | 3 | -1 | 1 21 |
| 29 | uuccacagcuuu | Phvul.002G250000.1 | 3 | -1 | 1 21 |
| 30 | uuccacagcuuu | Phvul.002G250000.1 | 3 | -1 | 1 22 |
| 31 | uuccacagcuuu | Phvul.003G014900.1 | 3 | -1 | 1 21 |
| 32 | uuccacagcuuu | Phvul.003G014900.1 | 3 | -1 | 1 21 |
| 33 | uuccacagcuuu | Phvul.003G014900.1 | 3 | -1 | 1 21 |
| 34 | uuccacagcuuu | Phvul.003G014900.1 | 3 | -1 | 1 21 |
| 35 | uuccacagcuuu | Phvul.003G014900.1 | 3 | -1 | 1 21 |
| 36 | uuccacagcuuu | Phvul.003G014900.1 | 3 | -1 | 1 21 |
| 37 | uuccacagcuuu | Phvul.003G014900.1 | 3 | -1 | 1 21 |
| 38 | uuccacagcuuu | Phvul.003G014900.1 | 3 | -1 | 1 21 |
| 39 | uuccacagcuuu | Phvul.003G014900.1 | 3 | -1 | 1 21 |
| 40 | uuccacagcuuu | Phvul.003G014900.1 | 3 | -1 | 1 21 |
| 41 | uuccacagcuuu | Phvul.003G014900.1 | 3 | -1 | 1 21 |
| 42 | uuccacagcuuu | Phvul.003G014900.1 | 3 | -1 | 1 21 |
| 43 | uuccacagcuuu | Phvul.003G014900.1 | 3 | -1 | 1 21 |
| 44 | uuccacagcuuu | Phvul.003G014900.1 | 3 | -1 | 1 21 |
| 45 | uuccacagcuuu | Phvul.003G014900.1 | 3 | -1 | 1 22 |
| 46 | uuccacagcuuu | Phvul.003G014900.1 | 3 | -1 | 1 21 |
| 47 | uuccacagcuuu | Phvul.003G131800.1 | 3 | -1 | 1 21 |
| 48 | uuccacagcuuu | Phvul.003G131800.1 | 3 | -1 | 1 21 |
| 49 | uuccacagcuuu | Phvul.003G131800.1 | 3 | -1 | 1 21 |
| 50 | uuccacagcuuu | Phvul.003G131800.1 | 3 | -1 | 1 21 |
| 51 | uuccacagcuuu | Phvul.003G131800.1 | 3 | -1 | 1 21 |
| 52 | uuccacagcuuu | Phvul.003G131800.1 | 3 | -1 | 1 21 |
| 53 | uuccacagcuuu | Phvul.003G131800.1 | 3 | -1 | 1 21 |
| 54 | uuccacagcuuu | Phvul.003G131800.1 | 3 | -1 | 1 21 |
| 55 | uuccacagcuuu | Phvul.003G131800.1 | 3 | -1 | 1 21 |
| 56 | uuccacagcuuu | Phvul.003G131800.1 | 3 | -1 | 1 21 |
| 57 | uuccacagcuuu | Phvul.003G131800.1 | 3 | -1 | 1 21 |
| 58 | uuccacagcuuu | Phvul.003G131800.1 | 3 | -1 | 1 21 |
| 59 | uuccacagcuuu | Phvul.003G131800.1 | 3 | -1 | 1 21 |
| 60 | uuccacagcuuu | Phvul.003G131800.1 | 3 | -1 | 1 21 |
| | uuccacagcuuu | Phvul.003G131800.1 | 3 | -1 | 1 22 |

| | | | | | | |
|----|--------------|--------------------|---|----|---|----|
| 1 | | | | | | |
| 2 | uuccacagcuuu | Phvul.003G154800.1 | 3 | -1 | 1 | 21 |
| 3 | uuccacagcuuu | Phvul.003G154800.1 | 3 | -1 | 1 | 21 |
| 4 | uuccacagcuuu | Phvul.003G154800.1 | 3 | -1 | 1 | 21 |
| 5 | uuccacagcuuu | Phvul.003G154800.1 | 3 | -1 | 1 | 21 |
| 6 | uuccacagcuuu | Phvul.003G154800.1 | 3 | -1 | 1 | 21 |
| 7 | uuccacagcuuu | Phvul.003G154800.1 | 3 | -1 | 1 | 21 |
| 8 | uuccacagcuuu | Phvul.003G154800.1 | 3 | -1 | 1 | 21 |
| 9 | uuccacagcuuu | Phvul.003G154800.1 | 3 | -1 | 1 | 21 |
| 10 | uuccacagcuuu | Phvul.003G154800.1 | 3 | -1 | 1 | 21 |
| 11 | uuccacagcuuu | Phvul.003G154800.1 | 3 | -1 | 1 | 21 |
| 12 | uuccacagcuuu | Phvul.003G154800.1 | 3 | -1 | 1 | 21 |
| 13 | uuccacagcuuu | Phvul.003G154800.1 | 3 | -1 | 1 | 21 |
| 14 | uuccacagcuuu | Phvul.003G154800.1 | 3 | -1 | 1 | 21 |
| 15 | uuccacagcuuu | Phvul.003G154800.1 | 3 | -1 | 1 | 21 |
| 16 | uuccacagcuuu | Phvul.003G154800.1 | 3 | -1 | 1 | 22 |
| 17 | uuccacagcuuu | Phvul.006G102400.1 | 3 | -1 | 1 | 21 |
| 18 | uuccacagcuuu | Phvul.006G102400.1 | 3 | -1 | 1 | 21 |
| 19 | uuccacagcuuu | Phvul.006G102400.1 | 3 | -1 | 1 | 21 |
| 20 | uuccacagcuuu | Phvul.006G102400.1 | 3 | -1 | 1 | 21 |
| 21 | uuccacagcuuu | Phvul.006G102400.1 | 3 | -1 | 1 | 21 |
| 22 | uuccacagcuuu | Phvul.006G102400.1 | 3 | -1 | 1 | 21 |
| 23 | uuccacagcuuu | Phvul.006G102400.1 | 3 | -1 | 1 | 21 |
| 24 | uuccacagcuuu | Phvul.006G102400.1 | 3 | -1 | 1 | 21 |
| 25 | uuccacagcuuu | Phvul.006G102400.1 | 3 | -1 | 1 | 21 |
| 26 | uuccacagcuuu | Phvul.006G102400.1 | 3 | -1 | 1 | 21 |
| 27 | uuccacagcuuu | Phvul.006G102400.1 | 3 | -1 | 1 | 21 |
| 28 | uuccacagcuuu | Phvul.006G102400.1 | 3 | -1 | 1 | 21 |
| 29 | uuccacagcuuu | Phvul.006G102400.1 | 3 | -1 | 1 | 21 |
| 30 | uuccacagcuuu | Phvul.006G102400.1 | 3 | -1 | 1 | 21 |
| 31 | uuccacagcuuu | Phvul.006G102400.1 | 3 | -1 | 1 | 21 |
| 32 | uuccacagcuuu | Phvul.006G102400.1 | 3 | -1 | 1 | 22 |
| 33 | uuccacagcuuu | Phvul.006G191600.1 | 3 | -1 | 1 | 21 |
| 34 | uuccacagcuuu | Phvul.006G191600.1 | 3 | -1 | 1 | 21 |
| 35 | uuccacagcuuu | Phvul.006G191600.1 | 3 | -1 | 1 | 21 |
| 36 | uuccacagcuuu | Phvul.006G191600.1 | 3 | -1 | 1 | 21 |
| 37 | uuccacagcuuu | Phvul.006G191600.1 | 3 | -1 | 1 | 21 |
| 38 | uuccacagcuuu | Phvul.006G191600.1 | 3 | -1 | 1 | 21 |
| 39 | uuccacagcuuu | Phvul.006G191600.1 | 3 | -1 | 1 | 21 |
| 40 | uuccacagcuuu | Phvul.006G191600.1 | 3 | -1 | 1 | 21 |
| 41 | uuccacagcuuu | Phvul.006G191600.1 | 3 | -1 | 1 | 21 |
| 42 | uuccacagcuuu | Phvul.006G191600.1 | 3 | -1 | 1 | 21 |
| 43 | uuccacagcuuu | Phvul.006G191600.1 | 3 | -1 | 1 | 21 |
| 44 | uuccacagcuuu | Phvul.006G191600.1 | 3 | -1 | 1 | 21 |
| 45 | uuccacagcuuu | Phvul.006G191600.1 | 3 | -1 | 1 | 21 |
| 46 | uuccacagcuuu | Phvul.006G191600.1 | 3 | -1 | 1 | 21 |
| 47 | uuccacagcuuu | Phvul.006G191600.1 | 3 | -1 | 1 | 21 |
| 48 | uuccacagcuuu | Phvul.006G191600.1 | 3 | -1 | 1 | 22 |
| 49 | uuccacagcuuu | Phvul.007G222300.1 | 3 | -1 | 1 | 21 |
| 50 | uuccacagcuuu | Phvul.007G222300.1 | 3 | -1 | 1 | 21 |
| 51 | uuccacagcuuu | Phvul.007G222300.1 | 3 | -1 | 1 | 21 |
| 52 | uuccacagcuuu | Phvul.007G222300.1 | 3 | -1 | 1 | 21 |
| 53 | uuccacagcuuu | Phvul.007G222300.1 | 3 | -1 | 1 | 21 |
| 54 | uuccacagcuuu | Phvul.007G222300.1 | 3 | -1 | 1 | 21 |
| 55 | uuccacagcuuu | Phvul.007G222300.1 | 3 | -1 | 1 | 21 |
| 56 | uuccacagcuuu | Phvul.007G222300.1 | 3 | -1 | 1 | 21 |
| 57 | uuccacagcuuu | Phvul.007G222300.1 | 3 | -1 | 1 | 21 |
| 58 | uuccacagcuuu | Phvul.007G222300.1 | 3 | -1 | 1 | 21 |
| 59 | uuccacagcuuu | Phvul.007G222300.1 | 3 | -1 | 1 | 21 |
| 60 | uuccacagcuuu | Phvul.007G222300.1 | 3 | -1 | 1 | 21 |
| | uuccacagcuuu | Phvul.007G222300.1 | 3 | -1 | 1 | 21 |

| | | | | | | |
|----|--------------|--------------------|---|----|---|----|
| 1 | | | | | | |
| 2 | uuccacagcuuu | Phvul.007G222300.1 | 3 | -1 | 1 | 21 |
| 3 | uuccacagcuuu | Phvul.007G222300.1 | 3 | -1 | 1 | 22 |
| 4 | uuccacagcuuu | Phvul.008G203800.1 | 3 | -1 | 1 | 21 |
| 5 | uuccacagcuuu | Phvul.008G203800.1 | 3 | -1 | 1 | 21 |
| 6 | uuccacagcuuu | Phvul.008G203800.1 | 3 | -1 | 1 | 21 |
| 7 | uuccacagcuuu | Phvul.008G203800.1 | 3 | -1 | 1 | 21 |
| 8 | uuccacagcuuu | Phvul.008G203800.1 | 3 | -1 | 1 | 21 |
| 9 | uuccacagcuuu | Phvul.008G203800.1 | 3 | -1 | 1 | 21 |
| 10 | uuccacagcuuu | Phvul.008G203800.1 | 3 | -1 | 1 | 21 |
| 11 | uuccacagcuuu | Phvul.008G203800.1 | 3 | -1 | 1 | 21 |
| 12 | uuccacagcuuu | Phvul.008G203800.1 | 3 | -1 | 1 | 21 |
| 13 | uuccacagcuuu | Phvul.008G203800.1 | 3 | -1 | 1 | 21 |
| 14 | uuccacagcuuu | Phvul.008G203800.1 | 3 | -1 | 1 | 21 |
| 15 | uuccacagcuuu | Phvul.008G203800.1 | 3 | -1 | 1 | 21 |
| 16 | uuccacagcuuu | Phvul.008G203800.1 | 3 | -1 | 1 | 21 |
| 17 | uuccacagcuuu | Phvul.008G203800.1 | 3 | -1 | 1 | 21 |
| 18 | uuccacagcuuu | Phvul.008G203800.1 | 3 | -1 | 1 | 21 |
| 19 | uuccacagcuuu | Phvul.008G203800.1 | 3 | -1 | 1 | 22 |
| 20 | uuccacagcuuu | Phvul.008G204100.1 | 3 | -1 | 1 | 21 |
| 21 | uuccacagcuuu | Phvul.008G204100.1 | 3 | -1 | 1 | 21 |
| 22 | uuccacagcuuu | Phvul.008G204100.1 | 3 | -1 | 1 | 21 |
| 23 | uuccacagcuuu | Phvul.008G204100.1 | 3 | -1 | 1 | 21 |
| 24 | uuccacagcuuu | Phvul.008G204100.1 | 3 | -1 | 1 | 21 |
| 25 | uuccacagcuuu | Phvul.008G204100.1 | 3 | -1 | 1 | 21 |
| 26 | uuccacagcuuu | Phvul.008G204100.1 | 3 | -1 | 1 | 21 |
| 27 | uuccacagcuuu | Phvul.008G204100.1 | 3 | -1 | 1 | 21 |
| 28 | uuccacagcuuu | Phvul.008G204100.1 | 3 | -1 | 1 | 21 |
| 29 | uuccacagcuuu | Phvul.008G204100.1 | 3 | -1 | 1 | 21 |
| 30 | uuccacagcuuu | Phvul.008G204100.1 | 3 | -1 | 1 | 21 |
| 31 | uuccacagcuuu | Phvul.008G204100.1 | 3 | -1 | 1 | 21 |
| 32 | uuccacagcuuu | Phvul.008G204100.1 | 3 | -1 | 1 | 21 |
| 33 | uuccacagcuuu | Phvul.008G204100.1 | 3 | -1 | 1 | 21 |
| 34 | uuccacagcuuu | Phvul.008G204100.1 | 3 | -1 | 1 | 21 |
| 35 | uuccacagcuuu | Phvul.008G204100.1 | 3 | -1 | 1 | 22 |
| 36 | uuccacagcuuu | Phvul.009G047000.9 | 3 | -1 | 1 | 21 |
| 37 | uuccacagcuuu | Phvul.009G047000.8 | 3 | -1 | 1 | 21 |
| 38 | uuccacagcuuu | Phvul.009G047000.7 | 3 | -1 | 1 | 21 |
| 39 | uuccacagcuuu | Phvul.009G047000.4 | 3 | -1 | 1 | 21 |
| 40 | uuccacagcuuu | Phvul.009G047000.1 | 3 | -1 | 1 | 21 |
| 41 | uuccacagcuuu | Phvul.009G047000.6 | 3 | -1 | 1 | 21 |
| 42 | uuccacagcuuu | Phvul.009G047000.5 | 3 | -1 | 1 | 21 |
| 43 | uuccacagcuuu | Phvul.009G047000.2 | 3 | -1 | 1 | 21 |
| 44 | uuccacagcuuu | Phvul.009G047000.3 | 3 | -1 | 1 | 21 |
| 45 | uuccacagcuuu | Phvul.009G047000.9 | 3 | -1 | 1 | 21 |
| 46 | uuccacagcuuu | Phvul.009G047000.8 | 3 | -1 | 1 | 21 |
| 47 | uuccacagcuuu | Phvul.009G047000.7 | 3 | -1 | 1 | 21 |
| 48 | uuccacagcuuu | Phvul.009G047000.4 | 3 | -1 | 1 | 21 |
| 49 | uuccacagcuuu | Phvul.009G047000.1 | 3 | -1 | 1 | 21 |
| 50 | uuccacagcuuu | Phvul.009G047000.6 | 3 | -1 | 1 | 21 |
| 51 | uuccacagcuuu | Phvul.009G047000.5 | 3 | -1 | 1 | 21 |
| 52 | uuccacagcuuu | Phvul.009G047000.2 | 3 | -1 | 1 | 21 |
| 53 | uuccacagcuuu | Phvul.009G047000.3 | 3 | -1 | 1 | 21 |
| 54 | uuccacagcuuu | Phvul.009G047000.9 | 3 | -1 | 1 | 21 |
| 55 | uuccacagcuuu | Phvul.009G047000.8 | 3 | -1 | 1 | 21 |
| 56 | uuccacagcuuu | Phvul.009G047000.7 | 3 | -1 | 1 | 21 |
| 57 | uuccacagcuuu | Phvul.009G047000.4 | 3 | -1 | 1 | 21 |
| 58 | uuccacagcuuu | Phvul.009G047000.1 | 3 | -1 | 1 | 21 |
| 59 | uuccacagcuuu | Phvul.009G047000.6 | 3 | -1 | 1 | 21 |
| 60 | uuccacagcuuu | Phvul.009G047000.5 | 3 | -1 | 1 | 21 |
| | uuccacagcuuu | Phvul.009G047000.2 | 3 | -1 | 1 | 21 |
| | uuccacagcuuu | Phvul.009G047000.3 | 3 | -1 | 1 | 21 |
| | uuccacagcuuu | Phvul.009G047000.9 | 3 | -1 | 1 | 21 |
| | uuccacagcuuu | Phvul.009G047000.8 | 3 | -1 | 1 | 21 |

| | | | | | |
|----|--------------|--------------------|---|----|------|
| 1 | | | | | |
| 2 | uuccacagcuuu | Phvul.009G047000.7 | 3 | -1 | 1 21 |
| 3 | uuccacagcuuu | Phvul.009G047000.4 | 3 | -1 | 1 21 |
| 4 | uuccacagcuuu | Phvul.009G047000.1 | 3 | -1 | 1 21 |
| 5 | uuccacagcuuu | Phvul.009G047000.6 | 3 | -1 | 1 21 |
| 6 | uuccacagcuuu | Phvul.009G047000.5 | 3 | -1 | 1 21 |
| 7 | uuccacagcuuu | Phvul.009G047000.2 | 3 | -1 | 1 21 |
| 8 | uuccacagcuuu | Phvul.009G047000.3 | 3 | -1 | 1 21 |
| 9 | uuccacagcuuu | Phvul.009G047000.9 | 3 | -1 | 1 21 |
| 10 | uuccacagcuuu | Phvul.009G047000.8 | 3 | -1 | 1 21 |
| 11 | uuccacagcuuu | Phvul.009G047000.7 | 3 | -1 | 1 21 |
| 12 | uuccacagcuuu | Phvul.009G047000.4 | 3 | -1 | 1 21 |
| 13 | uuccacagcuuu | Phvul.009G047000.1 | 3 | -1 | 1 21 |
| 14 | uuccacagcuuu | Phvul.009G047000.6 | 3 | -1 | 1 21 |
| 15 | uuccacagcuuu | Phvul.009G047000.5 | 3 | -1 | 1 21 |
| 16 | uuccacagcuuu | Phvul.009G047000.2 | 3 | -1 | 1 21 |
| 17 | uuccacagcuuu | Phvul.009G047000.3 | 3 | -1 | 1 21 |
| 18 | uuccacagcuuu | Phvul.009G047000.9 | 3 | -1 | 1 21 |
| 19 | uuccacagcuuu | Phvul.009G047000.8 | 3 | -1 | 1 21 |
| 20 | uuccacagcuuu | Phvul.009G047000.7 | 3 | -1 | 1 21 |
| 21 | uuccacagcuuu | Phvul.009G047000.4 | 3 | -1 | 1 21 |
| 22 | uuccacagcuuu | Phvul.009G047000.1 | 3 | -1 | 1 21 |
| 23 | uuccacagcuuu | Phvul.009G047000.6 | 3 | -1 | 1 21 |
| 24 | uuccacagcuuu | Phvul.009G047000.5 | 3 | -1 | 1 21 |
| 25 | uuccacagcuuu | Phvul.009G047000.2 | 3 | -1 | 1 21 |
| 26 | uuccacagcuuu | Phvul.009G047000.3 | 3 | -1 | 1 21 |
| 27 | uuccacagcuuu | Phvul.009G047000.9 | 3 | -1 | 1 21 |
| 28 | uuccacagcuuu | Phvul.009G047000.8 | 3 | -1 | 1 21 |
| 29 | uuccacagcuuu | Phvul.009G047000.7 | 3 | -1 | 1 21 |
| 30 | uuccacagcuuu | Phvul.009G047000.4 | 3 | -1 | 1 21 |
| 31 | uuccacagcuuu | Phvul.009G047000.1 | 3 | -1 | 1 21 |
| 32 | uuccacagcuuu | Phvul.009G047000.6 | 3 | -1 | 1 21 |
| 33 | uuccacagcuuu | Phvul.009G047000.5 | 3 | -1 | 1 21 |
| 34 | uuccacagcuuu | Phvul.009G047000.2 | 3 | -1 | 1 21 |
| 35 | uuccacagcuuu | Phvul.009G047000.3 | 3 | -1 | 1 21 |
| 36 | uuccacagcuuu | Phvul.009G047000.9 | 3 | -1 | 1 21 |
| 37 | uuccacagcuuu | Phvul.009G047000.8 | 3 | -1 | 1 21 |
| 38 | uuccacagcuuu | Phvul.009G047000.7 | 3 | -1 | 1 21 |
| 39 | uuccacagcuuu | Phvul.009G047000.4 | 3 | -1 | 1 21 |
| 40 | uuccacagcuuu | Phvul.009G047000.1 | 3 | -1 | 1 21 |
| 41 | uuccacagcuuu | Phvul.009G047000.6 | 3 | -1 | 1 21 |
| 42 | uuccacagcuuu | Phvul.009G047000.5 | 3 | -1 | 1 21 |
| 43 | uuccacagcuuu | Phvul.009G047000.2 | 3 | -1 | 1 21 |
| 44 | uuccacagcuuu | Phvul.009G047000.3 | 3 | -1 | 1 21 |
| 45 | uuccacagcuuu | Phvul.009G047000.9 | 3 | -1 | 1 21 |
| 46 | uuccacagcuuu | Phvul.009G047000.8 | 3 | -1 | 1 21 |
| 47 | uuccacagcuuu | Phvul.009G047000.7 | 3 | -1 | 1 21 |
| 48 | uuccacagcuuu | Phvul.009G047000.4 | 3 | -1 | 1 21 |
| 49 | uuccacagcuuu | Phvul.009G047000.1 | 3 | -1 | 1 21 |
| 50 | uuccacagcuuu | Phvul.009G047000.6 | 3 | -1 | 1 21 |
| 51 | uuccacagcuuu | Phvul.009G047000.5 | 3 | -1 | 1 21 |
| 52 | uuccacagcuuu | Phvul.009G047000.2 | 3 | -1 | 1 21 |
| 53 | uuccacagcuuu | Phvul.009G047000.3 | 3 | -1 | 1 21 |
| 54 | uuccacagcuuu | Phvul.009G047000.9 | 3 | -1 | 1 21 |
| 55 | uuccacagcuuu | Phvul.009G047000.8 | 3 | -1 | 1 21 |
| 56 | uuccacagcuuu | Phvul.009G047000.7 | 3 | -1 | 1 21 |
| 57 | uuccacagcuuu | Phvul.009G047000.4 | 3 | -1 | 1 21 |
| 58 | uuccacagcuuu | Phvul.009G047000.1 | 3 | -1 | 1 21 |
| 59 | uuccacagcuuu | Phvul.009G047000.6 | 3 | -1 | 1 21 |
| 60 | uuccacagcuuu | Phvul.009G047000.5 | 3 | -1 | 1 21 |
| | uuccacagcuuu | Phvul.009G047000.2 | 3 | -1 | 1 21 |
| | uuccacagcuuu | Phvul.009G047000.3 | 3 | -1 | 1 21 |
| | uuccacagcuuu | Phvul.009G047000.9 | 3 | -1 | 1 21 |
| | uuccacagcuuu | Phvul.009G047000.8 | 3 | -1 | 1 21 |
| | uuccacagcuuu | Phvul.009G047000.7 | 3 | -1 | 1 21 |

| | | | | | | |
|----|--------------|--------------------|---|----|---|----|
| 1 | | | | | | |
| 2 | uuccacagcuuu | Phvul.009G047000.4 | 3 | -1 | 1 | 21 |
| 3 | uuccacagcuuu | Phvul.009G047000.1 | 3 | -1 | 1 | 21 |
| 4 | uuccacagcuuu | Phvul.009G047000.6 | 3 | -1 | 1 | 21 |
| 5 | | | | | | |
| 6 | uuccacagcuuu | Phvul.009G047000.5 | 3 | -1 | 1 | 21 |
| 7 | uuccacagcuuu | Phvul.009G047000.2 | 3 | -1 | 1 | 21 |
| 8 | uuccacagcuuu | Phvul.009G047000.3 | 3 | -1 | 1 | 21 |
| 9 | | | | | | |
| 10 | uuccacagcuuu | Phvul.009G047000.9 | 3 | -1 | 1 | 21 |
| 11 | uuccacagcuuu | Phvul.009G047000.8 | 3 | -1 | 1 | 21 |
| 12 | uuccacagcuuu | Phvul.009G047000.7 | 3 | -1 | 1 | 21 |
| 13 | | | | | | |
| 14 | uuccacagcuuu | Phvul.009G047000.4 | 3 | -1 | 1 | 21 |
| 15 | uuccacagcuuu | Phvul.009G047000.1 | 3 | -1 | 1 | 21 |
| 16 | uuccacagcuuu | Phvul.009G047000.6 | 3 | -1 | 1 | 21 |
| 17 | | | | | | |
| 18 | uuccacagcuuu | Phvul.009G047000.5 | 3 | -1 | 1 | 21 |
| 19 | uuccacagcuuu | Phvul.009G047000.2 | 3 | -1 | 1 | 21 |
| 20 | uuccacagcuuu | Phvul.009G047000.3 | 3 | -1 | 1 | 21 |
| 21 | | | | | | |
| 22 | uuccacagcuuu | Phvul.009G047000.9 | 3 | -1 | 1 | 21 |
| 23 | uuccacagcuuu | Phvul.009G047000.8 | 3 | -1 | 1 | 21 |
| 24 | uuccacagcuuu | Phvul.009G047000.7 | 3 | -1 | 1 | 21 |
| 25 | | | | | | |
| 26 | uuccacagcuuu | Phvul.009G047000.4 | 3 | -1 | 1 | 21 |
| 27 | uuccacagcuuu | Phvul.009G047000.1 | 3 | -1 | 1 | 21 |
| 28 | uuccacagcuuu | Phvul.009G047000.6 | 3 | -1 | 1 | 21 |
| 29 | | | | | | |
| 30 | uuccacagcuuu | Phvul.009G047000.5 | 3 | -1 | 1 | 21 |
| 31 | uuccacagcuuu | Phvul.009G047000.2 | 3 | -1 | 1 | 21 |
| 32 | uuccacagcuuu | Phvul.009G047000.3 | 3 | -1 | 1 | 21 |
| 33 | | | | | | |
| 34 | uuccacagcuuu | Phvul.009G047000.9 | 3 | -1 | 1 | 21 |
| 35 | uuccacagcuuu | Phvul.009G047000.8 | 3 | -1 | 1 | 21 |
| 36 | uuccacagcuuu | Phvul.009G047000.7 | 3 | -1 | 1 | 21 |
| 37 | | | | | | |
| 38 | uuccacagcuuu | Phvul.009G047000.4 | 3 | -1 | 1 | 21 |
| 39 | uuccacagcuuu | Phvul.009G047000.1 | 3 | -1 | 1 | 21 |
| 40 | uuccacagcuuu | Phvul.009G047000.6 | 3 | -1 | 1 | 21 |
| 41 | | | | | | |
| 42 | uuccacagcuuu | Phvul.009G047000.5 | 3 | -1 | 1 | 21 |
| 43 | uuccacagcuuu | Phvul.009G047000.2 | 3 | -1 | 1 | 21 |
| 44 | uuccacagcuuu | Phvul.009G047000.3 | 3 | -1 | 1 | 21 |
| 45 | | | | | | |
| 46 | uuccacagcuuu | Phvul.009G047000.9 | 3 | -1 | 1 | 22 |
| 47 | uuccacagcuuu | Phvul.009G047000.8 | 3 | -1 | 1 | 22 |
| 48 | uuccacagcuuu | Phvul.009G047000.7 | 3 | -1 | 1 | 22 |
| 49 | | | | | | |
| 50 | uuccacagcuuu | Phvul.009G047000.4 | 3 | -1 | 1 | 22 |
| 51 | uuccacagcuuu | Phvul.009G047000.1 | 3 | -1 | 1 | 22 |
| 52 | uuccacagcuuu | Phvul.009G047000.6 | 3 | -1 | 1 | 22 |
| 53 | | | | | | |
| 54 | uuccacagcuuu | Phvul.009G047000.5 | 3 | -1 | 1 | 22 |
| 55 | uuccacagcuuu | Phvul.009G047000.2 | 3 | -1 | 1 | 22 |
| 56 | uuccacagcuuu | Phvul.009G047000.3 | 3 | -1 | 1 | 22 |
| 57 | | | | | | |
| 58 | uuccacagcuuu | Phvul.009G212100.1 | 3 | -1 | 1 | 21 |
| 59 | uuccacagcuuu | Phvul.009G212100.1 | 3 | -1 | 1 | 21 |
| 60 | uuccacagcuuu | Phvul.009G212100.1 | 3 | -1 | 1 | 21 |
| | uuccacagcuuu | Phvul.009G212100.1 | 3 | -1 | 1 | 21 |

| | | | | | |
|----|--------------|--------------------|---|----|------|
| 1 | | | | | |
| 2 | uuccacagcuuu | Phvul.009G212100.1 | 3 | -1 | 1 21 |
| 3 | uuccacagcuuu | Phvul.009G212100.1 | 3 | -1 | 1 21 |
| 4 | uuccacagcuuu | Phvul.009G212100.1 | 3 | -1 | 1 21 |
| 5 | uuccacagcuuu | Phvul.009G212100.1 | 3 | -1 | 1 21 |
| 6 | uuccacagcuuu | Phvul.009G212100.1 | 3 | -1 | 1 21 |
| 7 | uuccacagcuuu | Phvul.009G212100.1 | 3 | -1 | 1 21 |
| 8 | uuccacagcuuu | Phvul.009G212100.1 | 3 | -1 | 1 21 |
| 9 | uuccacagcuuu | Phvul.009G212100.1 | 3 | -1 | 1 21 |
| 10 | uuccacagcuuu | Phvul.009G212100.1 | 3 | -1 | 1 21 |
| 11 | uuccacagcuuu | Phvul.009G212100.1 | 3 | -1 | 1 22 |
| 12 | uuccacagcuuu | Phvul.009G228000.1 | 3 | -1 | 1 21 |
| 13 | uuccacagcuuu | Phvul.009G228000.2 | 3 | -1 | 1 21 |
| 14 | uuccacagcuuu | Phvul.009G228000.2 | 3 | -1 | 1 21 |
| 15 | uuccacagcuuu | Phvul.009G228000.1 | 3 | -1 | 1 21 |
| 16 | uuccacagcuuu | Phvul.009G228000.2 | 3 | -1 | 1 21 |
| 17 | uuccacagcuuu | Phvul.009G228000.2 | 3 | -1 | 1 21 |
| 18 | uuccacagcuuu | Phvul.009G228000.1 | 3 | -1 | 1 21 |
| 19 | uuccacagcuuu | Phvul.009G228000.2 | 3 | -1 | 1 21 |
| 20 | uuccacagcuuu | Phvul.009G228000.1 | 3 | -1 | 1 21 |
| 21 | uuccacagcuuu | Phvul.009G228000.1 | 3 | -1 | 1 21 |
| 22 | uuccacagcuuu | Phvul.009G228000.2 | 3 | -1 | 1 21 |
| 23 | uuccacagcuuu | Phvul.009G228000.1 | 3 | -1 | 1 21 |
| 24 | uuccacagcuuu | Phvul.009G228000.2 | 3 | -1 | 1 21 |
| 25 | uuccacagcuuu | Phvul.009G228000.1 | 3 | -1 | 1 21 |
| 26 | uuccacagcuuu | Phvul.009G228000.1 | 3 | -1 | 1 21 |
| 27 | uuccacagcuuu | Phvul.009G228000.2 | 3 | -1 | 1 21 |
| 28 | uuccacagcuuu | Phvul.009G228000.1 | 3 | -1 | 1 21 |
| 29 | uuccacagcuuu | Phvul.009G228000.1 | 3 | -1 | 1 21 |
| 30 | uuccacagcuuu | Phvul.009G228000.2 | 3 | -1 | 1 21 |
| 31 | uuccacagcuuu | Phvul.009G228000.1 | 3 | -1 | 1 21 |
| 32 | uuccacagcuuu | Phvul.009G228000.2 | 3 | -1 | 1 21 |
| 33 | uuccacagcuuu | Phvul.009G228000.1 | 3 | -1 | 1 21 |
| 34 | uuccacagcuuu | Phvul.009G228000.1 | 3 | -1 | 1 21 |
| 35 | uuccacagcuuu | Phvul.009G228000.2 | 3 | -1 | 1 21 |
| 36 | uuccacagcuuu | Phvul.009G228000.1 | 3 | -1 | 1 21 |
| 37 | uuccacagcuuu | Phvul.009G228000.2 | 3 | -1 | 1 21 |
| 38 | uuccacagcuuu | Phvul.009G228000.2 | 3 | -1 | 1 21 |
| 39 | uuccacagcuuu | Phvul.009G228000.1 | 3 | -1 | 1 21 |
| 40 | uuccacagcuuu | Phvul.009G228000.2 | 3 | -1 | 1 21 |
| 41 | uuccacagcuuu | Phvul.009G228000.1 | 3 | -1 | 1 22 |
| 42 | uuccacagcuuu | Phvul.009G228000.1 | 3 | -1 | 1 22 |
| 43 | uuccacagcuuu | Phvul.009G228000.2 | 3 | -1 | 1 22 |
| 44 | uuccacagcuuu | Phvul.010G048400.4 | 3 | -1 | 1 21 |
| 45 | uuccacagcuuu | Phvul.010G048400.3 | 3 | -1 | 1 21 |
| 46 | uuccacagcuuu | Phvul.010G048400.3 | 3 | -1 | 1 21 |
| 47 | uuccacagcuuu | Phvul.010G048400.1 | 3 | -1 | 1 21 |
| 48 | uuccacagcuuu | Phvul.010G048400.2 | 3 | -1 | 1 21 |
| 49 | uuccacagcuuu | Phvul.010G048400.4 | 3 | -1 | 1 21 |
| 50 | uuccacagcuuu | Phvul.010G048400.4 | 3 | -1 | 1 21 |
| 51 | uuccacagcuuu | Phvul.010G048400.3 | 3 | -1 | 1 21 |
| 52 | uuccacagcuuu | Phvul.010G048400.1 | 3 | -1 | 1 21 |
| 53 | uuccacagcuuu | Phvul.010G048400.2 | 3 | -1 | 1 21 |
| 54 | uuccacagcuuu | Phvul.010G048400.2 | 3 | -1 | 1 21 |
| 55 | uuccacagcuuu | Phvul.010G048400.4 | 3 | -1 | 1 21 |
| 56 | uuccacagcuuu | Phvul.010G048400.3 | 3 | -1 | 1 21 |
| 57 | uuccacagcuuu | Phvul.010G048400.1 | 3 | -1 | 1 21 |
| 58 | uuccacagcuuu | Phvul.010G048400.1 | 3 | -1 | 1 21 |
| 59 | uuccacagcuuu | Phvul.010G048400.2 | 3 | -1 | 1 21 |
| 60 | uuccacagcuuu | Phvul.010G048400.4 | 3 | -1 | 1 21 |
| | uuccacagcuuu | Phvul.010G048400.3 | 3 | -1 | 1 21 |

| | | | | | | |
|----|--------------|--------------------|---|----|---|----|
| 1 | | | | | | |
| 2 | uuccacagcuuu | Phvul.010G048400.1 | 3 | -1 | 1 | 21 |
| 3 | uuccacagcuuu | Phvul.010G048400.2 | 3 | -1 | 1 | 21 |
| 4 | uuccacagcuuu | Phvul.010G048400.4 | 3 | -1 | 1 | 21 |
| 5 | | | | | | |
| 6 | uuccacagcuuu | Phvul.010G048400.3 | 3 | -1 | 1 | 21 |
| 7 | uuccacagcuuu | Phvul.010G048400.1 | 3 | -1 | 1 | 21 |
| 8 | uuccacagcuuu | Phvul.010G048400.2 | 3 | -1 | 1 | 21 |
| 9 | | | | | | |
| 10 | uuccacagcuuu | Phvul.010G048400.4 | 3 | -1 | 1 | 21 |
| 11 | uuccacagcuuu | Phvul.010G048400.3 | 3 | -1 | 1 | 21 |
| 12 | uuccacagcuuu | Phvul.010G048400.1 | 3 | -1 | 1 | 21 |
| 13 | uuccacagcuuu | Phvul.010G048400.2 | 3 | -1 | 1 | 21 |
| 14 | uuccacagcuuu | Phvul.010G048400.4 | 3 | -1 | 1 | 21 |
| 15 | uuccacagcuuu | Phvul.010G048400.3 | 3 | -1 | 1 | 21 |
| 16 | uuccacagcuuu | Phvul.010G048400.1 | 3 | -1 | 1 | 21 |
| 17 | uuccacagcuuu | Phvul.010G048400.2 | 3 | -1 | 1 | 21 |
| 18 | uuccacagcuuu | Phvul.010G048400.4 | 3 | -1 | 1 | 21 |
| 19 | uuccacagcuuu | Phvul.010G048400.3 | 3 | -1 | 1 | 21 |
| 20 | uuccacagcuuu | Phvul.010G048400.1 | 3 | -1 | 1 | 21 |
| 21 | uuccacagcuuu | Phvul.010G048400.2 | 3 | -1 | 1 | 21 |
| 22 | uuccacagcuuu | Phvul.010G048400.4 | 3 | -1 | 1 | 21 |
| 23 | uuccacagcuuu | Phvul.010G048400.3 | 3 | -1 | 1 | 21 |
| 24 | uuccacagcuuu | Phvul.010G048400.1 | 3 | -1 | 1 | 21 |
| 25 | uuccacagcuuu | Phvul.010G048400.2 | 3 | -1 | 1 | 21 |
| 26 | uuccacagcuuu | Phvul.010G048400.4 | 3 | -1 | 1 | 21 |
| 27 | uuccacagcuuu | Phvul.010G048400.3 | 3 | -1 | 1 | 21 |
| 28 | uuccacagcuuu | Phvul.010G048400.1 | 3 | -1 | 1 | 21 |
| 29 | uuccacagcuuu | Phvul.010G048400.2 | 3 | -1 | 1 | 21 |
| 30 | uuccacagcuuu | Phvul.010G048400.4 | 3 | -1 | 1 | 21 |
| 31 | uuccacagcuuu | Phvul.010G048400.3 | 3 | -1 | 1 | 21 |
| 32 | uuccacagcuuu | Phvul.010G048400.1 | 3 | -1 | 1 | 21 |
| 33 | uuccacagcuuu | Phvul.010G048400.2 | 3 | -1 | 1 | 21 |
| 34 | uuccacagcuuu | Phvul.010G048400.4 | 3 | -1 | 1 | 21 |
| 35 | uuccacagcuuu | Phvul.010G048400.3 | 3 | -1 | 1 | 21 |
| 36 | uuccacagcuuu | Phvul.010G048400.1 | 3 | -1 | 1 | 21 |
| 37 | uuccacagcuuu | Phvul.010G048400.2 | 3 | -1 | 1 | 21 |
| 38 | uuccacagcuuu | Phvul.010G048400.4 | 3 | -1 | 1 | 21 |
| 39 | uuccacagcuuu | Phvul.010G048400.3 | 3 | -1 | 1 | 21 |
| 40 | uuccacagcuuu | Phvul.010G048400.1 | 3 | -1 | 1 | 21 |
| 41 | uuccacagcuuu | Phvul.010G048400.2 | 3 | -1 | 1 | 21 |
| 42 | uuccacagcuuu | Phvul.010G048400.4 | 3 | -1 | 1 | 22 |
| 43 | uuccacagcuuu | Phvul.010G048400.3 | 3 | -1 | 1 | 22 |
| 44 | uuccacagcuuu | Phvul.010G048400.1 | 3 | -1 | 1 | 22 |
| 45 | uuccacagcuuu | Phvul.010G048400.2 | 3 | -1 | 1 | 22 |
| 46 | uuccacagcuuu | Phvul.010G130000.1 | 3 | -1 | 1 | 21 |
| 47 | uuccacagcuuu | Phvul.010G130000.1 | 3 | -1 | 1 | 21 |
| 48 | uuccacagcuuu | Phvul.010G130000.1 | 3 | -1 | 1 | 21 |
| 49 | uuccacagcuuu | Phvul.010G130000.1 | 3 | -1 | 1 | 21 |
| 50 | uuccacagcuuu | Phvul.010G130000.1 | 3 | -1 | 1 | 21 |
| 51 | uuccacagcuuu | Phvul.010G130000.1 | 3 | -1 | 1 | 21 |
| 52 | uuccacagcuuu | Phvul.010G130000.1 | 3 | -1 | 1 | 21 |
| 53 | uuccacagcuuu | Phvul.010G130000.1 | 3 | -1 | 1 | 21 |
| 54 | uuccacagcuuu | Phvul.010G130000.1 | 3 | -1 | 1 | 21 |
| 55 | uuccacagcuuu | Phvul.010G130000.1 | 3 | -1 | 1 | 21 |
| 56 | uuccacagcuuu | Phvul.010G130000.1 | 3 | -1 | 1 | 21 |
| 57 | uuccacagcuuu | Phvul.010G130000.1 | 3 | -1 | 1 | 21 |
| 58 | uuccacagcuuu | Phvul.010G130000.1 | 3 | -1 | 1 | 21 |
| 59 | uuccacagcuuu | Phvul.010G130000.1 | 3 | -1 | 1 | 21 |
| 60 | uuccacagcuuu | Phvul.010G130000.1 | 3 | -1 | 1 | 21 |
| | uuccacagcuuu | Phvul.010G130000.1 | 3 | -1 | 1 | 22 |

| | | | | | | |
|----|--------------|--------------------|-----|----|---|----|
| 1 | | | | | | |
| 2 | uuccacagcuuu | Phvul.010G135701.1 | 3 | -1 | 1 | 21 |
| 3 | uuccacagcuuu | Phvul.010G135701.1 | 3 | -1 | 1 | 21 |
| 4 | uuccacagcuuu | Phvul.010G135701.1 | 3 | -1 | 1 | 21 |
| 5 | uuccacagcuuu | Phvul.010G135701.1 | 3 | -1 | 1 | 21 |
| 6 | uuccacagcuuu | Phvul.010G135701.1 | 3 | -1 | 1 | 21 |
| 7 | uuccacagcuuu | Phvul.010G135701.1 | 3 | -1 | 1 | 21 |
| 8 | uuccacagcuuu | Phvul.010G135701.1 | 3 | -1 | 1 | 21 |
| 9 | uuccacagcuuu | Phvul.010G135701.1 | 3 | -1 | 1 | 21 |
| 10 | uuccacagcuuu | Phvul.010G135701.1 | 3 | -1 | 1 | 21 |
| 11 | uuccacagcuuu | Phvul.010G135701.1 | 3 | -1 | 1 | 21 |
| 12 | uuccacagcuuu | Phvul.010G135701.1 | 3 | -1 | 1 | 21 |
| 13 | uuccacagcuuu | Phvul.010G135701.1 | 3 | -1 | 1 | 21 |
| 14 | uuccacagcuuu | Phvul.010G135701.1 | 3 | -1 | 1 | 21 |
| 15 | uuccacagcuuu | Phvul.010G135701.1 | 3 | -1 | 1 | 21 |
| 16 | uuccacagcuuu | Phvul.010G135701.1 | 3 | -1 | 1 | 22 |
| 17 | uuccacagcuuu | Phvul.010G135701.1 | 3 | -1 | 1 | 21 |
| 18 | uuccacagcuuu | Phvul.011G017700.1 | 3 | -1 | 1 | 21 |
| 19 | uuccacagcuuu | Phvul.011G017700.1 | 3 | -1 | 1 | 21 |
| 20 | uuccacagcuuu | Phvul.011G017700.1 | 3 | -1 | 1 | 21 |
| 21 | uuccacagcuuu | Phvul.011G017700.1 | 3 | -1 | 1 | 21 |
| 22 | uuccacagcuuu | Phvul.011G017700.1 | 3 | -1 | 1 | 21 |
| 23 | uuccacagcuuu | Phvul.011G017700.1 | 3 | -1 | 1 | 21 |
| 24 | uuccacagcuuu | Phvul.011G017700.1 | 3 | -1 | 1 | 21 |
| 25 | uuccacagcuuu | Phvul.011G017700.1 | 3 | -1 | 1 | 21 |
| 26 | uuccacagcuuu | Phvul.011G017700.1 | 3 | -1 | 1 | 21 |
| 27 | uuccacagcuuu | Phvul.011G017700.1 | 3 | -1 | 1 | 21 |
| 28 | uuccacagcuuu | Phvul.011G017700.1 | 3 | -1 | 1 | 21 |
| 29 | uuccacagcuuu | Phvul.011G017700.1 | 3 | -1 | 1 | 21 |
| 30 | uuccacagcuuu | Phvul.011G017700.1 | 3 | -1 | 1 | 21 |
| 31 | uuccacagcuuu | Phvul.011G017700.1 | 3 | -1 | 1 | 21 |
| 32 | uuccacagcuuu | Phvul.011G017700.1 | 3 | -1 | 1 | 22 |
| 33 | uuccacagcuuu | Phvul.011G017700.1 | 3 | -1 | 1 | 21 |
| 34 | uuccacagcuuu | Phvul.001G220500.1 | 3.5 | -1 | 1 | 21 |
| 35 | uuccacagcuuu | Phvul.001G220500.1 | 3.5 | -1 | 1 | 21 |
| 36 | uuccacagcuuu | Phvul.001G220500.1 | 3.5 | -1 | 1 | 21 |
| 37 | uuccacagcuuu | Phvul.001G220500.1 | 3.5 | -1 | 1 | 21 |
| 38 | uuccacagcuuu | Phvul.001G220500.1 | 3.5 | -1 | 1 | 21 |
| 39 | uuccacagcuuu | Phvul.001G220500.1 | 3.5 | -1 | 1 | 21 |
| 40 | uuccacagcuuu | Phvul.001G220500.1 | 3.5 | -1 | 1 | 21 |
| 41 | uuccacagcuuu | Phvul.001G220500.1 | 3.5 | -1 | 1 | 21 |
| 42 | uuccacagcuuu | Phvul.001G220500.1 | 3.5 | -1 | 1 | 21 |
| 43 | uuccacagcuuu | Phvul.001G220500.1 | 3.5 | -1 | 1 | 21 |
| 44 | uuccacagcuuu | Phvul.001G220500.1 | 3.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuu | Phvul.001G220500.1 | 3.5 | -1 | 1 | 21 |
| 46 | uuccacagcuuu | Phvul.001G220500.1 | 3.5 | -1 | 1 | 21 |
| 47 | uuccacagcuuu | Phvul.001G220500.1 | 3.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuu | Phvul.001G220500.1 | 3.5 | -1 | 1 | 22 |
| 49 | uuccacagcuuu | Phvul.001G261400.1 | 3.5 | -1 | 1 | 21 |
| 50 | uuccacagcuuu | Phvul.001G261400.1 | 3.5 | -1 | 1 | 21 |
| 51 | uuccacagcuuu | Phvul.001G261400.1 | 3.5 | -1 | 1 | 21 |
| 52 | uuccacagcuuu | Phvul.001G261400.1 | 3.5 | -1 | 1 | 21 |
| 53 | uuccacagcuuu | Phvul.001G261400.1 | 3.5 | -1 | 1 | 21 |
| 54 | uuccacagcuuu | Phvul.001G261400.1 | 3.5 | -1 | 1 | 21 |
| 55 | uuccacagcuuu | Phvul.001G261400.1 | 3.5 | -1 | 1 | 21 |
| 56 | uuccacagcuuu | Phvul.001G261400.1 | 3.5 | -1 | 1 | 21 |
| 57 | uuccacagcuuu | Phvul.001G261400.1 | 3.5 | -1 | 1 | 21 |
| 58 | uuccacagcuuu | Phvul.001G261400.1 | 3.5 | -1 | 1 | 21 |
| 59 | uuccacagcuuu | Phvul.001G261400.1 | 3.5 | -1 | 1 | 21 |
| 60 | uuccacagcuuu | Phvul.001G261400.1 | 3.5 | -1 | 1 | 21 |
| | uuccacagcuuu | Phvul.001G261400.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.001G261400.1 | 3.5 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.001G261400.1 | 3.5 | -1 | 1 | 22 |
| 4 | uuccacagcuuu Phvul.002G000300.1 | 3.5 | -1 | 1 | 21 |
| 5 | uuccacagcuuu Phvul.002G000300.1 | 3.5 | -1 | 1 | 21 |
| 6 | uuccacagcuuu Phvul.002G000300.2 | 3.5 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.002G000300.1 | 3.5 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.002G000300.2 | 3.5 | -1 | 1 | 21 |
| 9 | uuccacagcuuu Phvul.002G000300.1 | 3.5 | -1 | 1 | 21 |
| 10 | uuccacagcuuu Phvul.002G000300.1 | 3.5 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.002G000300.2 | 3.5 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.002G000300.1 | 3.5 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.002G000300.1 | 3.5 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.002G000300.2 | 3.5 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.002G000300.1 | 3.5 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.002G000300.2 | 3.5 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.002G000300.1 | 3.5 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.002G000300.1 | 3.5 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.002G000300.2 | 3.5 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.002G000300.1 | 3.5 | -1 | 1 | 21 |
| 21 | uuccacagcuuu Phvul.002G000300.1 | 3.5 | -1 | 1 | 21 |
| 22 | uuccacagcuuu Phvul.002G000300.2 | 3.5 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.002G000300.1 | 3.5 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.002G000300.2 | 3.5 | -1 | 1 | 21 |
| 25 | uuccacagcuuu Phvul.002G000300.1 | 3.5 | -1 | 1 | 21 |
| 26 | uuccacagcuuu Phvul.002G000300.1 | 3.5 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.002G000300.2 | 3.5 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.002G000300.1 | 3.5 | -1 | 1 | 21 |
| 29 | uuccacagcuuu Phvul.002G000300.2 | 3.5 | -1 | 1 | 21 |
| 30 | uuccacagcuuu Phvul.002G000300.2 | 3.5 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.002G000300.1 | 3.5 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.002G000300.2 | 3.5 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.002G000300.1 | 3.5 | -1 | 1 | 22 |
| 34 | uuccacagcuuu Phvul.002G000300.1 | 3.5 | -1 | 1 | 22 |
| 35 | uuccacagcuuu Phvul.002G000300.2 | 3.5 | -1 | 1 | 22 |
| 36 | uuccacagcuuu Phvul.002G167300.1 | 3.5 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.002G167300.1 | 3.5 | -1 | 1 | 21 |
| 38 | uuccacagcuuu Phvul.002G167300.1 | 3.5 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.002G167300.1 | 3.5 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.002G167300.1 | 3.5 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.002G167300.1 | 3.5 | -1 | 1 | 21 |
| 42 | uuccacagcuuu Phvul.002G167300.1 | 3.5 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.002G167300.1 | 3.5 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.002G167300.1 | 3.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.002G167300.1 | 3.5 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.002G167300.1 | 3.5 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.002G167300.1 | 3.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.002G167300.1 | 3.5 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.002G167300.1 | 3.5 | -1 | 1 | 21 |
| 50 | uuccacagcuuu Phvul.002G167300.1 | 3.5 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.002G167300.1 | 3.5 | -1 | 1 | 22 |
| 52 | uuccacagcuuu Phvul.002G248200.1 | 3.5 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.002G248200.1 | 3.5 | -1 | 1 | 21 |
| 54 | uuccacagcuuu Phvul.002G248200.1 | 3.5 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.002G248200.1 | 3.5 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.002G248200.1 | 3.5 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.002G248200.1 | 3.5 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.002G248200.1 | 3.5 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.002G248200.1 | 3.5 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.002G248200.1 | 3.5 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.002G248200.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.002G248200.1 | 3.5 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.002G248200.1 | 3.5 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.002G248200.1 | 3.5 | -1 | 1 | 21 |
| 5 | uuccacagcuuu Phvul.002G248200.1 | 3.5 | -1 | 1 | 21 |
| 6 | uuccacagcuuu Phvul.002G330600.1 | 3.5 | -1 | 1 | 22 |
| 7 | uuccacagcuuu Phvul.003G105600.1 | 3.5 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.003G105600.1 | 3.5 | -1 | 1 | 21 |
| 9 | uuccacagcuuu Phvul.003G105600.1 | 3.5 | -1 | 1 | 21 |
| 10 | uuccacagcuuu Phvul.003G105600.1 | 3.5 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.003G105600.1 | 3.5 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.003G105600.1 | 3.5 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.003G105600.1 | 3.5 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.003G105600.1 | 3.5 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.003G105600.1 | 3.5 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.003G105600.1 | 3.5 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.003G105600.1 | 3.5 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.003G105600.1 | 3.5 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.003G105600.1 | 3.5 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.003G105600.1 | 3.5 | -1 | 1 | 21 |
| 21 | uuccacagcuuu Phvul.003G105600.1 | 3.5 | -1 | 1 | 21 |
| 22 | uuccacagcuuu Phvul.003G105600.1 | 3.5 | -1 | 1 | 22 |
| 23 | uuccacagcuuu Phvul.003G127400.1 | 3.5 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.003G127400.1 | 3.5 | -1 | 1 | 21 |
| 25 | uuccacagcuuu Phvul.003G127400.1 | 3.5 | -1 | 1 | 21 |
| 26 | uuccacagcuuu Phvul.003G127400.1 | 3.5 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.003G127400.1 | 3.5 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.003G127400.1 | 3.5 | -1 | 1 | 21 |
| 29 | uuccacagcuuu Phvul.003G127400.1 | 3.5 | -1 | 1 | 21 |
| 30 | uuccacagcuuu Phvul.003G127400.1 | 3.5 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.003G127400.1 | 3.5 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.003G127400.1 | 3.5 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.003G127400.1 | 3.5 | -1 | 1 | 21 |
| 34 | uuccacagcuuu Phvul.003G127400.1 | 3.5 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.003G127400.1 | 3.5 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.003G127400.1 | 3.5 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.003G140200.2 | 3.5 | -1 | 1 | 21 |
| 38 | uuccacagcuuu Phvul.003G140200.2 | 3.5 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.003G140200.1 | 3.5 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.003G140200.2 | 3.5 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.003G140200.1 | 3.5 | -1 | 1 | 21 |
| 42 | uuccacagcuuu Phvul.003G140200.2 | 3.5 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.003G140200.1 | 3.5 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.003G140200.2 | 3.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.003G140200.1 | 3.5 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.003G140200.2 | 3.5 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.003G140200.1 | 3.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.003G140200.2 | 3.5 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.003G140200.1 | 3.5 | -1 | 1 | 21 |
| 50 | uuccacagcuuu Phvul.003G140200.2 | 3.5 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.003G140200.1 | 3.5 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.003G140200.2 | 3.5 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.003G140200.1 | 3.5 | -1 | 1 | 21 |
| 54 | uuccacagcuuu Phvul.003G140200.2 | 3.5 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.003G140200.1 | 3.5 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.003G140200.2 | 3.5 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.003G140200.1 | 3.5 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.003G140200.2 | 3.5 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.003G140200.1 | 3.5 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.003G140200.2 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.003G140200.1 | 3.5 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.003G140200.2 | 3.5 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.003G140200.1 | 3.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uuccacagcuuu Phvul.003G140200.2 | 3.5 | -1 | 1 | 22 |
| 7 | uuccacagcuuu Phvul.003G140200.1 | 3.5 | -1 | 1 | 22 |
| 8 | uuccacagcuuu Phvul.003G205600.1 | 3.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uuccacagcuuu Phvul.003G205600.1 | 3.5 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.003G205600.1 | 3.5 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.003G205600.1 | 3.5 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.003G205600.1 | 3.5 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.003G205600.1 | 3.5 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.003G205600.1 | 3.5 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.003G205600.1 | 3.5 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.003G205600.1 | 3.5 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.003G205600.1 | 3.5 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.003G205600.1 | 3.5 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.003G205600.1 | 3.5 | -1 | 1 | 21 |
| 21 | uuccacagcuuu Phvul.003G205600.1 | 3.5 | -1 | 1 | 21 |
| 22 | uuccacagcuuu Phvul.003G205600.1 | 3.5 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.003G205600.1 | 3.5 | -1 | 1 | 22 |
| 24 | uuccacagcuuu Phvul.004G012700.2 | 3.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uuccacagcuuu Phvul.004G012700.2 | 3.5 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.004G012700.2 | 3.5 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.004G012700.2 | 3.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uuccacagcuuu Phvul.004G012700.2 | 3.5 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.004G012700.2 | 3.5 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.004G012700.2 | 3.5 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.004G012700.2 | 3.5 | -1 | 1 | 21 |
| 34 | uuccacagcuuu Phvul.004G012700.2 | 3.5 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.004G012700.2 | 3.5 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.004G012700.2 | 3.5 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.004G012700.2 | 3.5 | -1 | 1 | 21 |
| 38 | uuccacagcuuu Phvul.004G012700.2 | 3.5 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.004G012700.2 | 3.5 | -1 | 1 | 22 |
| 40 | uuccacagcuuu Phvul.005G126400.1 | 3.5 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.005G126400.1 | 3.5 | -1 | 1 | 21 |
| 42 | uuccacagcuuu Phvul.005G126400.1 | 3.5 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.005G126400.1 | 3.5 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.005G126400.1 | 3.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.005G126400.1 | 3.5 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.005G126400.1 | 3.5 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.005G126400.1 | 3.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.005G126400.1 | 3.5 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.005G126400.1 | 3.5 | -1 | 1 | 21 |
| 50 | uuccacagcuuu Phvul.005G126400.1 | 3.5 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.005G126400.1 | 3.5 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.005G126400.1 | 3.5 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.005G126400.1 | 3.5 | -1 | 1 | 21 |
| 54 | uuccacagcuuu Phvul.005G126400.1 | 3.5 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.005G126400.1 | 3.5 | -1 | 1 | 22 |
| 56 | uuccacagcuuu Phvul.006G200700.1 | 3.5 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.006G200700.1 | 3.5 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.006G200700.1 | 3.5 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.006G200700.1 | 3.5 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.006G200700.1 | 3.5 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.006G200700.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.006G200700.1 | 3.5 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.006G200700.1 | 3.5 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.006G200700.1 | 3.5 | -1 | 1 | 21 |
| 5 | uuccacagcuuu Phvul.006G200700.1 | 3.5 | -1 | 1 | 21 |
| 6 | uuccacagcuuu Phvul.006G200700.1 | 3.5 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.006G200700.1 | 3.5 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.006G200700.1 | 3.5 | -1 | 1 | 21 |
| 9 | uuccacagcuuu Phvul.006G200700.1 | 3.5 | -1 | 1 | 21 |
| 10 | uuccacagcuuu Phvul.006G200700.1 | 3.5 | -1 | 1 | 22 |
| 11 | uuccacagcuuu Phvul.007G188900.1 | 3.5 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.007G188900.1 | 3.5 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.007G188900.1 | 3.5 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.007G188900.1 | 3.5 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.007G188900.1 | 3.5 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.007G188900.1 | 3.5 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.007G188900.1 | 3.5 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.007G188900.1 | 3.5 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.007G188900.1 | 3.5 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.007G188900.1 | 3.5 | -1 | 1 | 21 |
| 21 | uuccacagcuuu Phvul.007G188900.1 | 3.5 | -1 | 1 | 21 |
| 22 | uuccacagcuuu Phvul.007G188900.1 | 3.5 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.007G188900.1 | 3.5 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.007G188900.1 | 3.5 | -1 | 1 | 21 |
| 25 | uuccacagcuuu Phvul.007G189100.1 | 3.5 | -1 | 1 | 21 |
| 26 | uuccacagcuuu Phvul.007G189100.1 | 3.5 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.007G189100.1 | 3.5 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.007G189100.1 | 3.5 | -1 | 1 | 21 |
| 29 | uuccacagcuuu Phvul.007G189100.1 | 3.5 | -1 | 1 | 21 |
| 30 | uuccacagcuuu Phvul.007G189100.1 | 3.5 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.007G189100.1 | 3.5 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.007G189100.1 | 3.5 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.007G189100.1 | 3.5 | -1 | 1 | 21 |
| 34 | uuccacagcuuu Phvul.007G189100.1 | 3.5 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.007G189100.1 | 3.5 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.007G189100.1 | 3.5 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.007G189100.1 | 3.5 | -1 | 1 | 21 |
| 38 | uuccacagcuuu Phvul.007G189100.1 | 3.5 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.007G189100.1 | 3.5 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.007G189100.1 | 3.5 | -1 | 1 | 22 |
| 41 | uuccacagcuuu Phvul.007G212500.1 | 3.5 | -1 | 1 | 21 |
| 42 | uuccacagcuuu Phvul.007G212500.1 | 3.5 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.007G212500.1 | 3.5 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.007G212500.1 | 3.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.007G212500.1 | 3.5 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.007G212500.1 | 3.5 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.007G212500.1 | 3.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.007G212500.1 | 3.5 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.007G212500.1 | 3.5 | -1 | 1 | 21 |
| 50 | uuccacagcuuu Phvul.007G212500.1 | 3.5 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.007G212500.1 | 3.5 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.007G212500.1 | 3.5 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.007G212500.1 | 3.5 | -1 | 1 | 21 |
| 54 | uuccacagcuuu Phvul.007G212500.1 | 3.5 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.007G212500.1 | 3.5 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.007G212500.1 | 3.5 | -1 | 1 | 22 |
| 57 | uuccacagcuuu Phvul.007G225200.2 | 3.5 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.007G225200.1 | 3.5 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.007G225200.1 | 3.5 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.007G225200.2 | 3.5 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.007G225200.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|--------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuuPhvul.007G225200.2 | 3.5 | -1 | 1 | 21 |
| 3 | uuccacagcuuuPhvul.007G225200.1 | 3.5 | -1 | 1 | 21 |
| 4 | uuccacagcuuuPhvul.007G225200.2 | 3.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uuccacagcuuuPhvul.007G225200.1 | 3.5 | -1 | 1 | 21 |
| 7 | uuccacagcuuuPhvul.007G225200.2 | 3.5 | -1 | 1 | 21 |
| 8 | uuccacagcuuuPhvul.007G225200.1 | 3.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uuccacagcuuuPhvul.007G225200.2 | 3.5 | -1 | 1 | 21 |
| 11 | uuccacagcuuuPhvul.007G225200.1 | 3.5 | -1 | 1 | 21 |
| 12 | uuccacagcuuuPhvul.007G225200.2 | 3.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uuccacagcuuuPhvul.007G225200.1 | 3.5 | -1 | 1 | 21 |
| 15 | uuccacagcuuuPhvul.007G225200.2 | 3.5 | -1 | 1 | 21 |
| 16 | uuccacagcuuuPhvul.007G225200.1 | 3.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uuccacagcuuuPhvul.007G225200.2 | 3.5 | -1 | 1 | 21 |
| 19 | uuccacagcuuuPhvul.007G225200.1 | 3.5 | -1 | 1 | 21 |
| 20 | uuccacagcuuuPhvul.007G225200.2 | 3.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uuccacagcuuuPhvul.007G225200.1 | 3.5 | -1 | 1 | 21 |
| 23 | uuccacagcuuuPhvul.007G225200.2 | 3.5 | -1 | 1 | 21 |
| 24 | uuccacagcuuuPhvul.007G225200.1 | 3.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uuccacagcuuuPhvul.007G225200.2 | 3.5 | -1 | 1 | 22 |
| 27 | uuccacagcuuuPhvul.007G225200.1 | 3.5 | -1 | 1 | 22 |
| 28 | uuccacagcuuuPhvul.007G280800.1 | 3.5 | -1 | 1 | 21 |
| 29 | uuccacagcuuuPhvul.007G280800.1 | 3.5 | -1 | 1 | 21 |
| 30 | uuccacagcuuuPhvul.007G280800.1 | 3.5 | -1 | 1 | 21 |
| 31 | uuccacagcuuuPhvul.007G280800.1 | 3.5 | -1 | 1 | 21 |
| 32 | uuccacagcuuuPhvul.007G280800.1 | 3.5 | -1 | 1 | 21 |
| 33 | uuccacagcuuuPhvul.007G280800.1 | 3.5 | -1 | 1 | 21 |
| 34 | uuccacagcuuuPhvul.007G280800.1 | 3.5 | -1 | 1 | 21 |
| 35 | uuccacagcuuuPhvul.007G280800.1 | 3.5 | -1 | 1 | 21 |
| 36 | uuccacagcuuuPhvul.007G280800.1 | 3.5 | -1 | 1 | 21 |
| 37 | uuccacagcuuuPhvul.007G280800.1 | 3.5 | -1 | 1 | 21 |
| 38 | uuccacagcuuuPhvul.007G280800.1 | 3.5 | -1 | 1 | 21 |
| 39 | uuccacagcuuuPhvul.007G280800.1 | 3.5 | -1 | 1 | 21 |
| 40 | uuccacagcuuuPhvul.007G280800.1 | 3.5 | -1 | 1 | 21 |
| 41 | uuccacagcuuuPhvul.007G280800.1 | 3.5 | -1 | 1 | 21 |
| 42 | uuccacagcuuuPhvul.007G280800.1 | 3.5 | -1 | 1 | 21 |
| 43 | uuccacagcuuuPhvul.007G280800.1 | 3.5 | -1 | 1 | 22 |
| 44 | uuccacagcuuuPhvul.008G020700.1 | 3.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuuPhvul.008G020700.1 | 3.5 | -1 | 1 | 21 |
| 46 | uuccacagcuuuPhvul.008G020700.1 | 3.5 | -1 | 1 | 21 |
| 47 | uuccacagcuuuPhvul.008G020700.1 | 3.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuuPhvul.008G020700.1 | 3.5 | -1 | 1 | 21 |
| 49 | uuccacagcuuuPhvul.008G020700.1 | 3.5 | -1 | 1 | 21 |
| 50 | uuccacagcuuuPhvul.008G020700.1 | 3.5 | -1 | 1 | 21 |
| 51 | uuccacagcuuuPhvul.008G020700.1 | 3.5 | -1 | 1 | 21 |
| 52 | uuccacagcuuuPhvul.008G020700.1 | 3.5 | -1 | 1 | 21 |
| 53 | uuccacagcuuuPhvul.008G020700.1 | 3.5 | -1 | 1 | 21 |
| 54 | uuccacagcuuuPhvul.008G020700.1 | 3.5 | -1 | 1 | 21 |
| 55 | uuccacagcuuuPhvul.008G020700.1 | 3.5 | -1 | 1 | 21 |
| 56 | uuccacagcuuuPhvul.008G020700.1 | 3.5 | -1 | 1 | 21 |
| 57 | uuccacagcuuuPhvul.008G020700.1 | 3.5 | -1 | 1 | 21 |
| 58 | uuccacagcuuuPhvul.008G020700.1 | 3.5 | -1 | 1 | 21 |
| 59 | uuccacagcuuuPhvul.008G046300.1 | 3.5 | -1 | 1 | 21 |
| 60 | uuccacagcuuuPhvul.008G046300.2 | 3.5 | -1 | 1 | 21 |
| | uuccacagcuuuPhvul.008G046300.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.008G046300.2 | 3.5 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.008G046300.1 | 3.5 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.008G046300.2 | 3.5 | -1 | 1 | 21 |
| 5 | uuccacagcuuu Phvul.008G046300.1 | 3.5 | -1 | 1 | 21 |
| 6 | uuccacagcuuu Phvul.008G046300.1 | 3.5 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.008G046300.2 | 3.5 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.008G046300.1 | 3.5 | -1 | 1 | 21 |
| 9 | uuccacagcuuu Phvul.008G046300.1 | 3.5 | -1 | 1 | 21 |
| 10 | uuccacagcuuu Phvul.008G046300.2 | 3.5 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.008G046300.1 | 3.5 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.008G046300.2 | 3.5 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.008G046300.1 | 3.5 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.008G046300.1 | 3.5 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.008G046300.2 | 3.5 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.008G046300.1 | 3.5 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.008G046300.1 | 3.5 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.008G046300.2 | 3.5 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.008G046300.1 | 3.5 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.008G046300.2 | 3.5 | -1 | 1 | 21 |
| 21 | uuccacagcuuu Phvul.008G046300.2 | 3.5 | -1 | 1 | 21 |
| 22 | uuccacagcuuu Phvul.008G046300.1 | 3.5 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.008G046300.2 | 3.5 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.008G046300.1 | 3.5 | -1 | 1 | 21 |
| 25 | uuccacagcuuu Phvul.008G046300.2 | 3.5 | -1 | 1 | 21 |
| 26 | uuccacagcuuu Phvul.008G046300.2 | 3.5 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.008G118100.3 | 3.5 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.008G118100.1 | 3.5 | -1 | 1 | 21 |
| 29 | uuccacagcuuu Phvul.008G118100.2 | 3.5 | -1 | 1 | 21 |
| 30 | uuccacagcuuu Phvul.008G118100.2 | 3.5 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.008G118100.3 | 3.5 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.008G118100.1 | 3.5 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.008G118100.2 | 3.5 | -1 | 1 | 21 |
| 34 | uuccacagcuuu Phvul.008G118100.2 | 3.5 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.008G118100.3 | 3.5 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.008G118100.1 | 3.5 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.008G118100.2 | 3.5 | -1 | 1 | 21 |
| 38 | uuccacagcuuu Phvul.008G118100.2 | 3.5 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.008G118100.3 | 3.5 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.008G118100.1 | 3.5 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.008G118100.2 | 3.5 | -1 | 1 | 21 |
| 42 | uuccacagcuuu Phvul.008G118100.2 | 3.5 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.008G118100.3 | 3.5 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.008G118100.1 | 3.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.008G118100.2 | 3.5 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.008G118100.2 | 3.5 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.008G118100.3 | 3.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.008G118100.1 | 3.5 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.008G118100.2 | 3.5 | -1 | 1 | 21 |
| 50 | uuccacagcuuu Phvul.008G118100.2 | 3.5 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.008G118100.3 | 3.5 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.008G118100.1 | 3.5 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.008G118100.2 | 3.5 | -1 | 1 | 21 |
| 54 | uuccacagcuuu Phvul.008G118100.2 | 3.5 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.008G118100.3 | 3.5 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.008G118100.1 | 3.5 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.008G118100.2 | 3.5 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.008G118100.2 | 3.5 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.008G118100.3 | 3.5 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.008G118100.1 | 3.5 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.008G118100.2 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.008G118100.3 | 3.5 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.008G118100.1 | 3.5 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.008G118100.2 | 3.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uuccacagcuuu Phvul.008G118100.3 | 3.5 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.008G118100.1 | 3.5 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.008G118100.2 | 3.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uuccacagcuuu Phvul.008G143300.2 | 3.5 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.008G143300.2 | 3.5 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.008G143300.2 | 3.5 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.008G143300.2 | 3.5 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.008G143300.2 | 3.5 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.008G143300.2 | 3.5 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.008G143300.2 | 3.5 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.008G143300.2 | 3.5 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.008G143300.2 | 3.5 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.008G143300.2 | 3.5 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.008G143300.2 | 3.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uuccacagcuuu Phvul.008G143300.2 | 3.5 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.008G143300.2 | 3.5 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.009G019500.2 | 3.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uuccacagcuuu Phvul.009G019500.1 | 3.5 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.009G019500.2 | 3.5 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.009G019500.1 | 3.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uuccacagcuuu Phvul.009G019500.2 | 3.5 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.009G019500.1 | 3.5 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.009G019500.2 | 3.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uuccacagcuuu Phvul.009G019500.1 | 3.5 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.009G019500.2 | 3.5 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.009G019500.1 | 3.5 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.009G019500.2 | 3.5 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | uuccacagcuuu Phvul.009G019500.1 | 3.5 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.009G019500.2 | 3.5 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.009G019500.1 | 3.5 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uuccacagcuuu Phvul.009G019500.2 | 3.5 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.009G019500.1 | 3.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.009G019500.2 | 3.5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uuccacagcuuu Phvul.009G019500.1 | 3.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.009G019500.2 | 3.5 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.009G019500.1 | 3.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uuccacagcuuu Phvul.009G019500.2 | 3.5 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.009G019500.1 | 3.5 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.009G019500.2 | 3.5 | -1 | 1 | 22 |
| 54 | | | | | |
| 55 | uuccacagcuuu Phvul.009G019500.1 | 3.5 | -1 | 1 | 22 |
| 56 | uuccacagcuuu Phvul.009G037300.1 | 3.5 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.009G037300.1 | 3.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uuccacagcuuu Phvul.009G037300.1 | 3.5 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.009G037300.1 | 3.5 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.009G037300.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.009G037300.1 | 3.5 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.009G037300.1 | 3.5 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.009G037300.1 | 3.5 | -1 | 1 | 21 |
| 5 | uuccacagcuuu Phvul.009G037300.1 | 3.5 | -1 | 1 | 21 |
| 6 | uuccacagcuuu Phvul.009G037300.1 | 3.5 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.009G037300.1 | 3.5 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.009G037300.1 | 3.5 | -1 | 1 | 21 |
| 9 | uuccacagcuuu Phvul.009G037300.1 | 3.5 | -1 | 1 | 21 |
| 10 | uuccacagcuuu Phvul.009G037300.1 | 3.5 | -1 | 1 | 22 |
| 11 | uuccacagcuuu Phvul.009G065100.1 | 3.5 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.009G065100.1 | 3.5 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.009G065100.1 | 3.5 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.009G065100.1 | 3.5 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.009G065100.1 | 3.5 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.009G065100.1 | 3.5 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.009G065100.1 | 3.5 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.009G065100.1 | 3.5 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.009G065100.1 | 3.5 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.009G065100.1 | 3.5 | -1 | 1 | 21 |
| 21 | uuccacagcuuu Phvul.009G065100.1 | 3.5 | -1 | 1 | 21 |
| 22 | uuccacagcuuu Phvul.009G065100.1 | 3.5 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.009G065100.1 | 3.5 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.009G065100.1 | 3.5 | -1 | 1 | 21 |
| 25 | uuccacagcuuu Phvul.009G065100.1 | 3.5 | -1 | 1 | 21 |
| 26 | uuccacagcuuu Phvul.009G230000.2 | 3.5 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.009G230000.1 | 3.5 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.009G230000.2 | 3.5 | -1 | 1 | 21 |
| 29 | uuccacagcuuu Phvul.009G230000.2 | 3.5 | -1 | 1 | 21 |
| 30 | uuccacagcuuu Phvul.009G230000.1 | 3.5 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.009G230000.2 | 3.5 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.009G230000.1 | 3.5 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.009G230000.2 | 3.5 | -1 | 1 | 21 |
| 34 | uuccacagcuuu Phvul.009G230000.2 | 3.5 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.009G230000.1 | 3.5 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.009G230000.2 | 3.5 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.009G230000.1 | 3.5 | -1 | 1 | 21 |
| 38 | uuccacagcuuu Phvul.009G230000.1 | 3.5 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.009G230000.2 | 3.5 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.009G230000.1 | 3.5 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.009G230000.2 | 3.5 | -1 | 1 | 21 |
| 42 | uuccacagcuuu Phvul.009G230000.2 | 3.5 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.009G230000.1 | 3.5 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.009G230000.2 | 3.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.009G230000.1 | 3.5 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.009G230000.1 | 3.5 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.009G230000.2 | 3.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.009G230000.1 | 3.5 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.009G230000.2 | 3.5 | -1 | 1 | 21 |
| 50 | uuccacagcuuu Phvul.009G230000.2 | 3.5 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.009G230000.1 | 3.5 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.009G230000.2 | 3.5 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.009G230000.1 | 3.5 | -1 | 1 | 21 |
| 54 | uuccacagcuuu Phvul.009G230000.1 | 3.5 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.009G230000.2 | 3.5 | -1 | 1 | 22 |
| 56 | uuccacagcuuu Phvul.009G230000.1 | 3.5 | -1 | 1 | 22 |
| 57 | uuccacagcuuu Phvul.009G246000.2 | 3.5 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.009G246000.1 | 3.5 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.009G246000.2 | 3.5 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.009G246000.2 | 3.5 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.009G246000.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.009G246000.2 | 3.5 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.009G246000.1 | 3.5 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.009G246000.2 | 3.5 | -1 | 1 | 21 |
| 5 | uuccacagcuuu Phvul.009G246000.2 | 3.5 | -1 | 1 | 21 |
| 6 | uuccacagcuuu Phvul.009G246000.1 | 3.5 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.009G246000.2 | 3.5 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.009G246000.1 | 3.5 | -1 | 1 | 21 |
| 9 | uuccacagcuuu Phvul.009G246000.2 | 3.5 | -1 | 1 | 21 |
| 10 | uuccacagcuuu Phvul.009G246000.2 | 3.5 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.009G246000.1 | 3.5 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.009G246000.2 | 3.5 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.009G246000.1 | 3.5 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.009G246000.1 | 3.5 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.009G246000.2 | 3.5 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.009G246000.1 | 3.5 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.009G246000.2 | 3.5 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.009G246000.2 | 3.5 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.009G246000.1 | 3.5 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.009G246000.2 | 3.5 | -1 | 1 | 21 |
| 21 | uuccacagcuuu Phvul.009G246000.2 | 3.5 | -1 | 1 | 21 |
| 22 | uuccacagcuuu Phvul.009G246000.1 | 3.5 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.009G246000.2 | 3.5 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.009G246000.1 | 3.5 | -1 | 1 | 21 |
| 25 | uuccacagcuuu Phvul.009G246000.2 | 3.5 | -1 | 1 | 21 |
| 26 | uuccacagcuuu Phvul.009G246000.2 | 3.5 | -1 | 1 | 22 |
| 27 | uuccacagcuuu Phvul.009G246000.1 | 3.5 | -1 | 1 | 22 |
| 28 | uuccacagcuuu Phvul.010G135101.1 | 3.5 | -1 | 1 | 22 |
| 29 | uuccacagcuuu Phvul.010G135151.1 | 3.5 | -1 | 1 | 22 |
| 30 | uuccacagcuuu Phvul.011G014000.1 | 3.5 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.011G014000.1 | 3.5 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.011G014000.1 | 3.5 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.011G014000.1 | 3.5 | -1 | 1 | 21 |
| 34 | uuccacagcuuu Phvul.011G014000.1 | 3.5 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.011G014000.1 | 3.5 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.011G014000.1 | 3.5 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.011G014000.1 | 3.5 | -1 | 1 | 21 |
| 38 | uuccacagcuuu Phvul.011G014000.1 | 3.5 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.011G014000.1 | 3.5 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.011G014000.1 | 3.5 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.011G014000.1 | 3.5 | -1 | 1 | 21 |
| 42 | uuccacagcuuu Phvul.011G014000.1 | 3.5 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.011G014000.1 | 3.5 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.011G014000.1 | 3.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.011G087500.1 | 3.5 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.011G087500.1 | 3.5 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.011G087500.1 | 3.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.011G087500.1 | 3.5 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.011G087500.1 | 3.5 | -1 | 1 | 21 |
| 50 | uuccacagcuuu Phvul.011G087500.1 | 3.5 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.011G087500.1 | 3.5 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.011G087500.1 | 3.5 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.011G087500.1 | 3.5 | -1 | 1 | 21 |
| 54 | uuccacagcuuu Phvul.011G087500.1 | 3.5 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.011G087500.1 | 3.5 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.011G087500.1 | 3.5 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.011G087500.1 | 3.5 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.011G087500.1 | 3.5 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.011G087500.1 | 3.5 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.011G087500.1 | 3.5 | -1 | 1 | 22 |
| | uuccacagcuuu Phvul.001G021800.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.001G021800.2 | 4 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.001G021800.1 | 4 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.001G021800.2 | 4 | -1 | 1 | 21 |
| 5 | uuccacagcuuu Phvul.001G021800.1 | 4 | -1 | 1 | 21 |
| 6 | uuccacagcuuu Phvul.001G021800.1 | 4 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.001G021800.2 | 4 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.001G021800.1 | 4 | -1 | 1 | 21 |
| 9 | uuccacagcuuu Phvul.001G021800.1 | 4 | -1 | 1 | 21 |
| 10 | uuccacagcuuu Phvul.001G021800.2 | 4 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.001G021800.1 | 4 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.001G021800.2 | 4 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.001G021800.1 | 4 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.001G021800.1 | 4 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.001G021800.2 | 4 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.001G021800.1 | 4 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.001G021800.1 | 4 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.001G021800.2 | 4 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.001G021800.1 | 4 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.001G021800.2 | 4 | -1 | 1 | 21 |
| 21 | uuccacagcuuu Phvul.001G021800.2 | 4 | -1 | 1 | 21 |
| 22 | uuccacagcuuu Phvul.001G021800.1 | 4 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.001G021800.2 | 4 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.001G021800.1 | 4 | -1 | 1 | 21 |
| 25 | uuccacagcuuu Phvul.001G021800.2 | 4 | -1 | 1 | 21 |
| 26 | uuccacagcuuu Phvul.001G021800.2 | 4 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.001G021800.1 | 4 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.001G021800.2 | 4 | -1 | 1 | 21 |
| 29 | uuccacagcuuu Phvul.001G021800.2 | 4 | -1 | 1 | 21 |
| 30 | uuccacagcuuu Phvul.001G055000.1 | 4 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.001G055000.1 | 4 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.001G055000.1 | 4 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.001G055000.1 | 4 | -1 | 1 | 21 |
| 34 | uuccacagcuuu Phvul.001G055000.1 | 4 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.001G055000.1 | 4 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.001G055000.1 | 4 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.001G055000.1 | 4 | -1 | 1 | 21 |
| 38 | uuccacagcuuu Phvul.001G055000.1 | 4 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.001G055000.1 | 4 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.001G055000.1 | 4 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.001G055000.1 | 4 | -1 | 1 | 21 |
| 42 | uuccacagcuuu Phvul.001G055000.1 | 4 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.001G055000.1 | 4 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.001G055000.1 | 4 | -1 | 1 | 22 |
| 45 | uuccacagcuuu Phvul.001G103833.1 | 4 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.001G103833.1 | 4 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.001G103833.1 | 4 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.001G103833.1 | 4 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.001G103833.1 | 4 | -1 | 1 | 21 |
| 50 | uuccacagcuuu Phvul.001G103833.1 | 4 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.001G103833.1 | 4 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.001G103833.1 | 4 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.001G103833.1 | 4 | -1 | 1 | 21 |
| 54 | uuccacagcuuu Phvul.001G103833.1 | 4 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.001G103833.1 | 4 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.001G103833.1 | 4 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.001G103833.1 | 4 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.001G103833.1 | 4 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.001G103833.1 | 4 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.001G109780.1 | 4 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.001G109780.2 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|--------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuuPhvul.001G109780.1 | 4 | -1 | 1 | 21 |
| 3 | uuccacagcuuuPhvul.001G109780.2 | 4 | -1 | 1 | 21 |
| 4 | uuccacagcuuuPhvul.001G109780.1 | 4 | -1 | 1 | 21 |
| 5 | uuccacagcuuuPhvul.001G109780.2 | 4 | -1 | 1 | 21 |
| 6 | uuccacagcuuuPhvul.001G109780.1 | 4 | -1 | 1 | 21 |
| 7 | uuccacagcuuuPhvul.001G109780.2 | 4 | -1 | 1 | 21 |
| 8 | uuccacagcuuuPhvul.001G109780.1 | 4 | -1 | 1 | 21 |
| 9 | uuccacagcuuuPhvul.001G109780.2 | 4 | -1 | 1 | 21 |
| 10 | uuccacagcuuuPhvul.001G109780.1 | 4 | -1 | 1 | 21 |
| 11 | uuccacagcuuuPhvul.001G109780.2 | 4 | -1 | 1 | 21 |
| 12 | uuccacagcuuuPhvul.001G109780.1 | 4 | -1 | 1 | 21 |
| 13 | uuccacagcuuuPhvul.001G109780.2 | 4 | -1 | 1 | 21 |
| 14 | uuccacagcuuuPhvul.001G109780.1 | 4 | -1 | 1 | 21 |
| 15 | uuccacagcuuuPhvul.001G109780.2 | 4 | -1 | 1 | 21 |
| 16 | uuccacagcuuuPhvul.001G109780.1 | 4 | -1 | 1 | 21 |
| 17 | uuccacagcuuuPhvul.001G109780.2 | 4 | -1 | 1 | 21 |
| 18 | uuccacagcuuuPhvul.001G109780.1 | 4 | -1 | 1 | 21 |
| 19 | uuccacagcuuuPhvul.001G109780.2 | 4 | -1 | 1 | 21 |
| 20 | uuccacagcuuuPhvul.001G109780.1 | 4 | -1 | 1 | 21 |
| 21 | uuccacagcuuuPhvul.001G109780.2 | 4 | -1 | 1 | 21 |
| 22 | uuccacagcuuuPhvul.001G109780.1 | 4 | -1 | 1 | 21 |
| 23 | uuccacagcuuuPhvul.001G109780.2 | 4 | -1 | 1 | 21 |
| 24 | uuccacagcuuuPhvul.001G109780.1 | 4 | -1 | 1 | 21 |
| 25 | uuccacagcuuuPhvul.001G109780.2 | 4 | -1 | 1 | 21 |
| 26 | uuccacagcuuuPhvul.001G109780.1 | 4 | -1 | 1 | 21 |
| 27 | uuccacagcuuuPhvul.001G109780.2 | 4 | -1 | 1 | 21 |
| 28 | uuccacagcuuuPhvul.001G229200.1 | 4 | -1 | 1 | 21 |
| 29 | uuccacagcuuuPhvul.001G229200.1 | 4 | -1 | 1 | 21 |
| 30 | uuccacagcuuuPhvul.001G229200.1 | 4 | -1 | 1 | 21 |
| 31 | uuccacagcuuuPhvul.001G229200.1 | 4 | -1 | 1 | 21 |
| 32 | uuccacagcuuuPhvul.001G229200.1 | 4 | -1 | 1 | 21 |
| 33 | uuccacagcuuuPhvul.001G229200.1 | 4 | -1 | 1 | 21 |
| 34 | uuccacagcuuuPhvul.001G229200.1 | 4 | -1 | 1 | 21 |
| 35 | uuccacagcuuuPhvul.001G229200.1 | 4 | -1 | 1 | 21 |
| 36 | uuccacagcuuuPhvul.001G229200.1 | 4 | -1 | 1 | 21 |
| 37 | uuccacagcuuuPhvul.001G229200.1 | 4 | -1 | 1 | 21 |
| 38 | uuccacagcuuuPhvul.001G229200.1 | 4 | -1 | 1 | 21 |
| 39 | uuccacagcuuuPhvul.001G229200.1 | 4 | -1 | 1 | 21 |
| 40 | uuccacagcuuuPhvul.001G229200.1 | 4 | -1 | 1 | 21 |
| 41 | uuccacagcuuuPhvul.001G229200.1 | 4 | -1 | 1 | 21 |
| 42 | uuccacagcuuuPhvul.001G229200.1 | 4 | -1 | 1 | 21 |
| 43 | uuccacagcuuuPhvul.001G229200.1 | 4 | -1 | 1 | 22 |
| 44 | uuccacagcuuuPhvul.001G261800.1 | 4 | -1 | 1 | 21 |
| 45 | uuccacagcuuuPhvul.001G261800.2 | 4 | -1 | 1 | 21 |
| 46 | uuccacagcuuuPhvul.001G261800.1 | 4 | -1 | 1 | 21 |
| 47 | uuccacagcuuuPhvul.001G261800.2 | 4 | -1 | 1 | 21 |
| 48 | uuccacagcuuuPhvul.001G261800.1 | 4 | -1 | 1 | 21 |
| 49 | uuccacagcuuuPhvul.001G261800.2 | 4 | -1 | 1 | 21 |
| 50 | uuccacagcuuuPhvul.001G261800.1 | 4 | -1 | 1 | 21 |
| 51 | uuccacagcuuuPhvul.001G261800.2 | 4 | -1 | 1 | 21 |
| 52 | uuccacagcuuuPhvul.001G261800.1 | 4 | -1 | 1 | 21 |
| 53 | uuccacagcuuuPhvul.001G261800.2 | 4 | -1 | 1 | 21 |
| 54 | uuccacagcuuuPhvul.001G261800.1 | 4 | -1 | 1 | 21 |
| 55 | uuccacagcuuuPhvul.001G261800.2 | 4 | -1 | 1 | 21 |
| 56 | uuccacagcuuuPhvul.001G261800.1 | 4 | -1 | 1 | 21 |
| 57 | uuccacagcuuuPhvul.001G261800.2 | 4 | -1 | 1 | 21 |
| 58 | uuccacagcuuuPhvul.001G261800.1 | 4 | -1 | 1 | 21 |
| 59 | uuccacagcuuuPhvul.001G261800.2 | 4 | -1 | 1 | 21 |
| 60 | uuccacagcuuuPhvul.001G261800.1 | 4 | -1 | 1 | 21 |
| | uuccacagcuuuPhvul.001G261800.2 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|--------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuuPhvul.001G261800.1 | 4 | -1 | 1 | 21 |
| 3 | uuccacagcuuuPhvul.001G261800.2 | 4 | -1 | 1 | 21 |
| 4 | uuccacagcuuuPhvul.001G261800.1 | 4 | -1 | 1 | 21 |
| 5 | uuccacagcuuuPhvul.001G261800.2 | 4 | -1 | 1 | 21 |
| 6 | uuccacagcuuuPhvul.001G261800.1 | 4 | -1 | 1 | 21 |
| 7 | uuccacagcuuuPhvul.001G261800.2 | 4 | -1 | 1 | 21 |
| 8 | uuccacagcuuuPhvul.001G261800.1 | 4 | -1 | 1 | 21 |
| 9 | uuccacagcuuuPhvul.001G261800.2 | 4 | -1 | 1 | 21 |
| 10 | uuccacagcuuuPhvul.001G261800.1 | 4 | -1 | 1 | 21 |
| 11 | uuccacagcuuuPhvul.001G261800.2 | 4 | -1 | 1 | 21 |
| 12 | uuccacagcuuuPhvul.002G026300.2 | 4 | -1 | 1 | 21 |
| 13 | uuccacagcuuuPhvul.002G026300.1 | 4 | -1 | 1 | 21 |
| 14 | uuccacagcuuuPhvul.002G026300.2 | 4 | -1 | 1 | 21 |
| 15 | uuccacagcuuuPhvul.002G026300.1 | 4 | -1 | 1 | 21 |
| 16 | uuccacagcuuuPhvul.002G026300.2 | 4 | -1 | 1 | 21 |
| 17 | uuccacagcuuuPhvul.002G026300.1 | 4 | -1 | 1 | 21 |
| 18 | uuccacagcuuuPhvul.002G026300.2 | 4 | -1 | 1 | 21 |
| 19 | uuccacagcuuuPhvul.002G026300.1 | 4 | -1 | 1 | 21 |
| 20 | uuccacagcuuuPhvul.002G026300.2 | 4 | -1 | 1 | 21 |
| 21 | uuccacagcuuuPhvul.002G026300.1 | 4 | -1 | 1 | 21 |
| 22 | uuccacagcuuuPhvul.002G026300.2 | 4 | -1 | 1 | 21 |
| 23 | uuccacagcuuuPhvul.002G026300.1 | 4 | -1 | 1 | 21 |
| 24 | uuccacagcuuuPhvul.002G026300.2 | 4 | -1 | 1 | 21 |
| 25 | uuccacagcuuuPhvul.002G026300.1 | 4 | -1 | 1 | 21 |
| 26 | uuccacagcuuuPhvul.002G026300.2 | 4 | -1 | 1 | 21 |
| 27 | uuccacagcuuuPhvul.002G026300.1 | 4 | -1 | 1 | 21 |
| 28 | uuccacagcuuuPhvul.002G026300.2 | 4 | -1 | 1 | 21 |
| 29 | uuccacagcuuuPhvul.002G026300.1 | 4 | -1 | 1 | 21 |
| 30 | uuccacagcuuuPhvul.002G026300.2 | 4 | -1 | 1 | 21 |
| 31 | uuccacagcuuuPhvul.002G026300.1 | 4 | -1 | 1 | 21 |
| 32 | uuccacagcuuuPhvul.002G026300.2 | 4 | -1 | 1 | 21 |
| 33 | uuccacagcuuuPhvul.002G026300.1 | 4 | -1 | 1 | 21 |
| 34 | uuccacagcuuuPhvul.002G026300.2 | 4 | -1 | 1 | 21 |
| 35 | uuccacagcuuuPhvul.002G026300.1 | 4 | -1 | 1 | 21 |
| 36 | uuccacagcuuuPhvul.002G026300.2 | 4 | -1 | 1 | 21 |
| 37 | uuccacagcuuuPhvul.002G026300.1 | 4 | -1 | 1 | 21 |
| 38 | uuccacagcuuuPhvul.002G026300.2 | 4 | -1 | 1 | 21 |
| 39 | uuccacagcuuuPhvul.002G026300.1 | 4 | -1 | 1 | 21 |
| 40 | uuccacagcuuuPhvul.002G026300.2 | 4 | -1 | 1 | 21 |
| 41 | uuccacagcuuuPhvul.002G026300.1 | 4 | -1 | 1 | 21 |
| 42 | uuccacagcuuuPhvul.002G202700.1 | 4 | -1 | 1 | 21 |
| 43 | uuccacagcuuuPhvul.002G202700.1 | 4 | -1 | 1 | 21 |
| 44 | uuccacagcuuuPhvul.002G202700.1 | 4 | -1 | 1 | 21 |
| 45 | uuccacagcuuuPhvul.002G202700.1 | 4 | -1 | 1 | 21 |
| 46 | uuccacagcuuuPhvul.002G202700.1 | 4 | -1 | 1 | 21 |
| 47 | uuccacagcuuuPhvul.002G202700.1 | 4 | -1 | 1 | 21 |
| 48 | uuccacagcuuuPhvul.002G202700.1 | 4 | -1 | 1 | 21 |
| 49 | uuccacagcuuuPhvul.002G202700.1 | 4 | -1 | 1 | 21 |
| 50 | uuccacagcuuuPhvul.002G202700.1 | 4 | -1 | 1 | 21 |
| 51 | uuccacagcuuuPhvul.002G202700.1 | 4 | -1 | 1 | 21 |
| 52 | uuccacagcuuuPhvul.002G202700.1 | 4 | -1 | 1 | 21 |
| 53 | uuccacagcuuuPhvul.002G202700.1 | 4 | -1 | 1 | 21 |
| 54 | uuccacagcuuuPhvul.002G202700.1 | 4 | -1 | 1 | 21 |
| 55 | uuccacagcuuuPhvul.002G202700.1 | 4 | -1 | 1 | 21 |
| 56 | uuccacagcuuuPhvul.002G326600.1 | 4 | -1 | 1 | 21 |
| 57 | uuccacagcuuuPhvul.002G326600.2 | 4 | -1 | 1 | 21 |
| 58 | uuccacagcuuuPhvul.002G326600.1 | 4 | -1 | 1 | 21 |
| 59 | uuccacagcuuuPhvul.002G326600.2 | 4 | -1 | 1 | 21 |
| 60 | uuccacagcuuuPhvul.002G326600.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.002G326600.2 | 4 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.002G326600.1 | 4 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.002G326600.2 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uuccacagcuuu Phvul.002G326600.1 | 4 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.002G326600.2 | 4 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.002G326600.1 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uuccacagcuuu Phvul.002G326600.2 | 4 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.002G326600.1 | 4 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.002G326600.2 | 4 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uuccacagcuuu Phvul.002G326600.1 | 4 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.002G326600.2 | 4 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.002G326600.1 | 4 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uuccacagcuuu Phvul.002G326600.2 | 4 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.002G326600.1 | 4 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.002G326600.2 | 4 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uuccacagcuuu Phvul.002G326600.1 | 4 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.002G326600.2 | 4 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.002G326600.1 | 4 | -1 | 1 | 22 |
| 25 | | | | | |
| 26 | uuccacagcuuu Phvul.002G326600.2 | 4 | -1 | 1 | 22 |
| 27 | uuccacagcuuu Phvul.003G078600.1 | 4 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.003G078600.1 | 4 | -1 | 1 | 21 |
| 29 | uuccacagcuuu Phvul.003G078600.1 | 4 | -1 | 1 | 21 |
| 30 | uuccacagcuuu Phvul.003G078600.1 | 4 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.003G078600.1 | 4 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.003G078600.1 | 4 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.003G078600.1 | 4 | -1 | 1 | 21 |
| 34 | uuccacagcuuu Phvul.003G078600.1 | 4 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.003G078600.1 | 4 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.003G078600.1 | 4 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.003G078600.1 | 4 | -1 | 1 | 21 |
| 38 | uuccacagcuuu Phvul.003G078600.1 | 4 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.003G078600.1 | 4 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.003G078600.1 | 4 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.003G146200.1 | 4 | -1 | 1 | 21 |
| 42 | uuccacagcuuu Phvul.003G146200.1 | 4 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.003G146200.1 | 4 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.003G146200.1 | 4 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.003G146200.1 | 4 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.003G146200.1 | 4 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.003G146200.1 | 4 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.003G146200.1 | 4 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.003G146200.1 | 4 | -1 | 1 | 21 |
| 50 | uuccacagcuuu Phvul.003G146200.1 | 4 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.003G146200.1 | 4 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.003G146200.1 | 4 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.003G146200.1 | 4 | -1 | 1 | 21 |
| 54 | uuccacagcuuu Phvul.003G146200.1 | 4 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.003G146200.1 | 4 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.003G146200.1 | 4 | -1 | 1 | 22 |
| 57 | uuccacagcuuu Phvul.003G195900.2 | 4 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.003G195900.1 | 4 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.003G195900.2 | 4 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.003G195900.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.003G195900.2 | 4 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.003G195900.1 | 4 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.003G195900.2 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uuccacagcuuu Phvul.003G195900.1 | 4 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.003G195900.2 | 4 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.003G195900.1 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uuccacagcuuu Phvul.003G195900.2 | 4 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.003G195900.1 | 4 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.003G195900.2 | 4 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uuccacagcuuu Phvul.003G195900.1 | 4 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.003G195900.2 | 4 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.003G195900.1 | 4 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uuccacagcuuu Phvul.003G195900.2 | 4 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.003G195900.1 | 4 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.003G195900.2 | 4 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uuccacagcuuu Phvul.003G195900.1 | 4 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.003G195900.2 | 4 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.003G195900.1 | 4 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uuccacagcuuu Phvul.003G195900.2 | 4 | -1 | 1 | 22 |
| 27 | uuccacagcuuu Phvul.003G195900.1 | 4 | -1 | 1 | 22 |
| 28 | uuccacagcuuu Phvul.003G207600.1 | 4 | -1 | 1 | 21 |
| 29 | uuccacagcuuu Phvul.003G207600.1 | 4 | -1 | 1 | 21 |
| 30 | | | | | |
| 31 | uuccacagcuuu Phvul.003G207600.1 | 4 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.003G207600.1 | 4 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uuccacagcuuu Phvul.003G207600.1 | 4 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.003G207600.1 | 4 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.003G207600.1 | 4 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.003G207600.1 | 4 | -1 | 1 | 21 |
| 38 | uuccacagcuuu Phvul.003G207600.1 | 4 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.003G207600.1 | 4 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.003G207600.1 | 4 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.003G207600.1 | 4 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uuccacagcuuu Phvul.003G218500.3 | 4 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.003G218500.2 | 4 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.003G218500.1 | 4 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uuccacagcuuu Phvul.003G218500.3 | 4 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.003G218500.2 | 4 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.003G218500.1 | 4 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uuccacagcuuu Phvul.003G218500.3 | 4 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.003G218500.2 | 4 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.003G218500.1 | 4 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uuccacagcuuu Phvul.003G218500.3 | 4 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.003G218500.2 | 4 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.003G218500.1 | 4 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uuccacagcuuu Phvul.003G218500.3 | 4 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.003G218500.2 | 4 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.003G218500.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|--------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuuPhvul.003G218500.3 | 4 | -1 | 1 | 21 |
| 3 | uuccacagcuuuPhvul.003G218500.2 | 4 | -1 | 1 | 21 |
| 4 | uuccacagcuuuPhvul.003G218500.1 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uuccacagcuuuPhvul.003G218500.3 | 4 | -1 | 1 | 21 |
| 7 | uuccacagcuuuPhvul.003G218500.2 | 4 | -1 | 1 | 21 |
| 8 | uuccacagcuuuPhvul.003G218500.1 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uuccacagcuuuPhvul.003G218500.3 | 4 | -1 | 1 | 21 |
| 11 | uuccacagcuuuPhvul.003G218500.2 | 4 | -1 | 1 | 21 |
| 12 | uuccacagcuuuPhvul.003G218500.1 | 4 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uuccacagcuuuPhvul.003G218500.3 | 4 | -1 | 1 | 21 |
| 15 | uuccacagcuuuPhvul.003G218500.2 | 4 | -1 | 1 | 21 |
| 16 | uuccacagcuuuPhvul.003G218500.1 | 4 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uuccacagcuuuPhvul.003G218500.3 | 4 | -1 | 1 | 21 |
| 19 | uuccacagcuuuPhvul.003G218500.2 | 4 | -1 | 1 | 21 |
| 20 | uuccacagcuuuPhvul.003G218500.1 | 4 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uuccacagcuuuPhvul.003G218500.3 | 4 | -1 | 1 | 21 |
| 23 | uuccacagcuuuPhvul.003G218500.2 | 4 | -1 | 1 | 21 |
| 24 | uuccacagcuuuPhvul.003G218500.1 | 4 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uuccacagcuuuPhvul.003G218500.3 | 4 | -1 | 1 | 22 |
| 27 | uuccacagcuuuPhvul.003G218500.2 | 4 | -1 | 1 | 22 |
| 28 | uuccacagcuuuPhvul.003G218500.1 | 4 | -1 | 1 | 22 |
| 29 | | | | | |
| 30 | uuccacagcuuuPhvul.003G225400.1 | 4 | -1 | 1 | 22 |
| 31 | uuccacagcuuuPhvul.003G240800.1 | 4 | -1 | 1 | 21 |
| 32 | uuccacagcuuuPhvul.003G240800.1 | 4 | -1 | 1 | 21 |
| 33 | uuccacagcuuuPhvul.003G240800.1 | 4 | -1 | 1 | 21 |
| 34 | | | | | |
| 35 | uuccacagcuuuPhvul.003G240800.1 | 4 | -1 | 1 | 21 |
| 36 | uuccacagcuuuPhvul.003G240800.1 | 4 | -1 | 1 | 21 |
| 37 | uuccacagcuuuPhvul.003G240800.1 | 4 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | uuccacagcuuuPhvul.003G240800.1 | 4 | -1 | 1 | 21 |
| 40 | uuccacagcuuuPhvul.003G240800.1 | 4 | -1 | 1 | 21 |
| 41 | uuccacagcuuuPhvul.003G240800.1 | 4 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uuccacagcuuuPhvul.003G240800.1 | 4 | -1 | 1 | 21 |
| 44 | uuccacagcuuuPhvul.003G240800.1 | 4 | -1 | 1 | 21 |
| 45 | uuccacagcuuuPhvul.003G240800.1 | 4 | -1 | 1 | 22 |
| 46 | | | | | |
| 47 | uuccacagcuuuPhvul.003G248700.1 | 4 | -1 | 1 | 22 |
| 48 | uuccacagcuuuPhvul.003G249000.1 | 4 | -1 | 1 | 22 |
| 49 | uuccacagcuuuPhvul.003G273400.1 | 4 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uuccacagcuuuPhvul.003G273400.1 | 4 | -1 | 1 | 21 |
| 52 | uuccacagcuuuPhvul.003G273400.1 | 4 | -1 | 1 | 21 |
| 53 | uuccacagcuuuPhvul.003G273400.1 | 4 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uuccacagcuuuPhvul.003G273400.1 | 4 | -1 | 1 | 21 |
| 56 | uuccacagcuuuPhvul.003G273400.1 | 4 | -1 | 1 | 21 |
| 57 | uuccacagcuuuPhvul.003G273400.1 | 4 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uuccacagcuuuPhvul.003G273400.1 | 4 | -1 | 1 | 21 |
| 60 | uuccacagcuuuPhvul.003G273400.1 | 4 | -1 | 1 | 21 |
| | uuccacagcuuuPhvul.003G273400.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.003G273400.1 | 4 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.003G273400.1 | 4 | -1 | 1 | 22 |
| 4 | uuccacagcuuu Phvul.005G101400.3 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uuccacagcuuu Phvul.005G101400.2 | 4 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.005G101400.1 | 4 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.005G101400.3 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uuccacagcuuu Phvul.005G101400.2 | 4 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.005G101400.1 | 4 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.005G101400.3 | 4 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uuccacagcuuu Phvul.005G101400.2 | 4 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.005G101400.1 | 4 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.005G101400.3 | 4 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uuccacagcuuu Phvul.005G101400.2 | 4 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.005G101400.1 | 4 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.005G101400.3 | 4 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uuccacagcuuu Phvul.005G101400.2 | 4 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.005G101400.1 | 4 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.005G101400.3 | 4 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uuccacagcuuu Phvul.005G101400.2 | 4 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.005G101400.1 | 4 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.005G101400.3 | 4 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uuccacagcuuu Phvul.005G101400.2 | 4 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.005G101400.1 | 4 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.005G101400.3 | 4 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uuccacagcuuu Phvul.005G101400.2 | 4 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.005G101400.1 | 4 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.005G101400.3 | 4 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uuccacagcuuu Phvul.005G101400.2 | 4 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.005G101400.1 | 4 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.005G101400.3 | 4 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uuccacagcuuu Phvul.005G101400.2 | 4 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.005G101400.1 | 4 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.005G101400.3 | 4 | -1 | 1 | 21 |
| 45 | | | | | |
| 46 | uuccacagcuuu Phvul.005G101400.2 | 4 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.005G101400.1 | 4 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.005G101400.3 | 4 | -1 | 1 | 22 |
| 49 | uuccacagcuuu Phvul.005G101400.2 | 4 | -1 | 1 | 22 |
| 50 | | | | | |
| 51 | uuccacagcuuu Phvul.005G101400.1 | 4 | -1 | 1 | 22 |
| 52 | uuccacagcuuu Phvul.006G060500.3 | 4 | -1 | 1 | 22 |
| 53 | uuccacagcuuu Phvul.006G174400.2 | 4 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uuccacagcuuu Phvul.006G174400.1 | 4 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.006G174400.2 | 4 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.006G174400.1 | 4 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uuccacagcuuu Phvul.006G174400.2 | 4 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.006G174400.1 | 4 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.006G174400.2 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.006G174400.1 | 4 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.006G174400.2 | 4 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.006G174400.1 | 4 | -1 | 1 | 21 |
| 5 | uuccacagcuuu Phvul.006G174400.2 | 4 | -1 | 1 | 21 |
| 6 | uuccacagcuuu Phvul.006G174400.2 | 4 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.006G174400.1 | 4 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.006G174400.2 | 4 | -1 | 1 | 21 |
| 9 | uuccacagcuuu Phvul.006G174400.1 | 4 | -1 | 1 | 21 |
| 10 | uuccacagcuuu Phvul.006G174400.1 | 4 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.006G174400.2 | 4 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.006G174400.1 | 4 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.006G174400.2 | 4 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.006G174400.2 | 4 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.006G174400.1 | 4 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.006G174400.2 | 4 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.006G174400.2 | 4 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.006G174400.1 | 4 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.006G174400.2 | 4 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.006G174400.1 | 4 | -1 | 1 | 21 |
| 21 | uuccacagcuuu Phvul.006G174400.1 | 4 | -1 | 1 | 21 |
| 22 | uuccacagcuuu Phvul.006G174400.2 | 4 | -1 | 1 | 22 |
| 23 | uuccacagcuuu Phvul.006G174400.1 | 4 | -1 | 1 | 22 |
| 24 | uuccacagcuuu Phvul.007G136300.1 | 4 | -1 | 1 | 21 |
| 25 | uuccacagcuuu Phvul.007G136300.1 | 4 | -1 | 1 | 21 |
| 26 | uuccacagcuuu Phvul.007G136300.1 | 4 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.007G136300.1 | 4 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.007G136300.1 | 4 | -1 | 1 | 21 |
| 29 | uuccacagcuuu Phvul.007G136300.1 | 4 | -1 | 1 | 21 |
| 30 | uuccacagcuuu Phvul.007G136300.1 | 4 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.007G136300.1 | 4 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.007G136300.1 | 4 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.007G136300.1 | 4 | -1 | 1 | 21 |
| 34 | uuccacagcuuu Phvul.007G136300.1 | 4 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.007G136300.1 | 4 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.007G136300.1 | 4 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.007G136300.1 | 4 | -1 | 1 | 21 |
| 38 | uuccacagcuuu Phvul.007G136300.1 | 4 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.007G161800.2 | 4 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.007G161800.2 | 4 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.007G161800.2 | 4 | -1 | 1 | 21 |
| 42 | uuccacagcuuu Phvul.007G161800.2 | 4 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.007G161800.2 | 4 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.007G161800.2 | 4 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.007G161800.2 | 4 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.007G161800.2 | 4 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.007G161800.2 | 4 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.007G161800.2 | 4 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.007G161800.2 | 4 | -1 | 1 | 21 |
| 50 | uuccacagcuuu Phvul.007G161800.2 | 4 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.007G161800.2 | 4 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.007G161800.2 | 4 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.007G166500.6 | 4 | -1 | 1 | 21 |
| 54 | uuccacagcuuu Phvul.007G166500.5 | 4 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.007G166500.4 | 4 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.007G166500.4 | 4 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.007G166500.3 | 4 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.007G166500.3 | 4 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.007G166500.6 | 4 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.007G166500.5 | 4 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.007G166500.4 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.007G166500.3 | 4 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.007G166500.6 | 4 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.007G166500.5 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uuccacagcuuu Phvul.007G166500.4 | 4 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.007G166500.3 | 4 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.007G166500.6 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uuccacagcuuu Phvul.007G166500.5 | 4 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.007G166500.4 | 4 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.007G166500.3 | 4 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uuccacagcuuu Phvul.007G166500.6 | 4 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.007G166500.5 | 4 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.007G166500.4 | 4 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uuccacagcuuu Phvul.007G166500.3 | 4 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.007G166500.6 | 4 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.007G166500.5 | 4 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uuccacagcuuu Phvul.007G166500.4 | 4 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.007G166500.3 | 4 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.007G166500.6 | 4 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uuccacagcuuu Phvul.007G166500.5 | 4 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.007G166500.4 | 4 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.007G166500.3 | 4 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uuccacagcuuu Phvul.007G166500.6 | 4 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.007G166500.5 | 4 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.007G166500.4 | 4 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uuccacagcuuu Phvul.007G166500.3 | 4 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.007G166500.6 | 4 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.007G166500.5 | 4 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.007G166500.4 | 4 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | uuccacagcuuu Phvul.007G166500.3 | 4 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.007G166500.6 | 4 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.007G166500.5 | 4 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uuccacagcuuu Phvul.007G166500.4 | 4 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.007G166500.3 | 4 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.007G166500.6 | 4 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.007G166500.5 | 4 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.007G166500.4 | 4 | -1 | 1 | 21 |
| 48 | | | | | |
| 49 | uuccacagcuuu Phvul.007G166500.3 | 4 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uuccacagcuuu Phvul.007G184400.6 | 4 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.007G184400.2 | 4 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.007G184400.5 | 4 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uuccacagcuuu Phvul.007G184400.3 | 4 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.007G184400.6 | 4 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.007G184400.2 | 4 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uuccacagcuuu Phvul.007G184400.5 | 4 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.007G184400.3 | 4 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.007G184400.6 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.007G184400.2 | 4 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.007G184400.5 | 4 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.007G184400.3 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uuccacagcuuu Phvul.007G184400.6 | 4 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.007G184400.2 | 4 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.007G184400.5 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uuccacagcuuu Phvul.007G184400.3 | 4 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.007G184400.6 | 4 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.007G184400.2 | 4 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uuccacagcuuu Phvul.007G184400.5 | 4 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.007G184400.3 | 4 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.007G184400.6 | 4 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uuccacagcuuu Phvul.007G184400.2 | 4 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.007G184400.5 | 4 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.007G184400.3 | 4 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uuccacagcuuu Phvul.007G184400.6 | 4 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.007G184400.2 | 4 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.007G184400.5 | 4 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uuccacagcuuu Phvul.007G184400.3 | 4 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.007G184400.6 | 4 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.007G184400.2 | 4 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uuccacagcuuu Phvul.007G184400.5 | 4 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.007G184400.3 | 4 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.007G184400.6 | 4 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uuccacagcuuu Phvul.007G184400.2 | 4 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.007G184400.5 | 4 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.007G184400.3 | 4 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uuccacagcuuu Phvul.007G184400.6 | 4 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.007G184400.2 | 4 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.007G184400.5 | 4 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uuccacagcuuu Phvul.007G184400.3 | 4 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.007G184400.6 | 4 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.007G184400.2 | 4 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.007G184400.5 | 4 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uuccacagcuuu Phvul.007G184400.3 | 4 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.007G184400.6 | 4 | -1 | 1 | 22 |
| 49 | uuccacagcuuu Phvul.007G184400.2 | 4 | -1 | 1 | 22 |
| 50 | | | | | |
| 51 | uuccacagcuuu Phvul.007G184400.5 | 4 | -1 | 1 | 22 |
| 52 | uuccacagcuuu Phvul.007G184400.3 | 4 | -1 | 1 | 22 |
| 53 | uuccacagcuuu Phvul.007G207200.1 | 4 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uuccacagcuuu Phvul.007G207200.1 | 4 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.007G207200.1 | 4 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.007G207200.1 | 4 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uuccacagcuuu Phvul.007G207200.1 | 4 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.007G207200.1 | 4 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.007G207200.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.007G207200.1 | 4 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.007G207200.1 | 4 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.007G207200.1 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uuccacagcuuu Phvul.007G207200.1 | 4 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.008G012100.1 | 4 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.008G012100.2 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uuccacagcuuu Phvul.008G012100.1 | 4 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.008G012100.2 | 4 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.008G012100.1 | 4 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uuccacagcuuu Phvul.008G012100.2 | 4 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.008G012100.1 | 4 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.008G012100.2 | 4 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uuccacagcuuu Phvul.008G012100.1 | 4 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.008G012100.2 | 4 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.008G012100.1 | 4 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uuccacagcuuu Phvul.008G012100.2 | 4 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.008G012100.1 | 4 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.008G012100.2 | 4 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uuccacagcuuu Phvul.008G012100.1 | 4 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.008G012100.2 | 4 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.008G012100.1 | 4 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uuccacagcuuu Phvul.008G012100.2 | 4 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.008G012100.1 | 4 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.008G012100.2 | 4 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uuccacagcuuu Phvul.008G012100.1 | 4 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.008G012100.2 | 4 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.008G012100.1 | 4 | -1 | 1 | 22 |
| 37 | uuccacagcuuu Phvul.008G012100.2 | 4 | -1 | 1 | 22 |
| 38 | | | | | |
| 39 | uuccacagcuuu Phvul.008G151600.1 | 4 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.008G151600.1 | 4 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.008G151600.1 | 4 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uuccacagcuuu Phvul.008G151600.1 | 4 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.008G151600.1 | 4 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.008G151600.1 | 4 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.008G151600.1 | 4 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.008G151600.1 | 4 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.008G151600.1 | 4 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.008G151600.1 | 4 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uuccacagcuuu Phvul.008G151600.1 | 4 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.008G151600.1 | 4 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.008G206200.1 | 4 | -1 | 1 | 21 |
| 54 | uuccacagcuuu Phvul.008G206200.1 | 4 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.008G206200.1 | 4 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.008G206200.1 | 4 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.008G206200.1 | 4 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.008G206200.1 | 4 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.008G206200.1 | 4 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.008G206200.1 | 4 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.008G206200.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.008G206200.1 | 4 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.008G206200.1 | 4 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.008G206200.1 | 4 | -1 | 1 | 21 |
| 5 | uuccacagcuuu Phvul.008G206200.1 | 4 | -1 | 1 | 21 |
| 6 | uuccacagcuuu Phvul.008G206200.1 | 4 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.008G206200.1 | 4 | -1 | 1 | 22 |
| 8 | uuccacagcuuu Phvul.008G212400.1 | 4 | -1 | 1 | 21 |
| 9 | uuccacagcuuu Phvul.008G212400.1 | 4 | -1 | 1 | 21 |
| 10 | uuccacagcuuu Phvul.008G212400.1 | 4 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.008G212400.1 | 4 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.008G212400.1 | 4 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.008G212400.1 | 4 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.008G212400.1 | 4 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.008G212400.1 | 4 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.008G212400.1 | 4 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.008G212400.1 | 4 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.008G212400.1 | 4 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.008G212400.1 | 4 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.008G212400.1 | 4 | -1 | 1 | 21 |
| 21 | uuccacagcuuu Phvul.008G212400.1 | 4 | -1 | 1 | 21 |
| 22 | uuccacagcuuu Phvul.008G212400.1 | 4 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.008G237800.1 | 4 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.008G237800.1 | 4 | -1 | 1 | 21 |
| 25 | uuccacagcuuu Phvul.008G237800.1 | 4 | -1 | 1 | 21 |
| 26 | uuccacagcuuu Phvul.008G237800.1 | 4 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.008G237800.1 | 4 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.008G237800.1 | 4 | -1 | 1 | 21 |
| 29 | uuccacagcuuu Phvul.008G237800.1 | 4 | -1 | 1 | 21 |
| 30 | uuccacagcuuu Phvul.008G237800.1 | 4 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.008G237800.1 | 4 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.008G237800.1 | 4 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.008G237800.1 | 4 | -1 | 1 | 21 |
| 34 | uuccacagcuuu Phvul.008G237800.1 | 4 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.008G237800.1 | 4 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.008G237800.1 | 4 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.008G237800.1 | 4 | -1 | 1 | 22 |
| 38 | uuccacagcuuu Phvul.008G237800.1 | 4 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.009G010400.1 | 4 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.009G010400.1 | 4 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.009G010400.1 | 4 | -1 | 1 | 21 |
| 42 | uuccacagcuuu Phvul.009G010400.1 | 4 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.009G010400.1 | 4 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.009G010400.1 | 4 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.009G010400.1 | 4 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.009G010400.1 | 4 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.009G010400.1 | 4 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.009G010400.1 | 4 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.009G010400.1 | 4 | -1 | 1 | 21 |
| 50 | uuccacagcuuu Phvul.009G010400.1 | 4 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.009G010400.1 | 4 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.009G010400.1 | 4 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.009G010400.1 | 4 | -1 | 1 | 22 |
| 54 | uuccacagcuuu Phvul.009G010400.1 | 4 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.009G013500.1 | 4 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.009G013500.1 | 4 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.009G013500.1 | 4 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.009G013500.1 | 4 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.009G013500.1 | 4 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.009G013500.1 | 4 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.009G013500.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.009G013500.1 | 4 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.009G013500.1 | 4 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.009G013500.1 | 4 | -1 | 1 | 21 |
| 5 | uuccacagcuuu Phvul.009G013500.1 | 4 | -1 | 1 | 21 |
| 6 | uuccacagcuuu Phvul.009G013500.1 | 4 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.009G013500.1 | 4 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.009G080600.1 | 4 | -1 | 1 | 21 |
| 9 | uuccacagcuuu Phvul.009G080600.1 | 4 | -1 | 1 | 21 |
| 10 | uuccacagcuuu Phvul.009G080600.1 | 4 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.009G080600.1 | 4 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.009G080600.1 | 4 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.009G080600.1 | 4 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.009G080600.1 | 4 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.009G080600.1 | 4 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.009G080600.1 | 4 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.009G080600.1 | 4 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.009G080600.1 | 4 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.009G080600.1 | 4 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.009G080600.1 | 4 | -1 | 1 | 21 |
| 21 | uuccacagcuuu Phvul.009G080600.1 | 4 | -1 | 1 | 21 |
| 22 | uuccacagcuuu Phvul.009G080600.1 | 4 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.009G080600.1 | 4 | -1 | 1 | 22 |
| 24 | uuccacagcuuu Phvul.009G100700.1 | 4 | -1 | 1 | 21 |
| 25 | uuccacagcuuu Phvul.009G100700.1 | 4 | -1 | 1 | 21 |
| 26 | uuccacagcuuu Phvul.009G100700.1 | 4 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.009G100700.1 | 4 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.009G100700.1 | 4 | -1 | 1 | 21 |
| 29 | uuccacagcuuu Phvul.009G100700.1 | 4 | -1 | 1 | 21 |
| 30 | uuccacagcuuu Phvul.009G100700.1 | 4 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.009G100700.1 | 4 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.009G100700.1 | 4 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.009G100700.1 | 4 | -1 | 1 | 21 |
| 34 | uuccacagcuuu Phvul.009G100700.1 | 4 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.009G100700.1 | 4 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.009G100700.1 | 4 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.009G100700.1 | 4 | -1 | 1 | 21 |
| 38 | uuccacagcuuu Phvul.009G100700.1 | 4 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.009G100700.1 | 4 | -1 | 1 | 22 |
| 40 | uuccacagcuuu Phvul.009G138700.2 | 4 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.009G138700.2 | 4 | -1 | 1 | 21 |
| 42 | uuccacagcuuu Phvul.009G138700.2 | 4 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.009G138700.2 | 4 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.009G138700.2 | 4 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.009G138700.2 | 4 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.009G138700.2 | 4 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.009G138700.2 | 4 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.009G138700.2 | 4 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.009G138700.2 | 4 | -1 | 1 | 21 |
| 50 | uuccacagcuuu Phvul.009G138700.2 | 4 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.009G138700.2 | 4 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.009G138700.2 | 4 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.009G138700.2 | 4 | -1 | 1 | 21 |
| 54 | uuccacagcuuu Phvul.009G138700.2 | 4 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.009G141200.3 | 4 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.009G141200.2 | 4 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.009G141200.3 | 4 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.009G141200.3 | 4 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.009G141200.2 | 4 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.009G141200.3 | 4 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.009G141200.2 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.009G141200.3 | 4 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.009G141200.2 | 4 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.009G141200.3 | 4 | -1 | 1 | 21 |
| 5 | uuccacagcuuu Phvul.009G141200.2 | 4 | -1 | 1 | 21 |
| 6 | uuccacagcuuu Phvul.009G141200.3 | 4 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.009G141200.2 | 4 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.009G141200.3 | 4 | -1 | 1 | 21 |
| 9 | uuccacagcuuu Phvul.009G141200.2 | 4 | -1 | 1 | 21 |
| 10 | uuccacagcuuu Phvul.009G141200.3 | 4 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.009G141200.2 | 4 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.009G141200.3 | 4 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.009G141200.2 | 4 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.009G141200.3 | 4 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.009G141200.2 | 4 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.009G141200.3 | 4 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.009G141200.2 | 4 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.009G141200.3 | 4 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.009G141200.2 | 4 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.009G141200.3 | 4 | -1 | 1 | 21 |
| 21 | uuccacagcuuu Phvul.009G141200.2 | 4 | -1 | 1 | 21 |
| 22 | uuccacagcuuu Phvul.010G066800.1 | 4 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.010G066800.1 | 4 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.010G066800.1 | 4 | -1 | 1 | 21 |
| 25 | uuccacagcuuu Phvul.010G066800.1 | 4 | -1 | 1 | 21 |
| 26 | uuccacagcuuu Phvul.010G066800.1 | 4 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.010G066800.1 | 4 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.010G066800.1 | 4 | -1 | 1 | 21 |
| 29 | uuccacagcuuu Phvul.010G066800.1 | 4 | -1 | 1 | 21 |
| 30 | uuccacagcuuu Phvul.010G066800.1 | 4 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.010G066800.1 | 4 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.010G066800.1 | 4 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.010G066800.1 | 4 | -1 | 1 | 21 |
| 34 | uuccacagcuuu Phvul.010G066800.1 | 4 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.010G066800.1 | 4 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.010G066800.1 | 4 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.010G066800.1 | 4 | -1 | 1 | 22 |
| 38 | uuccacagcuuu Phvul.010G066900.1 | 4 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.010G066900.1 | 4 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.010G066900.1 | 4 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.010G066900.1 | 4 | -1 | 1 | 21 |
| 42 | uuccacagcuuu Phvul.010G066900.1 | 4 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.010G066900.1 | 4 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.010G066900.1 | 4 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.010G066900.1 | 4 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.010G066900.1 | 4 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.010G066900.1 | 4 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.010G066900.1 | 4 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.010G066900.1 | 4 | -1 | 1 | 21 |
| 50 | uuccacagcuuu Phvul.010G066900.1 | 4 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.010G066900.1 | 4 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.010G066900.1 | 4 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.010G066900.1 | 4 | -1 | 1 | 22 |
| 54 | uuccacagcuuu Phvul.010G073200.2 | 4 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.010G073200.1 | 4 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.010G073200.3 | 4 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.010G073200.2 | 4 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.010G073200.1 | 4 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.010G073200.3 | 4 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.010G073200.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|--------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuuPhvul.010G073200.2 | 4 | -1 | 1 | 21 |
| 3 | uuccacagcuuuPhvul.010G073200.1 | 4 | -1 | 1 | 21 |
| 4 | uuccacagcuuuPhvul.010G073200.3 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uuccacagcuuuPhvul.010G073200.2 | 4 | -1 | 1 | 21 |
| 7 | uuccacagcuuuPhvul.010G073200.1 | 4 | -1 | 1 | 21 |
| 8 | uuccacagcuuuPhvul.010G073200.3 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uuccacagcuuuPhvul.010G073200.2 | 4 | -1 | 1 | 21 |
| 11 | uuccacagcuuuPhvul.010G073200.1 | 4 | -1 | 1 | 21 |
| 12 | uuccacagcuuuPhvul.010G073200.3 | 4 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uuccacagcuuuPhvul.010G073200.2 | 4 | -1 | 1 | 21 |
| 15 | uuccacagcuuuPhvul.010G073200.1 | 4 | -1 | 1 | 21 |
| 16 | uuccacagcuuuPhvul.010G073200.3 | 4 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uuccacagcuuuPhvul.010G073200.2 | 4 | -1 | 1 | 21 |
| 19 | uuccacagcuuuPhvul.010G073200.1 | 4 | -1 | 1 | 21 |
| 20 | uuccacagcuuuPhvul.010G073200.3 | 4 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uuccacagcuuuPhvul.010G073200.2 | 4 | -1 | 1 | 21 |
| 23 | uuccacagcuuuPhvul.010G073200.1 | 4 | -1 | 1 | 21 |
| 24 | uuccacagcuuuPhvul.010G073200.3 | 4 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uuccacagcuuuPhvul.010G073200.2 | 4 | -1 | 1 | 21 |
| 27 | uuccacagcuuuPhvul.010G073200.1 | 4 | -1 | 1 | 21 |
| 28 | uuccacagcuuuPhvul.010G073200.3 | 4 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uuccacagcuuuPhvul.010G073200.2 | 4 | -1 | 1 | 21 |
| 31 | uuccacagcuuuPhvul.010G073200.1 | 4 | -1 | 1 | 21 |
| 32 | uuccacagcuuuPhvul.010G073200.3 | 4 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uuccacagcuuuPhvul.010G073200.2 | 4 | -1 | 1 | 21 |
| 35 | uuccacagcuuuPhvul.010G073200.1 | 4 | -1 | 1 | 21 |
| 36 | uuccacagcuuuPhvul.010G073200.3 | 4 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uuccacagcuuuPhvul.011G077500.1 | 4 | -1 | 1 | 21 |
| 39 | uuccacagcuuuPhvul.011G077500.1 | 4 | -1 | 1 | 21 |
| 40 | uuccacagcuuuPhvul.011G077500.1 | 4 | -1 | 1 | 21 |
| 41 | uuccacagcuuuPhvul.011G077500.1 | 4 | -1 | 1 | 21 |
| 42 | uuccacagcuuuPhvul.011G077500.1 | 4 | -1 | 1 | 21 |
| 43 | uuccacagcuuuPhvul.011G077500.1 | 4 | -1 | 1 | 21 |
| 44 | uuccacagcuuuPhvul.011G077500.1 | 4 | -1 | 1 | 21 |
| 45 | uuccacagcuuuPhvul.011G077500.1 | 4 | -1 | 1 | 21 |
| 46 | uuccacagcuuuPhvul.011G077500.1 | 4 | -1 | 1 | 21 |
| 47 | uuccacagcuuuPhvul.011G077500.1 | 4 | -1 | 1 | 21 |
| 48 | uuccacagcuuuPhvul.011G077500.1 | 4 | -1 | 1 | 21 |
| 49 | uuccacagcuuuPhvul.011G077500.1 | 4 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uuccacagcuuuPhvul.011G077500.1 | 4 | -1 | 1 | 21 |
| 52 | uuccacagcuuuPhvul.011G112400.1 | 4 | -1 | 1 | 21 |
| 53 | uuccacagcuuuPhvul.011G112400.1 | 4 | -1 | 1 | 21 |
| 54 | uuccacagcuuuPhvul.011G112400.1 | 4 | -1 | 1 | 21 |
| 55 | uuccacagcuuuPhvul.011G112400.1 | 4 | -1 | 1 | 21 |
| 56 | uuccacagcuuuPhvul.011G112400.1 | 4 | -1 | 1 | 21 |
| 57 | uuccacagcuuuPhvul.011G112400.1 | 4 | -1 | 1 | 21 |
| 58 | uuccacagcuuuPhvul.011G112400.1 | 4 | -1 | 1 | 21 |
| 59 | uuccacagcuuuPhvul.011G112400.1 | 4 | -1 | 1 | 21 |
| 60 | uuccacagcuuuPhvul.011G112400.1 | 4 | -1 | 1 | 21 |
| | uuccacagcuuuPhvul.011G112400.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|--------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuuPhvul.011G112400.1 | 4 | -1 | 1 | 21 |
| 3 | uuccacagcuuuPhvul.011G112400.1 | 4 | -1 | 1 | 21 |
| 4 | uuccacagcuuuPhvul.011G112400.1 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uuccacagcuuuPhvul.011G156800.1 | 4 | -1 | 1 | 21 |
| 7 | uuccacagcuuuPhvul.011G156800.1 | 4 | -1 | 1 | 21 |
| 8 | uuccacagcuuuPhvul.011G156800.1 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uuccacagcuuuPhvul.011G156800.1 | 4 | -1 | 1 | 21 |
| 11 | uuccacagcuuuPhvul.011G156800.1 | 4 | -1 | 1 | 21 |
| 12 | uuccacagcuuuPhvul.011G156800.1 | 4 | -1 | 1 | 21 |
| 13 | uuccacagcuuuPhvul.011G156800.1 | 4 | -1 | 1 | 21 |
| 14 | uuccacagcuuuPhvul.011G156800.1 | 4 | -1 | 1 | 21 |
| 15 | uuccacagcuuuPhvul.011G156800.1 | 4 | -1 | 1 | 21 |
| 16 | uuccacagcuuuPhvul.011G156800.1 | 4 | -1 | 1 | 21 |
| 17 | uuccacagcuuuPhvul.011G156800.1 | 4 | -1 | 1 | 21 |
| 18 | uuccacagcuuuPhvul.011G156800.1 | 4 | -1 | 1 | 21 |
| 19 | uuccacagcuuuPhvul.011G156800.1 | 4 | -1 | 1 | 21 |
| 20 | uuccacagcuuuPhvul.011G156800.1 | 4 | -1 | 1 | 22 |
| 21 | | | | | |
| 22 | uuccacagcuuuPhvul.001G024500.1 | 4.5 | -1 | 1 | 21 |
| 23 | uuccacagcuuuPhvul.001G024500.1 | 4.5 | -1 | 1 | 21 |
| 24 | uuccacagcuuuPhvul.001G024500.1 | 4.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uuccacagcuuuPhvul.001G024500.1 | 4.5 | -1 | 1 | 21 |
| 27 | uuccacagcuuuPhvul.001G024500.1 | 4.5 | -1 | 1 | 21 |
| 28 | uuccacagcuuuPhvul.001G024500.1 | 4.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uuccacagcuuuPhvul.001G024500.1 | 4.5 | -1 | 1 | 21 |
| 31 | uuccacagcuuuPhvul.001G024500.1 | 4.5 | -1 | 1 | 21 |
| 32 | uuccacagcuuuPhvul.001G024500.1 | 4.5 | -1 | 1 | 21 |
| 33 | uuccacagcuuuPhvul.001G024500.1 | 4.5 | -1 | 1 | 21 |
| 34 | uuccacagcuuuPhvul.001G024500.1 | 4.5 | -1 | 1 | 21 |
| 35 | uuccacagcuuuPhvul.001G024500.1 | 4.5 | -1 | 1 | 21 |
| 36 | uuccacagcuuuPhvul.001G024500.1 | 4.5 | -1 | 1 | 22 |
| 37 | uuccacagcuuuPhvul.001G095200.3 | 4.5 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | uuccacagcuuuPhvul.001G095200.2 | 4.5 | -1 | 1 | 21 |
| 40 | uuccacagcuuuPhvul.001G095200.3 | 4.5 | -1 | 1 | 21 |
| 41 | uuccacagcuuuPhvul.001G095200.2 | 4.5 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uuccacagcuuuPhvul.001G095200.3 | 4.5 | -1 | 1 | 21 |
| 44 | uuccacagcuuuPhvul.001G095200.2 | 4.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuuPhvul.001G095200.3 | 4.5 | -1 | 1 | 21 |
| 46 | uuccacagcuuuPhvul.001G095200.2 | 4.5 | -1 | 1 | 21 |
| 47 | uuccacagcuuuPhvul.001G095200.2 | 4.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuuPhvul.001G095200.3 | 4.5 | -1 | 1 | 21 |
| 49 | uuccacagcuuuPhvul.001G095200.2 | 4.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uuccacagcuuuPhvul.001G095200.3 | 4.5 | -1 | 1 | 21 |
| 52 | uuccacagcuuuPhvul.001G095200.2 | 4.5 | -1 | 1 | 21 |
| 53 | uuccacagcuuuPhvul.001G095200.3 | 4.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uuccacagcuuuPhvul.001G095200.2 | 4.5 | -1 | 1 | 21 |
| 56 | uuccacagcuuuPhvul.001G095200.3 | 4.5 | -1 | 1 | 21 |
| 57 | uuccacagcuuuPhvul.001G095200.2 | 4.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uuccacagcuuuPhvul.001G095200.3 | 4.5 | -1 | 1 | 21 |
| 60 | uuccacagcuuuPhvul.001G095200.2 | 4.5 | -1 | 1 | 21 |
| | uuccacagcuuuPhvul.001G095200.3 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|--------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuuPhvul.001G095200.2 | 4.5 | -1 | 1 | 21 |
| 3 | uuccacagcuuuPhvul.001G095200.3 | 4.5 | -1 | 1 | 21 |
| 4 | uuccacagcuuuPhvul.001G095200.2 | 4.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uuccacagcuuuPhvul.001G095200.3 | 4.5 | -1 | 1 | 22 |
| 7 | uuccacagcuuuPhvul.001G198800.1 | 4.5 | -1 | 1 | 21 |
| 8 | uuccacagcuuuPhvul.001G198800.1 | 4.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uuccacagcuuuPhvul.001G198800.1 | 4.5 | -1 | 1 | 21 |
| 11 | uuccacagcuuuPhvul.001G198800.1 | 4.5 | -1 | 1 | 21 |
| 12 | uuccacagcuuuPhvul.001G198800.1 | 4.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uuccacagcuuuPhvul.001G198800.1 | 4.5 | -1 | 1 | 21 |
| 15 | uuccacagcuuuPhvul.001G198800.1 | 4.5 | -1 | 1 | 21 |
| 16 | uuccacagcuuuPhvul.001G198800.1 | 4.5 | -1 | 1 | 21 |
| 17 | uuccacagcuuuPhvul.001G198800.1 | 4.5 | -1 | 1 | 21 |
| 18 | uuccacagcuuuPhvul.001G198800.1 | 4.5 | -1 | 1 | 21 |
| 19 | uuccacagcuuuPhvul.001G198800.1 | 4.5 | -1 | 1 | 21 |
| 20 | uuccacagcuuuPhvul.001G198800.1 | 4.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uuccacagcuuuPhvul.001G198800.1 | 4.5 | -1 | 1 | 22 |
| 23 | uuccacagcuuuPhvul.002G119401.1 | 4.5 | -1 | 1 | 21 |
| 24 | uuccacagcuuuPhvul.002G119401.1 | 4.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uuccacagcuuuPhvul.002G119401.1 | 4.5 | -1 | 1 | 21 |
| 27 | uuccacagcuuuPhvul.002G119401.1 | 4.5 | -1 | 1 | 21 |
| 28 | uuccacagcuuuPhvul.002G119401.1 | 4.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uuccacagcuuuPhvul.002G119401.1 | 4.5 | -1 | 1 | 21 |
| 31 | uuccacagcuuuPhvul.002G119401.1 | 4.5 | -1 | 1 | 21 |
| 32 | uuccacagcuuuPhvul.002G119401.1 | 4.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uuccacagcuuuPhvul.002G119401.1 | 4.5 | -1 | 1 | 21 |
| 35 | uuccacagcuuuPhvul.002G119401.1 | 4.5 | -1 | 1 | 21 |
| 36 | uuccacagcuuuPhvul.002G119401.1 | 4.5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uuccacagcuuuPhvul.002G119401.1 | 4.5 | -1 | 1 | 22 |
| 39 | uuccacagcuuuPhvul.002G123300.1 | 4.5 | -1 | 1 | 22 |
| 40 | uuccacagcuuuPhvul.002G123300.2 | 4.5 | -1 | 1 | 22 |
| 41 | | | | | |
| 42 | uuccacagcuuuPhvul.002G327900.1 | 4.5 | -1 | 1 | 22 |
| 43 | uuccacagcuuuPhvul.003G136300.2 | 4.5 | -1 | 1 | 21 |
| 44 | uuccacagcuuuPhvul.003G136300.1 | 4.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuuPhvul.003G136300.2 | 4.5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uuccacagcuuuPhvul.003G136300.1 | 4.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuuPhvul.003G136300.2 | 4.5 | -1 | 1 | 21 |
| 49 | uuccacagcuuuPhvul.003G136300.1 | 4.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uuccacagcuuuPhvul.003G136300.2 | 4.5 | -1 | 1 | 21 |
| 52 | uuccacagcuuuPhvul.003G136300.1 | 4.5 | -1 | 1 | 21 |
| 53 | uuccacagcuuuPhvul.003G136300.2 | 4.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uuccacagcuuuPhvul.003G136300.1 | 4.5 | -1 | 1 | 21 |
| 56 | uuccacagcuuuPhvul.003G136300.2 | 4.5 | -1 | 1 | 21 |
| 57 | uuccacagcuuuPhvul.003G136300.1 | 4.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uuccacagcuuuPhvul.003G136300.2 | 4.5 | -1 | 1 | 21 |
| 60 | uuccacagcuuuPhvul.003G136300.1 | 4.5 | -1 | 1 | 21 |
| | uuccacagcuuuPhvul.003G136300.2 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.003G136300.1 | 4.5 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.003G136300.2 | 4.5 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.003G136300.1 | 4.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uuccacagcuuu Phvul.003G136300.2 | 4.5 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.003G136300.1 | 4.5 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.003G136300.2 | 4.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uuccacagcuuu Phvul.003G136300.1 | 4.5 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uuccacagcuuu Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uuccacagcuuu Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uuccacagcuuu Phvul.003G154400.1 | 4.5 | -1 | 1 | 22 |
| 27 | uuccacagcuuu Phvul.003G195900.2 | 4.5 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.003G195900.1 | 4.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uuccacagcuuu Phvul.003G195900.2 | 4.5 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.003G195900.1 | 4.5 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.003G195900.2 | 4.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uuccacagcuuu Phvul.003G195900.1 | 4.5 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.003G195900.2 | 4.5 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.003G195900.1 | 4.5 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.003G195900.2 | 4.5 | -1 | 1 | 21 |
| 38 | uuccacagcuuu Phvul.003G195900.2 | 4.5 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.003G195900.1 | 4.5 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.003G195900.2 | 4.5 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.003G195900.1 | 4.5 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uuccacagcuuu Phvul.003G195900.2 | 4.5 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.003G195900.1 | 4.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.003G195900.2 | 4.5 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.003G195900.1 | 4.5 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.003G195900.1 | 4.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.003G195900.2 | 4.5 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.003G195900.1 | 4.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uuccacagcuuu Phvul.003G195900.2 | 4.5 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.003G195900.1 | 4.5 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.003G195900.2 | 4.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uuccacagcuuu Phvul.003G195900.1 | 4.5 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.003G195900.2 | 4.5 | -1 | 1 | 22 |
| 57 | uuccacagcuuu Phvul.003G195900.1 | 4.5 | -1 | 1 | 22 |
| 58 | | | | | |
| 59 | uuccacagcuuu Phvul.003G255900.1 | 4.5 | -1 | 1 | 22 |
| 60 | uuccacagcuuu Phvul.003G292800.1 | 4.5 | -1 | 1 | 22 |
| | uuccacagcuuu Phvul.004G026100.2 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.004G026100.1 | 4.5 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.004G026100.2 | 4.5 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.004G026100.1 | 4.5 | -1 | 1 | 21 |
| 5 | uuccacagcuuu Phvul.004G026100.2 | 4.5 | -1 | 1 | 21 |
| 6 | uuccacagcuuu Phvul.004G026100.2 | 4.5 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.004G026100.1 | 4.5 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.004G026100.2 | 4.5 | -1 | 1 | 21 |
| 9 | uuccacagcuuu Phvul.004G026100.1 | 4.5 | -1 | 1 | 21 |
| 10 | uuccacagcuuu Phvul.004G026100.1 | 4.5 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.004G026100.2 | 4.5 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.004G026100.1 | 4.5 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.004G026100.2 | 4.5 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.004G026100.2 | 4.5 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.004G026100.1 | 4.5 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.004G026100.2 | 4.5 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.004G026100.2 | 4.5 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.004G026100.1 | 4.5 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.004G026100.2 | 4.5 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.004G026100.1 | 4.5 | -1 | 1 | 21 |
| 21 | uuccacagcuuu Phvul.004G026100.1 | 4.5 | -1 | 1 | 21 |
| 22 | uuccacagcuuu Phvul.004G026100.2 | 4.5 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.004G026100.1 | 4.5 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.004G026100.2 | 4.5 | -1 | 1 | 21 |
| 25 | uuccacagcuuu Phvul.004G026100.1 | 4.5 | -1 | 1 | 21 |
| 26 | uuccacagcuuu Phvul.004G026100.1 | 4.5 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.004G026100.2 | 4.5 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.004G026100.1 | 4.5 | -1 | 1 | 21 |
| 29 | uuccacagcuuu Phvul.004G026100.2 | 4.5 | -1 | 1 | 21 |
| 30 | uuccacagcuuu Phvul.004G026100.2 | 4.5 | -1 | 1 | 22 |
| 31 | uuccacagcuuu Phvul.004G026100.1 | 4.5 | -1 | 1 | 22 |
| 32 | uuccacagcuuu Phvul.005G172300.2 | 4.5 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.005G172300.1 | 4.5 | -1 | 1 | 21 |
| 34 | uuccacagcuuu Phvul.005G172300.1 | 4.5 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.005G172300.2 | 4.5 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.005G172300.1 | 4.5 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.005G172300.2 | 4.5 | -1 | 1 | 21 |
| 38 | uuccacagcuuu Phvul.005G172300.2 | 4.5 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.005G172300.1 | 4.5 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.005G172300.2 | 4.5 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.005G172300.1 | 4.5 | -1 | 1 | 21 |
| 42 | uuccacagcuuu Phvul.005G172300.1 | 4.5 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.005G172300.2 | 4.5 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.005G172300.1 | 4.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.005G172300.2 | 4.5 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.005G172300.1 | 4.5 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.005G172300.1 | 4.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.005G172300.2 | 4.5 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.005G172300.1 | 4.5 | -1 | 1 | 21 |
| 50 | uuccacagcuuu Phvul.005G172300.1 | 4.5 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.005G172300.2 | 4.5 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.005G172300.1 | 4.5 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.005G172300.2 | 4.5 | -1 | 1 | 21 |
| 54 | uuccacagcuuu Phvul.005G172300.2 | 4.5 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.005G172300.1 | 4.5 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.005G172300.2 | 4.5 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.005G172300.1 | 4.5 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.005G172300.1 | 4.5 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.005G172300.2 | 4.5 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.005G172300.1 | 4.5 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.005G172300.2 | 4.5 | -1 | 1 | 22 |

| | | | | | |
|----|--------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuuPhvul.005G172300.1 | 4.5 | -1 | 1 | 22 |
| 3 | uuccacagcuuuPhvul.006G052200.1 | 4.5 | -1 | 1 | 21 |
| 4 | uuccacagcuuuPhvul.006G052200.1 | 4.5 | -1 | 1 | 21 |
| 5 | uuccacagcuuuPhvul.006G052200.1 | 4.5 | -1 | 1 | 21 |
| 6 | uuccacagcuuuPhvul.006G052200.1 | 4.5 | -1 | 1 | 21 |
| 7 | uuccacagcuuuPhvul.006G052200.1 | 4.5 | -1 | 1 | 21 |
| 8 | uuccacagcuuuPhvul.006G052200.1 | 4.5 | -1 | 1 | 21 |
| 9 | uuccacagcuuuPhvul.006G052200.1 | 4.5 | -1 | 1 | 21 |
| 10 | uuccacagcuuuPhvul.006G052200.1 | 4.5 | -1 | 1 | 21 |
| 11 | uuccacagcuuuPhvul.006G052200.1 | 4.5 | -1 | 1 | 21 |
| 12 | uuccacagcuuuPhvul.006G052200.1 | 4.5 | -1 | 1 | 21 |
| 13 | uuccacagcuuuPhvul.006G052200.1 | 4.5 | -1 | 1 | 21 |
| 14 | uuccacagcuuuPhvul.006G052200.1 | 4.5 | -1 | 1 | 21 |
| 15 | uuccacagcuuuPhvul.006G052200.1 | 4.5 | -1 | 1 | 21 |
| 16 | uuccacagcuuuPhvul.006G052200.1 | 4.5 | -1 | 1 | 21 |
| 17 | uuccacagcuuuPhvul.006G052200.1 | 4.5 | -1 | 1 | 21 |
| 18 | uuccacagcuuuPhvul.006G052200.1 | 4.5 | -1 | 1 | 22 |
| 19 | uuccacagcuuuPhvul.006G056000.2 | 4.5 | -1 | 1 | 21 |
| 20 | uuccacagcuuuPhvul.006G056000.2 | 4.5 | -1 | 1 | 21 |
| 21 | uuccacagcuuuPhvul.006G056000.2 | 4.5 | -1 | 1 | 21 |
| 22 | uuccacagcuuuPhvul.006G056000.2 | 4.5 | -1 | 1 | 21 |
| 23 | uuccacagcuuuPhvul.006G056000.2 | 4.5 | -1 | 1 | 21 |
| 24 | uuccacagcuuuPhvul.006G056000.2 | 4.5 | -1 | 1 | 21 |
| 25 | uuccacagcuuuPhvul.006G056000.2 | 4.5 | -1 | 1 | 21 |
| 26 | uuccacagcuuuPhvul.006G056000.2 | 4.5 | -1 | 1 | 21 |
| 27 | uuccacagcuuuPhvul.006G056000.2 | 4.5 | -1 | 1 | 21 |
| 28 | uuccacagcuuuPhvul.006G056000.2 | 4.5 | -1 | 1 | 21 |
| 29 | uuccacagcuuuPhvul.006G056000.2 | 4.5 | -1 | 1 | 21 |
| 30 | uuccacagcuuuPhvul.006G056000.2 | 4.5 | -1 | 1 | 21 |
| 31 | uuccacagcuuuPhvul.006G056000.2 | 4.5 | -1 | 1 | 21 |
| 32 | uuccacagcuuuPhvul.006G056000.2 | 4.5 | -1 | 1 | 21 |
| 33 | uuccacagcuuuPhvul.006G056000.2 | 4.5 | -1 | 1 | 21 |
| 34 | uuccacagcuuuPhvul.006G056000.2 | 4.5 | -1 | 1 | 22 |
| 35 | uuccacagcuuuPhvul.007G244900.1 | 4.5 | -1 | 1 | 22 |
| 36 | uuccacagcuuuPhvul.008G003600.2 | 4.5 | -1 | 1 | 21 |
| 37 | uuccacagcuuuPhvul.008G003600.1 | 4.5 | -1 | 1 | 21 |
| 38 | uuccacagcuuuPhvul.008G003600.1 | 4.5 | -1 | 1 | 21 |
| 39 | uuccacagcuuuPhvul.008G003600.2 | 4.5 | -1 | 1 | 21 |
| 40 | uuccacagcuuuPhvul.008G003600.1 | 4.5 | -1 | 1 | 21 |
| 41 | uuccacagcuuuPhvul.008G003600.2 | 4.5 | -1 | 1 | 21 |
| 42 | uuccacagcuuuPhvul.008G003600.1 | 4.5 | -1 | 1 | 21 |
| 43 | uuccacagcuuuPhvul.008G003600.1 | 4.5 | -1 | 1 | 21 |
| 44 | uuccacagcuuuPhvul.008G003600.2 | 4.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuuPhvul.008G003600.1 | 4.5 | -1 | 1 | 21 |
| 46 | uuccacagcuuuPhvul.008G003600.1 | 4.5 | -1 | 1 | 21 |
| 47 | uuccacagcuuuPhvul.008G003600.2 | 4.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuuPhvul.008G003600.1 | 4.5 | -1 | 1 | 21 |
| 49 | uuccacagcuuuPhvul.008G003600.2 | 4.5 | -1 | 1 | 21 |
| 50 | uuccacagcuuuPhvul.008G003600.1 | 4.5 | -1 | 1 | 21 |
| 51 | uuccacagcuuuPhvul.008G003600.1 | 4.5 | -1 | 1 | 21 |
| 52 | uuccacagcuuuPhvul.008G003600.2 | 4.5 | -1 | 1 | 21 |
| 53 | uuccacagcuuuPhvul.008G003600.1 | 4.5 | -1 | 1 | 21 |
| 54 | uuccacagcuuuPhvul.008G003600.1 | 4.5 | -1 | 1 | 21 |
| 55 | uuccacagcuuuPhvul.008G003600.2 | 4.5 | -1 | 1 | 21 |
| 56 | uuccacagcuuuPhvul.008G003600.1 | 4.5 | -1 | 1 | 21 |
| 57 | uuccacagcuuuPhvul.008G003600.2 | 4.5 | -1 | 1 | 21 |
| 58 | uuccacagcuuuPhvul.008G003600.2 | 4.5 | -1 | 1 | 21 |
| 59 | uuccacagcuuuPhvul.008G003600.1 | 4.5 | -1 | 1 | 21 |
| 60 | uuccacagcuuuPhvul.008G003600.2 | 4.5 | -1 | 1 | 21 |
| | uuccacagcuuuPhvul.008G003600.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.008G003600.2 | 4.5 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.008G003600.1 | 4.5 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.008G003600.2 | 4.5 | -1 | 1 | 22 |
| 5 | | | | | |
| 6 | uuccacagcuuu Phvul.008G003600.1 | 4.5 | -1 | 1 | 22 |
| 7 | uuccacagcuuu Phvul.008G055200.1 | 4.5 | -1 | 1 | 22 |
| 8 | uuccacagcuuu Phvul.008G162900.1 | 4.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uuccacagcuuu Phvul.008G162900.1 | 4.5 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.008G162900.1 | 4.5 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.008G162900.1 | 4.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uuccacagcuuu Phvul.008G162900.1 | 4.5 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.008G162900.1 | 4.5 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.008G162900.1 | 4.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uuccacagcuuu Phvul.008G162900.1 | 4.5 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.008G162900.1 | 4.5 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.008G162900.1 | 4.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uuccacagcuuu Phvul.008G162900.1 | 4.5 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.008G162900.1 | 4.5 | -1 | 1 | 22 |
| 24 | uuccacagcuuu Phvul.008G192200.1 | 4.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uuccacagcuuu Phvul.008G192200.1 | 4.5 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.008G192200.1 | 4.5 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.008G192200.1 | 4.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uuccacagcuuu Phvul.008G192200.1 | 4.5 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.008G192200.1 | 4.5 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.008G192200.1 | 4.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uuccacagcuuu Phvul.008G192200.1 | 4.5 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.008G192200.1 | 4.5 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.008G192200.1 | 4.5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uuccacagcuuu Phvul.008G192200.1 | 4.5 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.008G192200.1 | 4.5 | -1 | 1 | 22 |
| 40 | uuccacagcuuu Phvul.008G277900.1 | 4.5 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.008G277900.1 | 4.5 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uuccacagcuuu Phvul.008G277900.1 | 4.5 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.008G277900.1 | 4.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.008G277900.1 | 4.5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uuccacagcuuu Phvul.008G277900.1 | 4.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.008G277900.1 | 4.5 | -1 | 1 | 21 |
| 49 | | | | | |
| 50 | uuccacagcuuu Phvul.008G277900.1 | 4.5 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.008G277900.1 | 4.5 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.008G277900.1 | 4.5 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.008G277900.1 | 4.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uuccacagcuuu Phvul.008G277900.1 | 4.5 | -1 | 1 | 22 |
| 56 | uuccacagcuuu Phvul.008G283700.1 | 4.5 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.008G283700.1 | 4.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uuccacagcuuu Phvul.008G283700.1 | 4.5 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.008G283700.1 | 4.5 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.008G283700.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.008G283700.1 | 4.5 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.008G283700.1 | 4.5 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.008G283700.1 | 4.5 | -1 | 1 | 21 |
| 5 | uuccacagcuuu Phvul.008G283700.1 | 4.5 | -1 | 1 | 21 |
| 6 | uuccacagcuuu Phvul.008G283700.1 | 4.5 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.008G283700.1 | 4.5 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.008G283700.1 | 4.5 | -1 | 1 | 21 |
| 9 | uuccacagcuuu Phvul.008G283700.1 | 4.5 | -1 | 1 | 21 |
| 10 | uuccacagcuuu Phvul.008G283700.1 | 4.5 | -1 | 1 | 22 |
| 11 | uuccacagcuuu Phvul.009G086300.2 | 4.5 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.009G086300.1 | 4.5 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.009G086300.2 | 4.5 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.009G086300.2 | 4.5 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.009G086300.1 | 4.5 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.009G086300.2 | 4.5 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.009G086300.2 | 4.5 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.009G086300.1 | 4.5 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.009G086300.2 | 4.5 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.009G086300.1 | 4.5 | -1 | 1 | 21 |
| 21 | uuccacagcuuu Phvul.009G086300.1 | 4.5 | -1 | 1 | 21 |
| 22 | uuccacagcuuu Phvul.009G086300.2 | 4.5 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.009G086300.1 | 4.5 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.009G086300.2 | 4.5 | -1 | 1 | 21 |
| 25 | uuccacagcuuu Phvul.009G086300.1 | 4.5 | -1 | 1 | 21 |
| 26 | uuccacagcuuu Phvul.009G086300.1 | 4.5 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.009G086300.2 | 4.5 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.009G086300.1 | 4.5 | -1 | 1 | 21 |
| 29 | uuccacagcuuu Phvul.009G086300.2 | 4.5 | -1 | 1 | 21 |
| 30 | uuccacagcuuu Phvul.009G086300.2 | 4.5 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.009G086300.1 | 4.5 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.009G086300.2 | 4.5 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.009G086300.1 | 4.5 | -1 | 1 | 21 |
| 34 | uuccacagcuuu Phvul.009G086300.1 | 4.5 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.009G086300.2 | 4.5 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.009G086300.1 | 4.5 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.009G086300.2 | 4.5 | -1 | 1 | 21 |
| 38 | uuccacagcuuu Phvul.009G086300.2 | 4.5 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.009G086300.1 | 4.5 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.009G140900.1 | 4.5 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.009G140900.1 | 4.5 | -1 | 1 | 21 |
| 42 | uuccacagcuuu Phvul.009G140900.1 | 4.5 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.009G140900.1 | 4.5 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.009G140900.1 | 4.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.009G140900.1 | 4.5 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.009G140900.1 | 4.5 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.009G140900.1 | 4.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.009G140900.1 | 4.5 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.009G140900.1 | 4.5 | -1 | 1 | 21 |
| 50 | uuccacagcuuu Phvul.009G140900.1 | 4.5 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.009G140900.1 | 4.5 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.009G140900.1 | 4.5 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.009G140900.1 | 4.5 | -1 | 1 | 21 |
| 54 | uuccacagcuuu Phvul.009G140900.1 | 4.5 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.009G140900.1 | 4.5 | -1 | 1 | 22 |
| 56 | uuccacagcuuu Phvul.010G131100.2 | 4.5 | -1 | 1 | 22 |
| 57 | uuccacagcuuu Phvul.010G140600.2 | 4.5 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.010G140600.2 | 4.5 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.010G140600.2 | 4.5 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.010G140600.2 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.010G140600.2 | 4.5 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.010G140600.2 | 4.5 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.010G140600.2 | 4.5 | -1 | 1 | 21 |
| 5 | uuccacagcuuu Phvul.010G140600.2 | 4.5 | -1 | 1 | 21 |
| 6 | uuccacagcuuu Phvul.010G140600.2 | 4.5 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.010G140600.2 | 4.5 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.010G140600.2 | 4.5 | -1 | 1 | 21 |
| 9 | uuccacagcuuu Phvul.010G140600.2 | 4.5 | -1 | 1 | 21 |
| 10 | uuccacagcuuu Phvul.010G140600.2 | 4.5 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.010G140600.2 | 4.5 | -1 | 1 | 22 |
| 12 | uuccacagcuuu Phvul.011G014800.1 | 4.5 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.011G014800.1 | 4.5 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.011G014800.1 | 4.5 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.011G014800.1 | 4.5 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.011G014800.1 | 4.5 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.011G014800.1 | 4.5 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.011G014800.1 | 4.5 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.011G014800.1 | 4.5 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.011G014800.1 | 4.5 | -1 | 1 | 21 |
| 21 | uuccacagcuuu Phvul.011G014800.1 | 4.5 | -1 | 1 | 21 |
| 22 | uuccacagcuuu Phvul.011G014800.1 | 4.5 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.011G014800.1 | 4.5 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.011G014800.1 | 4.5 | -1 | 1 | 21 |
| 25 | uuccacagcuuu Phvul.011G014800.1 | 4.5 | -1 | 1 | 21 |
| 26 | uuccacagcuuu Phvul.011G014800.1 | 4.5 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.011G031600.2 | 4.5 | -1 | 1 | 22 |
| 28 | uuccacagcuuu Phvul.011G031600.1 | 4.5 | -1 | 1 | 22 |
| 29 | uuccacagcuuu Phvul.011G092600.2 | 4.5 | -1 | 1 | 21 |
| 30 | uuccacagcuuu Phvul.011G092600.2 | 4.5 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.011G092600.1 | 4.5 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.011G092600.2 | 4.5 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.011G092600.1 | 4.5 | -1 | 1 | 21 |
| 34 | uuccacagcuuu Phvul.011G092600.1 | 4.5 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.011G092600.2 | 4.5 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.011G092600.1 | 4.5 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.011G092600.2 | 4.5 | -1 | 1 | 21 |
| 38 | uuccacagcuuu Phvul.011G092600.2 | 4.5 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.011G092600.1 | 4.5 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.011G092600.2 | 4.5 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.011G092600.1 | 4.5 | -1 | 1 | 21 |
| 42 | uuccacagcuuu Phvul.011G092600.1 | 4.5 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.011G092600.2 | 4.5 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.011G092600.1 | 4.5 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.011G092600.2 | 4.5 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.011G092600.1 | 4.5 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.011G092600.1 | 4.5 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.011G092600.2 | 4.5 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.011G092600.1 | 4.5 | -1 | 1 | 21 |
| 50 | uuccacagcuuu Phvul.011G092600.1 | 4.5 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.011G092600.2 | 4.5 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.011G092600.1 | 4.5 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.011G092600.2 | 4.5 | -1 | 1 | 21 |
| 54 | uuccacagcuuu Phvul.011G092600.2 | 4.5 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.011G092600.1 | 4.5 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.011G092600.2 | 4.5 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.011G092600.1 | 4.5 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.011G092600.1 | 4.5 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.003G066900.3 | 5 | -1 | 1 | 22 |
| 60 | uuccacagcuuu Phvul.003G066900.2 | 5 | -1 | 1 | 22 |
| | uuccacagcuuu Phvul.003G146400.1 | 5 | -1 | 1 | 22 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.003G253800.1 | 5 | -1 | 1 | 22 |
| 3 | uuccacagcuuu Phvul.003G253800.2 | 5 | -1 | 1 | 22 |
| 4 | uuccacagcuuu Phvul.004G037600.3 | 5 | -1 | 1 | 22 |
| 5 | | | | | |
| 6 | uuccacagcuuu Phvul.004G037600.2 | 5 | -1 | 1 | 22 |
| 7 | uuccacagcuuu Phvul.005G029100.2 | 5 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.005G029100.2 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uuccacagcuuu Phvul.005G029100.2 | 5 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.005G029100.2 | 5 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.005G029100.2 | 5 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.005G029100.2 | 5 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.005G029100.2 | 5 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.005G029100.2 | 5 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.005G029100.2 | 5 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.005G029100.2 | 5 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.005G029100.2 | 5 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.005G029100.2 | 5 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.005G029100.2 | 5 | -1 | 1 | 21 |
| 21 | uuccacagcuuu Phvul.005G029100.2 | 5 | -1 | 1 | 21 |
| 22 | uuccacagcuuu Phvul.005G029100.2 | 5 | -1 | 1 | 22 |
| 23 | uuccacagcuuu Phvul.005G075200.1 | 5 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.005G075200.2 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uuccacagcuuu Phvul.005G075200.1 | 5 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.005G075200.2 | 5 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.005G075200.1 | 5 | -1 | 1 | 21 |
| 29 | uuccacagcuuu Phvul.005G075200.2 | 5 | -1 | 1 | 21 |
| 30 | uuccacagcuuu Phvul.005G075200.2 | 5 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.005G075200.1 | 5 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.005G075200.2 | 5 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.005G075200.1 | 5 | -1 | 1 | 21 |
| 34 | uuccacagcuuu Phvul.005G075200.1 | 5 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.005G075200.2 | 5 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.005G075200.1 | 5 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.005G075200.2 | 5 | -1 | 1 | 21 |
| 38 | uuccacagcuuu Phvul.005G075200.2 | 5 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.005G075200.1 | 5 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.005G075200.2 | 5 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.005G075200.1 | 5 | -1 | 1 | 21 |
| 42 | uuccacagcuuu Phvul.005G075200.1 | 5 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.005G075200.2 | 5 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.005G075200.1 | 5 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.005G075200.2 | 5 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.005G075200.1 | 5 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.005G075200.1 | 5 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.005G075200.2 | 5 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.005G075200.1 | 5 | -1 | 1 | 21 |
| 50 | uuccacagcuuu Phvul.005G075200.1 | 5 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.005G075200.2 | 5 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.005G075200.1 | 5 | -1 | 1 | 22 |
| 53 | uuccacagcuuu Phvul.005G075200.2 | 5 | -1 | 1 | 22 |
| 54 | uuccacagcuuu Phvul.005G105400.1 | 5 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.005G105400.1 | 5 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.005G105400.1 | 5 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.005G105400.1 | 5 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.005G105400.1 | 5 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.005G105400.1 | 5 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.005G105400.1 | 5 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.005G105400.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.005G105400.1 | 5 | -1 | 1 | 21 |
| 3 | uuccacagcuuu Phvul.005G105400.1 | 5 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.005G105400.1 | 5 | -1 | 1 | 21 |
| 5 | uuccacagcuuu Phvul.005G105400.1 | 5 | -1 | 1 | 21 |
| 6 | uuccacagcuuu Phvul.005G105400.1 | 5 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.005G105400.1 | 5 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.005G105400.1 | 5 | -1 | 1 | 22 |
| 9 | uuccacagcuuu Phvul.006G142000.1 | 5 | -1 | 1 | 21 |
| 10 | uuccacagcuuu Phvul.006G142000.1 | 5 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.006G142000.1 | 5 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.006G142000.1 | 5 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.006G142000.1 | 5 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.006G142000.1 | 5 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.006G142000.1 | 5 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.006G142000.1 | 5 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.006G142000.1 | 5 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.006G142000.1 | 5 | -1 | 1 | 21 |
| 19 | uuccacagcuuu Phvul.006G142000.1 | 5 | -1 | 1 | 21 |
| 20 | uuccacagcuuu Phvul.006G142000.1 | 5 | -1 | 1 | 21 |
| 21 | uuccacagcuuu Phvul.006G142000.1 | 5 | -1 | 1 | 21 |
| 22 | uuccacagcuuu Phvul.006G142000.1 | 5 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.006G142000.1 | 5 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.006G142000.1 | 5 | -1 | 1 | 22 |
| 25 | uuccacagcuuu Phvul.006G157700.1 | 5 | -1 | 1 | 21 |
| 26 | uuccacagcuuu Phvul.006G157700.1 | 5 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.006G157700.1 | 5 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.006G157700.1 | 5 | -1 | 1 | 21 |
| 29 | uuccacagcuuu Phvul.006G157700.1 | 5 | -1 | 1 | 21 |
| 30 | uuccacagcuuu Phvul.006G157700.1 | 5 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.006G157700.1 | 5 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.006G157700.1 | 5 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.006G157700.1 | 5 | -1 | 1 | 21 |
| 34 | uuccacagcuuu Phvul.006G157700.1 | 5 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.006G157700.1 | 5 | -1 | 1 | 21 |
| 36 | uuccacagcuuu Phvul.006G157700.1 | 5 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.006G157700.1 | 5 | -1 | 1 | 21 |
| 38 | uuccacagcuuu Phvul.006G157700.1 | 5 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.006G157700.1 | 5 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.006G157700.1 | 5 | -1 | 1 | 22 |
| 41 | uuccacagcuuu Phvul.006G200900.1 | 5 | -1 | 1 | 22 |
| 42 | uuccacagcuuu Phvul.007G083600.1 | 5 | -1 | 1 | 22 |
| 43 | uuccacagcuuu Phvul.007G083600.1 | 5 | -1 | 1 | 22 |
| 44 | uuccacagcuuu Phvul.007G083600.2 | 5 | -1 | 1 | 22 |
| 45 | uuccacagcuuu Phvul.007G136300.1 | 5 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.007G136300.1 | 5 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.007G136300.1 | 5 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.007G136300.1 | 5 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.007G136300.1 | 5 | -1 | 1 | 21 |
| 50 | uuccacagcuuu Phvul.007G136300.1 | 5 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.007G136300.1 | 5 | -1 | 1 | 21 |
| 52 | uuccacagcuuu Phvul.007G136300.1 | 5 | -1 | 1 | 21 |
| 53 | uuccacagcuuu Phvul.007G136300.1 | 5 | -1 | 1 | 21 |
| 54 | uuccacagcuuu Phvul.007G136300.1 | 5 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.007G136300.1 | 5 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.007G136300.1 | 5 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.007G136300.1 | 5 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.007G136300.1 | 5 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.007G136300.1 | 5 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.007G175300.2 | 5 | -1 | 1 | 22 |
| | uuccacagcuuu Phvul.007G175300.3 | 5 | -1 | 1 | 22 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuu Phvul.007G175300.1 | 5 | -1 | 1 | 22 |
| 3 | uuccacagcuuu Phvul.007G177900.1 | 5 | -1 | 1 | 21 |
| 4 | uuccacagcuuu Phvul.007G177900.1 | 5 | -1 | 1 | 21 |
| 5 | uuccacagcuuu Phvul.007G177900.1 | 5 | -1 | 1 | 21 |
| 6 | uuccacagcuuu Phvul.007G177900.1 | 5 | -1 | 1 | 21 |
| 7 | uuccacagcuuu Phvul.007G177900.1 | 5 | -1 | 1 | 21 |
| 8 | uuccacagcuuu Phvul.007G177900.1 | 5 | -1 | 1 | 21 |
| 9 | uuccacagcuuu Phvul.007G177900.1 | 5 | -1 | 1 | 21 |
| 10 | uuccacagcuuu Phvul.007G177900.1 | 5 | -1 | 1 | 21 |
| 11 | uuccacagcuuu Phvul.007G177900.1 | 5 | -1 | 1 | 21 |
| 12 | uuccacagcuuu Phvul.007G177900.1 | 5 | -1 | 1 | 21 |
| 13 | uuccacagcuuu Phvul.007G177900.1 | 5 | -1 | 1 | 21 |
| 14 | uuccacagcuuu Phvul.007G177900.1 | 5 | -1 | 1 | 21 |
| 15 | uuccacagcuuu Phvul.007G177900.1 | 5 | -1 | 1 | 21 |
| 16 | uuccacagcuuu Phvul.007G177900.1 | 5 | -1 | 1 | 21 |
| 17 | uuccacagcuuu Phvul.007G177900.1 | 5 | -1 | 1 | 21 |
| 18 | uuccacagcuuu Phvul.007G177900.1 | 5 | -1 | 1 | 22 |
| 19 | uuccacagcuuu Phvul.008G106100.1 | 5 | -1 | 1 | 22 |
| 20 | uuccacagcuuu Phvul.010G112800.1 | 5 | -1 | 1 | 21 |
| 21 | uuccacagcuuu Phvul.010G112800.1 | 5 | -1 | 1 | 21 |
| 22 | uuccacagcuuu Phvul.010G112800.1 | 5 | -1 | 1 | 21 |
| 23 | uuccacagcuuu Phvul.010G112800.1 | 5 | -1 | 1 | 21 |
| 24 | uuccacagcuuu Phvul.010G112800.1 | 5 | -1 | 1 | 21 |
| 25 | uuccacagcuuu Phvul.010G112800.1 | 5 | -1 | 1 | 21 |
| 26 | uuccacagcuuu Phvul.010G112800.1 | 5 | -1 | 1 | 21 |
| 27 | uuccacagcuuu Phvul.010G112800.1 | 5 | -1 | 1 | 21 |
| 28 | uuccacagcuuu Phvul.010G112800.1 | 5 | -1 | 1 | 21 |
| 29 | uuccacagcuuu Phvul.010G112800.1 | 5 | -1 | 1 | 21 |
| 30 | uuccacagcuuu Phvul.010G112800.1 | 5 | -1 | 1 | 21 |
| 31 | uuccacagcuuu Phvul.010G112800.1 | 5 | -1 | 1 | 21 |
| 32 | uuccacagcuuu Phvul.010G112800.1 | 5 | -1 | 1 | 21 |
| 33 | uuccacagcuuu Phvul.010G112800.1 | 5 | -1 | 1 | 21 |
| 34 | uuccacagcuuu Phvul.010G112800.1 | 5 | -1 | 1 | 21 |
| 35 | uuccacagcuuu Phvul.010G112800.1 | 5 | -1 | 1 | 22 |
| 36 | uuccacagcuuu Phvul.010G123900.1 | 5 | -1 | 1 | 21 |
| 37 | uuccacagcuuu Phvul.010G123900.1 | 5 | -1 | 1 | 21 |
| 38 | uuccacagcuuu Phvul.010G123900.1 | 5 | -1 | 1 | 21 |
| 39 | uuccacagcuuu Phvul.010G123900.1 | 5 | -1 | 1 | 21 |
| 40 | uuccacagcuuu Phvul.010G123900.1 | 5 | -1 | 1 | 21 |
| 41 | uuccacagcuuu Phvul.010G123900.1 | 5 | -1 | 1 | 21 |
| 42 | uuccacagcuuu Phvul.010G123900.1 | 5 | -1 | 1 | 21 |
| 43 | uuccacagcuuu Phvul.010G123900.1 | 5 | -1 | 1 | 21 |
| 44 | uuccacagcuuu Phvul.010G123900.1 | 5 | -1 | 1 | 21 |
| 45 | uuccacagcuuu Phvul.010G123900.1 | 5 | -1 | 1 | 21 |
| 46 | uuccacagcuuu Phvul.010G123900.1 | 5 | -1 | 1 | 21 |
| 47 | uuccacagcuuu Phvul.010G123900.1 | 5 | -1 | 1 | 21 |
| 48 | uuccacagcuuu Phvul.010G123900.1 | 5 | -1 | 1 | 21 |
| 49 | uuccacagcuuu Phvul.010G123900.1 | 5 | -1 | 1 | 21 |
| 50 | uuccacagcuuu Phvul.010G123900.1 | 5 | -1 | 1 | 21 |
| 51 | uuccacagcuuu Phvul.010G123900.1 | 5 | -1 | 1 | 22 |
| 52 | uuccacagcuuu Phvul.010G144000.1 | 5 | -1 | 1 | 22 |
| 53 | uuccacagcuuu Phvul.011G090600.1 | 5 | -1 | 1 | 21 |
| 54 | uuccacagcuuu Phvul.011G090600.1 | 5 | -1 | 1 | 21 |
| 55 | uuccacagcuuu Phvul.011G090600.1 | 5 | -1 | 1 | 21 |
| 56 | uuccacagcuuu Phvul.011G090600.1 | 5 | -1 | 1 | 21 |
| 57 | uuccacagcuuu Phvul.011G090600.1 | 5 | -1 | 1 | 21 |
| 58 | uuccacagcuuu Phvul.011G090600.1 | 5 | -1 | 1 | 21 |
| 59 | uuccacagcuuu Phvul.011G090600.1 | 5 | -1 | 1 | 21 |
| 60 | uuccacagcuuu Phvul.011G090600.1 | 5 | -1 | 1 | 21 |
| | uuccacagcuuu Phvul.011G090600.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|--------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uuccacagcuuuPhvul.011G090600.1 | 5 | -1 | 1 | 21 |
| 3 | uuccacagcuuuPhvul.011G090600.1 | 5 | -1 | 1 | 21 |
| 4 | uuccacagcuuuPhvul.011G090600.1 | 5 | -1 | 1 | 21 |
| 5 | uuccacagcuuuPhvul.011G090600.1 | 5 | -1 | 1 | 21 |
| 6 | uuccacagcuuuPhvul.011G090600.1 | 5 | -1 | 1 | 21 |
| 7 | uuccacagcuuuPhvul.L001616.1 | 5 | -1 | 1 | 21 |
| 8 | uuccacagcuuuPhvul.L001616.1 | 5 | -1 | 1 | 21 |
| 9 | uuccacagcuuuPhvul.L001616.1 | 5 | -1 | 1 | 21 |
| 10 | uuccacagcuuuPhvul.L001616.1 | 5 | -1 | 1 | 21 |
| 11 | uuccacagcuuuPhvul.L001616.1 | 5 | -1 | 1 | 21 |
| 12 | uuccacagcuuuPhvul.L001616.1 | 5 | -1 | 1 | 21 |
| 13 | uuccacagcuuuPhvul.L001616.1 | 5 | -1 | 1 | 21 |
| 14 | uuccacagcuuuPhvul.L001616.1 | 5 | -1 | 1 | 21 |
| 15 | uuccacagcuuuPhvul.L001616.1 | 5 | -1 | 1 | 21 |
| 16 | uuccacagcuuuPhvul.L001616.1 | 5 | -1 | 1 | 21 |
| 17 | uuccacagcuuuPhvul.L001616.1 | 5 | -1 | 1 | 21 |
| 18 | uuccacagcuuuPhvul.L001616.1 | 5 | -1 | 1 | 21 |
| 19 | uuccacagcuuuPhvul.L001616.1 | 5 | -1 | 1 | 21 |
| 20 | uuccacagcuuuPhvul.L001616.1 | 5 | -1 | 1 | 21 |
| 21 | uuccacagcuuuPhvul.L001616.1 | 5 | -1 | 1 | 21 |
| 22 | uuccacagcuuuPhvul.L001616.1 | 5 | -1 | 1 | 22 |
| 23 | | | | | |
| 24 | | | | | |
| 25 | | | | | |
| 26 | | | | | |
| 27 | | | | | |
| 28 | | | | | |
| 29 | | | | | |
| 30 | | | | | |
| 31 | | | | | |
| 32 | | | | | |
| 33 | | | | | |
| 34 | | | | | |
| 35 | | | | | |
| 36 | | | | | |
| 37 | | | | | |
| 38 | | | | | |
| 39 | | | | | |
| 40 | | | | | |
| 41 | | | | | |
| 42 | | | | | |
| 43 | | | | | |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

Do not distribute

| | | | | |
|----|-----|---------------|---------------------|--------------|
| 1 | | | | |
| 2 | 235 | 256 UCCACA-GC | UCGUUCAAG/Cleavage | pacid=371782 |
| 3 | 670 | 691 UCCACA-GC | UCGUUCAAG/Cleavage | pacid=371782 |
| 4 | 235 | 256 UCCACA-GC | UCGUUCAAG/Cleavage | pacid=371782 |
| 5 | 670 | 691 UCCACA-GC | UCGUUCAAG/Cleavage | pacid=371782 |
| 6 | 235 | 256 UCCACA-GC | UCGUUCAAG/Cleavage | pacid=371782 |
| 7 | 670 | 691 UCCACA-GC | UCGUUCAAG/Cleavage | pacid=371782 |
| 8 | 234 | 256 UCCACA-GC | AUCGUUCAAC/Cleavage | pacid=371782 |
| 9 | 669 | 691 UCCACA-GC | AUCGUUCAAC/Cleavage | pacid=371782 |
| 10 | 794 | 814 UCCACAGCL | CGGUUCAAG/Cleavage | pacid=371752 |
| 11 | 794 | 814 UCCACAGCL | CGGUUCAAG/Cleavage | pacid=371752 |
| 12 | 794 | 814 UCCACAGCL | CGGUUCAAG/Cleavage | pacid=371752 |
| 13 | 794 | 814 UCCACAGCL | CGGUUCAAG/Cleavage | pacid=371752 |
| 14 | 794 | 814 UCCACAGCL | CGGUUCAAG/Cleavage | pacid=371752 |
| 15 | 794 | 814 UCCACAGCL | CGGUUCAAG/Cleavage | pacid=371752 |
| 16 | 794 | 814 UCCACAGCL | CGGUUCAAG/Cleavage | pacid=371752 |
| 17 | 794 | 814 UCCACAGCL | CGGUUCAAG/Cleavage | pacid=371752 |
| 18 | 794 | 814 UCCACAGCL | CGGUUCAAG/Cleavage | pacid=371752 |
| 19 | 794 | 814 UCCACAGCL | CGGUUCAAG/Cleavage | pacid=371752 |
| 20 | 794 | 814 UCCACAGCL | CGGUUCAAG/Cleavage | pacid=371752 |
| 21 | 794 | 814 UCCACAGCL | CGGUUCAAG/Cleavage | pacid=371752 |
| 22 | 794 | 814 UCCACAGCL | CGGUUCAAG/Cleavage | pacid=371752 |
| 23 | 794 | 814 UCCACAGCL | CGGUUCAAG/Cleavage | pacid=371752 |
| 24 | 794 | 814 UCCACAGCL | CGGUUCAAG/Cleavage | pacid=371752 |
| 25 | 794 | 814 UCCACAGCL | CGGUUCAAG/Cleavage | pacid=371752 |
| 26 | 793 | 814 UCCACAGCL | CCGGUUCAAC/Cleavage | pacid=371752 |
| 27 | 496 | 517 UCCACA-GC | CCGUUCAAG/Cleavage | pacid=371780 |
| 28 | 496 | 517 UCCACA-GC | CCGUUCAAG/Cleavage | pacid=371780 |
| 29 | 496 | 517 UCCACA-GC | CCGUUCAAG/Cleavage | pacid=371780 |
| 30 | 496 | 517 UCCACA-GC | CCGUUCAAG/Cleavage | pacid=371780 |
| 31 | 496 | 517 UCCACA-GC | CCGUUCAAG/Cleavage | pacid=371780 |
| 32 | 496 | 517 UCCACA-GC | CCGUUCAAG/Cleavage | pacid=371780 |
| 33 | 496 | 517 UCCACA-GC | CCGUUCAAG/Cleavage | pacid=371780 |
| 34 | 496 | 517 UCCACA-GC | CCGUUCAAG/Cleavage | pacid=371780 |
| 35 | 496 | 517 UCCACA-GC | CCGUUCAAG/Cleavage | pacid=371780 |
| 36 | 496 | 517 UCCACA-GC | CCGUUCAAG/Cleavage | pacid=371780 |
| 37 | 496 | 517 UCCACA-GC | CCGUUCAAG/Cleavage | pacid=371780 |
| 38 | 496 | 517 UCCACA-GC | CCGUUCAAG/Cleavage | pacid=371780 |
| 39 | 496 | 517 UCCACA-GC | CCGUUCAAG/Cleavage | pacid=371780 |
| 40 | 496 | 517 UCCACA-GC | CCGUUCAAG/Cleavage | pacid=371780 |
| 41 | 496 | 517 UCCACA-GC | CCGUUCAAG/Cleavage | pacid=371780 |
| 42 | 495 | 517 UCCACA-GC | ACCGUUCAAC/Cleavage | pacid=371780 |
| 43 | 483 | 503 UCCACAGCL | CUCUUCAAG/Cleavage | pacid=371758 |
| 44 | 483 | 503 UCCACAGCL | CUCUUCAAG/Cleavage | pacid=371758 |
| 45 | 483 | 503 UCCACAGCL | CUCUUCAAG/Cleavage | pacid=371758 |
| 46 | 483 | 503 UCCACAGCL | CUCUUCAAG/Cleavage | pacid=371758 |
| 47 | 483 | 503 UCCACAGCL | CUCUUCAAG/Cleavage | pacid=371758 |
| 48 | 483 | 503 UCCACAGCL | CUCUUCAAG/Cleavage | pacid=371758 |
| 49 | 483 | 503 UCCACAGCL | CUCUUCAAG/Cleavage | pacid=371758 |
| 50 | 483 | 503 UCCACAGCL | CUCUUCAAG/Cleavage | pacid=371758 |
| 51 | 483 | 503 UCCACAGCL | CUCUUCAAG/Cleavage | pacid=371758 |
| 52 | 483 | 503 UCCACAGCL | CUCUUCAAG/Cleavage | pacid=371758 |
| 53 | 483 | 503 UCCACAGCL | CUCUUCAAG/Cleavage | pacid=371758 |
| 54 | 483 | 503 UCCACAGCL | CUCUUCAAG/Cleavage | pacid=371758 |
| 55 | 483 | 503 UCCACAGCL | CUCUUCAAG/Cleavage | pacid=371758 |
| 56 | 483 | 503 UCCACAGCL | CUCUUCAAG/Cleavage | pacid=371758 |
| 57 | 483 | 503 UCCACAGCL | CUCUUCAAG/Cleavage | pacid=371758 |
| 58 | 482 | 503 UCCACAGCL | GCUCUUCAAC/Cleavage | pacid=371758 |
| 59 | 906 | 926 UCCACAGCL | GUGUACGAG/Cleavage | pacid=371778 |
| 60 | 906 | 926 UCCACAGCL | GUGUACGAG/Cleavage | pacid=371778 |

| | | | |
|----|------|--|--------------|
| 1 | | | |
| 2 | 394 | 415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 3 | 860 | 881 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 4 | 862 | 883 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 5 | | | |
| 6 | 1029 | 1050 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 7 | 1032 | 1053 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 8 | 1028 | 1049 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 9 | | | |
| 10 | 1031 | 1052 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 11 | 394 | 415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 12 | 349 | 370 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 13 | | | |
| 14 | 394 | 415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 15 | 860 | 881 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 16 | 862 | 883 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 17 | | | |
| 18 | 1029 | 1050 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 19 | 1032 | 1053 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 20 | 1028 | 1049 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 21 | | | |
| 22 | 1031 | 1052 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 23 | 394 | 415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 24 | 349 | 370 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 25 | | | |
| 26 | 394 | 415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 27 | 860 | 881 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 28 | 862 | 883 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 29 | | | |
| 30 | 1029 | 1050 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 31 | 1032 | 1053 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 32 | 1028 | 1049 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 33 | | | |
| 34 | 1031 | 1052 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 35 | 394 | 415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 36 | 349 | 370 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 37 | | | |
| 38 | 394 | 415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 39 | 860 | 881 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 40 | 862 | 883 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 41 | | | |
| 42 | 1029 | 1050 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 43 | 1032 | 1053 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 44 | 1028 | 1049 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 45 | | | |
| 46 | 1031 | 1052 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 47 | 394 | 415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 48 | 349 | 370 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 49 | | | |
| 50 | 394 | 415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 51 | 860 | 881 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 52 | 862 | 883 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 53 | | | |
| 54 | 1029 | 1050 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 55 | 1032 | 1053 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 56 | 1028 | 1049 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 57 | | | |
| 58 | 1031 | 1052 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 59 | 394 | 415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| 60 | 349 | 370 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |
| | 394 | 415 UCCACA-GCl: ::::::::::: ::::: CCGUUCAAG ^A Cleavage | pacid=371509 |

| | | | | |
|----|------|------------------------------------|---------------------------------|--------------|
| 1 | | | | |
| 2 | 860 | 881 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 3 | 862 | 883 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 4 | 1029 | 1050 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 5 | 1032 | 1053 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 6 | 1028 | 1049 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 7 | 1031 | 1052 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 8 | | | | |
| 9 | 394 | 415 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 10 | 349 | 370 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 11 | 394 | 415 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 12 | | | | |
| 13 | 860 | 881 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 14 | 862 | 883 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 15 | 1029 | 1050 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 16 | 1032 | 1053 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 17 | 1028 | 1049 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 18 | 1031 | 1052 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 19 | | | | |
| 20 | 394 | 415 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 21 | 349 | 370 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 22 | 394 | 415 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 23 | | | | |
| 24 | 860 | 881 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 25 | 862 | 883 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 26 | 1029 | 1050 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 27 | 1032 | 1053 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 28 | 1028 | 1049 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 29 | 1031 | 1052 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 30 | | | | |
| 31 | 394 | 415 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 32 | 349 | 370 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 33 | 394 | 415 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 34 | | | | |
| 35 | 860 | 881 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 36 | 862 | 883 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 37 | 1029 | 1050 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 38 | 1032 | 1053 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 39 | 1028 | 1049 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 40 | 1031 | 1052 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 41 | | | | |
| 42 | 394 | 415 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 43 | 349 | 370 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 44 | 394 | 415 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 45 | | | | |
| 46 | 860 | 881 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 47 | 862 | 883 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 48 | 1029 | 1050 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 49 | 1032 | 1053 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 50 | 1028 | 1049 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 51 | 1031 | 1052 UCCACA-GCl: ::::::::::: ::::: | CCGUUCAAG ^A Cleavage | pacid=371509 |
| 52 | | | | |
| 53 | 393 | 415 UCCACA-GCl: ::::::::::: ::::: | CCCGUUCAAC Cleavage | pacid=371509 |
| 54 | 348 | 370 UCCACA-GCl: ::::::::::: ::::: | CCCGUUCAAC Cleavage | pacid=371509 |
| 55 | 393 | 415 UCCACA-GCl: ::::::::::: ::::: | CCCGUUCAAC Cleavage | pacid=371509 |
| 56 | | | | |
| 57 | 859 | 881 UCCACA-GCl: ::::::::::: ::::: | CCCGUUCAAC Cleavage | pacid=371509 |
| 58 | 861 | 883 UCCACA-GCl: ::::::::::: ::::: | CCCGUUCAAC Cleavage | pacid=371509 |
| 59 | 1028 | 1050 UCCACA-GCl: ::::::::::: ::::: | CCCGUUCAAC Cleavage | pacid=371509 |
| 60 | 1031 | 1053 UCCACA-GCl: ::::::::::: ::::: | CCCGUUCAAC Cleavage | pacid=371509 |
| | 1027 | 1049 UCCACA-GCl: ::::::::::: ::::: | CCCGUUCAAC Cleavage | pacid=371509 |
| | 1030 | 1052 UCCACA-GCl: ::::::::::: ::::: | CCCGUUCAAC Cleavage | pacid=371509 |
| | 1177 | 1197 UCCACAGCL : ::::::::::: ::::: | CCCUAAAG ^A Cleavage | pacid=371498 |
| | 1177 | 1197 UCCACAGCL : ::::::::::: ::::: | CCCUAAAG ^A Cleavage | pacid=371498 |
| | 1177 | 1197 UCCACAGCL : ::::::::::: ::::: | CCCUAAAG ^A Cleavage | pacid=371498 |
| | 1177 | 1197 UCCACAGCL : ::::::::::: ::::: | CCCUAAAG ^A Cleavage | pacid=371498 |

| | | | | |
|----|------|------------------|---------------------------------|--------------|
| 1 | | | | |
| 2 | 760 | 781 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 3 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 4 | 760 | 781 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371426 |
| 5 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 6 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 7 | 760 | 781 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 8 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 9 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 10 | 760 | 781 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371426 |
| 11 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 12 | 760 | 781 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 13 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 14 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 15 | 760 | 781 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371426 |
| 16 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 17 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 18 | 760 | 781 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 19 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 20 | 760 | 781 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371426 |
| 21 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 22 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 23 | 760 | 781 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 24 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 25 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 26 | 760 | 781 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371426 |
| 27 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 28 | 760 | 781 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 29 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 30 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 31 | 760 | 781 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371426 |
| 32 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 33 | 760 | 781 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 34 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 35 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 36 | 760 | 781 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371426 |
| 37 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 38 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 39 | 760 | 781 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 40 | 766 | 787 UCCACA-GCl | UCGUUCAAG/Cleavage | pacid=371425 |
| 41 | 759 | 781 UCCACA-GCl: | AUCGUUCAAC Cleavage | pacid=371426 |
| 42 | 765 | 787 UCCACA-GCl: | AUCGUUCAAC Cleavage | pacid=371425 |
| 43 | 765 | 787 UCCACA-GCl: | AUCGUUCAAC Cleavage | pacid=371425 |
| 44 | 759 | 781 UCCACA-GCl: | AUCGUUCAAC Cleavage | pacid=371425 |
| 45 | 765 | 787 UCCACA-GCl: | AUCGUUCAAC Cleavage | pacid=371425 |
| 46 | 765 | 787 UCCACA-GCl: | AUCGUUCAAC Cleavage | pacid=371425 |
| 47 | 1938 | 1959 UCCACA-GCl: | CCGUUCAAG ^A Cleavage | pacid=371432 |
| 48 | 1938 | 1959 UCCACA-GCl: | CCGUUCAAG ^A Cleavage | pacid=371432 |
| 49 | 1938 | 1959 UCCACA-GCl: | CCGUUCAAG ^A Cleavage | pacid=371432 |
| 50 | 1938 | 1959 UCCACA-GCl: | CCGUUCAAG ^A Cleavage | pacid=371432 |
| 51 | 1938 | 1959 UCCACA-GCl: | CCGUUCAAG ^A Cleavage | pacid=371432 |
| 52 | 1938 | 1959 UCCACA-GCl: | CCGUUCAAG ^A Cleavage | pacid=371432 |
| 53 | 1938 | 1959 UCCACA-GCl: | CCGUUCAAG ^A Cleavage | pacid=371432 |
| 54 | 1938 | 1959 UCCACA-GCl: | CCGUUCAAG ^A Cleavage | pacid=371432 |
| 55 | 1938 | 1959 UCCACA-GCl: | CCGUUCAAG ^A Cleavage | pacid=371432 |
| 56 | 1938 | 1959 UCCACA-GCl: | CCGUUCAAG ^A Cleavage | pacid=371432 |
| 57 | 1938 | 1959 UCCACA-GCl: | CCGUUCAAG ^A Cleavage | pacid=371432 |
| 58 | 1938 | 1959 UCCACA-GCl: | CCGUUCAAG ^A Cleavage | pacid=371432 |
| 59 | 1938 | 1959 UCCACA-GCl: | CCGUUCAAG ^A Cleavage | pacid=371432 |
| 60 | 1938 | 1959 UCCACA-GCl: | CCGUUCAAG ^A Cleavage | pacid=371432 |
| | 1937 | 1959 UCCACA-GCl: | ACCGUUCAAC Cleavage | pacid=371432 |

| | | | | | |
|----|------|----------------|---------------------|-------------|--------------|
| 1 | | | | | |
| 2 | 579 | 599 UCCACAGCL | :: ::::: GUCUCAUG/ | Cleavage | pacid=371777 |
| 3 | 579 | 599 UCCACAGCL | :: ::::: GUCUCAUG/ | Cleavage | pacid=371777 |
| 4 | 579 | 599 UCCACAGCL | :: ::::: GUCUCAUG/ | Cleavage | pacid=371777 |
| 5 | | | | | |
| 6 | 930 | 951 UCCACAGCL | :: ::::: AUGGUUUUC | Cleavage | pacid=371771 |
| 7 | 591 | 611 UCCACAGCL | :: ::::: GUAUUCAAG/ | Cleavage | pacid=371446 |
| 8 | 591 | 611 UCCACAGCL | :: ::::: GUAUUCAAG/ | Cleavage | pacid=371446 |
| 9 | | | | | |
| 10 | 591 | 611 UCCACAGCL | :: ::::: GUAUUCAAG/ | Cleavage | pacid=371446 |
| 11 | 591 | 611 UCCACAGCL | :: ::::: GUAUUCAAG/ | Cleavage | pacid=371446 |
| 12 | 591 | 611 UCCACAGCL | :: ::::: GUAUUCAAG/ | Cleavage | pacid=371446 |
| 13 | | | | | |
| 14 | 591 | 611 UCCACAGCL | :: ::::: GUAUUCAAG/ | Cleavage | pacid=371446 |
| 15 | 591 | 611 UCCACAGCL | :: ::::: GUAUUCAAG/ | Cleavage | pacid=371446 |
| 16 | 591 | 611 UCCACAGCL | :: ::::: GUAUUCAAG/ | Cleavage | pacid=371446 |
| 17 | | | | | |
| 18 | 591 | 611 UCCACAGCL | :: ::::: GUAUUCAAG/ | Cleavage | pacid=371446 |
| 19 | 591 | 611 UCCACAGCL | :: ::::: GUAUUCAAG/ | Cleavage | pacid=371446 |
| 20 | 591 | 611 UCCACAGCL | :: ::::: GUAUUCAAG/ | Cleavage | pacid=371446 |
| 21 | | | | | |
| 22 | 590 | 611 UCCACAGCL | :: ::::: AGUAUCAA | Cleavage | pacid=371446 |
| 23 | 2330 | 2350 UCCACAGCL | :: ::::: AUGUUCAAG/ | Translation | pacid=371449 |
| 24 | 2330 | 2350 UCCACAGCL | :: ::::: AUGUUCAAG/ | Translation | pacid=371449 |
| 25 | | | | | |
| 26 | 2330 | 2350 UCCACAGCL | :: ::::: AUGUUCAAG/ | Translation | pacid=371449 |
| 27 | 2330 | 2350 UCCACAGCL | :: ::::: AUGUUCAAG/ | Translation | pacid=371449 |
| 28 | 2330 | 2350 UCCACAGCL | :: ::::: AUGUUCAAG/ | Translation | pacid=371449 |
| 29 | | | | | |
| 30 | 2330 | 2350 UCCACAGCL | :: ::::: AUGUUCAAG/ | Translation | pacid=371449 |
| 31 | 2330 | 2350 UCCACAGCL | :: ::::: AUGUUCAAG/ | Translation | pacid=371449 |
| 32 | 2330 | 2350 UCCACAGCL | :: ::::: AUGUUCAAG/ | Translation | pacid=371449 |
| 33 | | | | | |
| 34 | 2330 | 2350 UCCACAGCL | :: ::::: AUGUUCAAG/ | Translation | pacid=371449 |
| 35 | 2330 | 2350 UCCACAGCL | :: ::::: AUGUUCAAG/ | Translation | pacid=371449 |
| 36 | 2330 | 2350 UCCACAGCL | :: ::::: AUGUUCAAG/ | Translation | pacid=371449 |
| 37 | | | | | |
| 38 | 540 | 560 UCCACAGCL | :: ::::: CGGUUCAAG | Cleavage | pacid=371452 |
| 39 | 942 | 962 UCCACAGCL | :: ::::: CGGUUCAAG | Cleavage | pacid=371452 |
| 40 | 540 | 560 UCCACAGCL | :: ::::: CGGUUCAAG | Cleavage | pacid=371452 |
| 41 | | | | | |
| 42 | 942 | 962 UCCACAGCL | :: ::::: CGGUUCAAG | Cleavage | pacid=371452 |
| 43 | 540 | 560 UCCACAGCL | :: ::::: CGGUUCAAG | Cleavage | pacid=371452 |
| 44 | 942 | 962 UCCACAGCL | :: ::::: CGGUUCAAG | Cleavage | pacid=371452 |
| 45 | 540 | 560 UCCACAGCL | :: ::::: CGGUUCAAG | Cleavage | pacid=371452 |
| 46 | | | | | |
| 47 | 942 | 962 UCCACAGCL | :: ::::: CGGUUCAAG | Cleavage | pacid=371452 |
| 48 | 540 | 560 UCCACAGCL | :: ::::: CGGUUCAAG | Cleavage | pacid=371452 |
| 49 | 942 | 962 UCCACAGCL | :: ::::: CGGUUCAAG | Cleavage | pacid=371452 |
| 50 | | | | | |
| 51 | 540 | 560 UCCACAGCL | :: ::::: CGGUUCAAG | Cleavage | pacid=371452 |
| 52 | 942 | 962 UCCACAGCL | :: ::::: CGGUUCAAG | Cleavage | pacid=371452 |
| 53 | 540 | 560 UCCACAGCL | :: ::::: CGGUUCAAG | Cleavage | pacid=371452 |
| 54 | | | | | |
| 55 | 942 | 962 UCCACAGCL | :: ::::: CGGUUCAAG | Cleavage | pacid=371452 |
| 56 | 540 | 560 UCCACAGCL | :: ::::: CGGUUCAAG | Cleavage | pacid=371452 |
| 57 | 942 | 962 UCCACAGCL | :: ::::: CGGUUCAAG | Cleavage | pacid=371452 |
| 58 | | | | | |
| 59 | 540 | 560 UCCACAGCL | :: ::::: CGGUUCAAG | Cleavage | pacid=371452 |
| 60 | 942 | 962 UCCACAGCL | :: ::::: CGGUUCAAG | Cleavage | pacid=371452 |
| | 540 | 560 UCCACAGCL | :: ::::: CGGUUCAAG | Cleavage | pacid=371452 |

| | | | | |
|----|------|-----------------|------------------|-----------------------|
| 1 | | | | |
| 2 | 942 | 962 UUCCACAGCL | ::: :: CGGUUCAAG | Cleavage pacid=371452 |
| 3 | 540 | 560 UUCCACAGCL | ::: :: CGGUUCAAG | Cleavage pacid=371452 |
| 4 | 942 | 962 UUCCACAGCL | ::: :: CGGUUCAAG | Cleavage pacid=371452 |
| 5 | | | | |
| 6 | 539 | 560 UUCCACAGCL | ::: :: UCGGUUCAA | Cleavage pacid=371452 |
| 7 | 941 | 962 UUCCACAGCL | ::: :: UCGGUUCAA | Cleavage pacid=371452 |
| 8 | 984 | 1004 UUCCACAGCL | ::: :: GAGCUCAUG | Cleavage pacid=371455 |
| 9 | 984 | 1004 UUCCACAGCL | ::: :: GAGCUCAUG | Cleavage pacid=371455 |
| 10 | 984 | 1004 UUCCACAGCL | ::: :: GAGCUCAUG | Cleavage pacid=371455 |
| 11 | 984 | 1004 UUCCACAGCL | ::: :: GAGCUCAUG | Cleavage pacid=371455 |
| 12 | 984 | 1004 UUCCACAGCL | ::: :: GAGCUCAUG | Cleavage pacid=371455 |
| 13 | 984 | 1004 UUCCACAGCL | ::: :: GAGCUCAUG | Cleavage pacid=371455 |
| 14 | 984 | 1004 UUCCACAGCL | ::: :: GAGCUCAUG | Cleavage pacid=371455 |
| 15 | 984 | 1004 UUCCACAGCL | ::: :: GAGCUCAUG | Cleavage pacid=371455 |
| 16 | 984 | 1004 UUCCACAGCL | ::: :: GAGCUCAUG | Cleavage pacid=371455 |
| 17 | 984 | 1004 UUCCACAGCL | ::: :: GAGCUCAUG | Cleavage pacid=371455 |
| 18 | 984 | 1004 UUCCACAGCL | ::: :: GAGCUCAUG | Cleavage pacid=371455 |
| 19 | 984 | 1004 UUCCACAGCL | ::: :: GAGCUCAUG | Cleavage pacid=371455 |
| 20 | 984 | 1004 UUCCACAGCL | ::: :: GAGCUCAUG | Cleavage pacid=371455 |
| 21 | 984 | 1004 UUCCACAGCL | ::: :: GAGCUCAUG | Cleavage pacid=371455 |
| 22 | 984 | 1004 UUCCACAGCL | ::: :: GAGCUCAUG | Cleavage pacid=371455 |
| 23 | 983 | 1004 UUCCACAGCL | ::: :: CGAGCUCAU | Cleavage pacid=371455 |
| 24 | 1055 | 1075 UUCCACAGCL | ::: :: AUGGCCAAG | Cleavage pacid=371618 |
| 25 | 1055 | 1075 UUCCACAGCL | ::: :: AUGGCCAAG | Cleavage pacid=371618 |
| 26 | 1055 | 1075 UUCCACAGCL | ::: :: AUGGCCAAG | Cleavage pacid=371618 |
| 27 | 1055 | 1075 UUCCACAGCL | ::: :: AUGGCCAAG | Cleavage pacid=371618 |
| 28 | 1055 | 1075 UUCCACAGCL | ::: :: AUGGCCAAG | Cleavage pacid=371618 |
| 29 | 1055 | 1075 UUCCACAGCL | ::: :: AUGGCCAAG | Cleavage pacid=371618 |
| 30 | 1055 | 1075 UUCCACAGCL | ::: :: AUGGCCAAG | Cleavage pacid=371618 |
| 31 | 1055 | 1075 UUCCACAGCL | ::: :: AUGGCCAAG | Cleavage pacid=371618 |
| 32 | 1055 | 1075 UUCCACAGCL | ::: :: AUGGCCAAG | Cleavage pacid=371618 |
| 33 | 1055 | 1075 UUCCACAGCL | ::: :: AUGGCCAAG | Cleavage pacid=371618 |
| 34 | 1055 | 1075 UUCCACAGCL | ::: :: AUGGCCAAG | Cleavage pacid=371618 |
| 35 | 1055 | 1075 UUCCACAGCL | ::: :: AUGGCCAAG | Cleavage pacid=371618 |
| 36 | 1055 | 1075 UUCCACAGCL | ::: :: AUGGCCAAG | Cleavage pacid=371618 |
| 37 | 1055 | 1075 UUCCACAGCL | ::: :: AUGGCCAAG | Cleavage pacid=371618 |
| 38 | 1055 | 1075 UUCCACAGCL | ::: :: AUGGCCAAG | Cleavage pacid=371618 |
| 39 | 1054 | 1075 UUCCACAGCL | ::: :: AAUGGCCAA | Cleavage pacid=371618 |
| 40 | 149 | 169 UUCCACAGCL | ::: :: AAGUUCAAG | Cleavage pacid=371545 |
| 41 | 149 | 169 UUCCACAGCL | ::: :: AAGUUCAAG | Cleavage pacid=371545 |
| 42 | 149 | 169 UUCCACAGCL | ::: :: AAGUUCAAG | Cleavage pacid=371545 |
| 43 | 149 | 169 UUCCACAGCL | ::: :: AAGUUCAAG | Cleavage pacid=371545 |
| 44 | 149 | 169 UUCCACAGCL | ::: :: AAGUUCAAG | Cleavage pacid=371545 |
| 45 | 149 | 169 UUCCACAGCL | ::: :: AAGUUCAAG | Cleavage pacid=371545 |
| 46 | 149 | 169 UUCCACAGCL | ::: :: AAGUUCAAG | Cleavage pacid=371545 |
| 47 | 149 | 169 UUCCACAGCL | ::: :: AAGUUCAAG | Cleavage pacid=371545 |
| 48 | 149 | 169 UUCCACAGCL | ::: :: AAGUUCAAG | Cleavage pacid=371545 |
| 49 | 149 | 169 UUCCACAGCL | ::: :: AAGUUCAAG | Cleavage pacid=371545 |
| 50 | 149 | 169 UUCCACAGCL | ::: :: AAGUUCAAG | Cleavage pacid=371545 |
| 51 | 149 | 169 UUCCACAGCL | ::: :: AAGUUCAAG | Cleavage pacid=371545 |
| 52 | 149 | 169 UUCCACAGCL | ::: :: AAGUUCAAG | Cleavage pacid=371545 |
| 53 | 149 | 169 UUCCACAGCL | ::: :: AAGUUCAAG | Cleavage pacid=371545 |
| 54 | 149 | 169 UUCCACAGCL | ::: :: AAGUUCAAG | Cleavage pacid=371545 |
| 55 | 148 | 169 UUCCACAGCL | ::: :: UAAGUUCAA | Cleavage pacid=371545 |
| 56 | 574 | 594 UUCCACAGCL | ::: :: CAGAUUGAG | Cleavage pacid=371713 |
| 57 | 574 | 594 UUCCACAGCL | ::: :: CAGAUUGAG | Cleavage pacid=371713 |
| 58 | 574 | 594 UUCCACAGCL | ::: :: CAGAUUGAG | Cleavage pacid=371713 |
| 59 | 574 | 594 UUCCACAGCL | ::: :: CAGAUUGAG | Cleavage pacid=371713 |
| 60 | 574 | 594 UUCCACAGCL | ::: :: CAGAUUGAG | Cleavage pacid=371713 |

| | | | | |
|----|------|-----------------|---------------------|--------------|
| 1 | | | | |
| 2 | 574 | 594 UUCCACAGCL | ::: ::: CAGAUUGAG/ | pacid=371713 |
| 3 | 574 | 594 UUCCACAGCL | ::: ::: CAGAUUGAG/ | pacid=371713 |
| 4 | 574 | 594 UUCCACAGCL | ::: ::: CAGAUUGAG/ | pacid=371713 |
| 5 | 574 | 594 UUCCACAGCL | ::: ::: CAGAUUGAG/ | pacid=371713 |
| 6 | 574 | 594 UUCCACAGCL | ::: ::: CAGAUUGAG/ | pacid=371713 |
| 7 | 574 | 594 UUCCACAGCL | ::: ::: CAGAUUGAG/ | pacid=371713 |
| 8 | 574 | 594 UUCCACAGCL | ::: ::: CAGAUUGAG/ | pacid=371713 |
| 9 | 574 | 594 UUCCACAGCL | ::: ::: CAGAUUGAG/ | pacid=371713 |
| 10 | 573 | 594 UUCCACAGCL | ::: ::: UCAGAUUGA/ | pacid=371713 |
| 11 | 1411 | 1431 UUCCACAGCL | ::: ::: AGGUUGGAG | pacid=371667 |
| 12 | 1411 | 1431 UUCCACAGCL | ::: ::: AGGUUGGAG | pacid=371667 |
| 13 | 1411 | 1431 UUCCACAGCL | ::: ::: AGGUUGGAG | pacid=371667 |
| 14 | 1411 | 1431 UUCCACAGCL | ::: ::: AGGUUGGAG | pacid=371667 |
| 15 | 1411 | 1431 UUCCACAGCL | ::: ::: AGGUUGGAG | pacid=371667 |
| 16 | 1411 | 1431 UUCCACAGCL | ::: ::: AGGUUGGAG | pacid=371667 |
| 17 | 1411 | 1431 UUCCACAGCL | ::: ::: AGGUUGGAG | pacid=371667 |
| 18 | 1411 | 1431 UUCCACAGCL | ::: ::: AGGUUGGAG | pacid=371667 |
| 19 | 1411 | 1431 UUCCACAGCL | ::: ::: AGGUUGGAG | pacid=371667 |
| 20 | 1411 | 1431 UUCCACAGCL | ::: ::: AGGUUGGAG | pacid=371667 |
| 21 | 1411 | 1431 UUCCACAGCL | ::: ::: AGGUUGGAG | pacid=371667 |
| 22 | 1411 | 1431 UUCCACAGCL | ::: ::: AGGUUGGAG | pacid=371667 |
| 23 | 1411 | 1431 UUCCACAGCL | ::: ::: AGGUUGGAG | pacid=371667 |
| 24 | 1411 | 1431 UUCCACAGCL | ::: ::: AGGUUGGAG | pacid=371667 |
| 25 | 394 | 414 UUCCACAGCL | ::: ::: GGGUUGGAG | pacid=371647 |
| 26 | 394 | 414 UUCCACAGCL | ::: ::: GGGUUGGAG | pacid=371647 |
| 27 | 394 | 414 UUCCACAGCL | ::: ::: GGGUUGGAG | pacid=371647 |
| 28 | 394 | 414 UUCCACAGCL | ::: ::: GGGUUGGAG | pacid=371647 |
| 29 | 394 | 414 UUCCACAGCL | ::: ::: GGGUUGGAG | pacid=371647 |
| 30 | 394 | 414 UUCCACAGCL | ::: ::: GGGUUGGAG | pacid=371647 |
| 31 | 394 | 414 UUCCACAGCL | ::: ::: GGGUUGGAG | pacid=371647 |
| 32 | 394 | 414 UUCCACAGCL | ::: ::: GGGUUGGAG | pacid=371647 |
| 33 | 394 | 414 UUCCACAGCL | ::: ::: GGGUUGGAG | pacid=371647 |
| 34 | 394 | 414 UUCCACAGCL | ::: ::: GGGUUGGAG | pacid=371647 |
| 35 | 394 | 414 UUCCACAGCL | ::: ::: GGGUUGGAG | pacid=371647 |
| 36 | 394 | 414 UUCCACAGCL | ::: ::: GGGUUGGAG | pacid=371647 |
| 37 | 394 | 414 UUCCACAGCL | ::: ::: GGGUUGGAG | pacid=371647 |
| 38 | 394 | 414 UUCCACAGCL | ::: ::: GGGUUGGAG | pacid=371647 |
| 39 | 394 | 414 UUCCACAGCL | ::: ::: GGGUUGGAG | pacid=371647 |
| 40 | 393 | 414 UUCCACAGCL | ::: ::: UGGUUGGA | pacid=371647 |
| 41 | 985 | 1005 UUCCACAGCL | ::: ::: GGUAUCAAG/ | pacid=371660 |
| 42 | 985 | 1005 UUCCACAGCL | ::: ::: GGUAUCAAG/ | pacid=371660 |
| 43 | 985 | 1005 UUCCACAGCL | ::: ::: GGUAUCAAG/ | pacid=371660 |
| 44 | 985 | 1005 UUCCACAGCL | ::: ::: GGUAUCAAG/ | pacid=371660 |
| 45 | 985 | 1005 UUCCACAGCL | ::: ::: GGUAUCAAG/ | pacid=371660 |
| 46 | 985 | 1005 UUCCACAGCL | ::: ::: GGUAUCAAG/ | pacid=371660 |
| 47 | 985 | 1005 UUCCACAGCL | ::: ::: GGUAUCAAG/ | pacid=371660 |
| 48 | 985 | 1005 UUCCACAGCL | ::: ::: GGUAUCAAG/ | pacid=371660 |
| 49 | 985 | 1005 UUCCACAGCL | ::: ::: GGUAUCAAG/ | pacid=371660 |
| 50 | 985 | 1005 UUCCACAGCL | ::: ::: GGUAUCAAG/ | pacid=371660 |
| 51 | 985 | 1005 UUCCACAGCL | ::: ::: GGUAUCAAG/ | pacid=371660 |
| 52 | 985 | 1005 UUCCACAGCL | ::: ::: GGUAUCAAG/ | pacid=371660 |
| 53 | 985 | 1005 UUCCACAGCL | ::: ::: GGUAUCAAG/ | pacid=371660 |
| 54 | 985 | 1005 UUCCACAGCL | ::: ::: GGUAUCAAG/ | pacid=371660 |
| 55 | 985 | 1005 UUCCACAGCL | ::: ::: GGUAUCAAG/ | pacid=371660 |
| 56 | 984 | 1005 UUCCACAGCL | ::: ::: AGGUAUCAAG/ | pacid=371660 |
| 57 | 704 | 724 UUCCACAGCL | ::: ::: GCUGCUAAG/ | pacid=371671 |
| 58 | 704 | 724 UUCCACAGCL | ::: ::: GCUGCUAAG/ | pacid=371671 |
| 59 | 704 | 724 UUCCACAGCL | ::: ::: GCUGCUAAG/ | pacid=371671 |
| 60 | 704 | 724 UUCCACAGCL | ::: ::: GCUGCUAAG/ | pacid=371671 |

| | | | |
|----|------|--|--------------|
| 1 | | | |
| 2 | 491 | 511 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage | pacid=371463 |
| 3 | 750 | 770 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage | pacid=371463 |
| 4 | 790 | 810 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage | pacid=371463 |
| 5 | | | |
| 6 | 491 | 511 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage | pacid=371463 |
| 7 | 750 | 770 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage | pacid=371463 |
| 8 | 790 | 810 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage | pacid=371463 |
| 9 | | | |
| 10 | 491 | 511 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage | pacid=371463 |
| 11 | 750 | 770 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage | pacid=371463 |
| 12 | 790 | 810 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage | pacid=371463 |
| 13 | | | |
| 14 | 491 | 511 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage | pacid=371463 |
| 15 | 750 | 770 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage | pacid=371463 |
| 16 | 790 | 810 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage | pacid=371463 |
| 17 | | | |
| 18 | 491 | 511 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage | pacid=371463 |
| 19 | 750 | 770 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage | pacid=371463 |
| 20 | 790 | 810 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage | pacid=371463 |
| 21 | | | |
| 22 | 491 | 511 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage | pacid=371463 |
| 23 | 750 | 770 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage | pacid=371463 |
| 24 | 790 | 810 UUCCACAGCL :..... :.....: CGGUUCAAG/Cleavage | pacid=371463 |
| 25 | | | |
| 26 | 490 | 511 UUCCACAGCL :..... :.....:UCGGUUCAA(Cleavage | pacid=371463 |
| 27 | 749 | 770 UUCCACAGCL :..... :.....:UCGGUUCAA(Cleavage | pacid=371463 |
| 28 | 789 | 810 UUCCACAGCL :..... :.....:UCGGUUCAA(Cleavage | pacid=371463 |
| 29 | | | |
| 30 | 2392 | 2413 UUCCACAGCL:..... :.....:AUAGUGAGAI Cleavage | pacid=371483 |
| 31 | 556 | 576 UUCCACAGCL ::.....:: AAGAUCAAG(Cleavage | pacid=371476 |
| 32 | 556 | 576 UUCCACAGCL ::.....:: AAGAUCAAG(Cleavage | pacid=371476 |
| 33 | 556 | 576 UUCCACAGCL ::.....:: AAGAUCAAG(Cleavage | pacid=371476 |
| 34 | 556 | 576 UUCCACAGCL ::.....:: AAGAUCAAG(Cleavage | pacid=371476 |
| 35 | 556 | 576 UUCCACAGCL ::.....:: AAGAUCAAG(Cleavage | pacid=371476 |
| 36 | 556 | 576 UUCCACAGCL ::.....:: AAGAUCAAG(Cleavage | pacid=371476 |
| 37 | 556 | 576 UUCCACAGCL ::.....:: AAGAUCAAG(Cleavage | pacid=371476 |
| 38 | 556 | 576 UUCCACAGCL ::.....:: AAGAUCAAG(Cleavage | pacid=371476 |
| 39 | 556 | 576 UUCCACAGCL ::.....:: AAGAUCAAG(Cleavage | pacid=371476 |
| 40 | 556 | 576 UUCCACAGCL ::.....:: AAGAUCAAG(Cleavage | pacid=371476 |
| 41 | 556 | 576 UUCCACAGCL ::.....:: AAGAUCAAG(Cleavage | pacid=371476 |
| 42 | 556 | 576 UUCCACAGCL ::.....:: AAGAUCAAG(Cleavage | pacid=371476 |
| 43 | 556 | 576 UUCCACAGCL ::.....:: AAGAUCAAG(Cleavage | pacid=371476 |
| 44 | 556 | 576 UUCCACAGCL ::.....:: AAGAUCAAG(Cleavage | pacid=371476 |
| 45 | 555 | 576 UUCCACAGCL: ::.....::AAAGAUCAAG(Cleavage | pacid=371476 |
| 46 | | | |
| 47 | 3519 | 3540 UUCCACAGCL:.....:: :ACUGUUCAA(Cleavage | pacid=371474 |
| 48 | 3671 | 3692 UUCCACAGCL:.....:: :ACUGUUCAA(Cleavage | pacid=371451 |
| 49 | | | |
| 50 | 812 | 832 UUCCACAGCL :.....:: : GAGUUCGAG/Cleavage | pacid=371455 |
| 51 | 812 | 832 UUCCACAGCL :.....:: : GAGUUCGAG/Cleavage | pacid=371455 |
| 52 | 812 | 832 UUCCACAGCL :.....:: : GAGUUCGAG/Cleavage | pacid=371455 |
| 53 | 812 | 832 UUCCACAGCL :.....:: : GAGUUCGAG/Cleavage | pacid=371455 |
| 54 | 812 | 832 UUCCACAGCL :.....:: : GAGUUCGAG/Cleavage | pacid=371455 |
| 55 | 812 | 832 UUCCACAGCL :.....:: : GAGUUCGAG/Cleavage | pacid=371455 |
| 56 | 812 | 832 UUCCACAGCL :.....:: : GAGUUCGAG/Cleavage | pacid=371455 |
| 57 | 812 | 832 UUCCACAGCL :.....:: : GAGUUCGAG/Cleavage | pacid=371455 |
| 58 | 812 | 832 UUCCACAGCL :.....:: : GAGUUCGAG/Cleavage | pacid=371455 |
| 59 | 812 | 832 UUCCACAGCL :.....:: : GAGUUCGAG/Cleavage | pacid=371455 |
| 60 | 812 | 832 UUCCACAGCL :.....:: : GAGUUCGAG/Cleavage | pacid=371455 |
| | 812 | 832 UUCCACAGCL :.....:: : GAGUUCGAG/Cleavage | pacid=371455 |

| | | | | |
|----|------|----------------|---------------------|--------------|
| 1 | | | | |
| 2 | 908 | 928 UCCACAGCL | GGGUUGAG Cleavage | pacid=371658 |
| 3 | 908 | 928 UCCACAGCL | GGGUUGAG Cleavage | pacid=371658 |
| 4 | 908 | 928 UCCACAGCL | GGGUUGAG Cleavage | pacid=371658 |
| 5 | 908 | 928 UCCACAGCL | GGGUUGAG Cleavage | pacid=371658 |
| 6 | 908 | 928 UCCACAGCL | GGGUUGAG Cleavage | pacid=371658 |
| 7 | 486 | 506 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 8 | 482 | 502 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 9 | 486 | 506 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 10 | 482 | 502 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 11 | 486 | 506 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 12 | 482 | 502 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 13 | 486 | 506 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 14 | 482 | 502 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 15 | 486 | 506 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 16 | 482 | 502 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 17 | 486 | 506 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 18 | 482 | 502 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 19 | 486 | 506 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 20 | 482 | 502 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 21 | 486 | 506 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 22 | 482 | 502 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 23 | 486 | 506 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 24 | 482 | 502 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 25 | 486 | 506 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 26 | 482 | 502 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 27 | 486 | 506 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 28 | 482 | 502 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 29 | 486 | 506 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 30 | 482 | 502 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 31 | 486 | 506 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 32 | 482 | 502 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 33 | 486 | 506 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 34 | 482 | 502 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 35 | 486 | 506 UCCACAGCL | CGGUUCAA/ Cleavage | pacid=371606 |
| 36 | 485 | 506 UCCACAGCL | GCGGUCAA/ Cleavage | pacid=371606 |
| 37 | 481 | 502 UCCACAGCL | GCGGUCAA/ Cleavage | pacid=371606 |
| 38 | 327 | 347 UCCACAGCL | AAGCUUGAG/ Cleavage | pacid=371579 |
| 39 | 327 | 347 UCCACAGCL | AAGCUUGAG/ Cleavage | pacid=371579 |
| 40 | 327 | 347 UCCACAGCL | AAGCUUGAG/ Cleavage | pacid=371579 |
| 41 | 327 | 347 UCCACAGCL | AAGCUUGAG/ Cleavage | pacid=371579 |
| 42 | 327 | 347 UCCACAGCL | AAGCUUGAG/ Cleavage | pacid=371579 |
| 43 | 327 | 347 UCCACAGCL | AAGCUUGAG/ Cleavage | pacid=371579 |
| 44 | 327 | 347 UCCACAGCL | AAGCUUGAG/ Cleavage | pacid=371579 |
| 45 | 327 | 347 UCCACAGCL | AAGCUUGAG/ Cleavage | pacid=371579 |
| 46 | 327 | 347 UCCACAGCL | AAGCUUGAG/ Cleavage | pacid=371579 |
| 47 | 327 | 347 UCCACAGCL | AAGCUUGAG/ Cleavage | pacid=371579 |
| 48 | 327 | 347 UCCACAGCL | AAGCUUGAG/ Cleavage | pacid=371579 |
| 49 | 327 | 347 UCCACAGCL | AAGCUUGAG/ Cleavage | pacid=371579 |
| 50 | 327 | 347 UCCACAGCL | AAGCUUGAG/ Cleavage | pacid=371579 |
| 51 | 327 | 347 UCCACAGCL | AAGCUUGAG/ Cleavage | pacid=371579 |
| 52 | 327 | 347 UCCACAGCL | AAGCUUGAG/ Cleavage | pacid=371579 |
| 53 | 1064 | 1085 UCCACAGCL | GAGUCCA/ Cleavage | pacid=371592 |
| 54 | 1064 | 1085 UCCACAGCL | GAGUCCA/ Cleavage | pacid=371592 |
| 55 | 1064 | 1085 UCCACAGCL | GAGUCCA/ Cleavage | pacid=371592 |
| 56 | 1064 | 1085 UCCACAGCL | GAGUCCA/ Cleavage | pacid=371592 |
| 57 | 1064 | 1085 UCCACAGCL | GAGUCCA/ Cleavage | pacid=371592 |
| 58 | 1064 | 1085 UCCACAGCL | GAGUCCA/ Cleavage | pacid=371592 |
| 59 | 1064 | 1085 UCCACAGCL | GAGUCCA/ Cleavage | pacid=371592 |
| 60 | 1064 | 1085 UCCACAGCL | GAGUCCA/ Cleavage | pacid=371592 |

| | | | | |
|----|------|----------------|-----------------------------------|--------------|
| 1 | | | | |
| 2 | 892 | 912 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 3 | 994 | 1014 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 4 | 1474 | 1494 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 5 | | | | |
| 6 | 892 | 912 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 7 | 994 | 1014 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 8 | 1474 | 1494 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 9 | | | | |
| 10 | 892 | 912 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 11 | 994 | 1014 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 12 | 1474 | 1494 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 13 | | | | |
| 14 | 892 | 912 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 15 | 994 | 1014 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 16 | 1474 | 1494 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 17 | | | | |
| 18 | 892 | 912 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 19 | 994 | 1014 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 20 | 1474 | 1494 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 21 | | | | |
| 22 | 892 | 912 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 23 | 994 | 1014 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 24 | 1474 | 1494 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 25 | | | | |
| 26 | 892 | 912 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 27 | 994 | 1014 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 28 | 1474 | 1494 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 29 | | | | |
| 30 | 892 | 912 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 31 | 994 | 1014 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 32 | 1474 | 1494 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 33 | | | | |
| 34 | 892 | 912 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 35 | 994 | 1014 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 36 | 1474 | 1494 UCCACAGCL | :::~::~:~::~: AUUAUCGAG/ Cleavage | pacid=371423 |
| 37 | | | | |
| 38 | 430 | 450 UCCACAGCL | :::~::~:~::~: ACCAUCAACA Cleavage | pacid=371556 |
| 39 | 430 | 450 UCCACAGCL | :::~::~:~::~: ACCAUCAACA Cleavage | pacid=371556 |
| 40 | 430 | 450 UCCACAGCL | :::~::~:~::~: ACCAUCAACA Cleavage | pacid=371556 |
| 41 | 430 | 450 UCCACAGCL | :::~::~:~::~: ACCAUCAACA Cleavage | pacid=371556 |
| 42 | 430 | 450 UCCACAGCL | :::~::~:~::~: ACCAUCAACA Cleavage | pacid=371556 |
| 43 | 430 | 450 UCCACAGCL | :::~::~:~::~: ACCAUCAACA Cleavage | pacid=371556 |
| 44 | 430 | 450 UCCACAGCL | :::~::~:~::~: ACCAUCAACA Cleavage | pacid=371556 |
| 45 | 430 | 450 UCCACAGCL | :::~::~:~::~: ACCAUCAACA Cleavage | pacid=371556 |
| 46 | 430 | 450 UCCACAGCL | :::~::~:~::~: ACCAUCAACA Cleavage | pacid=371556 |
| 47 | 430 | 450 UCCACAGCL | :::~::~:~::~: ACCAUCAACA Cleavage | pacid=371556 |
| 48 | 430 | 450 UCCACAGCL | :::~::~:~::~: ACCAUCAACA Cleavage | pacid=371556 |
| 49 | 430 | 450 UCCACAGCL | :::~::~:~::~: ACCAUCAACA Cleavage | pacid=371556 |
| 50 | 430 | 450 UCCACAGCL | :::~::~:~::~: ACCAUCAACA Cleavage | pacid=371556 |
| 51 | 430 | 450 UCCACAGCL | :::~::~:~::~: ACCAUCAACA Cleavage | pacid=371556 |
| 52 | 291 | 311 UCCACAGCL | :::~::~:~::~: CCUAUUGAG(Cleavage | pacid=371564 |
| 53 | 291 | 311 UCCACAGCL | :::~::~:~::~: CCUAUUGAG(Cleavage | pacid=371564 |
| 54 | | | | |
| 55 | 291 | 311 UCCACAGCL | :::~::~:~::~: CCUAUUGAG(Cleavage | pacid=371564 |
| 56 | 291 | 311 UCCACAGCL | :::~::~:~::~: CCUAUUGAG(Cleavage | pacid=371564 |
| 57 | 291 | 311 UCCACAGCL | :::~::~:~::~: CCUAUUGAG(Cleavage | pacid=371564 |
| 58 | 291 | 311 UCCACAGCL | :::~::~:~::~: CCUAUUGAG(Cleavage | pacid=371564 |
| 59 | 291 | 311 UCCACAGCL | :::~::~:~::~: CCUAUUGAG(Cleavage | pacid=371564 |
| 60 | 291 | 311 UCCACAGCL | :::~::~:~::~: CCUAUUGAG(Cleavage | pacid=371564 |
| | 291 | 311 UCCACAGCL | :::~::~:~::~: CCUAUUGAG(Cleavage | pacid=371564 |

| | | | | |
|----|------|-----------------|------------------------------|--------------|
| 1 | | | | |
| 2 | 1805 | 1825 UUCCACAGCL | : : AAGUUCAGG/Cleavage | pacid=371449 |
| 3 | 1806 | 1826 UUCCACAGCL | : : AAGUUCAGG/Cleavage | pacid=371449 |
| 4 | 1805 | 1825 UUCCACAGCL | : : AAGUUCAGG/Cleavage | pacid=371449 |
| 5 | 1806 | 1826 UUCCACAGCL | : : AAGUUCAGG/Cleavage | pacid=371449 |
| 6 | 1805 | 1825 UUCCACAGCL | : : AAGUUCAGG/Cleavage | pacid=371449 |
| 7 | 1806 | 1826 UUCCACAGCL | : : AAGUUCAGG/Cleavage | pacid=371449 |
| 8 | 1805 | 1825 UUCCACAGCL | : : AAGUUCAGG/Cleavage | pacid=371449 |
| 9 | 1806 | 1826 UUCCACAGCL | : : AAGUUCAGG/Cleavage | pacid=371449 |
| 10 | 1805 | 1825 UUCCACAGCL | : : AAGUUCAGG/Cleavage | pacid=371449 |
| 11 | 1736 | 1756 UUCCACAGCL | : : CAGUUAGAG/Cleavage | pacid=371484 |
| 12 | 1736 | 1756 UUCCACAGCL | : : CAGUUAGAG/Cleavage | pacid=371484 |
| 13 | 1736 | 1756 UUCCACAGCL | : : CAGUUAGAG/Cleavage | pacid=371484 |
| 14 | 1736 | 1756 UUCCACAGCL | : : CAGUUAGAG/Cleavage | pacid=371484 |
| 15 | 1736 | 1756 UUCCACAGCL | : : CAGUUAGAG/Cleavage | pacid=371484 |
| 16 | 1736 | 1756 UUCCACAGCL | : : CAGUUAGAG/Cleavage | pacid=371484 |
| 17 | 1736 | 1756 UUCCACAGCL | : : CAGUUAGAG/Cleavage | pacid=371484 |
| 18 | 1736 | 1756 UUCCACAGCL | : : CAGUUAGAG/Cleavage | pacid=371484 |
| 19 | 1736 | 1756 UUCCACAGCL | : : CAGUUAGAG/Cleavage | pacid=371484 |
| 20 | 1736 | 1756 UUCCACAGCL | : : CAGUUAGAG/Cleavage | pacid=371484 |
| 21 | 1736 | 1756 UUCCACAGCL | : : CAGUUAGAG/Cleavage | pacid=371484 |
| 22 | 1736 | 1756 UUCCACAGCL | : : CAGUUAGAG/Cleavage | pacid=371484 |
| 23 | 1736 | 1756 UUCCACAGCL | : : CAGUUAGAG/Cleavage | pacid=371484 |
| 24 | 1736 | 1756 UUCCACAGCL | : : CAGUUAGAG/Cleavage | pacid=371484 |
| 25 | 1736 | 1756 UUCCACAGCL | : : CAGUUAGAG/Cleavage | pacid=371484 |
| 26 | 1735 | 1756 UUCCACAGCL | : : ACAGUUAGA/Cleavage | pacid=371484 |
| 27 | 1891 | 1911 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 28 | 1928 | 1948 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 29 | 1891 | 1911 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 30 | 1928 | 1948 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 31 | 1891 | 1911 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 32 | 1928 | 1948 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 33 | 1891 | 1911 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 34 | 1928 | 1948 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 35 | 1891 | 1911 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 36 | 1928 | 1948 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 37 | 1891 | 1911 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 38 | 1928 | 1948 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 39 | 1891 | 1911 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 40 | 1928 | 1948 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 41 | 1891 | 1911 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 42 | 1928 | 1948 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 43 | 1891 | 1911 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 44 | 1928 | 1948 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 45 | 1891 | 1911 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 46 | 1928 | 1948 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 47 | 1891 | 1911 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 48 | 1928 | 1948 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 49 | 1891 | 1911 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 50 | 1928 | 1948 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 51 | 1891 | 1911 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 52 | 1928 | 1948 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 53 | 1891 | 1911 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 54 | 1928 | 1948 UUCCACAGCL | : : AACCUUGAU/Cleavage | pacid=371447 |
| 55 | 1890 | 1911 UUCCACAGCL | : : UAACCUUGA/Cleavage | pacid=371447 |
| 56 | 1927 | 1948 UUCCACAGCL | : : UAACCUUGA/Cleavage | pacid=371447 |
| 57 | 1105 | 1126 UUCCACAGCL | : : ACAGUGCAU/Cleavage | pacid=371479 |
| 58 | 1131 | 1152 UUCCACAGCL | : : AUAUCUCAA/Cleavage | pacid=371448 |
| 59 | 627 | 647 UUCCACAGCL | : : CAGAUCAAG/Cleavage | pacid=371624 |

| | | | | |
|----|------|--|------------|-----------------------|
| 1 | | | | |
| 2 | 631 | 651 UCCACAGCL :: :::::::::::::: | CAUCUCAAGA | Cleavage pacid=371526 |
| 3 | 631 | 651 UCCACAGCL :: :::::::::::::: | CAUCUCAAGA | Cleavage pacid=371526 |
| 4 | 631 | 651 UCCACAGCL :: :::::::::::::: | CAUCUCAAGA | Cleavage pacid=371526 |
| 5 | 631 | 651 UCCACAGCL :: :::::::::::::: | CAUCUCAAGA | Cleavage pacid=371526 |
| 6 | 631 | 651 UCCACAGCL :: :::::::::::::: | CAUCUCAAGA | Cleavage pacid=371526 |
| 7 | 631 | 651 UCCACAGCL :: :::::::::::::: | CAUCUCAAGA | Cleavage pacid=371526 |
| 8 | 630 | 651 UCCACAGCL :: :::::::::::::: | UCAUCUCAAC | Cleavage pacid=371526 |
| 9 | | | | |
| 10 | 1758 | 1778 UCCACAGCL :::::::::::::: :: | CAGUUCGAG | Cleavage pacid=371726 |
| 11 | 1758 | 1778 UCCACAGCL :::::::::::::: :: | CAGUUCGAG | Cleavage pacid=371726 |
| 12 | 1758 | 1778 UCCACAGCL :::::::::::::: :: | CAGUUCGAG | Cleavage pacid=371726 |
| 13 | 1758 | 1778 UCCACAGCL :::::::::::::: :: | CAGUUCGAG | Cleavage pacid=371726 |
| 14 | 1758 | 1778 UCCACAGCL :::::::::::::: :: | CAGUUCGAG | Cleavage pacid=371726 |
| 15 | 1758 | 1778 UCCACAGCL :::::::::::::: :: | CAGUUCGAG | Cleavage pacid=371726 |
| 16 | 1758 | 1778 UCCACAGCL :::::::::::::: :: | CAGUUCGAG | Cleavage pacid=371726 |
| 17 | 1758 | 1778 UCCACAGCL :::::::::::::: :: | CAGUUCGAG | Cleavage pacid=371726 |
| 18 | 1758 | 1778 UCCACAGCL :::::::::::::: :: | CAGUUCGAG | Cleavage pacid=371726 |
| 19 | 1758 | 1778 UCCACAGCL :::::::::::::: :: | CAGUUCGAG | Cleavage pacid=371726 |
| 20 | 1758 | 1778 UCCACAGCL :::::::::::::: :: | CAGUUCGAG | Cleavage pacid=371726 |
| 21 | 1758 | 1778 UCCACAGCL :::::::::::::: :: | CAGUUCGAG | Cleavage pacid=371726 |
| 22 | 1758 | 1778 UCCACAGCL :::::::::::::: :: | CAGUUCGAG | Cleavage pacid=371726 |
| 23 | 1758 | 1778 UCCACAGCL :::::::::::::: :: | CAGUUCGAG | Cleavage pacid=371726 |
| 24 | 1757 | 1778 UCCACAGCL :::::::::::::: :: | UCAGUUCGA | Cleavage pacid=371726 |
| 25 | | | | |
| 26 | 863 | 884 UCCACAGCL :: :: :::::::::::::: | CAUUUCAAU | Cleavage pacid=371722 |
| 27 | 863 | 884 UCCACAGCL :: :: :::::::::::::: | CAUUUCAAU | Cleavage pacid=371722 |
| 28 | 863 | 884 UCCACAGCL :: :: :::::::::::::: | CAUUUCAAU | Cleavage pacid=371722 |
| 29 | 863 | 884 UCCACAGCL :: :: :::::::::::::: | CAUUUCAAU | Cleavage pacid=371722 |
| 30 | 863 | 884 UCCACAGCL :: :: :::::::::::::: | CAUUUCAAU | Cleavage pacid=371722 |
| 31 | 863 | 884 UCCACAGCL :: :: :::::::::::::: | CAUUUCAAU | Cleavage pacid=371722 |
| 32 | 863 | 884 UCCACAGCL :: :: :::::::::::::: | CAUUUCAAU | Cleavage pacid=371722 |
| 33 | 863 | 884 UCCACAGCL :: :: :::::::::::::: | CAUUUCAAU | Cleavage pacid=371722 |
| 34 | 863 | 884 UCCACAGCL :: :: :::::::::::::: | CAUUUCAAU | Cleavage pacid=371722 |
| 35 | 863 | 884 UCCACAGCL :: :: :::::::::::::: | CAUUUCAAU | Cleavage pacid=371722 |
| 36 | 863 | 884 UCCACAGCL :: :: :::::::::::::: | CAUUUCAAU | Cleavage pacid=371722 |
| 37 | 863 | 884 UCCACAGCL :: :: :::::::::::::: | CAUUUCAAU | Cleavage pacid=371722 |
| 38 | 863 | 884 UCCACAGCL :: :: :::::::::::::: | CAUUUCAAU | Cleavage pacid=371722 |
| 39 | 863 | 884 UCCACAGCL :: :: :::::::::::::: | CAUUUCAAU | Cleavage pacid=371722 |
| 40 | 862 | 884 UCCACAGCL :: :: :::::::::::::: | ACAUUUCAAL | Cleavage pacid=371722 |
| 41 | | | | |
| 42 | 939 | 960 UCCACAGCL :: :: :: :: :: :: :: :: | GCAGUUCG | Cleavage pacid=371713 |
| 43 | 603 | 623 UCCACAGCL :: :: :: :: :: :: :: :: | AUAGUUUAA | Cleavage pacid=371643 |
| 44 | 644 | 664 UCCACAGCL :: :: :: :: :: :: :: :: | AUAGUUUAA | Cleavage pacid=371643 |
| 45 | | | | |
| 46 | 4525 | 4545 UCCACAGCL :: :: :: :: :: :: :: :: | CGGAACAAG | Cleavage pacid=371668 |
| 47 | 4525 | 4545 UCCACAGCL :: :: :: :: :: :: :: :: | CGGAACAAG | Cleavage pacid=371668 |
| 48 | 4525 | 4545 UCCACAGCL :: :: :: :: :: :: :: :: | CGGAACAAG | Cleavage pacid=371668 |
| 49 | 4525 | 4545 UCCACAGCL :: :: :: :: :: :: :: :: | CGGAACAAG | Cleavage pacid=371668 |
| 50 | 4525 | 4545 UCCACAGCL :: :: :: :: :: :: :: :: | CGGAACAAG | Cleavage pacid=371668 |
| 51 | 4525 | 4545 UCCACAGCL :: :: :: :: :: :: :: :: | CGGAACAAG | Cleavage pacid=371668 |
| 52 | 4525 | 4545 UCCACAGCL :: :: :: :: :: :: :: :: | CGGAACAAG | Cleavage pacid=371668 |
| 53 | 4525 | 4545 UCCACAGCL :: :: :: :: :: :: :: :: | CGGAACAAG | Cleavage pacid=371668 |
| 54 | 4525 | 4545 UCCACAGCL :: :: :: :: :: :: :: :: | CGGAACAAG | Cleavage pacid=371668 |
| 55 | 4525 | 4545 UCCACAGCL :: :: :: :: :: :: :: :: | CGGAACAAG | Cleavage pacid=371668 |
| 56 | 4525 | 4545 UCCACAGCL :: :: :: :: :: :: :: :: | CGGAACAAG | Cleavage pacid=371668 |
| 57 | 4525 | 4545 UCCACAGCL :: :: :: :: :: :: :: :: | CGGAACAAG | Cleavage pacid=371668 |
| 58 | 4525 | 4545 UCCACAGCL :: :: :: :: :: :: :: :: | CGGAACAAG | Cleavage pacid=371668 |
| 59 | 4525 | 4545 UCCACAGCL :: :: :: :: :: :: :: :: | CGGAACAAG | Cleavage pacid=371668 |
| 60 | 1780 | 1801 UCCACAGCL :: :: :: :: :: :: :: :: | ACAGUACAAC | Cleavage pacid=371656 |
| | 1898 | 1919 UCCACAGCL :: :: :: :: :: :: :: :: | ACAGUACAAC | Cleavage pacid=371656 |

| | | | |
|----|------|--|--------------|
| 1 | | | |
| 2 | 685 | 703 UUCCACAGCL ::::: ::::::::::: CAGUU--AGA(Cleavage | pacid=371569 |
| 3 | 685 | 703 UUCCACAGCL ::::: ::::::::::: CAGUU--AGA(Cleavage | pacid=371569 |
| 4 | 685 | 703 UUCCACAGCL ::::: ::::::::::: CAGUU--AGA(Cleavage | pacid=371569 |
| 5 | 685 | 703 UUCCACAGCL ::::: ::::::::::: CAGUU--AGA(Cleavage | pacid=371569 |
| 6 | 685 | 703 UUCCACAGCL ::::: ::::::::::: CAGUU--AGA(Cleavage | pacid=371569 |
| 7 | 1397 | 1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage | pacid=371790 |
| 8 | 1397 | 1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage | pacid=371790 |
| 9 | 1397 | 1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage | pacid=371790 |
| 10 | 1397 | 1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage | pacid=371790 |
| 11 | 1397 | 1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage | pacid=371790 |
| 12 | 1397 | 1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage | pacid=371790 |
| 13 | 1397 | 1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage | pacid=371790 |
| 14 | 1397 | 1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage | pacid=371790 |
| 15 | 1397 | 1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage | pacid=371790 |
| 16 | 1397 | 1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage | pacid=371790 |
| 17 | 1397 | 1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage | pacid=371790 |
| 18 | 1397 | 1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage | pacid=371790 |
| 19 | 1397 | 1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage | pacid=371790 |
| 20 | 1397 | 1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage | pacid=371790 |
| 21 | 1397 | 1417 UUCCACAGCL ::::::::::: CGGUUCGGG(Cleavage | pacid=371790 |
| 22 | 1396 | 1417 UUCCACAGCL ::::::::::: UCGGUUCGG(Cleavage | pacid=371790 |
| 23 | | | |
| 24 | | | |
| 25 | | | |
| 26 | | | |
| 27 | | | |
| 28 | | | |
| 29 | | | |
| 30 | | | |
| 31 | | | |
| 32 | | | |
| 33 | | | |
| 34 | | | |
| 35 | | | |
| 36 | | | |
| 37 | | | |
| 38 | | | |
| 39 | | | |
| 40 | | | |
| 41 | | | |
| 42 | | | |
| 43 | | | |
| 44 | | | |
| 45 | | | |
| 46 | | | |
| 47 | | | |
| 48 | | | |
| 49 | | | |
| 50 | | | |
| 51 | | | |
| 52 | | | |
| 53 | | | |
| 54 | | | |
| 55 | | | |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

not distribute

| | | | | |
|----|---|--------------------|------------------|-------------------------------|
| 1 | | | | |
| 2 | 1 | Phvul.002G248200.1 | Phvul.002G248200 | Phvul.002G248200 PF13894 |
| 3 | 1 | Phvul.002G248200.1 | Phvul.002G248200 | Phvul.002G248200 PF13894 |
| 4 | 1 | Phvul.002G248200.1 | Phvul.002G248200 | Phvul.002G248200 PF13894 |
| 5 | | | | |
| 6 | 1 | Phvul.002G330600.1 | Phvul.002G330600 | Phvul.002G330600 PF08238 |
| 7 | 1 | Phvul.003G105600.1 | Phvul.003G105600 | Phvul.003G105600 PF06827,PF08 |
| 8 | 1 | Phvul.003G105600.1 | Phvul.003G105600 | Phvul.003G105600 PF06827,PF08 |
| 9 | | | | |
| 10 | 1 | Phvul.003G105600.1 | Phvul.003G105600 | Phvul.003G105600 PF06827,PF08 |
| 11 | 1 | Phvul.003G105600.1 | Phvul.003G105600 | Phvul.003G105600 PF06827,PF08 |
| 12 | 1 | Phvul.003G105600.1 | Phvul.003G105600 | Phvul.003G105600 PF06827,PF08 |
| 13 | | | | |
| 14 | 1 | Phvul.003G105600.1 | Phvul.003G105600 | Phvul.003G105600 PF06827,PF08 |
| 15 | 1 | Phvul.003G105600.1 | Phvul.003G105600 | Phvul.003G105600 PF06827,PF08 |
| 16 | 1 | Phvul.003G105600.1 | Phvul.003G105600 | Phvul.003G105600 PF06827,PF08 |
| 17 | | | | |
| 18 | 1 | Phvul.003G105600.1 | Phvul.003G105600 | Phvul.003G105600 PF06827,PF08 |
| 19 | 1 | Phvul.003G105600.1 | Phvul.003G105600 | Phvul.003G105600 PF06827,PF08 |
| 20 | 1 | Phvul.003G105600.1 | Phvul.003G105600 | Phvul.003G105600 PF06827,PF08 |
| 21 | | | | |
| 22 | 1 | Phvul.003G105600.1 | Phvul.003G105600 | Phvul.003G105600 PF06827,PF08 |
| 23 | 1 | Phvul.003G127400.1 | Phvul.003G127400 | Phvul.003G127400 PF11995,PF00 |
| 24 | 1 | Phvul.003G127400.1 | Phvul.003G127400 | Phvul.003G127400 PF11995,PF00 |
| 25 | | | | |
| 26 | 1 | Phvul.003G127400.1 | Phvul.003G127400 | Phvul.003G127400 PF11995,PF00 |
| 27 | 1 | Phvul.003G127400.1 | Phvul.003G127400 | Phvul.003G127400 PF11995,PF00 |
| 28 | 1 | Phvul.003G127400.1 | Phvul.003G127400 | Phvul.003G127400 PF11995,PF00 |
| 29 | | | | |
| 30 | 1 | Phvul.003G127400.1 | Phvul.003G127400 | Phvul.003G127400 PF11995,PF00 |
| 31 | 1 | Phvul.003G127400.1 | Phvul.003G127400 | Phvul.003G127400 PF11995,PF00 |
| 32 | 1 | Phvul.003G127400.1 | Phvul.003G127400 | Phvul.003G127400 PF11995,PF00 |
| 33 | | | | |
| 34 | 1 | Phvul.003G127400.1 | Phvul.003G127400 | Phvul.003G127400 PF11995,PF00 |
| 35 | 1 | Phvul.003G127400.1 | Phvul.003G127400 | Phvul.003G127400 PF11995,PF00 |
| 36 | 1 | Phvul.003G127400.1 | Phvul.003G127400 | Phvul.003G127400 PF11995,PF00 |
| 37 | 1 | Phvul.003G127400.1 | Phvul.003G127400 | Phvul.003G127400 PF11995,PF00 |
| 38 | 1 | Phvul.003G140200.2 | Phvul.003G140200 | Phvul.003G140200 PF00690,PF12 |
| 39 | 1 | Phvul.003G140200.1 | Phvul.003G140200 | Phvul.003G140200 PF00690,PF12 |
| 40 | 1 | Phvul.003G140200.2 | Phvul.003G140200 | Phvul.003G140200 PF00690,PF12 |
| 41 | 1 | Phvul.003G140200.1 | Phvul.003G140200 | Phvul.003G140200 PF00690,PF12 |
| 42 | | | | |
| 43 | 1 | Phvul.003G140200.2 | Phvul.003G140200 | Phvul.003G140200 PF00690,PF12 |
| 44 | 1 | Phvul.003G140200.1 | Phvul.003G140200 | Phvul.003G140200 PF00690,PF12 |
| 45 | 1 | Phvul.003G140200.2 | Phvul.003G140200 | Phvul.003G140200 PF00690,PF12 |
| 46 | | | | |
| 47 | 1 | Phvul.003G140200.1 | Phvul.003G140200 | Phvul.003G140200 PF00690,PF12 |
| 48 | 1 | Phvul.003G140200.2 | Phvul.003G140200 | Phvul.003G140200 PF00690,PF12 |
| 49 | 1 | Phvul.003G140200.1 | Phvul.003G140200 | Phvul.003G140200 PF00690,PF12 |
| 50 | | | | |
| 51 | 1 | Phvul.003G140200.2 | Phvul.003G140200 | Phvul.003G140200 PF00690,PF12 |
| 52 | 1 | Phvul.003G140200.1 | Phvul.003G140200 | Phvul.003G140200 PF00690,PF12 |
| 53 | | | | |
| 54 | 1 | Phvul.003G140200.2 | Phvul.003G140200 | Phvul.003G140200 PF00690,PF12 |
| 55 | 1 | Phvul.003G140200.1 | Phvul.003G140200 | Phvul.003G140200 PF00690,PF12 |
| 56 | 1 | Phvul.003G140200.2 | Phvul.003G140200 | Phvul.003G140200 PF00690,PF12 |
| 57 | 1 | Phvul.003G140200.1 | Phvul.003G140200 | Phvul.003G140200 PF00690,PF12 |
| 58 | | | | |
| 59 | 1 | Phvul.003G140200.2 | Phvul.003G140200 | Phvul.003G140200 PF00690,PF12 |
| 60 | 1 | Phvul.003G140200.1 | Phvul.003G140200 | Phvul.003G140200 PF00690,PF12 |
| | 1 | Phvul.003G140200.2 | Phvul.003G140200 | Phvul.003G140200 PF00690,PF12 |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | |
|----------------------|------------------|------------------|--------------|
| 1 Phvul.003G140200.1 | Phvul.003G140200 | Phvul.003G140200 | PF00690,PF12 |
| 1 Phvul.003G140200.2 | Phvul.003G140200 | Phvul.003G140200 | PF00690,PF12 |
| 1 Phvul.003G140200.1 | Phvul.003G140200 | Phvul.003G140200 | PF00690,PF12 |
| 1 Phvul.003G140200.2 | Phvul.003G140200 | Phvul.003G140200 | PF00690,PF12 |
| 1 Phvul.003G140200.1 | Phvul.003G140200 | Phvul.003G140200 | PF00690,PF12 |
| 1 Phvul.003G205600.1 | Phvul.003G205600 | Phvul.003G205600 | PF03144,PF03 |
| 1 Phvul.003G205600.1 | Phvul.003G205600 | Phvul.003G205600 | PF03144,PF03 |
| 1 Phvul.003G205600.1 | Phvul.003G205600 | Phvul.003G205600 | PF03144,PF03 |
| 1 Phvul.003G205600.1 | Phvul.003G205600 | Phvul.003G205600 | PF03144,PF03 |
| 1 Phvul.003G205600.1 | Phvul.003G205600 | Phvul.003G205600 | PF03144,PF03 |
| 1 Phvul.003G205600.1 | Phvul.003G205600 | Phvul.003G205600 | PF03144,PF03 |
| 1 Phvul.003G205600.1 | Phvul.003G205600 | Phvul.003G205600 | PF03144,PF03 |
| 1 Phvul.003G205600.1 | Phvul.003G205600 | Phvul.003G205600 | PF03144,PF03 |
| 1 Phvul.003G205600.1 | Phvul.003G205600 | Phvul.003G205600 | PF03144,PF03 |
| 1 Phvul.003G205600.1 | Phvul.003G205600 | Phvul.003G205600 | PF03144,PF03 |
| 1 Phvul.003G205600.1 | Phvul.003G205600 | Phvul.003G205600 | PF03144,PF03 |
| 1 Phvul.004G012700.2 | Phvul.004G012700 | Phvul.004G012700 | PF00122,PF12 |
| 1 Phvul.004G012700.2 | Phvul.004G012700 | Phvul.004G012700 | PF00122,PF12 |
| 1 Phvul.004G012700.2 | Phvul.004G012700 | Phvul.004G012700 | PF00122,PF12 |
| 1 Phvul.004G012700.2 | Phvul.004G012700 | Phvul.004G012700 | PF00122,PF12 |
| 1 Phvul.004G012700.2 | Phvul.004G012700 | Phvul.004G012700 | PF00122,PF12 |
| 1 Phvul.004G012700.2 | Phvul.004G012700 | Phvul.004G012700 | PF00122,PF12 |
| 1 Phvul.004G012700.2 | Phvul.004G012700 | Phvul.004G012700 | PF00122,PF12 |
| 1 Phvul.004G012700.2 | Phvul.004G012700 | Phvul.004G012700 | PF00122,PF12 |
| 1 Phvul.004G012700.2 | Phvul.004G012700 | Phvul.004G012700 | PF00122,PF12 |
| 1 Phvul.004G012700.2 | Phvul.004G012700 | Phvul.004G012700 | PF00122,PF12 |
| 1 Phvul.004G012700.2 | Phvul.004G012700 | Phvul.004G012700 | PF00122,PF12 |
| 1 Phvul.004G012700.2 | Phvul.004G012700 | Phvul.004G012700 | PF00122,PF12 |
| 1 Phvul.004G012700.2 | Phvul.004G012700 | Phvul.004G012700 | PF00122,PF12 |
| 1 Phvul.005G126400.1 | Phvul.005G126400 | Phvul.005G126400 | PF07876 |
| 1 Phvul.005G126400.1 | Phvul.005G126400 | Phvul.005G126400 | PF07876 |
| 1 Phvul.005G126400.1 | Phvul.005G126400 | Phvul.005G126400 | PF07876 |
| 1 Phvul.005G126400.1 | Phvul.005G126400 | Phvul.005G126400 | PF07876 |
| 1 Phvul.005G126400.1 | Phvul.005G126400 | Phvul.005G126400 | PF07876 |
| 1 Phvul.005G126400.1 | Phvul.005G126400 | Phvul.005G126400 | PF07876 |
| 1 Phvul.005G126400.1 | Phvul.005G126400 | Phvul.005G126400 | PF07876 |
| 1 Phvul.005G126400.1 | Phvul.005G126400 | Phvul.005G126400 | PF07876 |
| 1 Phvul.005G126400.1 | Phvul.005G126400 | Phvul.005G126400 | PF07876 |
| 1 Phvul.005G126400.1 | Phvul.005G126400 | Phvul.005G126400 | PF07876 |
| 1 Phvul.005G126400.1 | Phvul.005G126400 | Phvul.005G126400 | PF07876 |
| 1 Phvul.006G200700.1 | Phvul.006G200700 | Phvul.006G200700 | PF00400 |
| 1 Phvul.006G200700.1 | Phvul.006G200700 | Phvul.006G200700 | PF00400 |
| 1 Phvul.006G200700.1 | Phvul.006G200700 | Phvul.006G200700 | PF00400 |
| 1 Phvul.006G200700.1 | Phvul.006G200700 | Phvul.006G200700 | PF00400 |
| 1 Phvul.006G200700.1 | Phvul.006G200700 | Phvul.006G200700 | PF00400 |

| | | | | | |
|----|---|--------------------|------------------|------------------|---------|
| 1 | | | | | |
| 2 | 1 | Phvul.008G046300.2 | Phvul.008G046300 | Phvul.008G046300 | PF13041 |
| 3 | 1 | Phvul.008G046300.1 | Phvul.008G046300 | Phvul.008G046300 | PF13041 |
| 4 | 1 | Phvul.008G046300.2 | Phvul.008G046300 | Phvul.008G046300 | PF13041 |
| 5 | | | | | |
| 6 | 1 | Phvul.008G046300.1 | Phvul.008G046300 | Phvul.008G046300 | PF13041 |
| 7 | 1 | Phvul.008G046300.2 | Phvul.008G046300 | Phvul.008G046300 | PF13041 |
| 8 | 1 | Phvul.008G046300.1 | Phvul.008G046300 | Phvul.008G046300 | PF13041 |
| 9 | | | | | |
| 10 | 1 | Phvul.008G046300.2 | Phvul.008G046300 | Phvul.008G046300 | PF13041 |
| 11 | 1 | Phvul.008G046300.1 | Phvul.008G046300 | Phvul.008G046300 | PF13041 |
| 12 | 1 | Phvul.008G046300.2 | Phvul.008G046300 | Phvul.008G046300 | PF13041 |
| 13 | | | | | |
| 14 | 1 | Phvul.008G046300.1 | Phvul.008G046300 | Phvul.008G046300 | PF13041 |
| 15 | 1 | Phvul.008G046300.2 | Phvul.008G046300 | Phvul.008G046300 | PF13041 |
| 16 | 1 | Phvul.008G046300.1 | Phvul.008G046300 | Phvul.008G046300 | PF13041 |
| 17 | | | | | |
| 18 | 1 | Phvul.008G046300.2 | Phvul.008G046300 | Phvul.008G046300 | PF13041 |
| 19 | 1 | Phvul.008G046300.1 | Phvul.008G046300 | Phvul.008G046300 | PF13041 |
| 20 | 1 | Phvul.008G046300.2 | Phvul.008G046300 | Phvul.008G046300 | PF13041 |
| 21 | | | | | |
| 22 | 1 | Phvul.008G046300.1 | Phvul.008G046300 | Phvul.008G046300 | PF13041 |
| 23 | 1 | Phvul.008G046300.2 | Phvul.008G046300 | Phvul.008G046300 | PF13041 |
| 24 | 1 | Phvul.008G046300.1 | Phvul.008G046300 | Phvul.008G046300 | PF13041 |
| 25 | | | | | |
| 26 | 1 | Phvul.008G046300.2 | Phvul.008G046300 | Phvul.008G046300 | PF13041 |
| 27 | 1 | Phvul.008G118100.3 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 28 | 1 | Phvul.008G118100.1 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 29 | | | | | |
| 30 | 1 | Phvul.008G118100.2 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 31 | 1 | Phvul.008G118100.3 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 32 | 1 | Phvul.008G118100.1 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 33 | | | | | |
| 34 | 1 | Phvul.008G118100.2 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 35 | 1 | Phvul.008G118100.3 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 36 | 1 | Phvul.008G118100.1 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 37 | | | | | |
| 38 | 1 | Phvul.008G118100.2 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 39 | 1 | Phvul.008G118100.3 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 40 | 1 | Phvul.008G118100.1 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 41 | | | | | |
| 42 | 1 | Phvul.008G118100.2 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 43 | 1 | Phvul.008G118100.3 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 44 | 1 | Phvul.008G118100.1 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 45 | | | | | |
| 46 | 1 | Phvul.008G118100.2 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 47 | 1 | Phvul.008G118100.3 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 48 | 1 | Phvul.008G118100.1 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 49 | | | | | |
| 50 | 1 | Phvul.008G118100.2 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 51 | 1 | Phvul.008G118100.3 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 52 | 1 | Phvul.008G118100.1 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 53 | | | | | |
| 54 | 1 | Phvul.008G118100.2 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 55 | 1 | Phvul.008G118100.3 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 56 | 1 | Phvul.008G118100.1 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 57 | | | | | |
| 58 | 1 | Phvul.008G118100.2 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 59 | 1 | Phvul.008G118100.3 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 60 | 1 | Phvul.008G118100.1 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| | 1 | Phvul.008G118100.2 | Phvul.008G118100 | Phvul.008G118100 | 0 |

| | | | | | |
|----|---|--------------------|------------------|------------------|--------------|
| 1 | | | | | |
| 2 | 1 | Phvul.008G118100.3 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 3 | 1 | Phvul.008G118100.1 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 4 | 1 | Phvul.008G118100.2 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 5 | | | | | |
| 6 | 1 | Phvul.008G118100.3 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 7 | 1 | Phvul.008G118100.1 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 8 | 1 | Phvul.008G118100.2 | Phvul.008G118100 | Phvul.008G118100 | 0 |
| 9 | | | | | |
| 10 | 1 | Phvul.008G143300.2 | Phvul.008G143300 | Phvul.008G143300 | PF09749 |
| 11 | 1 | Phvul.008G143300.2 | Phvul.008G143300 | Phvul.008G143300 | PF09749 |
| 12 | 1 | Phvul.008G143300.2 | Phvul.008G143300 | Phvul.008G143300 | PF09749 |
| 13 | | | | | |
| 14 | 1 | Phvul.008G143300.2 | Phvul.008G143300 | Phvul.008G143300 | PF09749 |
| 15 | 1 | Phvul.008G143300.2 | Phvul.008G143300 | Phvul.008G143300 | PF09749 |
| 16 | 1 | Phvul.008G143300.2 | Phvul.008G143300 | Phvul.008G143300 | PF09749 |
| 17 | | | | | |
| 18 | 1 | Phvul.008G143300.2 | Phvul.008G143300 | Phvul.008G143300 | PF09749 |
| 19 | 1 | Phvul.008G143300.2 | Phvul.008G143300 | Phvul.008G143300 | PF09749 |
| 20 | 1 | Phvul.008G143300.2 | Phvul.008G143300 | Phvul.008G143300 | PF09749 |
| 21 | | | | | |
| 22 | 1 | Phvul.008G143300.2 | Phvul.008G143300 | Phvul.008G143300 | PF09749 |
| 23 | 1 | Phvul.008G143300.2 | Phvul.008G143300 | Phvul.008G143300 | PF09749 |
| 24 | 1 | Phvul.009G019500.2 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 25 | | | | | |
| 26 | 1 | Phvul.009G019500.1 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 27 | 1 | Phvul.009G019500.2 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 28 | 1 | Phvul.009G019500.1 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 29 | | | | | |
| 30 | 1 | Phvul.009G019500.2 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 31 | 1 | Phvul.009G019500.1 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 32 | 1 | Phvul.009G019500.2 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 33 | | | | | |
| 34 | 1 | Phvul.009G019500.1 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 35 | 1 | Phvul.009G019500.2 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 36 | 1 | Phvul.009G019500.1 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 37 | 1 | Phvul.009G019500.2 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 38 | | | | | |
| 39 | 1 | Phvul.009G019500.1 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 40 | 1 | Phvul.009G019500.2 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 41 | 1 | Phvul.009G019500.1 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 42 | | | | | |
| 43 | 1 | Phvul.009G019500.2 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 44 | 1 | Phvul.009G019500.1 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 45 | 1 | Phvul.009G019500.2 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 46 | | | | | |
| 47 | 1 | Phvul.009G019500.1 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 48 | 1 | Phvul.009G019500.2 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 49 | 1 | Phvul.009G019500.1 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 50 | | | | | |
| 51 | 1 | Phvul.009G019500.2 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 52 | 1 | Phvul.009G019500.1 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 53 | 1 | Phvul.009G019500.2 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 54 | | | | | |
| 55 | 1 | Phvul.009G019500.1 | Phvul.009G019500 | Phvul.009G019500 | PF01479,PF00 |
| 56 | 1 | Phvul.009G037300.1 | Phvul.009G037300 | Phvul.009G037300 | PF01486,PF00 |
| 57 | 1 | Phvul.009G037300.1 | Phvul.009G037300 | Phvul.009G037300 | PF01486,PF00 |
| 58 | | | | | |
| 59 | 1 | Phvul.009G037300.1 | Phvul.009G037300 | Phvul.009G037300 | PF01486,PF00 |
| 60 | 1 | Phvul.009G037300.1 | Phvul.009G037300 | Phvul.009G037300 | PF01486,PF00 |
| | 1 | Phvul.009G037300.1 | Phvul.009G037300 | Phvul.009G037300 | PF01486,PF00 |

| | | | | | |
|----|---|--------------------|------------------|------------------|---------|
| 1 | | | | | |
| 2 | 1 | Phvul.007G166500.3 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 3 | 1 | Phvul.007G166500.6 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 4 | 1 | Phvul.007G166500.5 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 5 | | | | | |
| 6 | 1 | Phvul.007G166500.4 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 7 | 1 | Phvul.007G166500.3 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 8 | 1 | Phvul.007G166500.6 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 9 | | | | | |
| 10 | 1 | Phvul.007G166500.5 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 11 | 1 | Phvul.007G166500.4 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 12 | 1 | Phvul.007G166500.3 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 13 | | | | | |
| 14 | 1 | Phvul.007G166500.6 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 15 | 1 | Phvul.007G166500.5 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 16 | 1 | Phvul.007G166500.4 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 17 | | | | | |
| 18 | 1 | Phvul.007G166500.3 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 19 | 1 | Phvul.007G166500.6 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 20 | 1 | Phvul.007G166500.5 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 21 | | | | | |
| 22 | 1 | Phvul.007G166500.4 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 23 | 1 | Phvul.007G166500.3 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 24 | 1 | Phvul.007G166500.6 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 25 | | | | | |
| 26 | 1 | Phvul.007G166500.5 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 27 | 1 | Phvul.007G166500.4 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 28 | 1 | Phvul.007G166500.3 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 29 | 1 | Phvul.007G166500.6 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 30 | | | | | |
| 31 | 1 | Phvul.007G166500.5 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 32 | 1 | Phvul.007G166500.4 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 33 | | | | | |
| 34 | 1 | Phvul.007G166500.3 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 35 | 1 | Phvul.007G166500.6 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 36 | 1 | Phvul.007G166500.5 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 37 | 1 | Phvul.007G166500.4 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 38 | | | | | |
| 39 | 1 | Phvul.007G166500.3 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 40 | 1 | Phvul.007G166500.6 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 41 | 1 | Phvul.007G166500.5 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 42 | | | | | |
| 43 | 1 | Phvul.007G166500.4 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 44 | 1 | Phvul.007G166500.3 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 45 | 1 | Phvul.007G166500.6 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 46 | | | | | |
| 47 | 1 | Phvul.007G166500.5 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 48 | 1 | Phvul.007G166500.4 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 49 | 1 | Phvul.007G166500.3 | Phvul.007G166500 | Phvul.007G166500 | PF13365 |
| 50 | | | | | |
| 51 | 1 | Phvul.007G184400.6 | Phvul.007G184400 | Phvul.007G184400 | PF00400 |
| 52 | 1 | Phvul.007G184400.2 | Phvul.007G184400 | Phvul.007G184400 | PF00400 |
| 53 | 1 | Phvul.007G184400.5 | Phvul.007G184400 | Phvul.007G184400 | PF00400 |
| 54 | | | | | |
| 55 | 1 | Phvul.007G184400.3 | Phvul.007G184400 | Phvul.007G184400 | PF00400 |
| 56 | 1 | Phvul.007G184400.6 | Phvul.007G184400 | Phvul.007G184400 | PF00400 |
| 57 | 1 | Phvul.007G184400.2 | Phvul.007G184400 | Phvul.007G184400 | PF00400 |
| 58 | | | | | |
| 59 | 1 | Phvul.007G184400.5 | Phvul.007G184400 | Phvul.007G184400 | PF00400 |
| 60 | 1 | Phvul.007G184400.3 | Phvul.007G184400 | Phvul.007G184400 | PF00400 |
| | 1 | Phvul.007G184400.6 | Phvul.007G184400 | Phvul.007G184400 | PF00400 |

| | | | | | |
|----|---|--------------------|------------------|------------------|--------------|
| 1 | | | | | |
| 2 | 1 | Phvul.001G095200.2 | Phvul.001G095200 | Phvul.001G095200 | PF12854,PF13 |
| 3 | 1 | Phvul.001G095200.3 | Phvul.001G095200 | Phvul.001G095200 | PF12854,PF13 |
| 4 | 1 | Phvul.001G095200.2 | Phvul.001G095200 | Phvul.001G095200 | PF12854,PF13 |
| 5 | | | | | |
| 6 | 1 | Phvul.001G095200.3 | Phvul.001G095200 | Phvul.001G095200 | PF12854,PF13 |
| 7 | 1 | Phvul.001G198800.1 | Phvul.001G198800 | Phvul.001G198800 | PF04576 |
| 8 | 1 | Phvul.001G198800.1 | Phvul.001G198800 | Phvul.001G198800 | PF04576 |
| 9 | | | | | |
| 10 | 1 | Phvul.001G198800.1 | Phvul.001G198800 | Phvul.001G198800 | PF04576 |
| 11 | 1 | Phvul.001G198800.1 | Phvul.001G198800 | Phvul.001G198800 | PF04576 |
| 12 | 1 | Phvul.001G198800.1 | Phvul.001G198800 | Phvul.001G198800 | PF04576 |
| 13 | | | | | |
| 14 | 1 | Phvul.001G198800.1 | Phvul.001G198800 | Phvul.001G198800 | PF04576 |
| 15 | 1 | Phvul.001G198800.1 | Phvul.001G198800 | Phvul.001G198800 | PF04576 |
| 16 | 1 | Phvul.001G198800.1 | Phvul.001G198800 | Phvul.001G198800 | PF04576 |
| 17 | | | | | |
| 18 | 1 | Phvul.001G198800.1 | Phvul.001G198800 | Phvul.001G198800 | PF04576 |
| 19 | 1 | Phvul.001G198800.1 | Phvul.001G198800 | Phvul.001G198800 | PF04576 |
| 20 | 1 | Phvul.001G198800.1 | Phvul.001G198800 | Phvul.001G198800 | PF04576 |
| 21 | | | | | |
| 22 | 1 | Phvul.001G198800.1 | Phvul.001G198800 | Phvul.001G198800 | PF04576 |
| 23 | 1 | Phvul.002G119401.1 | Phvul.002G119401 | Phvul.002G119401 | PF04434,PF10 |
| 24 | 1 | Phvul.002G119401.1 | Phvul.002G119401 | Phvul.002G119401 | PF04434,PF10 |
| 25 | | | | | |
| 26 | 1 | Phvul.002G119401.1 | Phvul.002G119401 | Phvul.002G119401 | PF04434,PF10 |
| 27 | 1 | Phvul.002G119401.1 | Phvul.002G119401 | Phvul.002G119401 | PF04434,PF10 |
| 28 | 1 | Phvul.002G119401.1 | Phvul.002G119401 | Phvul.002G119401 | PF04434,PF10 |
| 29 | | | | | |
| 30 | 1 | Phvul.002G119401.1 | Phvul.002G119401 | Phvul.002G119401 | PF04434,PF10 |
| 31 | 1 | Phvul.002G119401.1 | Phvul.002G119401 | Phvul.002G119401 | PF04434,PF10 |
| 32 | 1 | Phvul.002G119401.1 | Phvul.002G119401 | Phvul.002G119401 | PF04434,PF10 |
| 33 | | | | | |
| 34 | 1 | Phvul.002G119401.1 | Phvul.002G119401 | Phvul.002G119401 | PF04434,PF10 |
| 35 | 1 | Phvul.002G119401.1 | Phvul.002G119401 | Phvul.002G119401 | PF04434,PF10 |
| 36 | 1 | Phvul.002G119401.1 | Phvul.002G119401 | Phvul.002G119401 | PF04434,PF10 |
| 37 | | | | | |
| 38 | 1 | Phvul.002G119401.1 | Phvul.002G119401 | Phvul.002G119401 | PF04434,PF10 |
| 39 | 1 | Phvul.002G123300.1 | Phvul.002G123300 | Phvul.002G123300 | PF03759 |
| 40 | 1 | Phvul.002G123300.2 | Phvul.002G123300 | Phvul.002G123300 | PF03759 |
| 41 | | | | | |
| 42 | 1 | Phvul.002G327900.1 | Phvul.002G327900 | Phvul.002G327900 | PF00462 |
| 43 | 1 | Phvul.003G136300.2 | Phvul.003G136300 | Phvul.003G136300 | PF01985 |
| 44 | 1 | Phvul.003G136300.1 | Phvul.003G136300 | Phvul.003G136300 | PF01985 |
| 45 | 1 | Phvul.003G136300.2 | Phvul.003G136300 | Phvul.003G136300 | PF01985 |
| 46 | | | | | |
| 47 | 1 | Phvul.003G136300.1 | Phvul.003G136300 | Phvul.003G136300 | PF01985 |
| 48 | 1 | Phvul.003G136300.2 | Phvul.003G136300 | Phvul.003G136300 | PF01985 |
| 49 | | | | | |
| 50 | 1 | Phvul.003G136300.1 | Phvul.003G136300 | Phvul.003G136300 | PF01985 |
| 51 | 1 | Phvul.003G136300.2 | Phvul.003G136300 | Phvul.003G136300 | PF01985 |
| 52 | 1 | Phvul.003G136300.1 | Phvul.003G136300 | Phvul.003G136300 | PF01985 |
| 53 | | | | | |
| 54 | 1 | Phvul.003G136300.2 | Phvul.003G136300 | Phvul.003G136300 | PF01985 |
| 55 | 1 | Phvul.003G136300.1 | Phvul.003G136300 | Phvul.003G136300 | PF01985 |
| 56 | 1 | Phvul.003G136300.2 | Phvul.003G136300 | Phvul.003G136300 | PF01985 |
| 57 | | | | | |
| 58 | 1 | Phvul.003G136300.1 | Phvul.003G136300 | Phvul.003G136300 | PF01985 |
| 59 | 1 | Phvul.003G136300.2 | Phvul.003G136300 | Phvul.003G136300 | PF01985 |
| 60 | 1 | Phvul.003G136300.1 | Phvul.003G136300 | Phvul.003G136300 | PF01985 |
| | 1 | Phvul.003G136300.2 | Phvul.003G136300 | Phvul.003G136300 | PF01985 |

| | | | | | |
|----|---|--------------------|------------------|------------------|--------------|
| 1 | | | | | |
| 2 | 1 | Phvul.008G003600.2 | Phvul.008G003600 | Phvul.008G003600 | PF00923 |
| 3 | 1 | Phvul.008G003600.1 | Phvul.008G003600 | Phvul.008G003600 | PF00923 |
| 4 | 1 | Phvul.008G003600.2 | Phvul.008G003600 | Phvul.008G003600 | PF00923 |
| 5 | | | | | |
| 6 | 1 | Phvul.008G003600.1 | Phvul.008G003600 | Phvul.008G003600 | PF00923 |
| 7 | 1 | Phvul.008G055200.1 | Phvul.008G055200 | Phvul.008G055200 | PF03547 |
| 8 | 1 | Phvul.008G162900.1 | Phvul.008G162900 | Phvul.008G162900 | PF13245,PF13 |
| 9 | | | | | |
| 10 | 1 | Phvul.008G162900.1 | Phvul.008G162900 | Phvul.008G162900 | PF13245,PF13 |
| 11 | 1 | Phvul.008G162900.1 | Phvul.008G162900 | Phvul.008G162900 | PF13245,PF13 |
| 12 | 1 | Phvul.008G162900.1 | Phvul.008G162900 | Phvul.008G162900 | PF13245,PF13 |
| 13 | | | | | |
| 14 | 1 | Phvul.008G162900.1 | Phvul.008G162900 | Phvul.008G162900 | PF13245,PF13 |
| 15 | 1 | Phvul.008G162900.1 | Phvul.008G162900 | Phvul.008G162900 | PF13245,PF13 |
| 16 | 1 | Phvul.008G162900.1 | Phvul.008G162900 | Phvul.008G162900 | PF13245,PF13 |
| 17 | | | | | |
| 18 | 1 | Phvul.008G162900.1 | Phvul.008G162900 | Phvul.008G162900 | PF13245,PF13 |
| 19 | 1 | Phvul.008G162900.1 | Phvul.008G162900 | Phvul.008G162900 | PF13245,PF13 |
| 20 | 1 | Phvul.008G162900.1 | Phvul.008G162900 | Phvul.008G162900 | PF13245,PF13 |
| 21 | | | | | |
| 22 | 1 | Phvul.008G162900.1 | Phvul.008G162900 | Phvul.008G162900 | PF13245,PF13 |
| 23 | 1 | Phvul.008G162900.1 | Phvul.008G162900 | Phvul.008G162900 | PF13245,PF13 |
| 24 | 1 | Phvul.008G192200.1 | Phvul.008G192200 | Phvul.008G192200 | 0 |
| 25 | | | | | |
| 26 | 1 | Phvul.008G192200.1 | Phvul.008G192200 | Phvul.008G192200 | 0 |
| 27 | 1 | Phvul.008G192200.1 | Phvul.008G192200 | Phvul.008G192200 | 0 |
| 28 | 1 | Phvul.008G192200.1 | Phvul.008G192200 | Phvul.008G192200 | 0 |
| 29 | | | | | |
| 30 | 1 | Phvul.008G192200.1 | Phvul.008G192200 | Phvul.008G192200 | 0 |
| 31 | 1 | Phvul.008G192200.1 | Phvul.008G192200 | Phvul.008G192200 | 0 |
| 32 | 1 | Phvul.008G192200.1 | Phvul.008G192200 | Phvul.008G192200 | 0 |
| 33 | | | | | |
| 34 | 1 | Phvul.008G192200.1 | Phvul.008G192200 | Phvul.008G192200 | 0 |
| 35 | 1 | Phvul.008G192200.1 | Phvul.008G192200 | Phvul.008G192200 | 0 |
| 36 | 1 | Phvul.008G192200.1 | Phvul.008G192200 | Phvul.008G192200 | 0 |
| 37 | 1 | Phvul.008G192200.1 | Phvul.008G192200 | Phvul.008G192200 | 0 |
| 38 | | | | | |
| 39 | 1 | Phvul.008G192200.1 | Phvul.008G192200 | Phvul.008G192200 | 0 |
| 40 | 1 | Phvul.008G277900.1 | Phvul.008G277900 | Phvul.008G277900 | PF01095 |
| 41 | 1 | Phvul.008G277900.1 | Phvul.008G277900 | Phvul.008G277900 | PF01095 |
| 42 | | | | | |
| 43 | 1 | Phvul.008G277900.1 | Phvul.008G277900 | Phvul.008G277900 | PF01095 |
| 44 | 1 | Phvul.008G277900.1 | Phvul.008G277900 | Phvul.008G277900 | PF01095 |
| 45 | 1 | Phvul.008G277900.1 | Phvul.008G277900 | Phvul.008G277900 | PF01095 |
| 46 | | | | | |
| 47 | 1 | Phvul.008G277900.1 | Phvul.008G277900 | Phvul.008G277900 | PF01095 |
| 48 | 1 | Phvul.008G277900.1 | Phvul.008G277900 | Phvul.008G277900 | PF01095 |
| 49 | 1 | Phvul.008G277900.1 | Phvul.008G277900 | Phvul.008G277900 | PF01095 |
| 50 | | | | | |
| 51 | 1 | Phvul.008G277900.1 | Phvul.008G277900 | Phvul.008G277900 | PF01095 |
| 52 | 1 | Phvul.008G277900.1 | Phvul.008G277900 | Phvul.008G277900 | PF01095 |
| 53 | | | | | |
| 54 | 1 | Phvul.008G277900.1 | Phvul.008G277900 | Phvul.008G277900 | PF01095 |
| 55 | 1 | Phvul.008G277900.1 | Phvul.008G277900 | Phvul.008G277900 | PF01095 |
| 56 | 1 | Phvul.008G283700.1 | Phvul.008G283700 | Phvul.008G283700 | PF17048,PF04 |
| 57 | 1 | Phvul.008G283700.1 | Phvul.008G283700 | Phvul.008G283700 | PF17048,PF04 |
| 58 | | | | | |
| 59 | 1 | Phvul.008G283700.1 | Phvul.008G283700 | Phvul.008G283700 | PF17048,PF04 |
| 60 | 1 | Phvul.008G283700.1 | Phvul.008G283700 | Phvul.008G283700 | PF17048,PF04 |
| | 1 | Phvul.008G283700.1 | Phvul.008G283700 | Phvul.008G283700 | PF17048,PF04 |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | |
|----------------------|------------------|------------------|--------------|
| 1 Phvul.008G283700.1 | Phvul.008G283700 | Phvul.008G283700 | PF17048,PF04 |
| 1 Phvul.008G283700.1 | Phvul.008G283700 | Phvul.008G283700 | PF17048,PF04 |
| 1 Phvul.008G283700.1 | Phvul.008G283700 | Phvul.008G283700 | PF17048,PF04 |
| 1 Phvul.008G283700.1 | Phvul.008G283700 | Phvul.008G283700 | PF17048,PF04 |
| 1 Phvul.008G283700.1 | Phvul.008G283700 | Phvul.008G283700 | PF17048,PF04 |
| 1 Phvul.008G283700.1 | Phvul.008G283700 | Phvul.008G283700 | PF17048,PF04 |
| 1 Phvul.008G283700.1 | Phvul.008G283700 | Phvul.008G283700 | PF17048,PF04 |
| 1 Phvul.008G283700.1 | Phvul.008G283700 | Phvul.008G283700 | PF17048,PF04 |
| 1 Phvul.009G086300.2 | Phvul.009G086300 | Phvul.009G086300 | PF12776 |
| 1 Phvul.009G086300.1 | Phvul.009G086300 | Phvul.009G086300 | PF12776 |
| 1 Phvul.009G086300.2 | Phvul.009G086300 | Phvul.009G086300 | PF12776 |
| 1 Phvul.009G086300.1 | Phvul.009G086300 | Phvul.009G086300 | PF12776 |
| 1 Phvul.009G086300.2 | Phvul.009G086300 | Phvul.009G086300 | PF12776 |
| 1 Phvul.009G086300.1 | Phvul.009G086300 | Phvul.009G086300 | PF12776 |
| 1 Phvul.009G086300.2 | Phvul.009G086300 | Phvul.009G086300 | PF12776 |
| 1 Phvul.009G086300.1 | Phvul.009G086300 | Phvul.009G086300 | PF12776 |
| 1 Phvul.009G086300.2 | Phvul.009G086300 | Phvul.009G086300 | PF12776 |
| 1 Phvul.009G086300.1 | Phvul.009G086300 | Phvul.009G086300 | PF12776 |
| 1 Phvul.009G086300.2 | Phvul.009G086300 | Phvul.009G086300 | PF12776 |
| 1 Phvul.009G086300.1 | Phvul.009G086300 | Phvul.009G086300 | PF12776 |
| 1 Phvul.009G086300.2 | Phvul.009G086300 | Phvul.009G086300 | PF12776 |
| 1 Phvul.009G086300.1 | Phvul.009G086300 | Phvul.009G086300 | PF12776 |
| 1 Phvul.009G086300.2 | Phvul.009G086300 | Phvul.009G086300 | PF12776 |
| 1 Phvul.009G086300.1 | Phvul.009G086300 | Phvul.009G086300 | PF12776 |
| 1 Phvul.009G086300.2 | Phvul.009G086300 | Phvul.009G086300 | PF12776 |
| 1 Phvul.009G086300.1 | Phvul.009G086300 | Phvul.009G086300 | PF12776 |
| 1 Phvul.009G086300.2 | Phvul.009G086300 | Phvul.009G086300 | PF12776 |
| 1 Phvul.009G140900.1 | Phvul.009G140900 | Phvul.009G140900 | PF00860 |
| 1 Phvul.009G140900.1 | Phvul.009G140900 | Phvul.009G140900 | PF00860 |
| 1 Phvul.009G140900.1 | Phvul.009G140900 | Phvul.009G140900 | PF00860 |
| 1 Phvul.009G140900.1 | Phvul.009G140900 | Phvul.009G140900 | PF00860 |
| 1 Phvul.009G140900.1 | Phvul.009G140900 | Phvul.009G140900 | PF00860 |
| 1 Phvul.009G140900.1 | Phvul.009G140900 | Phvul.009G140900 | PF00860 |
| 1 Phvul.009G140900.1 | Phvul.009G140900 | Phvul.009G140900 | PF00860 |
| 1 Phvul.009G140900.1 | Phvul.009G140900 | Phvul.009G140900 | PF00860 |
| 1 Phvul.009G140900.1 | Phvul.009G140900 | Phvul.009G140900 | PF00860 |
| 1 Phvul.009G140900.1 | Phvul.009G140900 | Phvul.009G140900 | PF00860 |
| 1 Phvul.009G140900.1 | Phvul.009G140900 | Phvul.009G140900 | PF00860 |
| 1 Phvul.009G140900.1 | Phvul.009G140900 | Phvul.009G140900 | PF00860 |
| 1 Phvul.010G131100.2 | Phvul.010G131100 | Phvul.010G131100 | PF00067 |
| 1 Phvul.010G140600.2 | Phvul.010G140600 | Phvul.010G140600 | PF00664,PF00 |
| 1 Phvul.010G140600.2 | Phvul.010G140600 | Phvul.010G140600 | PF00664,PF00 |
| 1 Phvul.010G140600.2 | Phvul.010G140600 | Phvul.010G140600 | PF00664,PF00 |
| 1 Phvul.010G140600.2 | Phvul.010G140600 | Phvul.010G140600 | PF00664,PF00 |

| | | | | |
|----|---|--------------------|------------------|-------------------------------|
| 1 | | | | |
| 2 | 1 | Phvul.005G105400.1 | Phvul.005G105400 | Phvul.005G105400 PF03168 |
| 3 | 1 | Phvul.005G105400.1 | Phvul.005G105400 | Phvul.005G105400 PF03168 |
| 4 | 1 | Phvul.005G105400.1 | Phvul.005G105400 | Phvul.005G105400 PF03168 |
| 5 | | | | |
| 6 | 1 | Phvul.005G105400.1 | Phvul.005G105400 | Phvul.005G105400 PF03168 |
| 7 | 1 | Phvul.005G105400.1 | Phvul.005G105400 | Phvul.005G105400 PF03168 |
| 8 | 1 | Phvul.005G105400.1 | Phvul.005G105400 | Phvul.005G105400 PF03168 |
| 9 | | | | |
| 10 | 1 | Phvul.006G142000.1 | Phvul.006G142000 | Phvul.006G142000 PF00083 |
| 11 | 1 | Phvul.006G142000.1 | Phvul.006G142000 | Phvul.006G142000 PF00083 |
| 12 | 1 | Phvul.006G142000.1 | Phvul.006G142000 | Phvul.006G142000 PF00083 |
| 13 | | | | |
| 14 | 1 | Phvul.006G142000.1 | Phvul.006G142000 | Phvul.006G142000 PF00083 |
| 15 | 1 | Phvul.006G142000.1 | Phvul.006G142000 | Phvul.006G142000 PF00083 |
| 16 | 1 | Phvul.006G142000.1 | Phvul.006G142000 | Phvul.006G142000 PF00083 |
| 17 | | | | |
| 18 | 1 | Phvul.006G142000.1 | Phvul.006G142000 | Phvul.006G142000 PF00083 |
| 19 | 1 | Phvul.006G142000.1 | Phvul.006G142000 | Phvul.006G142000 PF00083 |
| 20 | 1 | Phvul.006G142000.1 | Phvul.006G142000 | Phvul.006G142000 PF00083 |
| 21 | | | | |
| 22 | 1 | Phvul.006G142000.1 | Phvul.006G142000 | Phvul.006G142000 PF00083 |
| 23 | 1 | Phvul.006G142000.1 | Phvul.006G142000 | Phvul.006G142000 PF00083 |
| 24 | 1 | Phvul.006G142000.1 | Phvul.006G142000 | Phvul.006G142000 PF00083 |
| 25 | | | | |
| 26 | 1 | Phvul.006G157700.1 | Phvul.006G157700 | Phvul.006G157700 PF12937,PF13 |
| 27 | 1 | Phvul.006G157700.1 | Phvul.006G157700 | Phvul.006G157700 PF12937,PF13 |
| 28 | 1 | Phvul.006G157700.1 | Phvul.006G157700 | Phvul.006G157700 PF12937,PF13 |
| 29 | | | | |
| 30 | 1 | Phvul.006G157700.1 | Phvul.006G157700 | Phvul.006G157700 PF12937,PF13 |
| 31 | 1 | Phvul.006G157700.1 | Phvul.006G157700 | Phvul.006G157700 PF12937,PF13 |
| 32 | 1 | Phvul.006G157700.1 | Phvul.006G157700 | Phvul.006G157700 PF12937,PF13 |
| 33 | | | | |
| 34 | 1 | Phvul.006G157700.1 | Phvul.006G157700 | Phvul.006G157700 PF12937,PF13 |
| 35 | 1 | Phvul.006G157700.1 | Phvul.006G157700 | Phvul.006G157700 PF12937,PF13 |
| 36 | 1 | Phvul.006G157700.1 | Phvul.006G157700 | Phvul.006G157700 PF12937,PF13 |
| 37 | 1 | Phvul.006G157700.1 | Phvul.006G157700 | Phvul.006G157700 PF12937,PF13 |
| 38 | | | | |
| 39 | 1 | Phvul.006G157700.1 | Phvul.006G157700 | Phvul.006G157700 PF12937,PF13 |
| 40 | 1 | Phvul.006G157700.1 | Phvul.006G157700 | Phvul.006G157700 PF12937,PF13 |
| 41 | 1 | Phvul.006G200900.1 | Phvul.006G200900 | Phvul.006G200900 PF04576 |
| 42 | | | | |
| 43 | 1 | Phvul.007G083600.1 | Phvul.007G083600 | Phvul.007G083600 PF10994 |
| 44 | 1 | Phvul.007G083600.2 | Phvul.007G083600 | Phvul.007G083600 PF10994 |
| 45 | 2 | Phvul.007G136300.1 | Phvul.007G136300 | Phvul.007G136300 PF00400,PF04 |
| 46 | 2 | Phvul.007G136300.1 | Phvul.007G136300 | Phvul.007G136300 PF00400,PF04 |
| 47 | 2 | Phvul.007G136300.1 | Phvul.007G136300 | Phvul.007G136300 PF00400,PF04 |
| 48 | 2 | Phvul.007G136300.1 | Phvul.007G136300 | Phvul.007G136300 PF00400,PF04 |
| 49 | 2 | Phvul.007G136300.1 | Phvul.007G136300 | Phvul.007G136300 PF00400,PF04 |
| 50 | | | | |
| 51 | 2 | Phvul.007G136300.1 | Phvul.007G136300 | Phvul.007G136300 PF00400,PF04 |
| 52 | 2 | Phvul.007G136300.1 | Phvul.007G136300 | Phvul.007G136300 PF00400,PF04 |
| 53 | 2 | Phvul.007G136300.1 | Phvul.007G136300 | Phvul.007G136300 PF00400,PF04 |
| 54 | 2 | Phvul.007G136300.1 | Phvul.007G136300 | Phvul.007G136300 PF00400,PF04 |
| 55 | 2 | Phvul.007G136300.1 | Phvul.007G136300 | Phvul.007G136300 PF00400,PF04 |
| 56 | 2 | Phvul.007G136300.1 | Phvul.007G136300 | Phvul.007G136300 PF00400,PF04 |
| 57 | 2 | Phvul.007G136300.1 | Phvul.007G136300 | Phvul.007G136300 PF00400,PF04 |
| 58 | 2 | Phvul.007G136300.1 | Phvul.007G136300 | Phvul.007G136300 PF00400,PF04 |
| 59 | 1 | Phvul.007G175300.2 | Phvul.007G175300 | Phvul.007G175300 PF13385,PF00 |
| 60 | 1 | Phvul.007G175300.3 | Phvul.007G175300 | Phvul.007G175300 PF13385,PF00 |

| | | | | |
|----|----------------------|------------------|------------------|--------------|
| 1 | | | | |
| 2 | 1 Phvul.011G090600.1 | Phvul.011G090600 | Phvul.011G090600 | PF00300 |
| 3 | 1 Phvul.011G090600.1 | Phvul.011G090600 | Phvul.011G090600 | PF00300 |
| 4 | 1 Phvul.011G090600.1 | Phvul.011G090600 | Phvul.011G090600 | PF00300 |
| 5 | | | | |
| 6 | 1 Phvul.011G090600.1 | Phvul.011G090600 | Phvul.011G090600 | PF00300 |
| 7 | 1 Phvul.L001616.1 | Phvul.L001616 | Phvul.L001616 | PF04564,PF00 |
| 8 | 1 Phvul.L001616.1 | Phvul.L001616 | Phvul.L001616 | PF04564,PF00 |
| 9 | | | | |
| 10 | 1 Phvul.L001616.1 | Phvul.L001616 | Phvul.L001616 | PF04564,PF00 |
| 11 | 1 Phvul.L001616.1 | Phvul.L001616 | Phvul.L001616 | PF04564,PF00 |
| 12 | 1 Phvul.L001616.1 | Phvul.L001616 | Phvul.L001616 | PF04564,PF00 |
| 13 | 1 Phvul.L001616.1 | Phvul.L001616 | Phvul.L001616 | PF04564,PF00 |
| 14 | 1 Phvul.L001616.1 | Phvul.L001616 | Phvul.L001616 | PF04564,PF00 |
| 15 | 1 Phvul.L001616.1 | Phvul.L001616 | Phvul.L001616 | PF04564,PF00 |
| 16 | 1 Phvul.L001616.1 | Phvul.L001616 | Phvul.L001616 | PF04564,PF00 |
| 17 | 1 Phvul.L001616.1 | Phvul.L001616 | Phvul.L001616 | PF04564,PF00 |
| 18 | 1 Phvul.L001616.1 | Phvul.L001616 | Phvul.L001616 | PF04564,PF00 |
| 19 | 1 Phvul.L001616.1 | Phvul.L001616 | Phvul.L001616 | PF04564,PF00 |
| 20 | 1 Phvul.L001616.1 | Phvul.L001616 | Phvul.L001616 | PF04564,PF00 |
| 21 | 1 Phvul.L001616.1 | Phvul.L001616 | Phvul.L001616 | PF04564,PF00 |
| 22 | 1 Phvul.L001616.1 | Phvul.L001616 | Phvul.L001616 | PF04564,PF00 |
| 23 | | | | |
| 24 | | | | |
| 25 | | | | |
| 26 | | | | |
| 27 | | | | |
| 28 | | | | |
| 29 | | | | |
| 30 | | | | |
| 31 | | | | |
| 32 | | | | |
| 33 | | | | |
| 34 | | | | |
| 35 | | | | |
| 36 | | | | |
| 37 | | | | |
| 38 | | | | |
| 39 | | | | |
| 40 | | | | |
| 41 | | | | |
| 42 | | | | |
| 43 | | | | |
| 44 | | | | |
| 45 | | | | |
| 46 | | | | |
| 47 | | | | |
| 48 | | | | |
| 49 | | | | |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

| | | | | | | | | |
|----|--------------------------------------|---|---------|--------|--------|--------------|-------------|---|
| 1 | | | | | | | | |
| 2 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 3 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 4 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 5 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 6 | PTHR33142,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G20898.1 | 0 |
| 7 | PTHR33142,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G20898.1 | 0 |
| 8 | PTHR33142,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G20898.1 | 0 |
| 9 | PTHR33142,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G20898.1 | 0 |
| 10 | PTHR33142,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G20898.1 | 0 |
| 11 | PTHR33142,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G20898.1 | 0 |
| 12 | PTHR33142,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G20898.1 | 0 |
| 13 | PTHR33142,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G20898.1 | 0 |
| 14 | PTHR33142,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G20898.1 | 0 |
| 15 | PTHR33142,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G20898.1 | 0 |
| 16 | PTHR33142,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G20898.1 | 0 |
| 17 | PTHR33142,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G20898.1 | 0 |
| 18 | PTHR33142,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G20898.1 | 0 |
| 19 | PTHR33142,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G20898.1 | 0 |
| 20 | PTHR33142,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G20898.1 | 0 |
| 21 | PTHR33142,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G20898.1 | 0 |
| 22 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | 0 | 0 | 0 | AT3G63380.1 | 0 |
| 23 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | 0 | 0 | 0 | AT3G63380.1 | 0 |
| 24 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | 0 | 0 | 0 | AT3G63380.1 | 0 |
| 25 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | 0 | 0 | 0 | AT3G63380.1 | 0 |
| 26 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | 0 | 0 | 0 | AT3G63380.1 | 0 |
| 27 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | 0 | 0 | 0 | AT3G63380.1 | 0 |
| 28 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | 0 | 0 | 0 | AT3G63380.1 | 0 |
| 29 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | 0 | 0 | 0 | AT3G63380.1 | 0 |
| 30 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | 0 | 0 | 0 | AT3G63380.1 | 0 |
| 31 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | 0 | 0 | 0 | AT3G63380.1 | 0 |
| 32 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | 0 | 0 | 0 | AT3G63380.1 | 0 |
| 33 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | 0 | 0 | 0 | AT3G63380.1 | 0 |
| 34 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | 0 | 0 | 0 | AT3G63380.1 | 0 |
| 35 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | 0 | 0 | 0 | AT3G63380.1 | 0 |
| 36 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | 0 | 0 | 0 | AT3G63380.1 | 0 |
| 37 | PTHR22904,P ⁻ KOG0548,KOC | | | 0 | K09527 | 0 | AT5G65160.1 | 0 |
| 38 | PTHR22904,P ⁻ KOG0548,KOC | | | 0 | K09527 | 0 | AT5G65160.1 | 0 |
| 39 | PTHR22904,P ⁻ KOG0548,KOC | | | 0 | K09527 | 0 | AT5G65160.1 | 0 |
| 40 | PTHR22904,P ⁻ KOG0548,KOC | | | 0 | K09527 | 0 | AT5G65160.1 | 0 |
| 41 | PTHR22904,P ⁻ KOG0548,KOC | | | 0 | K09527 | 0 | AT5G65160.1 | 0 |
| 42 | PTHR22904,P ⁻ KOG0548,KOC | | | 0 | K09527 | 0 | AT5G65160.1 | 0 |
| 43 | PTHR22904,P ⁻ KOG0548,KOC | | | 0 | K09527 | 0 | AT5G65160.1 | 0 |
| 44 | PTHR22904,P ⁻ KOG0548,KOC | | | 0 | K09527 | 0 | AT5G65160.1 | 0 |
| 45 | PTHR22904,P ⁻ KOG0548,KOC | | | 0 | K09527 | 0 | AT5G65160.1 | 0 |
| 46 | PTHR22904,P ⁻ KOG0548,KOC | | | 0 | K09527 | 0 | AT5G65160.1 | 0 |
| 47 | PTHR22904,P ⁻ KOG0548,KOC | | | 0 | K09527 | 0 | AT5G65160.1 | 0 |
| 48 | PTHR22904,P ⁻ KOG0548,KOC | | | 0 | K09527 | 0 | AT5G65160.1 | 0 |
| 49 | PTHR22904,P ⁻ KOG0548,KOC | | | 0 | K09527 | 0 | AT5G65160.1 | 0 |
| 50 | PTHR22904,P ⁻ KOG0548,KOC | | | 0 | K09527 | 0 | AT5G65160.1 | 0 |
| 51 | PTHR22904,P ⁻ KOG0548,KOC | | | 0 | K09527 | 0 | AT5G65160.1 | 0 |
| 52 | PTHR22904,P ⁻ KOG0548,KOC | | | 0 | K09527 | 0 | AT5G65160.1 | 0 |
| 53 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | K01537 | | GO:0046872,C | AT3G22910.1 | 0 |
| 54 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | K01537 | | GO:0046872,C | AT3G22910.1 | 0 |
| 55 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | K01537 | | GO:0046872,C | AT3G22910.1 | 0 |
| 56 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | K01537 | | GO:0046872,C | AT3G22910.1 | 0 |
| 57 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | K01537 | | GO:0046872,C | AT3G22910.1 | 0 |
| 58 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | K01537 | | GO:0046872,C | AT3G22910.1 | 0 |
| 59 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | K01537 | | GO:0046872,C | AT3G22910.1 | 0 |
| 60 | PTHR24093,P ⁻ | 0 | 3.6.3.8 | K01537 | | GO:0046872,C | AT3G22910.1 | 0 |
| | PTHR24093,P ⁻ | 0 | 3.6.3.8 | K01537 | | GO:0046872,C | AT3G22910.1 | 0 |

| | | | | | |
|----|--------------------------|-----------|----------|--|---|
| 1 | | | | | |
| 2 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | GO:0046872,C AT3G22910.1 | 0 |
| 3 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | GO:0046872,C AT3G22910.1 | 0 |
| 4 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | GO:0046872,C AT3G22910.1 | 0 |
| 5 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | GO:0046872,C AT3G22910.1 | 0 |
| 6 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | GO:0046872,C AT3G22910.1 | 0 |
| 7 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | GO:0046872,C AT3G22910.1 | 0 |
| 8 | PTHR11361,P ⁻ | 0 | 0 | 0 GO:0030983,C AT5G54090.1 | 0 |
| 9 | PTHR11361,P ⁻ | 0 | 0 | 0 GO:0030983,C AT5G54090.1 | 0 |
| 10 | PTHR11361,P ⁻ | 0 | 0 | 0 GO:0030983,C AT5G54090.1 | 0 |
| 11 | PTHR11361,P ⁻ | 0 | 0 | 0 GO:0030983,C AT5G54090.1 | 0 |
| 12 | PTHR11361,P ⁻ | 0 | 0 | 0 GO:0030983,C AT5G54090.1 | 0 |
| 13 | PTHR11361,P ⁻ | 0 | 0 | 0 GO:0030983,C AT5G54090.1 | 0 |
| 14 | PTHR11361,P ⁻ | 0 | 0 | 0 GO:0030983,C AT5G54090.1 | 0 |
| 15 | PTHR11361,P ⁻ | 0 | 0 | 0 GO:0030983,C AT5G54090.1 | 0 |
| 16 | PTHR11361,P ⁻ | 0 | 0 | 0 GO:0030983,C AT5G54090.1 | 0 |
| 17 | PTHR11361,P ⁻ | 0 | 0 | 0 GO:0030983,C AT5G54090.1 | 0 |
| 18 | PTHR11361,P ⁻ | 0 | 0 | 0 GO:0030983,C AT5G54090.1 | 0 |
| 19 | PTHR11361,P ⁻ | 0 | 0 | 0 GO:0030983,C AT5G54090.1 | 0 |
| 20 | PTHR11361,P ⁻ | 0 | 0 | 0 GO:0030983,C AT5G54090.1 | 0 |
| 21 | PTHR11361,P ⁻ | 0 | 0 | 0 GO:0030983,C AT5G54090.1 | 0 |
| 22 | PTHR11361,P ⁻ | 0 | 0 | 0 GO:0030983,C AT5G54090.1 | 0 |
| 23 | PTHR11361,P ⁻ | 0 | 0 | 0 GO:0030983,C AT5G54090.1 | 0 |
| 24 | PTHR12217,P ⁻ | 0 | 0 K15027 | GO:0006413,C AT1G71350.1 | 0 |
| 25 | PTHR12217,P ⁻ | 0 | 0 K15027 | GO:0006413,C AT1G71350.1 | 0 |
| 26 | PTHR12217,P ⁻ | 0 | 0 K15027 | GO:0006413,C AT1G71350.1 | 0 |
| 27 | PTHR12217,P ⁻ | 0 | 0 K15027 | GO:0006413,C AT1G71350.1 | 0 |
| 28 | PTHR12217,P ⁻ | 0 | 0 K15027 | GO:0006413,C AT1G71350.1 | 0 |
| 29 | PTHR12217,P ⁻ | 0 | 0 K15027 | GO:0006413,C AT1G71350.1 | 0 |
| 30 | PTHR12217,P ⁻ | 0 | 0 K15027 | GO:0006413,C AT1G71350.1 | 0 |
| 31 | PTHR12217,P ⁻ | 0 | 0 K15027 | GO:0006413,C AT1G71350.1 | 0 |
| 32 | PTHR12217,P ⁻ | 0 | 0 K15027 | GO:0006413,C AT1G71350.1 | 0 |
| 33 | PTHR12217,P ⁻ | 0 | 0 K15027 | GO:0006413,C AT1G71350.1 | 0 |
| 34 | PTHR12217,P ⁻ | 0 | 0 K15027 | GO:0006413,C AT1G71350.1 | 0 |
| 35 | PTHR12217,P ⁻ | 0 | 0 K15027 | GO:0006413,C AT1G71350.1 | 0 |
| 36 | PTHR12217,P ⁻ | 0 | 0 K15027 | GO:0006413,C AT1G71350.1 | 0 |
| 37 | PTHR12217,P ⁻ | 0 | 0 K15027 | GO:0006413,C AT1G71350.1 | 0 |
| 38 | PTHR12217,P ⁻ | 0 | 0 K15027 | GO:0006413,C AT1G71350.1 | 0 |
| 39 | PTHR12217,P ⁻ | 0 | 0 K15027 | GO:0006413,C AT1G71350.1 | 0 |
| 40 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1 | 0 |
| 41 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1 | 0 |
| 42 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1 | 0 |
| 43 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1 | 0 |
| 44 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1 | 0 |
| 45 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1 | 0 |
| 46 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1 | 0 |
| 47 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1 | 0 |
| 48 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1 | 0 |
| 49 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1 | 0 |
| 50 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1 | 0 |
| 51 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1 | 0 |
| 52 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1 | 0 |
| 53 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1 | 0 |
| 54 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1 | 0 |
| 55 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,C AT2G22840.1 AtGRF1,GRF1 | 0 |
| 56 | PTHR16019,P ⁻ | 0 | 0 | 0 AT1G03350.1 | 0 |
| 57 | PTHR16019,P ⁻ | 0 | 0 | 0 AT1G03350.1 | 0 |
| 58 | PTHR16019,P ⁻ | 0 | 0 | 0 AT1G03350.1 | 0 |
| 59 | PTHR16019,P ⁻ | 0 | 0 | 0 AT1G03350.1 | 0 |
| 60 | PTHR16019,P ⁻ | 0 | 0 | 0 AT1G03350.1 | 0 |
| | PTHR16019,P ⁻ | 0 | 0 | 0 AT1G03350.1 | 0 |

| | | | | | | |
|----|--------------------------|------------|----------|---------------------------------------|--|---|
| 1 | | | | | | |
| 2 | PTHR11246,P ⁻ | 0 | 0 K12869 | GO:0005515,(AT5G41770.1 | | 0 |
| 3 | PTHR11246,P ⁻ | 0 | 0 K12869 | GO:0005515,(AT5G41770.1 | | 0 |
| 4 | PTHR11246,P ⁻ | 0 | 0 K12869 | GO:0005515,(AT5G41770.1 | | 0 |
| 5 | PTHR11246,P ⁻ | 0 | 0 K12869 | GO:0005515,(AT5G41770.1 | | 0 |
| 6 | PTHR11246,P ⁻ | 0 | 0 K12869 | GO:0005515,(AT5G41770.1 | | 0 |
| 7 | PTHR11246,P ⁻ | 0 | 0 K12869 | GO:0005515,(AT5G41770.1 | | 0 |
| 8 | PTHR11246,P ⁻ | 0 | 0 K12869 | GO:0005515,(AT5G41770.1 | | 0 |
| 9 | PTHR11246,P ⁻ | 0 | 0 K12869 | GO:0005515,(AT5G41770.1 | | 0 |
| 10 | PTHR11246,P ⁻ | 0 | 0 K12869 | GO:0005515,(AT5G41770.1 | | 0 |
| 11 | PTHR11246,P ⁻ | 0 | 0 K12869 | GO:0005515,(AT5G41770.1 | | 0 |
| 12 | PTHR11246,P ⁻ | 0 | 0 K12869 | GO:0005515,(AT5G41770.1 | | 0 |
| 13 | PTHR11246,P ⁻ | 0 | 0 K12869 | GO:0005515,(AT5G41770.1 | | 0 |
| 14 | PTHR11246,P ⁻ | 0 | 0 K12869 | GO:0005515,(AT5G41770.1 | | 0 |
| 15 | PTHR23086,P ⁻ | 0 2.7.1.68 | K00889 | GO:0046488,(AT1G10900.1 | | 0 |
| 16 | PTHR23086,P ⁻ | 0 2.7.1.68 | K00889 | GO:0046488,(AT1G10900.1 | | 0 |
| 17 | PTHR23086,P ⁻ | 0 2.7.1.68 | K00889 | GO:0046488,(AT1G10900.1 | | 0 |
| 18 | PTHR23086,P ⁻ | 0 2.7.1.68 | K00889 | GO:0046488,(AT1G10900.1 | | 0 |
| 19 | PTHR23086,P ⁻ | 0 2.7.1.68 | K00889 | GO:0046488,(AT1G10900.1 | | 0 |
| 20 | PTHR23086,P ⁻ | 0 2.7.1.68 | K00889 | GO:0046488,(AT1G10900.1 | | 0 |
| 21 | PTHR23086,P ⁻ | 0 2.7.1.68 | K00889 | GO:0046488,(AT1G10900.1 | | 0 |
| 22 | PTHR23086,P ⁻ | 0 2.7.1.68 | K00889 | GO:0046488,(AT1G10900.1 | | 0 |
| 23 | PTHR23086,P ⁻ | 0 2.7.1.68 | K00889 | GO:0046488,(AT1G10900.1 | | 0 |
| 24 | PTHR23086,P ⁻ | 0 2.7.1.68 | K00889 | GO:0046488,(AT1G10900.1 | | 0 |
| 25 | PTHR23086,P ⁻ | 0 2.7.1.68 | K00889 | GO:0046488,(AT1G10900.1 | | 0 |
| 26 | PTHR23086,P ⁻ | 0 2.7.1.68 | K00889 | GO:0046488,(AT1G10900.1 | | 0 |
| 27 | PTHR23086,P ⁻ | 0 2.7.1.68 | K00889 | GO:0046488,(AT1G10900.1 | | 0 |
| 28 | PTHR23086,P ⁻ | 0 2.7.1.68 | K00889 | GO:0046488,(AT1G10900.1 | | 0 |
| 29 | PTHR23086,P ⁻ | 0 2.7.1.68 | K00889 | GO:0046488,(AT1G10900.1 | | 0 |
| 30 | PTHR23086,P ⁻ | 0 2.7.1.68 | K00889 | GO:0046488,(AT1G10900.1 | | 0 |
| 31 | PTHR24015,P ⁻ | 0 | 0 | 0 AT1G31430.1 | | 0 |
| 32 | PTHR24015,P ⁻ | 0 | 0 | 0 AT1G31430.1 | | 0 |
| 33 | PTHR24015,P ⁻ | 0 | 0 | 0 AT1G31430.1 | | 0 |
| 34 | PTHR24015,P ⁻ | 0 | 0 | 0 AT1G31430.1 | | 0 |
| 35 | PTHR24015,P ⁻ | 0 | 0 | 0 AT1G31430.1 | | 0 |
| 36 | PTHR24015,P ⁻ | 0 | 0 | 0 AT1G31430.1 | | 0 |
| 37 | PTHR24015,P ⁻ | 0 | 0 | 0 AT1G31430.1 | | 0 |
| 38 | PTHR24015,P ⁻ | 0 | 0 | 0 AT1G31430.1 | | 0 |
| 39 | PTHR24015,P ⁻ | 0 | 0 | 0 AT1G31430.1 | | 0 |
| 40 | PTHR24015,P ⁻ | 0 | 0 | 0 AT1G31430.1 | | 0 |
| 41 | PTHR24015,P ⁻ | 0 | 0 | 0 AT1G31430.1 | | 0 |
| 42 | PTHR24015,P ⁻ | 0 | 0 | 0 AT1G31430.1 | | 0 |
| 43 | PTHR24015,P ⁻ | 0 | 0 | 0 AT1G31430.1 | | 0 |
| 44 | PTHR24015,P ⁻ | 0 | 0 | 0 AT1G31430.1 | | 0 |
| 45 | PTHR24015,P ⁻ | 0 | 0 | 0 AT1G31430.1 | | 0 |
| 46 | PTHR24015,P ⁻ | 0 | 0 | 0 AT1G31430.1 | | 0 |
| 47 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 | | 0 |
| 48 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 | | 0 |
| 49 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 | | 0 |
| 50 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 | | 0 |
| 51 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 | | 0 |
| 52 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 | | 0 |
| 53 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 | | 0 |
| 54 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 | | 0 |
| 55 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 | | 0 |
| 56 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 | | 0 |
| 57 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 | | 0 |
| 58 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 | | 0 |
| 59 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 | | 0 |
| 60 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 | | 0 |
| | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 | | 0 |

| | | | | | | |
|----|----------------------------------|----------|----------------|--------------------------|---|--|
| 1 | | | | | | |
| 2 | PTHR19375,P ⁻ | 0 | 0 K03283 | 0 AT1G16030.1 Hsp70b | | |
| 3 | PTHR19375,P ⁻ | 0 | 0 K03283 | 0 AT1G16030.1 Hsp70b | | |
| 4 | PTHR19375,P ⁻ | 0 | 0 K03283 | 0 AT1G16030.1 Hsp70b | | |
| 5 | PTHR19375,P ⁻ | 0 | 0 K03283 | 0 AT1G16030.1 Hsp70b | | |
| 6 | PTHR19375,P ⁻ | 0 | 0 K03283 | 0 AT1G16030.1 Hsp70b | | |
| 7 | PTHR19375,P ⁻ | 0 | 0 K03283 | 0 AT1G16030.1 Hsp70b | | |
| 8 | PTHR19375,P ⁻ | 0 | 0 K03283 | 0 AT1G16030.1 Hsp70b | | |
| 9 | PTHR19375,P ⁻ | 0 | 0 K03283 | 0 AT1G16030.1 Hsp70b | | |
| 10 | PTHR19375,P ⁻ | 0 | 0 K03283 | 0 AT1G16030.1 Hsp70b | | |
| 11 | PTHR19375,P ⁻ | 0 | 0 K03283 | 0 AT1G16030.1 Hsp70b | | |
| 12 | PTHR19375,P ⁻ | 0 | 0 K03283 | 0 AT1G16030.1 Hsp70b | | |
| 13 | PTHR19375,P ⁻ | 0 | 0 K03283 | 0 AT1G16030.1 Hsp70b | | |
| 14 | PTHR19375,P ⁻ | 0 | 0 K03283 | 0 AT1G16030.1 Hsp70b | | |
| 15 | PTHR19375,P ⁻ | 0 | 0 K03283 | 0 AT1G16030.1 Hsp70b | | |
| 16 | PTHR19375,P ⁻ | 0 | 0 K03283 | 0 AT1G16030.1 Hsp70b | | |
| 17 | | | | | | |
| 18 | PTHR22904,P ⁻ KOG4412 | 0 | 0 GO:0005515 | AT3G04710.3 | 0 | |
| 19 | PTHR22904,P ⁻ KOG4412 | 0 | 0 GO:0005515 | AT3G04710.3 | 0 | |
| 20 | PTHR22904,P ⁻ KOG4412 | 0 | 0 GO:0005515 | AT3G04710.3 | 0 | |
| 21 | PTHR22904,P ⁻ KOG4412 | 0 | 0 GO:0005515 | AT3G04710.3 | 0 | |
| 22 | PTHR22904,P ⁻ KOG4412 | 0 | 0 GO:0005515 | AT3G04710.3 | 0 | |
| 23 | PTHR22904,P ⁻ KOG4412 | 0 | 0 GO:0005515 | AT3G04710.3 | 0 | |
| 24 | PTHR22904,P ⁻ KOG4412 | 0 | 0 GO:0005515 | AT3G04710.3 | 0 | |
| 25 | PTHR22904,P ⁻ KOG4412 | 0 | 0 GO:0005515 | AT3G04710.3 | 0 | |
| 26 | PTHR22904,P ⁻ KOG4412 | 0 | 0 GO:0005515 | AT3G04710.3 | 0 | |
| 27 | PTHR22904,P ⁻ KOG4412 | 0 | 0 GO:0005515 | AT3G04710.3 | 0 | |
| 28 | PTHR22904,P ⁻ KOG4412 | 0 | 0 GO:0005515 | AT3G04710.3 | 0 | |
| 29 | PTHR22904,P ⁻ KOG4412 | 0 | 0 GO:0005515 | AT3G04710.3 | 0 | |
| 30 | PTHR22904,P ⁻ KOG4412 | 0 | 0 GO:0005515 | AT3G04710.3 | 0 | |
| 31 | PTHR22904,P ⁻ KOG4412 | 0 | 0 GO:0005515 | AT3G04710.3 | 0 | |
| 32 | PTHR22904,P ⁻ KOG4412 | 0 | 0 GO:0005515 | AT3G04710.3 | 0 | |
| 33 | | | | | | |
| 34 | PTHR19957,P ⁻ KOG0810 | 0 K08486 | GO:0005515,C | AT1G61290.1 ATSYP124,SYP | | |
| 35 | PTHR19957,P ⁻ KOG0810 | 0 K08486 | GO:0005515,C | AT1G61290.1 ATSYP124,SYP | | |
| 36 | PTHR19957,P ⁻ KOG0810 | 0 K08486 | GO:0005515,C | AT1G61290.1 ATSYP124,SYP | | |
| 37 | PTHR19957,P ⁻ KOG0810 | 0 K08486 | GO:0005515,C | AT1G61290.1 ATSYP124,SYP | | |
| 38 | PTHR19957,P ⁻ KOG0810 | 0 K08486 | GO:0005515,C | AT1G61290.1 ATSYP124,SYP | | |
| 39 | PTHR19957,P ⁻ KOG0810 | 0 K08486 | GO:0005515,C | AT1G61290.1 ATSYP124,SYP | | |
| 40 | PTHR19957,P ⁻ KOG0810 | 0 K08486 | GO:0005515,C | AT1G61290.1 ATSYP124,SYP | | |
| 41 | PTHR19957,P ⁻ KOG0810 | 0 K08486 | GO:0005515,C | AT1G61290.1 ATSYP124,SYP | | |
| 42 | PTHR19957,P ⁻ KOG0810 | 0 K08486 | GO:0005515,C | AT1G61290.1 ATSYP124,SYP | | |
| 43 | PTHR19957,P ⁻ KOG0810 | 0 K08486 | GO:0005515,C | AT1G61290.1 ATSYP124,SYP | | |
| 44 | PTHR19957,P ⁻ KOG0810 | 0 K08486 | GO:0005515,C | AT1G61290.1 ATSYP124,SYP | | |
| 45 | PTHR19957,P ⁻ KOG0810 | 0 K08486 | GO:0005515,C | AT1G61290.1 ATSYP124,SYP | | |
| 46 | PTHR19957,P ⁻ KOG0810 | 0 K08486 | GO:0005515,C | AT1G61290.1 ATSYP124,SYP | | |
| 47 | PTHR19957,P ⁻ KOG0810 | 0 K08486 | GO:0005515,C | AT1G61290.1 ATSYP124,SYP | | |
| 48 | PTHR19957,P ⁻ KOG0810 | 0 K08486 | GO:0005515,C | AT1G61290.1 ATSYP124,SYP | | |
| 49 | | | | | | |
| 50 | PTHR31602,P ⁻ | 0 | 0 GO:0006355,C | AT2G36400.1 AtGRF3,GRF3 | | |
| 51 | PTHR31602,P ⁻ | 0 | 0 GO:0006355,C | AT2G36400.1 AtGRF3,GRF3 | | |
| 52 | PTHR31602,P ⁻ | 0 | 0 GO:0006355,C | AT2G36400.1 AtGRF3,GRF3 | | |
| 53 | PTHR31602,P ⁻ | 0 | 0 GO:0006355,C | AT2G36400.1 AtGRF3,GRF3 | | |
| 54 | PTHR31602,P ⁻ | 0 | 0 GO:0006355,C | AT2G36400.1 AtGRF3,GRF3 | | |
| 55 | PTHR31602,P ⁻ | 0 | 0 GO:0006355,C | AT2G36400.1 AtGRF3,GRF3 | | |
| 56 | PTHR31602,P ⁻ | 0 | 0 GO:0006355,C | AT2G36400.1 AtGRF3,GRF3 | | |
| 57 | PTHR31602,P ⁻ | 0 | 0 GO:0006355,C | AT2G36400.1 AtGRF3,GRF3 | | |
| 58 | PTHR31602,P ⁻ | 0 | 0 GO:0006355,C | AT2G36400.1 AtGRF3,GRF3 | | |
| 59 | PTHR31602,P ⁻ | 0 | 0 GO:0006355,C | AT2G36400.1 AtGRF3,GRF3 | | |
| 60 | PTHR31602,P ⁻ | 0 | 0 GO:0006355,C | AT2G36400.1 AtGRF3,GRF3 | | |
| | PTHR31602,P ⁻ | 0 | 0 GO:0006355,C | AT2G36400.1 AtGRF3,GRF3 | | |

| | | | | | | |
|----|--------------------------|---|---|---|--------------------------------------|---|
| 1 | | | | | | |
| 2 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT2G36400.1 AtGRF3,GRF3 | |
| 3 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT2G36400.1 AtGRF3,GRF3 | |
| 4 | PTHR24177 KOG4214 | | 0 | 0 | GO:0008270 AT3G54070.1 | 0 |
| 5 | | | | | | |
| 6 | PTHR24177 KOG4214 | | 0 | 0 | GO:0008270 AT3G54070.1 | 0 |
| 7 | PTHR24177 KOG4214 | | 0 | 0 | GO:0008270 AT3G54070.1 | 0 |
| 8 | PTHR24177 KOG4214 | | 0 | 0 | GO:0008270 AT3G54070.1 | 0 |
| 9 | | | | | | |
| 10 | PTHR24177 KOG4214 | | 0 | 0 | GO:0008270 AT3G54070.1 | 0 |
| 11 | PTHR24177 KOG4214 | | 0 | 0 | GO:0008270 AT3G54070.1 | 0 |
| 12 | PTHR24177 KOG4214 | | 0 | 0 | GO:0008270 AT3G54070.1 | 0 |
| 13 | | | | | | |
| 14 | PTHR24177 KOG4214 | | 0 | 0 | GO:0008270 AT3G54070.1 | 0 |
| 15 | PTHR24177 KOG4214 | | 0 | 0 | GO:0008270 AT3G54070.1 | 0 |
| 16 | PTHR24177 KOG4214 | | 0 | 0 | GO:0008270 AT3G54070.1 | 0 |
| 17 | PTHR24177 KOG4214 | | 0 | 0 | GO:0008270 AT3G54070.1 | 0 |
| 18 | PTHR24177 KOG4214 | | 0 | 0 | GO:0008270 AT3G54070.1 | 0 |
| 19 | PTHR24177 KOG4214 | | 0 | 0 | GO:0008270 AT3G54070.1 | 0 |
| 20 | PTHR24177 | 0 | 0 | 0 | AT3G54070.1 | 0 |
| 21 | PTHR24177 | 0 | 0 | 0 | AT3G54070.1 | 0 |
| 22 | PTHR24177 | 0 | 0 | 0 | AT3G54070.1 | 0 |
| 23 | PTHR24177 | 0 | 0 | 0 | AT3G54070.1 | 0 |
| 24 | PTHR24177 | 0 | 0 | 0 | AT3G54070.1 | 0 |
| 25 | PTHR24177 | 0 | 0 | 0 | AT3G54070.1 | 0 |
| 26 | PTHR24177 | 0 | 0 | 0 | AT3G54070.1 | 0 |
| 27 | PTHR24177 | 0 | 0 | 0 | AT3G54070.1 | 0 |
| 28 | PTHR24177 | 0 | 0 | 0 | AT3G54070.1 | 0 |
| 29 | PTHR24177 | 0 | 0 | 0 | AT3G54070.1 | 0 |
| 30 | PTHR24177 | 0 | 0 | 0 | AT3G54070.1 | 0 |
| 31 | PTHR24177 | 0 | 0 | 0 | AT3G54070.1 | 0 |
| 32 | PTHR24177 | 0 | 0 | 0 | AT3G54070.1 | 0 |
| 33 | PTHR24177 | 0 | 0 | 0 | AT3G54070.1 | 0 |
| 34 | PTHR24177 | 0 | 0 | 0 | AT3G54070.1 | 0 |
| 35 | PTHR24177 | 0 | 0 | 0 | AT3G54070.1 | 0 |
| 36 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 37 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 38 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 39 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 40 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 41 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 42 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 43 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 44 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 45 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 46 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 47 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 48 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 49 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 50 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 51 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 52 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 53 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 54 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 55 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 56 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 57 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 58 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 59 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| 60 | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |
| | PTHR31602,P ⁻ | 0 | 0 | 0 | GO:0006355,C AT4G37740.1 AtGRF2,GRF2 | |

| | | | | |
|----|----------------------------------|----------|------------|---------------------------------------|
| 1 | | | | |
| 2 | PTHR11771,P ⁻ | 0 | 1.13.11.58 | 0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1 |
| 3 | PTHR11771,P ⁻ | 0 | 1.13.11.58 | 0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1 |
| 4 | PTHR11771,P ⁻ | 0 | 1.13.11.58 | 0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1 |
| 5 | PTHR11771,P ⁻ | 0 | 1.13.11.58 | 0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1 |
| 6 | PTHR11771,P ⁻ | 0 | 1.13.11.58 | 0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1 |
| 7 | PTHR11771,P ⁻ | 0 | 1.13.11.58 | 0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1 |
| 8 | PTHR11771,P ⁻ | 0 | 1.13.11.58 | 0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1 |
| 9 | PTHR11771,P ⁻ | 0 | 1.13.11.58 | 0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1 |
| 10 | PTHR11771,P ⁻ | 0 | 1.13.11.58 | 0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1 |
| 11 | PTHR11771,P ⁻ | 0 | 1.13.11.58 | 0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1 |
| 12 | PTHR11771,P ⁻ | 0 | 1.13.11.58 | 0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1 |
| 13 | PTHR11771,P ⁻ | 0 | 1.13.11.58 | 0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1 |
| 14 | PTHR11771,P ⁻ | 0 | 1.13.11.58 | 0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1 |
| 15 | PTHR11771,P ⁻ | 0 | 1.13.11.58 | 0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1 |
| 16 | PTHR11771,P ⁻ | 0 | 1.13.11.58 | 0 GO:0055114,(AT1G55020.1 ATLOX1,LOX1 |
| 17 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 |
| 18 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 |
| 19 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 |
| 20 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 |
| 21 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 |
| 22 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 |
| 23 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 |
| 24 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 |
| 25 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 |
| 26 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 |
| 27 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 |
| 28 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 |
| 29 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 |
| 30 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 |
| 31 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 |
| 32 | PTHR31602,P ⁻ | 0 | 0 | 0 GO:0006355,(AT3G13960.1 AtGRF5,GRF5 |
| 33 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | | 0 GO:0016787,(AT5G26742.2 emb1138 |
| 34 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | | 0 GO:0016787,(AT5G26742.2 emb1138 |
| 35 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | | 0 GO:0016787,(AT5G26742.2 emb1138 |
| 36 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | | 0 GO:0016787,(AT5G26742.2 emb1138 |
| 37 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | | 0 GO:0016787,(AT5G26742.2 emb1138 |
| 38 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | | 0 GO:0016787,(AT5G26742.2 emb1138 |
| 39 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | | 0 GO:0016787,(AT5G26742.2 emb1138 |
| 40 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | | 0 GO:0016787,(AT5G26742.2 emb1138 |
| 41 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | | 0 GO:0016787,(AT5G26742.2 emb1138 |
| 42 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | | 0 GO:0016787,(AT5G26742.2 emb1138 |
| 43 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | | 0 GO:0016787,(AT5G26742.2 emb1138 |
| 44 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | | 0 GO:0016787,(AT5G26742.2 emb1138 |
| 45 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | | 0 GO:0016787,(AT5G26742.2 emb1138 |
| 46 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | | 0 GO:0016787,(AT5G26742.2 emb1138 |
| 47 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | | 0 GO:0016787,(AT5G26742.2 emb1138 |
| 48 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | | 0 GO:0016787,(AT5G26742.2 emb1138 |
| 49 | PTHR32409,P ⁻ | 0 | 0 | 0 GO:0045040,(AT3G27080.1 TOM20-3 |
| 50 | PTHR32409,P ⁻ | 0 | 0 | 0 GO:0045040,(AT3G27080.1 TOM20-3 |
| 51 | PTHR32409,P ⁻ | 0 | 0 | 0 GO:0045040,(AT3G27080.1 TOM20-3 |
| 52 | PTHR32409,P ⁻ | 0 | 0 | 0 GO:0045040,(AT3G27080.1 TOM20-3 |
| 53 | PTHR32409,P ⁻ | 0 | 0 | 0 GO:0045040,(AT3G27080.1 TOM20-3 |
| 54 | PTHR32409,P ⁻ | 0 | 0 | 0 GO:0045040,(AT3G27080.1 TOM20-3 |
| 55 | PTHR32409,P ⁻ | 0 | 0 | 0 GO:0045040,(AT3G27080.1 TOM20-3 |
| 56 | PTHR32409,P ⁻ | 0 | 0 | 0 GO:0045040,(AT3G27080.1 TOM20-3 |
| 57 | PTHR32409,P ⁻ | 0 | 0 | 0 GO:0045040,(AT3G27080.1 TOM20-3 |
| 58 | PTHR32409,P ⁻ | 0 | 0 | 0 GO:0045040,(AT3G27080.1 TOM20-3 |
| 59 | PTHR32409,P ⁻ | 0 | 0 | 0 GO:0045040,(AT3G27080.1 TOM20-3 |
| 60 | PTHR32409,P ⁻ | 0 | 0 | 0 GO:0045040,(AT3G27080.1 TOM20-3 |

| | | | | | | | |
|----|--------------------------|---------|-----------|--------|--------------|-------------|---------|
| 1 | | | | | | | |
| 2 | PTHR32409,P ⁻ | 0 | 0 | 0 | GO:0045040,C | AT3G27080.1 | TOM20-3 |
| 3 | PTHR32409,P ⁻ | 0 | 0 | 0 | GO:0045040,C | AT3G27080.1 | TOM20-3 |
| 4 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 5 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 6 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 7 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 8 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 9 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 10 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 11 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 12 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 13 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 14 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 15 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 16 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 17 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 18 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 19 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 20 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 21 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 22 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 23 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 24 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 25 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 26 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 27 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 28 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 29 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 30 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 31 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 32 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 33 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 34 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 35 | PTHR10589 | KOG1415 | 3.4.19.12 | 0 | GO:0006511,C | AT4G17510.1 | UCH3 |
| 36 | PTHR11727,P ⁻ | KOG0820 | 2.1.1.183 | K14191 | 0 | AT5G66360.2 | 0 |
| 37 | PTHR11727,P ⁻ | KOG0820 | 2.1.1.183 | K14191 | 0 | AT5G66360.2 | 0 |
| 38 | PTHR11727,P ⁻ | KOG0820 | 2.1.1.183 | K14191 | 0 | AT5G66360.2 | 0 |
| 39 | PTHR11727,P ⁻ | KOG0820 | 2.1.1.183 | K14191 | 0 | AT5G66360.2 | 0 |
| 40 | PTHR11727,P ⁻ | KOG0820 | 2.1.1.183 | K14191 | 0 | AT5G66360.2 | 0 |
| 41 | PTHR11727,P ⁻ | KOG0820 | 2.1.1.183 | K14191 | 0 | AT5G66360.2 | 0 |
| 42 | PTHR11727,P ⁻ | KOG0820 | 2.1.1.183 | K14191 | 0 | AT5G66360.2 | 0 |
| 43 | PTHR11727,P ⁻ | KOG0820 | 2.1.1.183 | K14191 | 0 | AT5G66360.2 | 0 |
| 44 | PTHR11727,P ⁻ | KOG0820 | 2.1.1.183 | K14191 | 0 | AT5G66360.2 | 0 |
| 45 | PTHR11727,P ⁻ | KOG0820 | 2.1.1.183 | K14191 | 0 | AT5G66360.2 | 0 |
| 46 | PTHR11727,P ⁻ | KOG0820 | 2.1.1.183 | K14191 | 0 | AT5G66360.2 | 0 |
| 47 | PTHR11727,P ⁻ | KOG0820 | 2.1.1.183 | K14191 | 0 | AT5G66360.2 | 0 |
| 48 | PTHR11727,P ⁻ | KOG0820 | 2.1.1.183 | K14191 | 0 | AT5G66360.2 | 0 |
| 49 | PTHR11727,P ⁻ | KOG0820 | 2.1.1.183 | K14191 | 0 | AT5G66360.2 | 0 |
| 50 | PTHR11727,P ⁻ | KOG0820 | 2.1.1.183 | K14191 | 0 | AT5G66360.2 | 0 |
| 51 | PTHR11727,P ⁻ | KOG0820 | 2.1.1.183 | K14191 | 0 | AT5G66360.2 | 0 |
| 52 | PTHR14003 | 0 | 0 | 0 | 0 | AT4G06634.1 | 0 |
| 53 | PTHR14003 | 0 | 0 | 0 | 0 | AT4G06634.1 | 0 |
| 54 | PTHR14003 | 0 | 0 | 0 | 0 | AT4G06634.1 | 0 |
| 55 | PTHR14003 | 0 | 0 | 0 | 0 | AT4G06634.1 | 0 |
| 56 | PTHR14003 | 0 | 0 | 0 | 0 | AT4G06634.1 | 0 |
| 57 | PTHR14003 | 0 | 0 | 0 | 0 | AT4G06634.1 | 0 |
| 58 | PTHR14003 | 0 | 0 | 0 | 0 | AT4G06634.1 | 0 |
| 59 | PTHR14003 | 0 | 0 | 0 | 0 | AT4G06634.1 | 0 |
| 60 | PTHR14003 | 0 | 0 | 0 | 0 | AT4G06634.1 | 0 |
| | PTHR14003 | 0 | 0 | 0 | 0 | AT4G06634.1 | 0 |

| | | | | | | |
|----|----------------------------------|-----------|----------|---|-------------------------------------|---|
| 1 | | | | | | |
| 2 | PTHR14003 | 0 | 0 | 0 | 0 AT4G06634.1 | 0 |
| 3 | PTHR14003 | 0 | 0 | 0 | 0 AT4G06634.1 | 0 |
| 4 | PTHR14003 | 0 | 0 | 0 | 0 AT4G06634.1 | 0 |
| 5 | | | | | | |
| 6 | PTHR11102,P ⁻ KOG1550 | | 0 K14026 | | 0 AT1G18260.1 | 0 |
| 7 | PTHR11946,P ⁻ | 0 6.1.1.5 | K01870 | | GO:0006418,(AT5G49030.3 OVA2 | |
| 8 | PTHR11946,P ⁻ | 0 6.1.1.5 | K01870 | | GO:0006418,(AT5G49030.3 OVA2 | |
| 9 | | | | | | |
| 10 | PTHR11946,P ⁻ | 0 6.1.1.5 | K01870 | | GO:0006418,(AT5G49030.3 OVA2 | |
| 11 | PTHR11946,P ⁻ | 0 6.1.1.5 | K01870 | | GO:0006418,(AT5G49030.3 OVA2 | |
| 12 | PTHR11946,P ⁻ | 0 6.1.1.5 | K01870 | | GO:0006418,(AT5G49030.3 OVA2 | |
| 13 | | | | | | |
| 14 | PTHR11946,P ⁻ | 0 6.1.1.5 | K01870 | | GO:0006418,(AT5G49030.3 OVA2 | |
| 15 | PTHR11946,P ⁻ | 0 6.1.1.5 | K01870 | | GO:0006418,(AT5G49030.3 OVA2 | |
| 16 | PTHR11946,P ⁻ | 0 6.1.1.5 | K01870 | | GO:0006418,(AT5G49030.3 OVA2 | |
| 17 | | | | | | |
| 18 | PTHR11946,P ⁻ | 0 6.1.1.5 | K01870 | | GO:0006418,(AT5G49030.3 OVA2 | |
| 19 | PTHR11946,P ⁻ | 0 6.1.1.5 | K01870 | | GO:0006418,(AT5G49030.3 OVA2 | |
| 20 | PTHR11946,P ⁻ | 0 6.1.1.5 | K01870 | | GO:0006418,(AT5G49030.3 OVA2 | |
| 21 | | | | | | |
| 22 | PTHR11946,P ⁻ | 0 6.1.1.5 | K01870 | | GO:0006418,(AT5G49030.3 OVA2 | |
| 23 | PTHR24115,P ⁻ KOG0242 | 3.6.4.4 | K11498 | | GO:0008017,(AT3G43210.1 ATNACK2,NAC | |
| 24 | PTHR24115,P ⁻ KOG0242 | 3.6.4.4 | K11498 | | GO:0008017,(AT3G43210.1 ATNACK2,NAC | |
| 25 | | | | | | |
| 26 | PTHR24115,P ⁻ KOG0242 | 3.6.4.4 | K11498 | | GO:0008017,(AT3G43210.1 ATNACK2,NAC | |
| 27 | PTHR24115,P ⁻ KOG0242 | 3.6.4.4 | K11498 | | GO:0008017,(AT3G43210.1 ATNACK2,NAC | |
| 28 | PTHR24115,P ⁻ KOG0242 | 3.6.4.4 | K11498 | | GO:0008017,(AT3G43210.1 ATNACK2,NAC | |
| 29 | | | | | | |
| 30 | PTHR24115,P ⁻ KOG0242 | 3.6.4.4 | K11498 | | GO:0008017,(AT3G43210.1 ATNACK2,NAC | |
| 31 | PTHR24115,P ⁻ KOG0242 | 3.6.4.4 | K11498 | | GO:0008017,(AT3G43210.1 ATNACK2,NAC | |
| 32 | PTHR24115,P ⁻ KOG0242 | 3.6.4.4 | K11498 | | GO:0008017,(AT3G43210.1 ATNACK2,NAC | |
| 33 | | | | | | |
| 34 | PTHR24115,P ⁻ KOG0242 | 3.6.4.4 | K11498 | | GO:0008017,(AT3G43210.1 ATNACK2,NAC | |
| 35 | PTHR24115,P ⁻ KOG0242 | 3.6.4.4 | K11498 | | GO:0008017,(AT3G43210.1 ATNACK2,NAC | |
| 36 | PTHR24115,P ⁻ KOG0242 | 3.6.4.4 | K11498 | | GO:0008017,(AT3G43210.1 ATNACK2,NAC | |
| 37 | | | | | | |
| 38 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT5G57110.2 ACA8,AT-ACA | |
| 39 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT5G57110.2 ACA8,AT-ACA | |
| 40 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT5G57110.2 ACA8,AT-ACA | |
| 41 | | | | | | |
| 42 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT5G57110.2 ACA8,AT-ACA | |
| 43 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT5G57110.2 ACA8,AT-ACA | |
| 44 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT5G57110.2 ACA8,AT-ACA | |
| 45 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT5G57110.2 ACA8,AT-ACA | |
| 46 | | | | | | |
| 47 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT5G57110.2 ACA8,AT-ACA | |
| 48 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT5G57110.2 ACA8,AT-ACA | |
| 49 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT5G57110.2 ACA8,AT-ACA | |
| 50 | | | | | | |
| 51 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT5G57110.2 ACA8,AT-ACA | |
| 52 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT5G57110.2 ACA8,AT-ACA | |
| 53 | | | | | | |
| 54 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT5G57110.2 ACA8,AT-ACA | |
| 55 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT5G57110.2 ACA8,AT-ACA | |
| 56 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT5G57110.2 ACA8,AT-ACA | |
| 57 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT5G57110.2 ACA8,AT-ACA | |
| 58 | | | | | | |
| 59 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT5G57110.2 ACA8,AT-ACA | |
| 60 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT5G57110.2 ACA8,AT-ACA | |
| | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | | GO:0005516,(AT5G57110.2 ACA8,AT-ACA | |

| | | | | | | |
|----|--------------------------|-----------|----------|---------------------------------------|--|---|
| 1 | | | | | | |
| 2 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | GO:0005516,(AT5G57110.2 ACA8,AT-ACA8 | | |
| 3 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | GO:0005516,(AT5G57110.2 ACA8,AT-ACA8 | | |
| 4 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | GO:0005516,(AT5G57110.2 ACA8,AT-ACA8 | | |
| 5 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | GO:0005516,(AT5G57110.2 ACA8,AT-ACA8 | | |
| 6 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | GO:0005516,(AT5G57110.2 ACA8,AT-ACA8 | | |
| 7 | PTHR24093,P ⁻ | 0 3.6.3.8 | K01537 | GO:0005516,(AT5G57110.2 ACA8,AT-ACA8 | | |
| 8 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02358 | GO:0005525 AT4G20360.1 ATRAB8D,ATR | | |
| 9 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02358 | GO:0005525 AT4G20360.1 ATRAB8D,ATR | | |
| 10 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02358 | GO:0005525 AT4G20360.1 ATRAB8D,ATR | | |
| 11 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02358 | GO:0005525 AT4G20360.1 ATRAB8D,ATR | | |
| 12 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02358 | GO:0005525 AT4G20360.1 ATRAB8D,ATR | | |
| 13 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02358 | GO:0005525 AT4G20360.1 ATRAB8D,ATR | | |
| 14 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02358 | GO:0005525 AT4G20360.1 ATRAB8D,ATR | | |
| 15 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02358 | GO:0005525 AT4G20360.1 ATRAB8D,ATR | | |
| 16 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02358 | GO:0005525 AT4G20360.1 ATRAB8D,ATR | | |
| 17 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02358 | GO:0005525 AT4G20360.1 ATRAB8D,ATR | | |
| 18 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02358 | GO:0005525 AT4G20360.1 ATRAB8D,ATR | | |
| 19 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02358 | GO:0005525 AT4G20360.1 ATRAB8D,ATR | | |
| 20 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02358 | GO:0005525 AT4G20360.1 ATRAB8D,ATR | | |
| 21 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02358 | GO:0005525 AT4G20360.1 ATRAB8D,ATR | | |
| 22 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02358 | GO:0005525 AT4G20360.1 ATRAB8D,ATR | | |
| 23 | PTHR23115,P ⁻ | 0 3.6.5.3 | K02358 | GO:0005525 AT4G20360.1 ATRAB8D,ATR | | |
| 24 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(AT3G27870.1 | | 0 |
| 25 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(AT3G27870.1 | | 0 |
| 26 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(AT3G27870.1 | | 0 |
| 27 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(AT3G27870.1 | | 0 |
| 28 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(AT3G27870.1 | | 0 |
| 29 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(AT3G27870.1 | | 0 |
| 30 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(AT3G27870.1 | | 0 |
| 31 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(AT3G27870.1 | | 0 |
| 32 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(AT3G27870.1 | | 0 |
| 33 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(AT3G27870.1 | | 0 |
| 34 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(AT3G27870.1 | | 0 |
| 35 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(AT3G27870.1 | | 0 |
| 36 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(AT3G27870.1 | | 0 |
| 37 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(AT3G27870.1 | | 0 |
| 38 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(AT3G27870.1 | | 0 |
| 39 | PTHR24092,P ⁻ | 0 3.6.3.1 | K01530 | GO:0046872,(AT3G27870.1 | | 0 |
| 40 | PTHR33178,P ⁻ | 0 | 0 | 0 AT5G22580.1 | | 0 |
| 41 | PTHR33178,P ⁻ | 0 | 0 | 0 AT5G22580.1 | | 0 |
| 42 | PTHR33178,P ⁻ | 0 | 0 | 0 AT5G22580.1 | | 0 |
| 43 | PTHR33178,P ⁻ | 0 | 0 | 0 AT5G22580.1 | | 0 |
| 44 | PTHR33178,P ⁻ | 0 | 0 | 0 AT5G22580.1 | | 0 |
| 45 | PTHR33178,P ⁻ | 0 | 0 | 0 AT5G22580.1 | | 0 |
| 46 | PTHR33178,P ⁻ | 0 | 0 | 0 AT5G22580.1 | | 0 |
| 47 | PTHR33178,P ⁻ | 0 | 0 | 0 AT5G22580.1 | | 0 |
| 48 | PTHR33178,P ⁻ | 0 | 0 | 0 AT5G22580.1 | | 0 |
| 49 | PTHR33178,P ⁻ | 0 | 0 | 0 AT5G22580.1 | | 0 |
| 50 | PTHR33178,P ⁻ | 0 | 0 | 0 AT5G22580.1 | | 0 |
| 51 | PTHR33178,P ⁻ | 0 | 0 | 0 AT5G22580.1 | | 0 |
| 52 | PTHR33178,P ⁻ | 0 | 0 | 0 AT5G22580.1 | | 0 |
| 53 | PTHR33178,P ⁻ | 0 | 0 | 0 AT5G22580.1 | | 0 |
| 54 | PTHR33178,P ⁻ | 0 | 0 | 0 AT5G22580.1 | | 0 |
| 55 | PTHR33178,P ⁻ | 0 | 0 | 0 AT5G22580.1 | | 0 |
| 56 | PTHR18359 | 0 | 0 K14553 | GO:0005515 AT5G14050.1 | | 0 |
| 57 | PTHR18359 | 0 | 0 K14553 | GO:0005515 AT5G14050.1 | | 0 |
| 58 | PTHR18359 | 0 | 0 K14553 | GO:0005515 AT5G14050.1 | | 0 |
| 59 | PTHR18359 | 0 | 0 K14553 | GO:0005515 AT5G14050.1 | | 0 |
| 60 | PTHR18359 | 0 | 0 K14553 | GO:0005515 AT5G14050.1 | | 0 |
| | PTHR18359 | 0 | 0 K14553 | GO:0005515 AT5G14050.1 | | 0 |

| | | | | | | |
|----|----------------------------------|-----------|----------|--------------|------------------------|---|
| 1 | | | | | | |
| 2 | PTHR18359 | 0 | 0 K14553 | GO:0005515 | AT5G14050.1 | 0 |
| 3 | PTHR18359 | 0 | 0 K14553 | GO:0005515 | AT5G14050.1 | 0 |
| 4 | PTHR18359 | 0 | 0 K14553 | GO:0005515 | AT5G14050.1 | 0 |
| 5 | PTHR18359 | 0 | 0 K14553 | GO:0005515 | AT5G14050.1 | 0 |
| 6 | PTHR18359 | 0 | 0 K14553 | GO:0005515 | AT5G14050.1 | 0 |
| 7 | PTHR18359 | 0 | 0 K14553 | GO:0005515 | AT5G14050.1 | 0 |
| 8 | PTHR18359 | 0 | 0 K14553 | GO:0005515 | AT5G14050.1 | 0 |
| 9 | PTHR18359 | 0 | 0 K14553 | GO:0005515 | AT5G14050.1 | 0 |
| 10 | PTHR18359 | 0 | 0 K14553 | GO:0005515 | AT5G14050.1 | 0 |
| 11 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 12 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 13 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 14 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 15 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 16 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 17 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 18 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 19 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 20 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 21 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 22 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 23 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 24 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 25 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 26 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 27 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 28 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 29 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 30 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 31 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 32 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 33 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 34 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 35 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 36 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 37 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 38 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 39 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 40 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G11460.1 | 0 |
| 41 | PTHR24096,P ⁻ | 0 6.2.1.3 | K01897 | GO:0008152,(| AT2G47240.1 CER8,LACS1 | |
| 42 | PTHR24096,P ⁻ | 0 6.2.1.3 | K01897 | GO:0008152,(| AT2G47240.1 CER8,LACS1 | |
| 43 | PTHR24096,P ⁻ | 0 6.2.1.3 | K01897 | GO:0008152,(| AT2G47240.1 CER8,LACS1 | |
| 44 | PTHR24096,P ⁻ | 0 6.2.1.3 | K01897 | GO:0008152,(| AT2G47240.1 CER8,LACS1 | |
| 45 | PTHR24096,P ⁻ | 0 6.2.1.3 | K01897 | GO:0008152,(| AT2G47240.1 CER8,LACS1 | |
| 46 | PTHR24096,P ⁻ | 0 6.2.1.3 | K01897 | GO:0008152,(| AT2G47240.1 CER8,LACS1 | |
| 47 | PTHR24096,P ⁻ | 0 6.2.1.3 | K01897 | GO:0008152,(| AT2G47240.1 CER8,LACS1 | |
| 48 | PTHR24096,P ⁻ | 0 6.2.1.3 | K01897 | GO:0008152,(| AT2G47240.1 CER8,LACS1 | |
| 49 | PTHR24096,P ⁻ | 0 6.2.1.3 | K01897 | GO:0008152,(| AT2G47240.1 CER8,LACS1 | |
| 50 | PTHR24096,P ⁻ | 0 6.2.1.3 | K01897 | GO:0008152,(| AT2G47240.1 CER8,LACS1 | |
| 51 | PTHR24096,P ⁻ | 0 6.2.1.3 | K01897 | GO:0008152,(| AT2G47240.1 CER8,LACS1 | |
| 52 | PTHR24096,P ⁻ | 0 6.2.1.3 | K01897 | GO:0008152,(| AT2G47240.1 CER8,LACS1 | |
| 53 | PTHR24096,P ⁻ | 0 6.2.1.3 | K01897 | GO:0008152,(| AT2G47240.1 CER8,LACS1 | |
| 54 | PTHR24096,P ⁻ | 0 6.2.1.3 | K01897 | GO:0008152,(| AT2G47240.1 CER8,LACS1 | |
| 55 | PTHR24096,P ⁻ | 0 6.2.1.3 | K01897 | GO:0008152,(| AT2G47240.1 CER8,LACS1 | |
| 56 | PTHR24096,P ⁻ | 0 6.2.1.3 | K01897 | GO:0008152,(| AT2G47240.1 CER8,LACS1 | |
| 57 | PTHR23241,P ⁻ KOG4744 | | 0 | 0 | 0 AT3G53040.1 | 0 |
| 58 | PTHR23241,P ⁻ KOG4744 | | 0 | 0 | 0 AT3G53040.1 | 0 |
| 59 | PTHR23241,P ⁻ KOG4744 | | 0 | 0 | 0 AT3G53040.1 | 0 |
| 60 | PTHR23241,P ⁻ KOG4744 | | 0 | 0 | 0 AT3G53040.1 | 0 |

| | | | | | |
|----|----------------------------------|-------------|---|------------------------|---|
| 1 | | | | | |
| 2 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 3 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 4 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 5 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 6 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 7 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 8 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 9 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 10 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 11 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 12 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 13 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 14 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 15 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 16 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 17 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 18 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 19 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 20 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 21 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 22 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 23 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 24 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 25 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 26 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 27 | PTHR23241,P ⁻ KOG4744 | 0 | 0 | 0 AT3G53040.1 | 0 |
| 28 | PTHR31642,P ⁻ | 0 2.3.1.196 | 0 | GO:0016747 AT5G17540.1 | 0 |
| 29 | PTHR31642,P ⁻ | 0 2.3.1.196 | 0 | GO:0016747 AT5G17540.1 | 0 |
| 30 | PTHR31642,P ⁻ | 0 2.3.1.196 | 0 | GO:0016747 AT5G17540.1 | 0 |
| 31 | PTHR31642,P ⁻ | 0 2.3.1.196 | 0 | GO:0016747 AT5G17540.1 | 0 |
| 32 | PTHR31642,P ⁻ | 0 2.3.1.196 | 0 | GO:0016747 AT5G17540.1 | 0 |
| 33 | PTHR31642,P ⁻ | 0 2.3.1.196 | 0 | GO:0016747 AT5G17540.1 | 0 |
| 34 | PTHR31642,P ⁻ | 0 2.3.1.196 | 0 | GO:0016747 AT5G17540.1 | 0 |
| 35 | PTHR31642,P ⁻ | 0 2.3.1.196 | 0 | GO:0016747 AT5G17540.1 | 0 |
| 36 | PTHR31642,P ⁻ | 0 2.3.1.196 | 0 | GO:0016747 AT5G17540.1 | 0 |
| 37 | PTHR31642,P ⁻ | 0 2.3.1.196 | 0 | GO:0016747 AT5G17540.1 | 0 |
| 38 | PTHR31642,P ⁻ | 0 2.3.1.196 | 0 | GO:0016747 AT5G17540.1 | 0 |
| 39 | PTHR31642,P ⁻ | 0 2.3.1.196 | 0 | GO:0016747 AT5G17540.1 | 0 |
| 40 | PTHR31642,P ⁻ | 0 2.3.1.196 | 0 | GO:0016747 AT5G17540.1 | 0 |
| 41 | PTHR31642,P ⁻ | 0 2.3.1.196 | 0 | GO:0016747 AT5G17540.1 | 0 |
| 42 | PTHR31642,P ⁻ | 0 2.3.1.196 | 0 | GO:0016747 AT5G17540.1 | 0 |
| 43 | PTHR31642,P ⁻ | 0 2.3.1.196 | 0 | GO:0016747 AT5G17540.1 | 0 |
| 44 | PTHR23155,P ⁻ KOG4658 | 0 | 0 | GO:0005515,CA4G10780.1 | 0 |
| 45 | PTHR23155,P ⁻ KOG4658 | 0 | 0 | GO:0005515,CA4G10780.1 | 0 |
| 46 | PTHR23155,P ⁻ KOG4658 | 0 | 0 | GO:0005515,CA4G10780.1 | 0 |
| 47 | PTHR23155,P ⁻ KOG4658 | 0 | 0 | GO:0005515,CA4G10780.1 | 0 |
| 48 | PTHR23155,P ⁻ KOG4658 | 0 | 0 | GO:0005515,CA4G10780.1 | 0 |
| 49 | PTHR23155,P ⁻ KOG4658 | 0 | 0 | GO:0005515,CA4G10780.1 | 0 |
| 50 | PTHR23155,P ⁻ KOG4658 | 0 | 0 | GO:0005515,CA4G10780.1 | 0 |
| 51 | PTHR23155,P ⁻ KOG4658 | 0 | 0 | GO:0005515,CA4G10780.1 | 0 |
| 52 | PTHR23155,P ⁻ KOG4658 | 0 | 0 | GO:0005515,CA4G10780.1 | 0 |
| 53 | PTHR23155,P ⁻ KOG4658 | 0 | 0 | GO:0005515,CA4G10780.1 | 0 |
| 54 | PTHR23155,P ⁻ KOG4658 | 0 | 0 | GO:0005515,CA4G10780.1 | 0 |
| 55 | PTHR23155,P ⁻ KOG4658 | 0 | 0 | GO:0005515,CA4G10780.1 | 0 |
| 56 | PTHR23155,P ⁻ KOG4658 | 0 | 0 | GO:0005515,CA4G10780.1 | 0 |
| 57 | PTHR23155,P ⁻ KOG4658 | 0 | 0 | GO:0005515,CA4G10780.1 | 0 |
| 58 | PTHR23155,P ⁻ KOG4658 | 0 | 0 | GO:0005515,CA4G10780.1 | 0 |
| 59 | PTHR24015,P ⁻ | 0 | 0 | 0 AT4G19890.1 | 0 |
| 60 | PTHR24015,P ⁻ | 0 | 0 | 0 AT4G19890.1 | 0 |
| | PTHR24015,P ⁻ | 0 | 0 | 0 AT4G19890.1 | 0 |

| | | | | | | |
|----|--------------------------|---|---|---|--------------------|---|
| 1 | | | | | | |
| 2 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 3 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 4 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 5 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 6 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 7 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 8 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 9 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 10 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 11 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 12 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 13 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 14 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 15 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 16 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 17 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 18 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 19 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 20 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 21 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 22 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 23 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 24 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 25 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 26 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT4G19890.1 | 0 |
| 27 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 28 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 29 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 30 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 31 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 32 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 33 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 34 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 35 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 36 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 37 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 38 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 39 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 40 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 41 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 42 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 43 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 44 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 45 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 46 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 47 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 48 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 49 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 50 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 51 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 52 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 53 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 54 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 55 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 56 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 57 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 58 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 59 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| 60 | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |
| | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 | |

| | | | | | | |
|----|--------------------------|---------|-----------|---|-------------------------------------|--------------------|
| 1 | | | | | | |
| 2 | | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 |
| 3 | | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 |
| 4 | | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 |
| 5 | | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 |
| 6 | | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 |
| 7 | | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 |
| 8 | | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 |
| 9 | | 0 | 0 | 0 | 0 | 0 AT5G02130.1 NDP1 |
| 10 | PTHR13522 | KOG3102 | | 0 | 0 GO:0034477,(AT5G51170.1 | 0 |
| 11 | PTHR13522 | KOG3102 | | 0 | 0 GO:0034477,(AT5G51170.1 | 0 |
| 12 | PTHR13522 | KOG3102 | | 0 | 0 GO:0034477,(AT5G51170.1 | 0 |
| 13 | PTHR13522 | KOG3102 | | 0 | 0 GO:0034477,(AT5G51170.1 | 0 |
| 14 | PTHR13522 | KOG3102 | | 0 | 0 GO:0034477,(AT5G51170.1 | 0 |
| 15 | PTHR13522 | KOG3102 | | 0 | 0 GO:0034477,(AT5G51170.1 | 0 |
| 16 | PTHR13522 | KOG3102 | | 0 | 0 GO:0034477,(AT5G51170.1 | 0 |
| 17 | PTHR13522 | KOG3102 | | 0 | 0 GO:0034477,(AT5G51170.1 | 0 |
| 18 | PTHR13522 | KOG3102 | | 0 | 0 GO:0034477,(AT5G51170.1 | 0 |
| 19 | PTHR13522 | KOG3102 | | 0 | 0 GO:0034477,(AT5G51170.1 | 0 |
| 20 | PTHR13522 | KOG3102 | | 0 | 0 GO:0034477,(AT5G51170.1 | 0 |
| 21 | PTHR13522 | KOG3102 | | 0 | 0 GO:0034477,(AT5G51170.1 | 0 |
| 22 | PTHR13522 | KOG3102 | | 0 | 0 GO:0034477,(AT5G51170.1 | 0 |
| 23 | PTHR13522 | KOG3102 | | 0 | 0 GO:0034477,(AT5G51170.1 | 0 |
| 24 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 25 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 26 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 27 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 28 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 29 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 30 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 31 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 32 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 33 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 34 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 35 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 36 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 37 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 38 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 39 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 40 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 41 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 42 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 43 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 44 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 45 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 46 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 47 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 48 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 49 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 50 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 51 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 52 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 53 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 54 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 55 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.23 | | 0 GO:0003723,(AT1G76050.2 | 0 |
| 56 | PTHR11945,P ⁻ | KOG0014 | | 0 | 0 GO:0006355,(AT2G22540.1 AGL22,SVP | |
| 57 | PTHR11945,P ⁻ | KOG0014 | | 0 | 0 GO:0006355,(AT2G22540.1 AGL22,SVP | |
| 58 | PTHR11945,P ⁻ | KOG0014 | | 0 | 0 GO:0006355,(AT2G22540.1 AGL22,SVP | |
| 59 | PTHR11945,P ⁻ | KOG0014 | | 0 | 0 GO:0006355,(AT2G22540.1 AGL22,SVP | |
| 60 | PTHR11945,P ⁻ | KOG0014 | | 0 | 0 GO:0006355,(AT2G22540.1 AGL22,SVP | |

| | | | | | | |
|----|----------------------------------|---|---|---|------------------------------------|---|
| 1 | | | | | | |
| 2 | PTHR11945,P ⁻ KOG0014 | | 0 | 0 | GO:0006355,C AT2G22540.1 AGL22,SVP | |
| 3 | PTHR11945,P ⁻ KOG0014 | | 0 | 0 | GO:0006355,C AT2G22540.1 AGL22,SVP | |
| 4 | PTHR11945,P ⁻ KOG0014 | | 0 | 0 | GO:0006355,C AT2G22540.1 AGL22,SVP | |
| 5 | PTHR11945,P ⁻ KOG0014 | | 0 | 0 | GO:0006355,C AT2G22540.1 AGL22,SVP | |
| 6 | PTHR11945,P ⁻ KOG0014 | | 0 | 0 | GO:0006355,C AT2G22540.1 AGL22,SVP | |
| 7 | PTHR11945,P ⁻ KOG0014 | | 0 | 0 | GO:0006355,C AT2G22540.1 AGL22,SVP | |
| 8 | PTHR11945,P ⁻ KOG0014 | | 0 | 0 | GO:0006355,C AT2G22540.1 AGL22,SVP | |
| 9 | PTHR11945,P ⁻ KOG0014 | | 0 | 0 | GO:0006355,C AT2G22540.1 AGL22,SVP | |
| 10 | PTHR11945,P ⁻ KOG0014 | | 0 | 0 | GO:0006355,C AT2G22540.1 AGL22,SVP | |
| 11 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT2G04860.1 | 0 |
| 12 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT2G04860.1 | 0 |
| 13 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT2G04860.1 | 0 |
| 14 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT2G04860.1 | 0 |
| 15 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT2G04860.1 | 0 |
| 16 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT2G04860.1 | 0 |
| 17 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT2G04860.1 | 0 |
| 18 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT2G04860.1 | 0 |
| 19 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT2G04860.1 | 0 |
| 20 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT2G04860.1 | 0 |
| 21 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT2G04860.1 | 0 |
| 22 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT2G04860.1 | 0 |
| 23 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT2G04860.1 | 0 |
| 24 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT2G04860.1 | 0 |
| 25 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT2G04860.1 | 0 |
| 26 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 27 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 28 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 29 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 30 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 31 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 32 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 33 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 34 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 35 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 36 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 37 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 38 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 39 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 40 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 41 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 42 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 43 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 44 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 45 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 46 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 47 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 48 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 49 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 50 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 51 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 52 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 53 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 54 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 55 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 56 | PTHR31115,P ⁻ | 0 | 0 | 0 | AT4G29790.1 | 0 |
| 57 | PTHR13780,P ⁻ | 0 | 0 | 0 | AT1G09020.1 ATSNF4,SNF4 | |
| 58 | PTHR13780,P ⁻ | 0 | 0 | 0 | AT1G09020.1 ATSNF4,SNF4 | |
| 59 | PTHR13780,P ⁻ | 0 | 0 | 0 | AT1G09020.1 ATSNF4,SNF4 | |
| 60 | PTHR13780,P ⁻ | 0 | 0 | 0 | AT1G09020.1 ATSNF4,SNF4 | |

| | | | | | |
|----|----------------------------------|--------------|----------|----------------|---------------------------|
| 1 | | | | | |
| 2 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 3 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 4 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 5 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 6 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 7 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 8 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 9 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 10 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 11 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 12 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 13 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 14 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 15 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 16 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 17 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 18 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 19 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 20 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 21 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 22 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 23 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 24 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 25 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 26 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 27 | PTHR13780,P ⁻ | 0 | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 28 | PTHR11771,P ⁻ | 0 1.13.11.58 | K15718 | GO:0005515,(| AT1G55020.1 ATLOX1,LOX1 |
| 29 | PTHR11771,P ⁻ | 0 1.13.11.58 | K15718 | GO:0005515,(| AT1G55020.1 ATLOX1,LOX1 |
| 30 | PTHR13878,P ⁻ | 0 1.5.99.12 | K00279 | GO:0055114,(| AT3G63440.1 ATCKX6,ATCK |
| 31 | PTHR13878,P ⁻ | 0 1.5.99.12 | K00279 | GO:0055114,(| AT3G63440.1 ATCKX6,ATCK |
| 32 | PTHR13878,P ⁻ | 0 1.5.99.12 | K00279 | GO:0055114,(| AT3G63440.1 ATCKX6,ATCK |
| 33 | PTHR13878,P ⁻ | 0 1.5.99.12 | K00279 | GO:0055114,(| AT3G63440.1 ATCKX6,ATCK |
| 34 | PTHR13878,P ⁻ | 0 1.5.99.12 | K00279 | GO:0055114,(| AT3G63440.1 ATCKX6,ATCK |
| 35 | PTHR13878,P ⁻ | 0 1.5.99.12 | K00279 | GO:0055114,(| AT3G63440.1 ATCKX6,ATCK |
| 36 | PTHR13878,P ⁻ | 0 1.5.99.12 | K00279 | GO:0055114,(| AT3G63440.1 ATCKX6,ATCK |
| 37 | PTHR13878,P ⁻ | 0 1.5.99.12 | K00279 | GO:0055114,(| AT3G63440.1 ATCKX6,ATCK |
| 38 | PTHR13878,P ⁻ | 0 1.5.99.12 | K00279 | GO:0055114,(| AT3G63440.1 ATCKX6,ATCK |
| 39 | PTHR13878,P ⁻ | 0 1.5.99.12 | K00279 | GO:0055114,(| AT3G63440.1 ATCKX6,ATCK |
| 40 | PTHR13878,P ⁻ | 0 1.5.99.12 | K00279 | GO:0055114,(| AT3G63440.1 ATCKX6,ATCK |
| 41 | PTHR13878,P ⁻ | 0 1.5.99.12 | K00279 | GO:0055114,(| AT3G63440.1 ATCKX6,ATCK |
| 42 | PTHR13878,P ⁻ | 0 1.5.99.12 | K00279 | GO:0055114,(| AT3G63440.1 ATCKX6,ATCK |
| 43 | PTHR13878,P ⁻ | 0 1.5.99.12 | K00279 | GO:0055114,(| AT3G63440.1 ATCKX6,ATCK |
| 44 | PTHR13878,P ⁻ | 0 1.5.99.12 | K00279 | GO:0055114,(| AT3G63440.1 ATCKX6,ATCK |
| 45 | PTHR23428 KOG1744 | | 0 K11252 | GO:0003677,(| AT1G08170.1 0 |
| 46 | PTHR23428 KOG1744 | | 0 K11252 | GO:0003677,(| AT1G08170.1 0 |
| 47 | PTHR23428 KOG1744 | | 0 K11252 | GO:0003677,(| AT1G08170.1 0 |
| 48 | PTHR23428 KOG1744 | | 0 K11252 | GO:0003677,(| AT1G08170.1 0 |
| 49 | PTHR23428 KOG1744 | | 0 K11252 | GO:0003677,(| AT1G08170.1 0 |
| 50 | PTHR23428 KOG1744 | | 0 K11252 | GO:0003677,(| AT1G08170.1 0 |
| 51 | PTHR23428 KOG1744 | | 0 K11252 | GO:0003677,(| AT1G08170.1 0 |
| 52 | PTHR23428 KOG1744 | | 0 K11252 | GO:0003677,(| AT1G08170.1 0 |
| 53 | PTHR23428 KOG1744 | | 0 K11252 | GO:0003677,(| AT1G08170.1 0 |
| 54 | PTHR23428 KOG1744 | | 0 K11252 | GO:0003677,(| AT1G08170.1 0 |
| 55 | PTHR23428 KOG1744 | | 0 K11252 | GO:0003677,(| AT1G08170.1 0 |
| 56 | PTHR23428 KOG1744 | | 0 K11252 | GO:0003677,(| AT1G08170.1 0 |
| 57 | PTHR23428 KOG1744 | | 0 K11252 | GO:0003677,(| AT1G08170.1 0 |
| 58 | PTHR23428 KOG1744 | | 0 K11252 | GO:0003677,(| AT1G08170.1 0 |
| 59 | PTHR23428 KOG1744 | | 0 K11252 | GO:0003677,(| AT1G08170.1 0 |
| 60 | PTHR23428 KOG1744 | | 0 K11252 | GO:0003677,(| AT1G08170.1 0 |
| | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | | 0 GO:0016757,(| AT4G33330.2 GUX2,PGSIP3 |

| | | | |
|----|----------------------------------|------------|--|
| 1 | | | |
| 2 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 3 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 4 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 5 | | | |
| 6 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 7 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 8 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 9 | | | |
| 10 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 11 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 12 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 13 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 14 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 15 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 16 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 17 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 18 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 19 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 20 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 21 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 22 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 23 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 24 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 25 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 26 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 27 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 28 | PTHR11183,P ⁻ KOG1950 | 2.4.1.17 | 0 GO:0016757,(AT4G33330.2 GUX2,PGSIP3 |
| 29 | | | |
| 30 | PTHR10209,P ⁻ KOG0143 | 0 K04124 | GO:0055114,(AT1G15550.1 ATGA3OX1,G/ |
| 31 | PTHR10209,P ⁻ KOG0143 | 0 K04124 | GO:0055114,(AT1G15550.1 ATGA3OX1,G/ |
| 32 | PTHR10209,P ⁻ KOG0143 | 0 K04124 | GO:0055114,(AT1G15550.1 ATGA3OX1,G/ |
| 33 | PTHR10209,P ⁻ KOG0143 | 0 K04124 | GO:0055114,(AT1G15550.1 ATGA3OX1,G/ |
| 34 | PTHR10209,P ⁻ KOG0143 | 0 K04124 | GO:0055114,(AT1G15550.1 ATGA3OX1,G/ |
| 35 | PTHR10209,P ⁻ KOG0143 | 0 K04124 | GO:0055114,(AT1G15550.1 ATGA3OX1,G/ |
| 36 | PTHR10209,P ⁻ KOG0143 | 0 K04124 | GO:0055114,(AT1G15550.1 ATGA3OX1,G/ |
| 37 | PTHR10209,P ⁻ KOG0143 | 0 K04124 | GO:0055114,(AT1G15550.1 ATGA3OX1,G/ |
| 38 | PTHR10209,P ⁻ KOG0143 | 0 K04124 | GO:0055114,(AT1G15550.1 ATGA3OX1,G/ |
| 39 | PTHR10209,P ⁻ KOG0143 | 0 K04124 | GO:0055114,(AT1G15550.1 ATGA3OX1,G/ |
| 40 | PTHR10209,P ⁻ KOG0143 | 0 K04124 | GO:0055114,(AT1G15550.1 ATGA3OX1,G/ |
| 41 | PTHR10209,P ⁻ KOG0143 | 0 K04124 | GO:0055114,(AT1G15550.1 ATGA3OX1,G/ |
| 42 | PTHR10209,P ⁻ KOG0143 | 0 K04124 | GO:0055114,(AT1G15550.1 ATGA3OX1,G/ |
| 43 | PTHR10209,P ⁻ KOG0143 | 0 K04124 | GO:0055114,(AT1G15550.1 ATGA3OX1,G/ |
| 44 | PTHR10209,P ⁻ KOG0143 | 0 K04124 | GO:0055114,(AT1G15550.1 ATGA3OX1,G/ |
| 45 | PTHR10277,P ⁻ | 0 2.3.3.13 | 0 GO:0009098,(AT1G18500.1 IPMS1,MAML |
| 46 | PTHR10277,P ⁻ | 0 2.3.3.13 | 0 GO:0009098,(AT1G18500.1 IPMS1,MAML |
| 47 | PTHR10277,P ⁻ | 0 2.3.3.13 | 0 GO:0009098,(AT1G18500.1 IPMS1,MAML |
| 48 | PTHR10277,P ⁻ | 0 2.3.3.13 | 0 GO:0009098,(AT1G18500.1 IPMS1,MAML |
| 49 | PTHR10277,P ⁻ | 0 2.3.3.13 | 0 GO:0009098,(AT1G18500.1 IPMS1,MAML |
| 50 | PTHR10277,P ⁻ | 0 2.3.3.13 | 0 GO:0009098,(AT1G18500.1 IPMS1,MAML |
| 51 | PTHR10277,P ⁻ | 0 2.3.3.13 | 0 GO:0009098,(AT1G18500.1 IPMS1,MAML |
| 52 | PTHR10277,P ⁻ | 0 2.3.3.13 | 0 GO:0009098,(AT1G18500.1 IPMS1,MAML |
| 53 | PTHR10277,P ⁻ | 0 2.3.3.13 | 0 GO:0009098,(AT1G18500.1 IPMS1,MAML |
| 54 | PTHR10277,P ⁻ | 0 2.3.3.13 | 0 GO:0009098,(AT1G18500.1 IPMS1,MAML |
| 55 | PTHR10277,P ⁻ | 0 2.3.3.13 | 0 GO:0009098,(AT1G18500.1 IPMS1,MAML |
| 56 | PTHR10277,P ⁻ | 0 2.3.3.13 | 0 GO:0009098,(AT1G18500.1 IPMS1,MAML |
| 57 | PTHR10277,P ⁻ | 0 2.3.3.13 | 0 GO:0009098,(AT1G18500.1 IPMS1,MAML |
| 58 | PTHR10277,P ⁻ | 0 2.3.3.13 | 0 GO:0009098,(AT1G18500.1 IPMS1,MAML |
| 59 | PTHR10277,P ⁻ | 0 2.3.3.13 | 0 GO:0009098,(AT1G18500.1 IPMS1,MAML |
| 60 | PTHR10277,P ⁻ | 0 2.3.3.14 | 0 GO:0009098,(AT1G74040.1 IMS1,IPMS2,N |
| | PTHR10277,P ⁻ | 0 2.3.3.14 | 0 GO:0009098,(AT1G74040.1 IMS1,IPMS2,N |

| | | | | | |
|----|----------------------------------|-----------|----------|---|---------------------------------------|
| 1 | | | | | |
| 2 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 3 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 4 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 5 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 6 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 7 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 8 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 9 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 10 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 11 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 12 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 13 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 14 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 15 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 16 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 17 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 18 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 19 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 20 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 21 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 22 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 23 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 24 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 25 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 26 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 27 | PTHR10277,P ⁻ | 0 | 2.3.3.14 | 0 | GO:0009098,C AT1G74040.1 IMS1,IPMS2,N |
| 28 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 | GO:0006508,C AT1G66180.1 0 |
| 29 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 | GO:0006508,C AT1G66180.1 0 |
| 30 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 | GO:0006508,C AT1G66180.1 0 |
| 31 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 | GO:0006508,C AT1G66180.1 0 |
| 32 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 | GO:0006508,C AT1G66180.1 0 |
| 33 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 | GO:0006508,C AT1G66180.1 0 |
| 34 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 | GO:0006508,C AT1G66180.1 0 |
| 35 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 | GO:0006508,C AT1G66180.1 0 |
| 36 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 | GO:0006508,C AT1G66180.1 0 |
| 37 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 | GO:0006508,C AT1G66180.1 0 |
| 38 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 | GO:0006508,C AT1G66180.1 0 |
| 39 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 | GO:0006508,C AT1G66180.1 0 |
| 40 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 | GO:0006508,C AT1G66180.1 0 |
| 41 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 | GO:0006508,C AT1G66180.1 0 |
| 42 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 | GO:0006508,C AT1G66180.1 0 |
| 43 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 | GO:0006508,C AT1G66180.1 0 |
| 44 | PTHR33732,P ⁻ | 0 | 0 | 0 | AT1G67360.2 0 |
| 45 | PTHR33732,P ⁻ | 0 | 0 | 0 | AT1G67360.2 0 |
| 46 | PTHR33732,P ⁻ | 0 | 0 | 0 | AT1G67360.2 0 |
| 47 | PTHR33732,P ⁻ | 0 | 0 | 0 | AT1G67360.2 0 |
| 48 | PTHR33732,P ⁻ | 0 | 0 | 0 | AT1G67360.2 0 |
| 49 | PTHR33732,P ⁻ | 0 | 0 | 0 | AT1G67360.2 0 |
| 50 | PTHR33732,P ⁻ | 0 | 0 | 0 | AT1G67360.2 0 |
| 51 | PTHR33732,P ⁻ | 0 | 0 | 0 | AT1G67360.2 0 |
| 52 | PTHR33732,P ⁻ | 0 | 0 | 0 | AT1G67360.2 0 |
| 53 | PTHR33732,P ⁻ | 0 | 0 | 0 | AT1G67360.2 0 |
| 54 | PTHR33732,P ⁻ | 0 | 0 | 0 | AT1G67360.2 0 |
| 55 | PTHR33732,P ⁻ | 0 | 0 | 0 | AT1G67360.2 0 |
| 56 | PTHR33732,P ⁻ | 0 | 0 | 0 | AT1G67360.2 0 |
| 57 | PTHR33732,P ⁻ | 0 | 0 | 0 | AT1G67360.2 0 |
| 58 | PTHR33732,P ⁻ | 0 | 0 | 0 | AT1G67360.2 0 |
| 59 | PTHR33732,P ⁻ | 0 | 0 | 0 | AT1G67360.2 0 |
| 60 | PTHR33732,P ⁻ | 0 | 0 | 0 | AT1G67360.2 0 |
| | PTHR33732,P ⁻ | 0 | 0 | 0 | AT1G67360.2 0 |

| | | | | | | |
|----|----------------------------------|-----------|--------|--------------------------------------|----------------------------------|---|
| 1 | | | | | | |
| 2 | PTHR33732,P ⁻ | 0 | 0 | 0 | 0 AT1G67360.2 | 0 |
| 3 | PTHR33732,P ⁻ | 0 | 0 | 0 | 0 AT1G67360.2 | 0 |
| 4 | PTHR33732,P ⁻ | 0 | 0 | 0 | 0 AT1G67360.2 | 0 |
| 5 | PTHR33732,P ⁻ | 0 | 0 | 0 | 0 AT1G67360.2 | 0 |
| 6 | PTHR33732,P ⁻ | 0 | 0 | 0 | 0 AT1G67360.2 | 0 |
| 7 | PTHR33732,P ⁻ | 0 | 0 | 0 | 0 AT1G67360.2 | 0 |
| 8 | PTHR33732,P ⁻ | 0 | 0 | 0 | 0 AT1G67360.2 | 0 |
| 9 | PTHR33732,P ⁻ | 0 | 0 | 0 | 0 AT1G67360.2 | 0 |
| 10 | PTHR33732,P ⁻ | 0 | 0 | 0 | 0 AT1G67360.2 | 0 |
| 11 | PTHR33732,P ⁻ | 0 | 0 | 0 | 0 AT1G67360.2 | 0 |
| 12 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 13 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 14 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 15 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 16 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 17 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 18 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 19 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 20 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 21 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 22 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 23 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 24 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 25 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 26 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 27 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 28 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 29 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 30 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 31 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 32 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 33 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 34 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 35 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 36 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 37 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 38 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 39 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 40 | PTHR31113,P ⁻ | 0 | 0 | 0 | 0 AT2G18630.1 | 0 |
| 41 | PTHR11679,P ⁻ | 0 | 0 | 0 | 0 GO:0016192,(AT2G17980.1 ATSLY1 | |
| 42 | PTHR11679,P ⁻ | 0 | 0 | 0 | 0 GO:0016192,(AT2G17980.1 ATSLY1 | |
| 43 | PTHR11679,P ⁻ | 0 | 0 | 0 | 0 GO:0016192,(AT2G17980.1 ATSLY1 | |
| 44 | PTHR11679,P ⁻ | 0 | 0 | 0 | 0 GO:0016192,(AT2G17980.1 ATSLY1 | |
| 45 | PTHR11679,P ⁻ | 0 | 0 | 0 | 0 GO:0016192,(AT2G17980.1 ATSLY1 | |
| 46 | PTHR11679,P ⁻ | 0 | 0 | 0 | 0 GO:0016192,(AT2G17980.1 ATSLY1 | |
| 47 | PTHR11679,P ⁻ | 0 | 0 | 0 | 0 GO:0016192,(AT2G17980.1 ATSLY1 | |
| 48 | PTHR11679,P ⁻ | 0 | 0 | 0 | 0 GO:0016192,(AT2G17980.1 ATSLY1 | |
| 49 | PTHR11679,P ⁻ | 0 | 0 | 0 | 0 GO:0016192,(AT2G17980.1 ATSLY1 | |
| 50 | PTHR11679,P ⁻ | 0 | 0 | 0 | 0 GO:0016192,(AT2G17980.1 ATSLY1 | |
| 51 | PTHR11679,P ⁻ | 0 | 0 | 0 | 0 GO:0016192,(AT2G17980.1 ATSLY1 | |
| 52 | PTHR11679,P ⁻ | 0 | 0 | 0 | 0 GO:0016192,(AT2G17980.1 ATSLY1 | |
| 53 | PTHR11679,P ⁻ | 0 | 0 | 0 | 0 GO:0016192,(AT2G17980.1 ATSLY1 | |
| 54 | PTHR11679,P ⁻ | 0 | 0 | 0 | 0 GO:0016192,(AT2G17980.1 ATSLY1 | |
| 55 | PTHR11679,P ⁻ | 0 | 0 | 0 | 0 GO:0016192,(AT2G17980.1 ATSLY1 | |
| 56 | PTHR10209,P ⁻ KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EF | | |
| 57 | PTHR10209,P ⁻ KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EF | | |
| 58 | PTHR10209,P ⁻ KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EF | | |
| 59 | PTHR10209,P ⁻ KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EF | | |
| 60 | PTHR10209,P ⁻ KOG0143 | 1.14.17.4 | K05933 | GO:0055114,(AT1G05010.1 ACO4,EAT1,EF | | |

| | | | | | | |
|----|----------------------------------|----------|---|---|--|---|
| 1 | | | | | | |
| 2 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 3 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 4 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 5 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 6 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 7 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 8 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 9 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 10 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 11 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 12 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 13 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 14 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 15 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 16 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 17 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 18 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 19 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 20 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 21 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 22 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 23 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 24 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 25 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 26 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 27 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 AT1G19010.1 | 0 |
| 28 | PTHR12626,P ⁻ | 0 | 0 | 0 | 0 AT5G63190.1 | 0 |
| 29 | PTHR12626,P ⁻ | 0 | 0 | 0 | 0 AT5G63190.1 | 0 |
| 30 | PTHR12626,P ⁻ | 0 | 0 | 0 | 0 AT5G63190.1 | 0 |
| 31 | PTHR12626,P ⁻ | 0 | 0 | 0 | 0 AT5G63190.1 | 0 |
| 32 | PTHR12626,P ⁻ | 0 | 0 | 0 | 0 AT5G63190.1 | 0 |
| 33 | PTHR12626,P ⁻ | 0 | 0 | 0 | 0 AT5G63190.1 | 0 |
| 34 | PTHR12626,P ⁻ | 0 | 0 | 0 | 0 AT5G63190.1 | 0 |
| 35 | PTHR12626,P ⁻ | 0 | 0 | 0 | 0 AT5G63190.1 | 0 |
| 36 | PTHR12626,P ⁻ | 0 | 0 | 0 | 0 AT5G63190.1 | 0 |
| 37 | PTHR12626,P ⁻ | 0 | 0 | 0 | 0 AT5G63190.1 | 0 |
| 38 | PTHR12626,P ⁻ | 0 | 0 | 0 | 0 AT5G63190.1 | 0 |
| 39 | PTHR12626,P ⁻ | 0 | 0 | 0 | 0 AT5G63190.1 | 0 |
| 40 | PTHR12626,P ⁻ | 0 | 0 | 0 | 0 AT5G63190.1 | 0 |
| 41 | PTHR12626,P ⁻ | 0 | 0 | 0 | 0 AT5G63190.1 | 0 |
| 42 | PTHR12626,P ⁻ | 0 | 0 | 0 | 0 AT5G63190.1 | 0 |
| 43 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | | | 0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C | |
| 44 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | | | 0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C | |
| 45 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | | | 0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C | |
| 46 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | | | 0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C | |
| 47 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | | | 0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C | |
| 48 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | | | 0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C | |
| 49 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | | | 0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C | |
| 50 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | | | 0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C | |
| 51 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | | | 0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C | |
| 52 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | | | 0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C | |
| 53 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | | | 0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C | |
| 54 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | | | 0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C | |
| 55 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | | | 0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C | |
| 56 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | | | 0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C | |
| 57 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | | | 0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C | |
| 58 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | | | 0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C | |
| 59 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | | | 0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C | |
| 60 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | | | 0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C | |
| | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | | | 0 GO:0016020,(AT1G12110.1 ATNRT1,B-1,C | |

| | | | | | |
|----|----------------------------------|------------|---|---------------------------------------|---|
| 1 | | | | | |
| 2 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 3 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 4 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 5 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 6 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 7 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 8 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 9 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 10 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 11 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 12 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 13 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 14 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 15 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 16 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 17 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 18 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 19 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 20 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 21 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 22 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 23 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 24 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 25 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 26 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 27 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 28 | PTHR11654,P ⁻ KOG1237 | 3.6.3.26 | 0 | GO:0016020,C AT1G12110.1 ATNRT1,B-1,C | |
| 29 | PTHR12029,P ⁻ | 0 2.1.1.34 | 0 | GO:0008173,C AT4G17610.1 | 0 |
| 30 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | 0 | GO:0008234,C AT3G19390.1 | 0 |
| 31 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | 0 | GO:0008234,C AT3G19390.1 | 0 |
| 32 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | 0 | GO:0008234,C AT3G19390.1 | 0 |
| 33 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | 0 | GO:0008234,C AT3G19390.1 | 0 |
| 34 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | 0 | GO:0008234,C AT3G19390.1 | 0 |
| 35 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | 0 | GO:0008234,C AT3G19390.1 | 0 |
| 36 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | 0 | GO:0008234,C AT3G19390.1 | 0 |
| 37 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | 0 | GO:0008234,C AT3G19390.1 | 0 |
| 38 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | 0 | GO:0008234,C AT3G19390.1 | 0 |
| 39 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | 0 | GO:0008234,C AT3G19390.1 | 0 |
| 40 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | 0 | GO:0008234,C AT3G19390.1 | 0 |
| 41 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | 0 | GO:0008234,C AT3G19390.1 | 0 |
| 42 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | 0 | GO:0008234,C AT3G19390.1 | 0 |
| 43 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | 0 | GO:0008234,C AT3G19390.1 | 0 |
| 44 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | 0 | GO:0008234,C AT3G19390.1 | 0 |
| 45 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | 0 | GO:0008234,C AT3G19390.1 | 0 |
| 46 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | 0 | GO:0008234,C AT3G19390.1 | 0 |
| 47 | PTHR14237,P ⁻ | 0 2.8.1.9 | 0 | AT2G23520.1 | 0 |
| 48 | PTHR14237,P ⁻ | 0 2.8.1.9 | 0 | AT2G23520.1 | 0 |
| 49 | PTHR23324,P ⁻ KOG1471 | 0 | 0 | AT1G55690.3 | 0 |
| 50 | PTHR23324,P ⁻ KOG1471 | 0 | 0 | AT1G55690.3 | 0 |
| 51 | PTHR23324,P ⁻ KOG1471 | 0 | 0 | AT1G55690.3 | 0 |
| 52 | PTHR23324,P ⁻ KOG1471 | 0 | 0 | AT1G55690.3 | 0 |
| 53 | PTHR23324,P ⁻ KOG1471 | 0 | 0 | AT1G55690.3 | 0 |
| 54 | PTHR23324,P ⁻ KOG1471 | 0 | 0 | AT1G55690.3 | 0 |
| 55 | PTHR23324,P ⁻ KOG1471 | 0 | 0 | AT1G55690.3 | 0 |
| 56 | PTHR23324,P ⁻ KOG1471 | 0 | 0 | AT1G55690.3 | 0 |
| 57 | PTHR23324,P ⁻ KOG1471 | 0 | 0 | AT1G55690.3 | 0 |
| 58 | PTHR23324,P ⁻ KOG1471 | 0 | 0 | AT1G55690.3 | 0 |
| 59 | PTHR23324,P ⁻ KOG1471 | 0 | 0 | AT1G55690.3 | 0 |
| 60 | PTHR23324,P ⁻ KOG1471 | 0 | 0 | AT1G55690.3 | 0 |
| | PTHR23324,P ⁻ KOG1471 | 0 | 0 | AT1G55690.3 | 0 |

| | | | | | |
|----|----------------------------------|----------|----------|--------------------------------------|---|
| 1 | | | | | |
| 2 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | K16911 | GO:0008270,C AT5G26742.2 emb1138 | |
| 3 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | K16911 | GO:0008270,C AT5G26742.2 emb1138 | |
| 4 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | K16911 | GO:0008270,C AT5G26742.2 emb1138 | |
| 5 | PTHR24031,P ⁻ KOG0331 | 3.6.4.13 | K16911 | GO:0008270,C AT5G26742.2 emb1138 | |
| 6 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 7 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 8 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 9 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 10 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 11 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 12 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 13 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 14 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 15 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 16 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 17 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 18 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 19 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 20 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 21 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 22 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 23 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 24 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 25 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 26 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 27 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 28 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 29 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 30 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 31 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 32 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 33 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 34 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 35 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 36 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 37 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 38 | PTHR10221,P ⁻ KOG2549 | | 0 K03131 | GO:0006352,C AT1G04950.1 ATTA6,TAF6, | |
| 39 | PTHR36795,P ⁻ | 0 | 0 | 0 AT5G14410.1 | 0 |
| 40 | PTHR36795,P ⁻ | 0 | 0 | 0 AT5G14410.1 | 0 |
| 41 | PTHR36795,P ⁻ | 0 | 0 | 0 AT5G14410.1 | 0 |
| 42 | PTHR36795,P ⁻ | 0 | 0 | 0 AT5G14410.1 | 0 |
| 43 | PTHR36795,P ⁻ | 0 | 0 | 0 AT5G14410.1 | 0 |
| 44 | PTHR36795,P ⁻ | 0 | 0 | 0 AT5G14410.1 | 0 |
| 45 | PTHR36795,P ⁻ | 0 | 0 | 0 AT5G14410.1 | 0 |
| 46 | PTHR36795,P ⁻ | 0 | 0 | 0 AT5G14410.1 | 0 |
| 47 | PTHR36795,P ⁻ | 0 | 0 | 0 AT5G14410.1 | 0 |
| 48 | PTHR36795,P ⁻ | 0 | 0 | 0 AT5G14410.1 | 0 |
| 49 | PTHR36795,P ⁻ | 0 | 0 | 0 AT5G14410.1 | 0 |
| 50 | PTHR36795,P ⁻ | 0 | 0 | 0 AT5G14410.1 | 0 |
| 51 | PTHR36795,P ⁻ | 0 | 0 | 0 AT5G14410.1 | 0 |
| 52 | PTHR36795,P ⁻ | 0 | 0 | 0 AT5G14410.1 | 0 |
| 53 | PTHR24012,P ⁻ KOG0131 | | 0 K12741 | GO:0003676 AT2G41060.2 | 0 |
| 54 | PTHR24012,P ⁻ KOG0131 | | 0 K12741 | GO:0003676 AT2G41060.2 | 0 |
| 55 | PTHR24012,P ⁻ KOG0131 | | 0 K12741 | GO:0003676 AT2G41060.2 | 0 |
| 56 | PTHR24012,P ⁻ KOG0131 | | 0 K12741 | GO:0003676 AT2G41060.2 | 0 |
| 57 | PTHR24012,P ⁻ KOG0131 | | 0 K12741 | GO:0003676 AT2G41060.2 | 0 |
| 58 | PTHR24012,P ⁻ KOG0131 | | 0 K12741 | GO:0003676 AT2G41060.2 | 0 |
| 59 | PTHR24012,P ⁻ KOG0131 | | 0 K12741 | GO:0003676 AT2G41060.2 | 0 |
| 60 | PTHR24012,P ⁻ KOG0131 | | 0 K12741 | GO:0003676 AT2G41060.2 | 0 |
| | PTHR24012,P ⁻ KOG0131 | | 0 K12741 | GO:0003676 AT2G41060.2 | 0 |

| | | | | | | | |
|----|----------------------------------|-----------|----------|----------------|---------------|---|---|
| 1 | | | | | | | |
| 2 | PTHR24012,P ⁻ KOG0131 | | 0 K12741 | GO:0003676 | AT2G41060.2 | | 0 |
| 3 | PTHR24012,P ⁻ KOG0131 | | 0 K12741 | GO:0003676 | AT2G41060.2 | | 0 |
| 4 | PTHR24012,P ⁻ KOG0131 | | 0 K12741 | GO:0003676 | AT2G41060.2 | | 0 |
| 5 | PTHR24012,P ⁻ KOG0131 | | 0 K12741 | GO:0003676 | AT2G41060.2 | | 0 |
| 6 | PTHR24012,P ⁻ KOG0131 | | 0 K12741 | GO:0003676 | AT2G41060.2 | | 0 |
| 7 | PTHR24012,P ⁻ KOG0131 | | 0 K12741 | GO:0003676 | AT2G41060.2 | | 0 |
| 8 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G02650.1 | | 0 |
| 9 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G02650.1 | | 0 |
| 10 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G02650.1 | | 0 |
| 11 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G02650.1 | | 0 |
| 12 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G02650.1 | | 0 |
| 13 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G02650.1 | | 0 |
| 14 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G02650.1 | | 0 |
| 15 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G02650.1 | | 0 |
| 16 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G02650.1 | | 0 |
| 17 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G02650.1 | | 0 |
| 18 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G02650.1 | | 0 |
| 19 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G02650.1 | | 0 |
| 20 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G02650.1 | | 0 |
| 21 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G02650.1 | | 0 |
| 22 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G02650.1 | | 0 |
| 23 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 GO:0006508,C | AT1G66180.1 | | 0 |
| 24 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 GO:0006508,C | AT1G66180.1 | | 0 |
| 25 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 GO:0006508,C | AT1G66180.1 | | 0 |
| 26 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 GO:0006508,C | AT1G66180.1 | | 0 |
| 27 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 GO:0006508,C | AT1G66180.1 | | 0 |
| 28 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 GO:0006508,C | AT1G66180.1 | | 0 |
| 29 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 GO:0006508,C | AT1G66180.1 | | 0 |
| 30 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 GO:0006508,C | AT1G66180.1 | | 0 |
| 31 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 GO:0006508,C | AT1G66180.1 | | 0 |
| 32 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 GO:0006508,C | AT1G66180.1 | | 0 |
| 33 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 GO:0006508,C | AT1G66180.1 | | 0 |
| 34 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 GO:0006508,C | AT1G66180.1 | | 0 |
| 35 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 GO:0006508,C | AT1G66180.1 | | 0 |
| 36 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 GO:0006508,C | AT1G66180.1 | | 0 |
| 37 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 GO:0006508,C | AT1G66180.1 | | 0 |
| 38 | PTHR13683,P ⁻ KOG1339 | 3.4.23.12 | | 0 GO:0006508,C | AT1G66180.1 | | 0 |
| 39 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 40 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 41 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 42 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 43 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 44 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 45 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 46 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 47 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 48 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 49 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 50 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 51 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 52 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 53 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 54 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 55 | PTHR10445,P ⁻ KOG2905 | 3.6.4.12 | K03139 | GO:0006367,C | AT1G75510.1 | | 0 |
| 56 | PTHR10445,P ⁻ KOG2905 | 3.6.4.12 | K03139 | GO:0006367,C | AT1G75510.1 | | 0 |
| 57 | PTHR10445,P ⁻ KOG2905 | 3.6.4.12 | K03139 | GO:0006367,C | AT1G75510.1 | | 0 |
| 58 | PTHR10445,P ⁻ KOG2905 | 3.6.4.12 | K03139 | GO:0006367,C | AT1G75510.1 | | 0 |
| 59 | PTHR10445,P ⁻ KOG2905 | 3.6.4.12 | K03139 | GO:0006367,C | AT1G75510.1 | | 0 |
| 60 | PTHR10445,P ⁻ KOG2905 | 3.6.4.12 | K03139 | GO:0006367,C | AT1G75510.1 | | 0 |
| | PTHR10445,P ⁻ KOG2905 | 3.6.4.12 | K03139 | GO:0006367,C | AT1G75510.1 | | 0 |

| | | | | | | |
|----|----------------------------------|------------|--------|--------------|--------------------------|---|
| 1 | | | | | | |
| 2 | PTHR10445,P ⁻ KOG2905 | 3.6.4.12 | K03139 | GO:0006367,C | AT1G75510.1 | 0 |
| 3 | PTHR10445,P ⁻ KOG2905 | 3.6.4.12 | K03139 | GO:0006367,C | AT1G75510.1 | 0 |
| 4 | PTHR10445,P ⁻ KOG2905 | 3.6.4.12 | K03139 | GO:0006367,C | AT1G75510.1 | 0 |
| 5 | PTHR10445,P ⁻ KOG2905 | 3.6.4.12 | K03139 | GO:0006367,C | AT1G75510.1 | 0 |
| 6 | PTHR10445,P ⁻ KOG2905 | 3.6.4.12 | K03139 | GO:0006367,C | AT1G75510.1 | 0 |
| 7 | PTHR10445,P ⁻ KOG2905 | 3.6.4.12 | K03139 | GO:0006367,C | AT1G75510.1 | 0 |
| 8 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G05670.2 | 0 |
| 9 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G05670.2 | 0 |
| 10 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G05670.2 | 0 |
| 11 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G05670.2 | 0 |
| 12 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G05670.2 | 0 |
| 13 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G05670.2 | 0 |
| 14 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G05670.2 | 0 |
| 15 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G05670.2 | 0 |
| 16 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G05670.2 | 0 |
| 17 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G05670.2 | 0 |
| 18 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G05670.2 | 0 |
| 19 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G05670.2 | 0 |
| 20 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G05670.2 | 0 |
| 21 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G05670.2 | 0 |
| 22 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G05670.2 | 0 |
| 23 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G05670.2 | 0 |
| 24 | PTHR10410,P ⁻ | 0 3.4.25.1 | K09613 | GO:0005515 | AT1G71230.1 AJH2,CSN5,CS | |
| 25 | PTHR10410,P ⁻ | 0 3.4.25.1 | K09613 | GO:0005515 | AT1G71230.1 AJH2,CSN5,CS | |
| 26 | PTHR10410,P ⁻ | 0 3.4.25.1 | K09613 | GO:0005515 | AT1G71230.1 AJH2,CSN5,CS | |
| 27 | PTHR10410,P ⁻ | 0 3.4.25.1 | K09613 | GO:0005515 | AT1G71230.1 AJH2,CSN5,CS | |
| 28 | PTHR10410,P ⁻ | 0 3.4.25.1 | K09613 | GO:0005515 | AT1G71230.1 AJH2,CSN5,CS | |
| 29 | PTHR10410,P ⁻ | 0 3.4.25.1 | K09613 | GO:0005515 | AT1G71230.1 AJH2,CSN5,CS | |
| 30 | PTHR10410,P ⁻ | 0 3.4.25.1 | K09613 | GO:0005515 | AT1G71230.1 AJH2,CSN5,CS | |
| 31 | PTHR10410,P ⁻ | 0 3.4.25.1 | K09613 | GO:0005515 | AT1G71230.1 AJH2,CSN5,CS | |
| 32 | PTHR10410,P ⁻ | 0 3.4.25.1 | K09613 | GO:0005515 | AT1G71230.1 AJH2,CSN5,CS | |
| 33 | PTHR10410,P ⁻ | 0 3.4.25.1 | K09613 | GO:0005515 | AT1G71230.1 AJH2,CSN5,CS | |
| 34 | PTHR10410,P ⁻ | 0 3.4.25.1 | K09613 | GO:0005515 | AT1G71230.1 AJH2,CSN5,CS | |
| 35 | PTHR10410,P ⁻ | 0 3.4.25.1 | K09613 | GO:0005515 | AT1G71230.1 AJH2,CSN5,CS | |
| 36 | PTHR10410,P ⁻ | 0 3.4.25.1 | K09613 | GO:0005515 | AT1G71230.1 AJH2,CSN5,CS | |
| 37 | PTHR10410,P ⁻ | 0 3.4.25.1 | K09613 | GO:0005515 | AT1G71230.1 AJH2,CSN5,CS | |
| 38 | PTHR10410,P ⁻ | 0 3.4.25.1 | K09613 | GO:0005515 | AT1G71230.1 AJH2,CSN5,CS | |
| 39 | PTHR10410,P ⁻ | 0 3.4.25.1 | K09613 | GO:0005515 | AT1G71230.1 AJH2,CSN5,CS | |
| 40 | PTHR26312,P ⁻ | 0 | 0 | 0 | 0 AT4G39470.1 | 0 |
| 41 | PTHR26312,P ⁻ | 0 | 0 | 0 | 0 AT4G39470.1 | 0 |
| 42 | PTHR26312,P ⁻ | 0 | 0 | 0 | 0 AT4G39470.1 | 0 |
| 43 | PTHR26312,P ⁻ | 0 | 0 | 0 | 0 AT4G39470.1 | 0 |
| 44 | PTHR26312,P ⁻ | 0 | 0 | 0 | 0 AT4G39470.1 | 0 |
| 45 | PTHR26312,P ⁻ | 0 | 0 | 0 | 0 AT4G39470.1 | 0 |
| 46 | PTHR26312,P ⁻ | 0 | 0 | 0 | 0 AT4G39470.1 | 0 |
| 47 | PTHR26312,P ⁻ | 0 | 0 | 0 | 0 AT4G39470.1 | 0 |
| 48 | PTHR26312,P ⁻ | 0 | 0 | 0 | 0 AT4G39470.1 | 0 |
| 49 | PTHR26312,P ⁻ | 0 | 0 | 0 | 0 AT4G39470.1 | 0 |
| 50 | PTHR26312,P ⁻ | 0 | 0 | 0 | 0 AT4G39470.1 | 0 |
| 51 | PTHR26312,P ⁻ | 0 | 0 | 0 | 0 AT4G39470.1 | 0 |
| 52 | PTHR26312,P ⁻ | 0 | 0 | 0 | 0 AT4G39470.1 | 0 |
| 53 | PTHR26312,P ⁻ | 0 | 0 | 0 | 0 AT4G39470.1 | 0 |
| 54 | PTHR26312,P ⁻ | 0 | 0 | 0 | 0 AT4G39470.1 | 0 |
| 55 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 56 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 57 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 58 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 59 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 60 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |

| | | | | | | |
|----|----------------------------------|------------|--------|----------------|------------------|---|
| 1 | | | | | | |
| 2 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 3 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 4 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 5 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 6 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 7 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 8 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 9 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 10 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 11 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 12 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 13 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 14 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 15 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 16 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 17 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 18 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 19 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 20 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 21 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 22 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G79540.1 | 0 |
| 23 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 24 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 25 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 26 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 27 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 28 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 29 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 30 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 31 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 32 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 33 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 34 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 35 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 36 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 37 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 38 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 39 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 40 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 41 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 42 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 43 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 44 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 45 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 46 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 47 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 48 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 49 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 50 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 51 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 52 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 53 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 54 | PTHR31388,P ⁻ | 0 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 |
| 55 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,(| AT5G01310.1 APTX | |
| 56 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,(| AT5G01310.1 APTX | |
| 57 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,(| AT5G01310.1 APTX | |
| 58 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,(| AT5G01310.1 APTX | |
| 59 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,(| AT5G01310.1 APTX | |
| 60 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,(| AT5G01310.1 APTX | |
| | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,(| AT5G01310.1 APTX | |

| | | | | |
|----|----------------------------------|-----------|----------|--------------------------------------|
| 1 | | | | |
| 2 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 3 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 4 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 5 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 6 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 7 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 8 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 9 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 10 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 11 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 12 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 13 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 14 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 15 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 16 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 17 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 18 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 19 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 20 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 21 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 22 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 23 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 24 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 25 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 26 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 27 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 28 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 29 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 30 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 31 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 32 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 33 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 34 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 35 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 36 | PTHR12486,P ⁻ KOG0562 | | 0 | 0 GO:0033699,C AT5G01310.1 APTX |
| 37 | PTHR10252,P ⁻ | 0 2.7.7.7 | 0 | 0 AT1G07980.1 NF-YC10 |
| 38 | PTHR10252,P ⁻ | 0 2.7.7.7 | 0 | 0 AT1G07980.1 NF-YC10 |
| 39 | PTHR10252,P ⁻ | 0 2.7.7.7 | 0 | 0 AT1G07980.1 NF-YC10 |
| 40 | PTHR10252,P ⁻ | 0 2.7.7.7 | 0 | 0 AT1G07980.1 NF-YC10 |
| 41 | PTHR10252,P ⁻ | 0 2.7.7.7 | 0 | 0 AT1G07980.1 NF-YC10 |
| 42 | PTHR10252,P ⁻ | 0 2.7.7.7 | 0 | 0 AT1G07980.1 NF-YC10 |
| 43 | PTHR10252,P ⁻ | 0 2.7.7.7 | 0 | 0 AT1G07980.1 NF-YC10 |
| 44 | PTHR10252,P ⁻ | 0 2.7.7.7 | 0 | 0 AT1G07980.1 NF-YC10 |
| 45 | PTHR10252,P ⁻ | 0 2.7.7.7 | 0 | 0 AT1G07980.1 NF-YC10 |
| 46 | PTHR10252,P ⁻ | 0 2.7.7.7 | 0 | 0 AT1G07980.1 NF-YC10 |
| 47 | PTHR10252,P ⁻ | 0 2.7.7.7 | 0 | 0 AT1G07980.1 NF-YC10 |
| 48 | PTHR10252,P ⁻ | 0 2.7.7.7 | 0 | 0 AT1G07980.1 NF-YC10 |
| 49 | PTHR10252,P ⁻ | 0 2.7.7.7 | 0 | 0 AT1G07980.1 NF-YC10 |
| 50 | PTHR10252,P ⁻ | 0 2.7.7.7 | 0 | 0 AT1G07980.1 NF-YC10 |
| 51 | PTHR10252,P ⁻ | 0 2.7.7.7 | 0 | 0 AT1G07980.1 NF-YC10 |
| 52 | PTHR31633 | 0 | 0 K14763 | GO:0042254,C AT1G03530.1 ATNAF1,NAF1 |
| 53 | PTHR31633 | 0 | 0 K14763 | GO:0042254,C AT1G03530.1 ATNAF1,NAF1 |
| 54 | PTHR31633 | 0 | 0 K14763 | GO:0042254,C AT1G03530.1 ATNAF1,NAF1 |
| 55 | PTHR31633 | 0 | 0 K14763 | GO:0042254,C AT1G03530.1 ATNAF1,NAF1 |
| 56 | PTHR31633 | 0 | 0 K14763 | GO:0042254,C AT1G03530.1 ATNAF1,NAF1 |
| 57 | PTHR31633 | 0 | 0 K14763 | GO:0042254,C AT1G03530.1 ATNAF1,NAF1 |
| 58 | PTHR31633 | 0 | 0 K14763 | GO:0042254,C AT1G03530.1 ATNAF1,NAF1 |
| 59 | PTHR31633 | 0 | 0 K14763 | GO:0042254,C AT1G03530.1 ATNAF1,NAF1 |
| 60 | PTHR31633 | 0 | 0 K14763 | GO:0042254,C AT1G03530.1 ATNAF1,NAF1 |
| | PTHR31633 | 0 | 0 K14763 | GO:0042254,C AT1G03530.1 ATNAF1,NAF1 |

| | | | | | | |
|----|----------------------------------|-----------|----------|----------------|-------------------------|---|
| 1 | | | | | | |
| 2 | PTHR31633 | 0 | 0 K14763 | GO:0042254,(| AT1G03530.1 ATNAF1,NAF1 | |
| 3 | PTHR31633 | 0 | 0 K14763 | GO:0042254,(| AT1G03530.1 ATNAF1,NAF1 | |
| 4 | PTHR31633 | 0 | 0 K14763 | GO:0042254,(| AT1G03530.1 ATNAF1,NAF1 | |
| 5 | | | | | | |
| 6 | PTHR24326,P ⁻ | 0 | 0 | 0 GO:0003677 | AT5G53980.1 ATHB52,HB52 | |
| 7 | PTHR24326,P ⁻ | 0 | 0 | 0 GO:0003677 | AT5G53980.1 ATHB52,HB52 | |
| 8 | PTHR24326,P ⁻ | 0 | 0 | 0 GO:0003677 | AT5G53980.1 ATHB52,HB52 | |
| 9 | | | | | | |
| 10 | PTHR24326,P ⁻ | 0 | 0 | 0 GO:0003677 | AT5G53980.1 ATHB52,HB52 | |
| 11 | PTHR24326,P ⁻ | 0 | 0 | 0 GO:0003677 | AT5G53980.1 ATHB52,HB52 | |
| 12 | PTHR24326,P ⁻ | 0 | 0 | 0 GO:0003677 | AT5G53980.1 ATHB52,HB52 | |
| 13 | | | | | | |
| 14 | PTHR24326,P ⁻ | 0 | 0 | 0 GO:0003677 | AT5G53980.1 ATHB52,HB52 | |
| 15 | PTHR24326,P ⁻ | 0 | 0 | 0 GO:0003677 | AT5G53980.1 ATHB52,HB52 | |
| 16 | PTHR24326,P ⁻ | 0 | 0 | 0 GO:0003677 | AT5G53980.1 ATHB52,HB52 | |
| 17 | | | | | | |
| 18 | PTHR24326,P ⁻ | 0 | 0 | 0 GO:0003677 | AT5G53980.1 ATHB52,HB52 | |
| 19 | PTHR24326,P ⁻ | 0 | 0 | 0 GO:0003677 | AT5G53980.1 ATHB52,HB52 | |
| 20 | PTHR24326,P ⁻ | 0 | 0 | 0 GO:0003677 | AT5G53980.1 ATHB52,HB52 | |
| 21 | | | | | | |
| 22 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | | 0 GO:0008234,(| AT1G47128.1 RD21,RD21A | |
| 23 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | | 0 GO:0008234,(| AT1G47128.1 RD21,RD21A | |
| 24 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | | 0 GO:0008234,(| AT1G47128.1 RD21,RD21A | |
| 25 | | | | | | |
| 26 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | | 0 GO:0008234,(| AT1G47128.1 RD21,RD21A | |
| 27 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | | 0 GO:0008234,(| AT1G47128.1 RD21,RD21A | |
| 28 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | | 0 GO:0008234,(| AT1G47128.1 RD21,RD21A | |
| 29 | | | | | | |
| 30 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | | 0 GO:0008234,(| AT1G47128.1 RD21,RD21A | |
| 31 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | | 0 GO:0008234,(| AT1G47128.1 RD21,RD21A | |
| 32 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | | 0 GO:0008234,(| AT1G47128.1 RD21,RD21A | |
| 33 | | | | | | |
| 34 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | | 0 GO:0008234,(| AT1G47128.1 RD21,RD21A | |
| 35 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | | 0 GO:0008234,(| AT1G47128.1 RD21,RD21A | |
| 36 | PTHR12411,P ⁻ KOG1543 | 3.4.22.14 | | 0 GO:0008234,(| AT1G47128.1 RD21,RD21A | |
| 37 | | | | | | |
| 38 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 39 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 40 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 41 | | | | | | |
| 42 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 43 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 44 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 45 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 46 | | | | | | |
| 47 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 48 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 49 | | | | | | |
| 50 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 51 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 52 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 53 | | | | | | |
| 54 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 55 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 56 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 57 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 58 | | | | | | |
| 59 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 60 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |

| | | | | | | |
|----|----------------------------------|---|--------|---|------------------------------------|---|
| 1 | | | | | | |
| 2 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 3 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 4 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 5 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 6 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G04130.2 | 0 |
| 7 | PTHR31422,P ⁻ | 0 | 0 | 0 | 0 AT5G06560.1 | 0 |
| 8 | PTHR31422,P ⁻ | 0 | 0 | 0 | 0 AT5G06560.1 | 0 |
| 9 | PTHR31422,P ⁻ | 0 | 0 | 0 | 0 AT5G06560.1 | 0 |
| 10 | PTHR31422,P ⁻ | 0 | 0 | 0 | 0 AT5G06560.1 | 0 |
| 11 | PTHR31422,P ⁻ | 0 | 0 | 0 | 0 AT5G06560.1 | 0 |
| 12 | PTHR31422,P ⁻ | 0 | 0 | 0 | 0 AT5G06560.1 | 0 |
| 13 | PTHR31422,P ⁻ | 0 | 0 | 0 | 0 AT5G06560.1 | 0 |
| 14 | PTHR31422,P ⁻ | 0 | 0 | 0 | 0 AT5G06560.1 | 0 |
| 15 | PTHR31422,P ⁻ | 0 | 0 | 0 | 0 AT5G06560.1 | 0 |
| 16 | PTHR31422,P ⁻ | 0 | 0 | 0 | 0 AT5G06560.1 | 0 |
| 17 | PTHR31422,P ⁻ | 0 | 0 | 0 | 0 AT5G06560.1 | 0 |
| 18 | PTHR31422,P ⁻ | 0 | 0 | 0 | 0 AT5G06560.1 | 0 |
| 19 | PTHR31422,P ⁻ | 0 | 0 | 0 | 0 AT5G06560.1 | 0 |
| 20 | PTHR31422,P ⁻ | 0 | 0 | 0 | 0 AT5G06560.1 | 0 |
| 21 | PTHR31422,P ⁻ | 0 | 0 | 0 | 0 AT5G06560.1 | 0 |
| 22 | PTHR31422,P ⁻ | 0 | 0 | 0 | 0 AT5G06560.1 | 0 |
| 23 | PTHR31669,P ⁻ | 0 | 0 | 0 | GO:0008270,C AT4G38180.1 FRS5 | |
| 24 | PTHR31669,P ⁻ | 0 | 0 | 0 | GO:0008270,C AT4G38180.1 FRS5 | |
| 25 | PTHR31669,P ⁻ | 0 | 0 | 0 | GO:0008270,C AT4G38180.1 FRS5 | |
| 26 | PTHR31669,P ⁻ | 0 | 0 | 0 | GO:0008270,C AT4G38180.1 FRS5 | |
| 27 | PTHR31669,P ⁻ | 0 | 0 | 0 | GO:0008270,C AT4G38180.1 FRS5 | |
| 28 | PTHR31669,P ⁻ | 0 | 0 | 0 | GO:0008270,C AT4G38180.1 FRS5 | |
| 29 | PTHR31669,P ⁻ | 0 | 0 | 0 | GO:0008270,C AT4G38180.1 FRS5 | |
| 30 | PTHR31669,P ⁻ | 0 | 0 | 0 | GO:0008270,C AT4G38180.1 FRS5 | |
| 31 | PTHR31669,P ⁻ | 0 | 0 | 0 | GO:0008270,C AT4G38180.1 FRS5 | |
| 32 | PTHR31669,P ⁻ | 0 | 0 | 0 | GO:0008270,C AT4G38180.1 FRS5 | |
| 33 | PTHR31669,P ⁻ | 0 | 0 | 0 | GO:0008270,C AT4G38180.1 FRS5 | |
| 34 | PTHR31669,P ⁻ | 0 | 0 | 0 | GO:0008270,C AT4G38180.1 FRS5 | |
| 35 | PTHR31669,P ⁻ | 0 | 0 | 0 | GO:0008270,C AT4G38180.1 FRS5 | |
| 36 | PTHR31669,P ⁻ | 0 | 0 | 0 | GO:0008270,C AT4G38180.1 FRS5 | |
| 37 | PTHR31669,P ⁻ | 0 | 0 | 0 | GO:0008270,C AT4G38180.1 FRS5 | |
| 38 | PTHR31669,P ⁻ | 0 | 0 | 0 | GO:0008270,C AT4G38180.1 FRS5 | |
| 39 | PTHR33101,P ⁻ | 0 | 0 | 0 | GO:0005089 AT1G31650.1 ATROPGEF14, | |
| 40 | PTHR33101,P ⁻ | 0 | 0 | 0 | GO:0005089 AT1G31650.1 ATROPGEF14, | |
| 41 | PTHR10168,P ⁻ KOG2824 | 0 | K17479 | 0 | GO:0045454,C AT4G10630.1 | 0 |
| 42 | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |
| 43 | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |
| 44 | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |
| 45 | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |
| 46 | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |
| 47 | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |
| 48 | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |
| 49 | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |
| 50 | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |
| 51 | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |
| 52 | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |
| 53 | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |
| 54 | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |
| 55 | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |
| 56 | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |
| 57 | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |
| 58 | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |
| 59 | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |
| 60 | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |
| | PTHR31846,P ⁻ KOG1990 | 0 | | 0 | GO:0003723 AT4G29750.1 | 0 |

| | | | | | | | |
|----|----------------------------------|---|-----------|--------|------------|-------------|-------------|
| 1 | | | | | | | |
| 2 | PTHR31846,P ⁻ KOG1990 | | 0 | 0 | GO:0003723 | AT4G29750.1 | 0 |
| 3 | PTHR31846,P ⁻ KOG1990 | | 0 | 0 | GO:0003723 | AT4G29750.1 | 0 |
| 4 | PTHR31846,P ⁻ KOG1990 | | 0 | 0 | GO:0003723 | AT4G29750.1 | 0 |
| 5 | PTHR31846,P ⁻ KOG1990 | | 0 | 0 | GO:0003723 | AT4G29750.1 | 0 |
| 6 | PTHR31846,P ⁻ KOG1990 | | 0 | 0 | GO:0003723 | AT4G29750.1 | 0 |
| 7 | PTHR31846,P ⁻ KOG1990 | | 0 | 0 | GO:0003723 | AT4G29750.1 | 0 |
| 8 | PTHR31846,P ⁻ KOG1990 | | 0 | 0 | GO:0003723 | AT4G29750.1 | 0 |
| 9 | PTHR31846,P ⁻ KOG1990 | | 0 | 0 | GO:0003723 | AT4G29750.1 | 0 |
| 10 | PTHR31846,P ⁻ KOG1990 | | 0 | 0 | GO:0003723 | AT4G29750.1 | 0 |
| 11 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | AT4G30700.1 | 0 |
| 12 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | AT4G30700.1 | 0 |
| 13 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | AT4G30700.1 | 0 |
| 14 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | AT4G30700.1 | 0 |
| 15 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | AT4G30700.1 | 0 |
| 16 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | AT4G30700.1 | 0 |
| 17 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | AT4G30700.1 | 0 |
| 18 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | AT4G30700.1 | 0 |
| 19 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | AT4G30700.1 | 0 |
| 20 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | AT4G30700.1 | 0 |
| 21 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | AT4G30700.1 | 0 |
| 22 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | AT4G30700.1 | 0 |
| 23 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | AT4G30700.1 | 0 |
| 24 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | AT4G30700.1 | 0 |
| 25 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | AT4G30700.1 | 0 |
| 26 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | AT4G30700.1 | 0 |
| 27 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 28 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 29 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 30 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 31 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 32 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 33 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 34 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 35 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 36 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 37 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 38 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 39 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 40 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 41 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 42 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 43 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 44 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 45 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 46 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 47 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 48 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 49 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 50 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 51 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 52 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 53 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 54 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 55 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 56 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 57 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 58 | PTHR34778,P ⁻ | 0 | 0 | 0 | 0 | AT1G19010.1 | 0 |
| 59 | PTHR31009,P ⁻ | 0 | 2.1.1.274 | K08241 | GO:0008168 | AT5G04380.1 | 0 |
| 60 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | AT2G15690.1 | 0 |
| | PTHR10264,P ⁻ KOG2620 | | 0 | 0 | GO:0016020 | AT5G62740.1 | ATHIR1,HIR1 |

| | | | | | | | | |
|----|----------------------------------|------------|--------|---|--------------------------|--------------------------|------------|---|
| 1 | | | | | | | | |
| 2 | PTHR12526,P ⁻ KOG0853 | | 0 | 0 | 0 | AT3G15940.2 | | 0 |
| 3 | PTHR24223,P ⁻ | 0 3.6.3.44 | | | 0 | GO:0055085,C AT3G13080.1 | ATMRP3,MRP | |
| 4 | PTHR24223,P ⁻ | 0 3.6.3.44 | | | 0 | GO:0055085,C AT3G13080.1 | ATMRP3,MRP | |
| 5 | PTHR24223,P ⁻ | 0 3.6.3.44 | | | 0 | GO:0055085,C AT3G13080.1 | ATMRP3,MRP | |
| 6 | PTHR24223,P ⁻ | 0 3.6.3.44 | | | 0 | GO:0055085,C AT3G13080.1 | ATMRP3,MRP | |
| 7 | PTHR24223,P ⁻ | 0 3.6.3.44 | | | 0 | GO:0055085,C AT3G13080.1 | ATMRP3,MRP | |
| 8 | PTHR24223,P ⁻ | 0 3.6.3.44 | | | 0 | GO:0055085,C AT3G13080.1 | ATMRP3,MRP | |
| 9 | PTHR24223,P ⁻ | 0 3.6.3.44 | | | 0 | GO:0055085,C AT3G13080.1 | ATMRP3,MRP | |
| 10 | PTHR24223,P ⁻ | 0 3.6.3.44 | | | 0 | GO:0055085,C AT3G13080.1 | ATMRP3,MRP | |
| 11 | PTHR24223,P ⁻ | 0 3.6.3.44 | | | 0 | GO:0055085,C AT3G13080.1 | ATMRP3,MRP | |
| 12 | PTHR24223,P ⁻ | 0 3.6.3.44 | | | 0 | GO:0055085,C AT3G13080.1 | ATMRP3,MRP | |
| 13 | PTHR24223,P ⁻ | 0 3.6.3.44 | | | 0 | GO:0055085,C AT3G13080.1 | ATMRP3,MRP | |
| 14 | PTHR24223,P ⁻ | 0 3.6.3.44 | | | 0 | GO:0055085,C AT3G13080.1 | ATMRP3,MRP | |
| 15 | PTHR24223,P ⁻ | 0 3.6.3.44 | | | 0 | GO:0055085,C AT3G13080.1 | ATMRP3,MRP | |
| 16 | PTHR24223,P ⁻ | 0 3.6.3.44 | | | 0 | GO:0055085,C AT3G13080.1 | ATMRP3,MRP | |
| 17 | PTHR24223,P ⁻ | 0 3.6.3.44 | | | 0 | GO:0055085,C AT3G13080.1 | ATMRP3,MRP | |
| 18 | PTHR24223,P ⁻ | 0 3.6.3.44 | | | 0 | GO:0055085,C AT3G13080.1 | ATMRP3,MRP | |
| 19 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 22 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 25 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 27 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 30 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 31 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 32 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 33 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 34 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 35 | PTHR11817,P ⁻ | 0 2.7.1.40 | K00873 | | GO:0030955,C AT3G52990.1 | | | 0 |
| 36 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 37 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 38 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 39 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 40 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 41 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 42 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 43 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 44 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 45 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 46 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 47 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 48 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 49 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 50 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 51 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 52 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 53 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 54 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 55 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 56 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 57 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 58 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 59 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| 60 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |
| | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | | 0 | GO:0005975 AT5G13420.1 | | 0 |

| | | | | | | |
|----|----------------------------------|------------|----------|--------------|-----------------------------|---|
| 1 | | | | | | |
| 2 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | 0 GO:0005975 | AT5G13420.1 | 0 |
| 3 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | 0 GO:0005975 | AT5G13420.1 | 0 |
| 4 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | 0 GO:0005975 | AT5G13420.1 | 0 |
| 5 | | | | | | |
| 6 | PTHR10683,P ⁻ KOG2772 | 2.2.1.2 | | 0 GO:0005975 | AT5G13420.1 | 0 |
| 7 | PTHR31752,P ⁻ | 0 | 0 K13947 | GO:0055085,C | AT5G16530.1 PIN5 | |
| 8 | PTHR10887,P ⁻ KOG1801 | | 0 K10706 | | 0 AT4G15570.1 MAA3 | |
| 9 | | | | | | |
| 10 | PTHR10887,P ⁻ KOG1801 | | 0 K10706 | | 0 AT4G15570.1 MAA3 | |
| 11 | PTHR10887,P ⁻ KOG1801 | | 0 K10706 | | 0 AT4G15570.1 MAA3 | |
| 12 | PTHR10887,P ⁻ KOG1801 | | 0 K10706 | | 0 AT4G15570.1 MAA3 | |
| 13 | | | | | | |
| 14 | PTHR10887,P ⁻ KOG1801 | | 0 K10706 | | 0 AT4G15570.1 MAA3 | |
| 15 | PTHR10887,P ⁻ KOG1801 | | 0 K10706 | | 0 AT4G15570.1 MAA3 | |
| 16 | PTHR10887,P ⁻ KOG1801 | | 0 K10706 | | 0 AT4G15570.1 MAA3 | |
| 17 | | | | | | |
| 18 | PTHR10887,P ⁻ KOG1801 | | 0 K10706 | | 0 AT4G15570.1 MAA3 | |
| 19 | PTHR10887,P ⁻ KOG1801 | | 0 K10706 | | 0 AT4G15570.1 MAA3 | |
| 20 | PTHR10887,P ⁻ KOG1801 | | 0 K10706 | | 0 AT4G15570.1 MAA3 | |
| 21 | | | | | | |
| 22 | PTHR10887,P ⁻ KOG1801 | | 0 K10706 | | 0 AT4G15570.1 MAA3 | |
| 23 | PTHR10887,P ⁻ KOG1801 | | 0 K10706 | | 0 AT4G15570.1 MAA3 | |
| 24 | PTHR24078,P ⁻ | 0 | 0 | 0 | 0 AT1G75250.1 ATRL6,RL6,RSI | |
| 25 | PTHR24078,P ⁻ | 0 | 0 | 0 | 0 AT1G75250.1 ATRL6,RL6,RSI | |
| 26 | PTHR24078,P ⁻ | 0 | 0 | 0 | 0 AT1G75250.1 ATRL6,RL6,RSI | |
| 27 | PTHR24078,P ⁻ | 0 | 0 | 0 | 0 AT1G75250.1 ATRL6,RL6,RSI | |
| 28 | PTHR24078,P ⁻ | 0 | 0 | 0 | 0 AT1G75250.1 ATRL6,RL6,RSI | |
| 29 | PTHR24078,P ⁻ | 0 | 0 | 0 | 0 AT1G75250.1 ATRL6,RL6,RSI | |
| 30 | PTHR24078,P ⁻ | 0 | 0 | 0 | 0 AT1G75250.1 ATRL6,RL6,RSI | |
| 31 | PTHR24078,P ⁻ | 0 | 0 | 0 | 0 AT1G75250.1 ATRL6,RL6,RSI | |
| 32 | PTHR24078,P ⁻ | 0 | 0 | 0 | 0 AT1G75250.1 ATRL6,RL6,RSI | |
| 33 | PTHR24078,P ⁻ | 0 | 0 | 0 | 0 AT1G75250.1 ATRL6,RL6,RSI | |
| 34 | PTHR24078,P ⁻ | 0 | 0 | 0 | 0 AT1G75250.1 ATRL6,RL6,RSI | |
| 35 | PTHR24078,P ⁻ | 0 | 0 | 0 | 0 AT1G75250.1 ATRL6,RL6,RSI | |
| 36 | PTHR24078,P ⁻ | 0 | 0 | 0 | 0 AT1G75250.1 ATRL6,RL6,RSI | |
| 37 | PTHR24078,P ⁻ | 0 | 0 | 0 | 0 AT1G75250.1 ATRL6,RL6,RSI | |
| 38 | PTHR24078,P ⁻ | 0 | 0 | 0 | 0 AT1G75250.1 ATRL6,RL6,RSI | |
| 39 | PTHR24078,P ⁻ | 0 | 0 | 0 | 0 AT1G75250.1 ATRL6,RL6,RSI | |
| 40 | PTHR31321,P ⁻ | 0 3.1.1.11 | K01051 | GO:0042545,C | AT5G55590.1 QRT1 | |
| 41 | PTHR31321,P ⁻ | 0 3.1.1.11 | K01051 | GO:0042545,C | AT5G55590.1 QRT1 | |
| 42 | PTHR31321,P ⁻ | 0 3.1.1.11 | K01051 | GO:0042545,C | AT5G55590.1 QRT1 | |
| 43 | PTHR31321,P ⁻ | 0 3.1.1.11 | K01051 | GO:0042545,C | AT5G55590.1 QRT1 | |
| 44 | PTHR31321,P ⁻ | 0 3.1.1.11 | K01051 | GO:0042545,C | AT5G55590.1 QRT1 | |
| 45 | PTHR31321,P ⁻ | 0 3.1.1.11 | K01051 | GO:0042545,C | AT5G55590.1 QRT1 | |
| 46 | PTHR31321,P ⁻ | 0 3.1.1.11 | K01051 | GO:0042545,C | AT5G55590.1 QRT1 | |
| 47 | PTHR31321,P ⁻ | 0 3.1.1.11 | K01051 | GO:0042545,C | AT5G55590.1 QRT1 | |
| 48 | PTHR31321,P ⁻ | 0 3.1.1.11 | K01051 | GO:0042545,C | AT5G55590.1 QRT1 | |
| 49 | PTHR31321,P ⁻ | 0 3.1.1.11 | K01051 | GO:0042545,C | AT5G55590.1 QRT1 | |
| 50 | PTHR31321,P ⁻ | 0 3.1.1.11 | K01051 | GO:0042545,C | AT5G55590.1 QRT1 | |
| 51 | PTHR31321,P ⁻ | 0 3.1.1.11 | K01051 | GO:0042545,C | AT5G55590.1 QRT1 | |
| 52 | PTHR31321,P ⁻ | 0 3.1.1.11 | K01051 | GO:0042545,C | AT5G55590.1 QRT1 | |
| 53 | PTHR31321,P ⁻ | 0 3.1.1.11 | K01051 | GO:0042545,C | AT5G55590.1 QRT1 | |
| 54 | PTHR31321,P ⁻ | 0 3.1.1.11 | K01051 | GO:0042545,C | AT5G55590.1 QRT1 | |
| 55 | PTHR31321,P ⁻ | 0 3.1.1.11 | K01051 | GO:0042545,C | AT5G55590.1 QRT1 | |
| 56 | PTHR12670,P ⁻ | 0 3.5.1.23 | K12349 | | 0 AT1G07380.1 | 0 |
| 57 | PTHR12670,P ⁻ | 0 3.5.1.23 | K12349 | | 0 AT1G07380.1 | 0 |
| 58 | PTHR12670,P ⁻ | 0 3.5.1.23 | K12349 | | 0 AT1G07380.1 | 0 |
| 59 | PTHR12670,P ⁻ | 0 3.5.1.23 | K12349 | | 0 AT1G07380.1 | 0 |
| 60 | PTHR12670,P ⁻ | 0 3.5.1.23 | K12349 | | 0 AT1G07380.1 | 0 |

| | | | | | | |
|----|--------------------------|---|----------|--------|--------------|-------------------------|
| 1 | | | | | | |
| 2 | PTHR12670,P ⁻ | 0 | 3.5.1.23 | K12349 | 0 | AT1G07380.1 |
| 3 | PTHR12670,P ⁻ | 0 | 3.5.1.23 | K12349 | 0 | AT1G07380.1 |
| 4 | PTHR12670,P ⁻ | 0 | 3.5.1.23 | K12349 | 0 | AT1G07380.1 |
| 5 | PTHR12670,P ⁻ | 0 | 3.5.1.23 | K12349 | 0 | AT1G07380.1 |
| 6 | PTHR12670,P ⁻ | 0 | 3.5.1.23 | K12349 | 0 | AT1G07380.1 |
| 7 | PTHR12670,P ⁻ | 0 | 3.5.1.23 | K12349 | 0 | AT1G07380.1 |
| 8 | PTHR12670,P ⁻ | 0 | 3.5.1.23 | K12349 | 0 | AT1G07380.1 |
| 9 | PTHR12670,P ⁻ | 0 | 3.5.1.23 | K12349 | 0 | AT1G07380.1 |
| 10 | PTHR12670,P ⁻ | 0 | 3.5.1.23 | K12349 | 0 | AT1G07380.1 |
| 11 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 12 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 13 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 14 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 15 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 16 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 17 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 18 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 19 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 20 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 21 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 22 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 23 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 24 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 25 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 26 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 27 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 28 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 29 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 30 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 31 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 32 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 33 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 34 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 35 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 36 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 37 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 38 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 39 | PTHR31704,P ⁻ | 0 | 0 | 0 | 0 | AT2G24960.2 |
| 40 | PTHR11119,P ⁻ | 0 | 0 | K06901 | GO:0055085,C | AT3G10960.1 ATAZG1,AZG1 |
| 41 | PTHR11119,P ⁻ | 0 | 0 | K06901 | GO:0055085,C | AT3G10960.1 ATAZG1,AZG1 |
| 42 | PTHR11119,P ⁻ | 0 | 0 | K06901 | GO:0055085,C | AT3G10960.1 ATAZG1,AZG1 |
| 43 | PTHR11119,P ⁻ | 0 | 0 | K06901 | GO:0055085,C | AT3G10960.1 ATAZG1,AZG1 |
| 44 | PTHR11119,P ⁻ | 0 | 0 | K06901 | GO:0055085,C | AT3G10960.1 ATAZG1,AZG1 |
| 45 | PTHR11119,P ⁻ | 0 | 0 | K06901 | GO:0055085,C | AT3G10960.1 ATAZG1,AZG1 |
| 46 | PTHR11119,P ⁻ | 0 | 0 | K06901 | GO:0055085,C | AT3G10960.1 ATAZG1,AZG1 |
| 47 | PTHR11119,P ⁻ | 0 | 0 | K06901 | GO:0055085,C | AT3G10960.1 ATAZG1,AZG1 |
| 48 | PTHR11119,P ⁻ | 0 | 0 | K06901 | GO:0055085,C | AT3G10960.1 ATAZG1,AZG1 |
| 49 | PTHR11119,P ⁻ | 0 | 0 | K06901 | GO:0055085,C | AT3G10960.1 ATAZG1,AZG1 |
| 50 | PTHR11119,P ⁻ | 0 | 0 | K06901 | GO:0055085,C | AT3G10960.1 ATAZG1,AZG1 |
| 51 | PTHR11119,P ⁻ | 0 | 0 | K06901 | GO:0055085,C | AT3G10960.1 ATAZG1,AZG1 |
| 52 | PTHR11119,P ⁻ | 0 | 0 | K06901 | GO:0055085,C | AT3G10960.1 ATAZG1,AZG1 |
| 53 | PTHR11119,P ⁻ | 0 | 0 | K06901 | GO:0055085,C | AT3G10960.1 ATAZG1,AZG1 |
| 54 | PTHR11119,P ⁻ | 0 | 0 | K06901 | GO:0055085,C | AT3G10960.1 ATAZG1,AZG1 |
| 55 | PTHR11119,P ⁻ | 0 | 0 | K06901 | GO:0055085,C | AT3G10960.1 ATAZG1,AZG1 |
| 56 | PTHR24286,P ⁻ | 0 | 0 | 0 | GO:0055114,C | AT1G05160.1 ATKAO1,CYP8 |
| 57 | PTHR24223,P ⁻ | 0 | 3.6.3.44 | 0 | GO:0055085,C | AT3G60160.1 ATMRP9,MRP |
| 58 | PTHR24223,P ⁻ | 0 | 3.6.3.44 | 0 | GO:0055085,C | AT3G60160.1 ATMRP9,MRP |
| 59 | PTHR24223,P ⁻ | 0 | 3.6.3.44 | 0 | GO:0055085,C | AT3G60160.1 ATMRP9,MRP |
| 60 | PTHR24223,P ⁻ | 0 | 3.6.3.44 | 0 | GO:0055085,C | AT3G60160.1 ATMRP9,MRP |

| | | | | |
|----|----------------------------------|-------------|----------|--|
| 1 | | | | |
| 2 | PTHR24223,P ⁻ | 0 3.6.3.44 | | 0 GO:0055085,C AT3G60160.1 ATM RP9,MRP |
| 3 | PTHR24223,P ⁻ | 0 3.6.3.44 | | 0 GO:0055085,C AT3G60160.1 ATM RP9,MRP |
| 4 | PTHR24223,P ⁻ | 0 3.6.3.44 | | 0 GO:0055085,C AT3G60160.1 ATM RP9,MRP |
| 5 | PTHR24223,P ⁻ | 0 3.6.3.44 | | 0 GO:0055085,C AT3G60160.1 ATM RP9,MRP |
| 6 | PTHR24223,P ⁻ | 0 3.6.3.44 | | 0 GO:0055085,C AT3G60160.1 ATM RP9,MRP |
| 7 | PTHR24223,P ⁻ | 0 3.6.3.44 | | 0 GO:0055085,C AT3G60160.1 ATM RP9,MRP |
| 8 | PTHR24223,P ⁻ | 0 3.6.3.44 | | 0 GO:0055085,C AT3G60160.1 ATM RP9,MRP |
| 9 | PTHR24223,P ⁻ | 0 3.6.3.44 | | 0 GO:0055085,C AT3G60160.1 ATM RP9,MRP |
| 10 | PTHR24223,P ⁻ | 0 3.6.3.44 | | 0 GO:0055085,C AT3G60160.1 ATM RP9,MRP |
| 11 | PTHR24223,P ⁻ | 0 3.6.3.44 | | 0 GO:0055085,C AT3G60160.1 ATM RP9,MRP |
| 12 | PTHR22953,P ⁻ KOG1378 | 3.1.4.1 | | 0 GO:0016787 AT4G24890.1 ATPAP24,PAP. |
| 13 | PTHR22953,P ⁻ KOG1378 | 3.1.4.1 | | 0 GO:0016787 AT4G24890.1 ATPAP24,PAP. |
| 14 | PTHR22953,P ⁻ KOG1378 | 3.1.4.1 | | 0 GO:0016787 AT4G24890.1 ATPAP24,PAP. |
| 15 | PTHR22953,P ⁻ KOG1378 | 3.1.4.1 | | 0 GO:0016787 AT4G24890.1 ATPAP24,PAP. |
| 16 | PTHR22953,P ⁻ KOG1378 | 3.1.4.1 | | 0 GO:0016787 AT4G24890.1 ATPAP24,PAP. |
| 17 | PTHR22953,P ⁻ KOG1378 | 3.1.4.1 | | 0 GO:0016787 AT4G24890.1 ATPAP24,PAP. |
| 18 | PTHR22953,P ⁻ KOG1378 | 3.1.4.1 | | 0 GO:0016787 AT4G24890.1 ATPAP24,PAP. |
| 19 | PTHR22953,P ⁻ KOG1378 | 3.1.4.1 | | 0 GO:0016787 AT4G24890.1 ATPAP24,PAP. |
| 20 | PTHR22953,P ⁻ KOG1378 | 3.1.4.1 | | 0 GO:0016787 AT4G24890.1 ATPAP24,PAP. |
| 21 | PTHR22953,P ⁻ KOG1378 | 3.1.4.1 | | 0 GO:0016787 AT4G24890.1 ATPAP24,PAP. |
| 22 | PTHR22953,P ⁻ KOG1378 | 3.1.4.1 | | 0 GO:0016787 AT4G24890.1 ATPAP24,PAP. |
| 23 | PTHR22953,P ⁻ KOG1378 | 3.1.4.1 | | 0 GO:0016787 AT4G24890.1 ATPAP24,PAP. |
| 24 | PTHR22953,P ⁻ KOG1378 | 3.1.4.1 | | 0 GO:0016787 AT4G24890.1 ATPAP24,PAP. |
| 25 | PTHR22953,P ⁻ KOG1378 | 3.1.4.1 | | 0 GO:0016787 AT4G24890.1 ATPAP24,PAP. |
| 26 | PTHR22953,P ⁻ KOG1378 | 3.1.4.1 | | 0 GO:0016787 AT4G24890.1 ATPAP24,PAP. |
| 27 | PTHR10774,P ⁻ | 0 | 0 | 0 GO:0005515 AT3G19830.1 NTMC2T5.2,N |
| 28 | PTHR10774,P ⁻ | 0 | 0 | 0 GO:0005515 AT3G19830.1 NTMC2T5.2,N |
| 29 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 30 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 31 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 32 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 33 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 34 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 35 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 36 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 37 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 38 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 39 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 40 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 41 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 42 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 43 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 44 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 45 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 46 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 47 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 48 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 49 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 50 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 51 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 52 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 53 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 54 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 55 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 56 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 57 | PTHR10795,P ⁻ | 0 3.4.14.10 | | 0 GO:0006508,C AT2G04160.1 AIR3 |
| 58 | PTHR22870,P ⁻ KOG1427 | | 0 | 0 GO:0046872 AT1G69710.1 |
| 59 | PTHR22870,P ⁻ KOG1427 | | 0 | 0 GO:0046872 AT1G69710.1 |
| 60 | PTHR23070,P ⁻ | 0 | 0 K08900 | GO:0005524,C AT5G57480.1 |

| | | | | | |
|----|----------------------------------|-------------|---|--------------------------------------|---|
| 1 | | | | | |
| 2 | PTHR11746,P ⁻ KOG1509 | | 0 | 0 GO:0005737 AT5G66550.1 | 0 |
| 3 | PTHR11746,P ⁻ KOG1509 | | 0 | 0 GO:0005737 AT5G66550.1 | 0 |
| 4 | PTHR27000,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 5 | | | | | |
| 6 | PTHR27000,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 7 | PTHR21330,P ⁻ | 0 | 0 | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 8 | PTHR21330,P ⁻ | 0 | 0 | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 9 | PTHR21330,P ⁻ | 0 | 0 | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 10 | PTHR21330,P ⁻ | 0 | 0 | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 11 | PTHR21330,P ⁻ | 0 | 0 | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 12 | PTHR21330,P ⁻ | 0 | 0 | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 13 | PTHR21330,P ⁻ | 0 | 0 | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 14 | PTHR21330,P ⁻ | 0 | 0 | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 15 | PTHR21330,P ⁻ | 0 | 0 | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 16 | PTHR21330,P ⁻ | 0 | 0 | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 17 | PTHR21330,P ⁻ | 0 | 0 | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 18 | PTHR21330,P ⁻ | 0 | 0 | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 19 | PTHR21330,P ⁻ | 0 | 0 | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 20 | PTHR21330,P ⁻ | 0 | 0 | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 21 | PTHR21330,P ⁻ | 0 | 0 | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 22 | PTHR21330,P ⁻ | 0 | 0 | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 23 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 24 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 25 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 26 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 27 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 28 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 29 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 30 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 31 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 32 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 33 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 34 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 35 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 36 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 37 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 38 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 39 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 40 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 41 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 42 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 43 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 44 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 45 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 46 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 47 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 48 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 49 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 50 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 51 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 52 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 53 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 54 | PTHR21330,P ⁻ | 0 3.4.22.16 | | 0 GO:0030915,(AT3G15150.1 ATMMS21,HP | |
| 55 | PTHR31852,P ⁻ | 0 | 0 | 0 AT2G35460.1 | 0 |
| 56 | PTHR31852,P ⁻ | 0 | 0 | 0 AT2G35460.1 | 0 |
| 57 | PTHR31852,P ⁻ | 0 | 0 | 0 AT2G35460.1 | 0 |
| 58 | PTHR31852,P ⁻ | 0 | 0 | 0 AT2G35460.1 | 0 |
| 59 | PTHR31852,P ⁻ | 0 | 0 | 0 AT2G35460.1 | 0 |
| 60 | PTHR31852,P ⁻ | 0 | 0 | 0 AT2G35460.1 | 0 |
| | PTHR31852,P ⁻ | 0 | 0 | 0 AT2G35460.1 | 0 |

| | | | | | | |
|----|----------------------------------|-----------|----------|---|--------------------------------------|---|
| 1 | | | | | | |
| 2 | PTHR31852,P ⁻ | 0 | 0 | 0 | 0 AT2G35460.1 | 0 |
| 3 | PTHR31852,P ⁻ | 0 | 0 | 0 | 0 AT2G35460.1 | 0 |
| 4 | PTHR31852,P ⁻ | 0 | 0 | 0 | 0 AT2G35460.1 | 0 |
| 5 | PTHR31852,P ⁻ | 0 | 0 | 0 | 0 AT2G35460.1 | 0 |
| 6 | PTHR31852,P ⁻ | 0 | 0 | 0 | 0 AT2G35460.1 | 0 |
| 7 | PTHR31852,P ⁻ | 0 | 0 | 0 | 0 AT2G35460.1 | 0 |
| 8 | PTHR31852,P ⁻ | 0 | 0 | 0 | 0 AT2G35460.1 | 0 |
| 9 | | | | | | |
| 10 | PTHR23500,P ⁻ KOG0254 | | 0 K08150 | | GO:0055085,C AT4G16480.1 ATINT4,INT4 | |
| 11 | PTHR23500,P ⁻ KOG0254 | | 0 K08150 | | GO:0055085,C AT4G16480.1 ATINT4,INT4 | |
| 12 | PTHR23500,P ⁻ KOG0254 | | 0 K08150 | | GO:0055085,C AT4G16480.1 ATINT4,INT4 | |
| 13 | PTHR23500,P ⁻ KOG0254 | | 0 K08150 | | GO:0055085,C AT4G16480.1 ATINT4,INT4 | |
| 14 | PTHR23500,P ⁻ KOG0254 | | 0 K08150 | | GO:0055085,C AT4G16480.1 ATINT4,INT4 | |
| 15 | PTHR23500,P ⁻ KOG0254 | | 0 K08150 | | GO:0055085,C AT4G16480.1 ATINT4,INT4 | |
| 16 | PTHR23500,P ⁻ KOG0254 | | 0 K08150 | | GO:0055085,C AT4G16480.1 ATINT4,INT4 | |
| 17 | PTHR23500,P ⁻ KOG0254 | | 0 K08150 | | GO:0055085,C AT4G16480.1 ATINT4,INT4 | |
| 18 | PTHR23500,P ⁻ KOG0254 | | 0 K08150 | | GO:0055085,C AT4G16480.1 ATINT4,INT4 | |
| 19 | PTHR23500,P ⁻ KOG0254 | | 0 K08150 | | GO:0055085,C AT4G16480.1 ATINT4,INT4 | |
| 20 | PTHR23500,P ⁻ KOG0254 | | 0 K08150 | | GO:0055085,C AT4G16480.1 ATINT4,INT4 | |
| 21 | PTHR23500,P ⁻ KOG0254 | | 0 K08150 | | GO:0055085,C AT4G16480.1 ATINT4,INT4 | |
| 22 | PTHR23500,P ⁻ KOG0254 | | 0 K08150 | | GO:0055085,C AT4G16480.1 ATINT4,INT4 | |
| 23 | PTHR23500,P ⁻ KOG0254 | | 0 K08150 | | GO:0055085,C AT4G16480.1 ATINT4,INT4 | |
| 24 | PTHR23500,P ⁻ KOG0254 | | 0 K08150 | | GO:0055085,C AT4G16480.1 ATINT4,INT4 | |
| 25 | PTHR24006,P ⁻ KOG1947 | | 0 K10268 | | GO:0005515 AT4G15475.1 | 0 |
| 26 | PTHR24006,P ⁻ KOG1947 | | 0 K10268 | | GO:0005515 AT4G15475.1 | 0 |
| 27 | PTHR24006,P ⁻ KOG1947 | | 0 K10268 | | GO:0005515 AT4G15475.1 | 0 |
| 28 | PTHR24006,P ⁻ KOG1947 | | 0 K10268 | | GO:0005515 AT4G15475.1 | 0 |
| 29 | PTHR24006,P ⁻ KOG1947 | | 0 K10268 | | GO:0005515 AT4G15475.1 | 0 |
| 30 | PTHR24006,P ⁻ KOG1947 | | 0 K10268 | | GO:0005515 AT4G15475.1 | 0 |
| 31 | PTHR24006,P ⁻ KOG1947 | | 0 K10268 | | GO:0005515 AT4G15475.1 | 0 |
| 32 | PTHR24006,P ⁻ KOG1947 | | 0 K10268 | | GO:0005515 AT4G15475.1 | 0 |
| 33 | PTHR24006,P ⁻ KOG1947 | | 0 K10268 | | GO:0005515 AT4G15475.1 | 0 |
| 34 | PTHR24006,P ⁻ KOG1947 | | 0 K10268 | | GO:0005515 AT4G15475.1 | 0 |
| 35 | PTHR24006,P ⁻ KOG1947 | | 0 K10268 | | GO:0005515 AT4G15475.1 | 0 |
| 36 | PTHR24006,P ⁻ KOG1947 | | 0 K10268 | | GO:0005515 AT4G15475.1 | 0 |
| 37 | PTHR24006,P ⁻ KOG1947 | | 0 K10268 | | GO:0005515 AT4G15475.1 | 0 |
| 38 | PTHR24006,P ⁻ KOG1947 | | 0 K10268 | | GO:0005515 AT4G15475.1 | 0 |
| 39 | PTHR24006,P ⁻ KOG1947 | | 0 K10268 | | GO:0005515 AT4G15475.1 | 0 |
| 40 | PTHR24006,P ⁻ KOG1947 | | 0 K10268 | | GO:0005515 AT4G15475.1 | 0 |
| 41 | PTHR31422,P ⁻ | 0 | 0 | 0 | 0 AT1G18265.1 | 0 |
| 42 | | | | | | |
| 43 | PTHR11532,P ⁻ KOG2649 | 3.4.17.22 | | 0 | 0 AT1G71696.1 SOL1 | |
| 44 | PTHR11532,P ⁻ KOG2649 | 3.4.17.22 | | 0 | 0 AT1G71696.1 SOL1 | |
| 45 | PTHR22849,P ⁻ KOG0279 | 2.7.11.7 | | 0 | GO:0005515,C AT3G06880.2 | 0 |
| 46 | PTHR22849,P ⁻ KOG0279 | 2.7.11.7 | | 0 | GO:0005515,C AT3G06880.2 | 0 |
| 47 | PTHR22849,P ⁻ KOG0279 | 2.7.11.7 | | 0 | GO:0005515,C AT3G06880.2 | 0 |
| 48 | PTHR22849,P ⁻ KOG0279 | 2.7.11.7 | | 0 | GO:0005515,C AT3G06880.2 | 0 |
| 49 | PTHR22849,P ⁻ KOG0279 | 2.7.11.7 | | 0 | GO:0005515,C AT3G06880.2 | 0 |
| 50 | PTHR22849,P ⁻ KOG0279 | 2.7.11.7 | | 0 | GO:0005515,C AT3G06880.2 | 0 |
| 51 | PTHR22849,P ⁻ KOG0279 | 2.7.11.7 | | 0 | GO:0005515,C AT3G06880.2 | 0 |
| 52 | PTHR22849,P ⁻ KOG0279 | 2.7.11.7 | | 0 | GO:0005515,C AT3G06880.2 | 0 |
| 53 | PTHR22849,P ⁻ KOG0279 | 2.7.11.7 | | 0 | GO:0005515,C AT3G06880.2 | 0 |
| 54 | PTHR22849,P ⁻ KOG0279 | 2.7.11.7 | | 0 | GO:0005515,C AT3G06880.2 | 0 |
| 55 | PTHR22849,P ⁻ KOG0279 | 2.7.11.7 | | 0 | GO:0005515,C AT3G06880.2 | 0 |
| 56 | PTHR22849,P ⁻ KOG0279 | 2.7.11.7 | | 0 | GO:0005515,C AT3G06880.2 | 0 |
| 57 | PTHR22849,P ⁻ KOG0279 | 2.7.11.7 | | 0 | GO:0005515,C AT3G06880.2 | 0 |
| 58 | PTHR22849,P ⁻ KOG0279 | 2.7.11.7 | | 0 | GO:0005515,C AT3G06880.2 | 0 |
| 59 | PTHR22849,P ⁻ KOG0279 | 2.7.11.7 | | 0 | GO:0005515,C AT3G06880.2 | 0 |
| 60 | PTHR13743,P ⁻ | 0 | 0 | 0 | GO:0005515 AT1G03060.1 SPI | |
| | PTHR13743,P ⁻ | 0 | 0 | 0 | GO:0005515 AT1G03060.1 SPI | |

| | | | | | | |
|----|----------------------------------|----------|----------------|--------|--------------------------------|---|
| 1 | | | | | | |
| 2 | PTHR13743,P ⁻ | 0 | 0 | 0 | GO:0005515 AT1G03060.1 SPI | |
| 3 | PTHR31282,P ⁻ | 0 | 0 | 0 | GO:0043565,CAT2G30590.1 WRKY21 | |
| 4 | PTHR31282,P ⁻ | 0 | 0 | 0 | GO:0043565,CAT2G30590.1 WRKY21 | |
| 5 | PTHR31282,P ⁻ | 0 | 0 | 0 | GO:0043565,CAT2G30590.1 WRKY21 | |
| 6 | PTHR31282,P ⁻ | 0 | 0 | 0 | GO:0043565,CAT2G30590.1 WRKY21 | |
| 7 | PTHR31282,P ⁻ | 0 | 0 | 0 | GO:0043565,CAT2G30590.1 WRKY21 | |
| 8 | PTHR31282,P ⁻ | 0 | 0 | 0 | GO:0043565,CAT2G30590.1 WRKY21 | |
| 9 | PTHR31282,P ⁻ | 0 | 0 | 0 | GO:0043565,CAT2G30590.1 WRKY21 | |
| 10 | PTHR31282,P ⁻ | 0 | 0 | 0 | GO:0043565,CAT2G30590.1 WRKY21 | |
| 11 | PTHR31282,P ⁻ | 0 | 0 | 0 | GO:0043565,CAT2G30590.1 WRKY21 | |
| 12 | PTHR31282,P ⁻ | 0 | 0 | 0 | GO:0043565,CAT2G30590.1 WRKY21 | |
| 13 | PTHR31282,P ⁻ | 0 | 0 | 0 | GO:0043565,CAT2G30590.1 WRKY21 | |
| 14 | PTHR31282,P ⁻ | 0 | 0 | 0 | GO:0043565,CAT2G30590.1 WRKY21 | |
| 15 | PTHR31282,P ⁻ | 0 | 0 | 0 | GO:0043565,CAT2G30590.1 WRKY21 | |
| 16 | PTHR31282,P ⁻ | 0 | 0 | 0 | GO:0043565,CAT2G30590.1 WRKY21 | |
| 17 | PTHR31282,P ⁻ | 0 | 0 | 0 | GO:0043565,CAT2G30590.1 WRKY21 | |
| 18 | PTHR31282,P ⁻ | 0 | 0 | 0 | GO:0043565,CAT2G30590.1 WRKY21 | |
| 19 | PTHR31549,P ⁻ | 0 | 0 | 0 | 0 AT4G31980.1 | 0 |
| 20 | PTHR24031,P ⁻ | 0 | 3.6.4.13 | K17679 | GO:0016787,CAT5G08610.1 | 0 |
| 21 | PTHR24031,P ⁻ | 0 | 3.6.4.13 | K17679 | GO:0016787,CAT5G08610.1 | 0 |
| 22 | PTHR24031,P ⁻ | 0 | 3.6.4.13 | K17679 | GO:0016787,CAT5G08610.1 | 0 |
| 23 | PTHR24031,P ⁻ | 0 | 3.6.4.13 | K17679 | GO:0016787,CAT5G08610.1 | 0 |
| 24 | PTHR24031,P ⁻ | 0 | 3.6.4.13 | K17679 | GO:0016787,CAT5G08610.1 | 0 |
| 25 | PTHR24031,P ⁻ | 0 | 3.6.4.13 | K17679 | GO:0016787,CAT5G08610.1 | 0 |
| 26 | PTHR24031,P ⁻ | 0 | 3.6.4.13 | K17679 | GO:0016787,CAT5G08610.1 | 0 |
| 27 | PTHR24031,P ⁻ | 0 | 3.6.4.13 | K17679 | GO:0016787,CAT5G08610.1 | 0 |
| 28 | PTHR24031,P ⁻ | 0 | 3.6.4.13 | K17679 | GO:0016787,CAT5G08610.1 | 0 |
| 29 | PTHR24031,P ⁻ | 0 | 3.6.4.13 | K17679 | GO:0016787,CAT5G08610.1 | 0 |
| 30 | PTHR24031,P ⁻ | 0 | 3.6.4.13 | K17679 | GO:0016787,CAT5G08610.1 | 0 |
| 31 | PTHR24031,P ⁻ | 0 | 3.6.4.13 | K17679 | GO:0016787,CAT5G08610.1 | 0 |
| 32 | PTHR24031,P ⁻ | 0 | 3.6.4.13 | K17679 | GO:0016787,CAT5G08610.1 | 0 |
| 33 | PTHR24031,P ⁻ | 0 | 3.6.4.13 | K17679 | GO:0016787,CAT5G08610.1 | 0 |
| 34 | PTHR24031,P ⁻ | 0 | 3.6.4.13 | K17679 | GO:0016787,CAT5G08610.1 | 0 |
| 35 | PTHR24031,P ⁻ | 0 | 3.6.4.13 | K17679 | GO:0016787,CAT5G08610.1 | 0 |
| 36 | PTHR22970,P ⁻ | 0 | 0 | 0 | GO:0003677 AT3G43240.1 | 0 |
| 37 | PTHR22970,P ⁻ | 0 | 0 | 0 | GO:0003677 AT3G43240.1 | 0 |
| 38 | PTHR22970,P ⁻ | 0 | 0 | 0 | GO:0003677 AT3G43240.1 | 0 |
| 39 | PTHR22970,P ⁻ | 0 | 0 | 0 | GO:0003677 AT3G43240.1 | 0 |
| 40 | PTHR22970,P ⁻ | 0 | 0 | 0 | GO:0003677 AT3G43240.1 | 0 |
| 41 | PTHR22970,P ⁻ | 0 | 0 | 0 | GO:0003677 AT3G43240.1 | 0 |
| 42 | PTHR22970,P ⁻ | 0 | 0 | 0 | GO:0003677 AT3G43240.1 | 0 |
| 43 | PTHR22970,P ⁻ | 0 | 0 | 0 | GO:0003677 AT3G43240.1 | 0 |
| 44 | PTHR22970,P ⁻ | 0 | 0 | 0 | GO:0003677 AT3G43240.1 | 0 |
| 45 | PTHR22970,P ⁻ | 0 | 0 | 0 | GO:0003677 AT3G43240.1 | 0 |
| 46 | PTHR22970,P ⁻ | 0 | 0 | 0 | GO:0003677 AT3G43240.1 | 0 |
| 47 | PTHR22970,P ⁻ | 0 | 0 | 0 | GO:0003677 AT3G43240.1 | 0 |
| 48 | PTHR22970,P ⁻ | 0 | 0 | 0 | GO:0003677 AT3G43240.1 | 0 |
| 49 | PTHR22970,P ⁻ | 0 | 0 | 0 | GO:0003677 AT3G43240.1 | 0 |
| 50 | PTHR22970,P ⁻ | 0 | 0 | 0 | GO:0003677 AT3G43240.1 | 0 |
| 51 | PTHR22970,P ⁻ | 0 | 0 | 0 | GO:0003677 AT3G43240.1 | 0 |
| 52 | PTHR11851,P ⁻ | 0 | 1.10.2.2,3.4.2 | K01412 | 0 AT1G51980.1 | 0 |
| 53 | PTHR23029,P ⁻ KOG0235 | 3.1.3.63 | K15634 | 0 | AT5G22620.1 | 0 |
| 54 | PTHR23029,P ⁻ KOG0235 | 3.1.3.63 | K15634 | 0 | AT5G22620.1 | 0 |
| 55 | PTHR23029,P ⁻ KOG0235 | 3.1.3.63 | K15634 | 0 | AT5G22620.1 | 0 |
| 56 | PTHR23029,P ⁻ KOG0235 | 3.1.3.63 | K15634 | 0 | AT5G22620.1 | 0 |
| 57 | PTHR23029,P ⁻ KOG0235 | 3.1.3.63 | K15634 | 0 | AT5G22620.1 | 0 |
| 58 | PTHR23029,P ⁻ KOG0235 | 3.1.3.63 | K15634 | 0 | AT5G22620.1 | 0 |
| 59 | PTHR23029,P ⁻ KOG0235 | 3.1.3.63 | K15634 | 0 | AT5G22620.1 | 0 |
| 60 | PTHR23029,P ⁻ KOG0235 | 3.1.3.63 | K15634 | 0 | AT5G22620.1 | 0 |
| | PTHR23029,P ⁻ KOG0235 | 3.1.3.63 | K15634 | 0 | AT5G22620.1 | 0 |

| | | | | | |
|----|----------------------------------|------------|--------|----------------------------|---|
| 1 | | | | | |
| 2 | PTHR23029,P ⁻ KOG0235 | 3.1.3.63 | K15634 | 0 AT5G22620.1 | 0 |
| 3 | PTHR23029,P ⁻ KOG0235 | 3.1.3.63 | K15634 | 0 AT5G22620.1 | 0 |
| 4 | PTHR23029,P ⁻ KOG0235 | 3.1.3.63 | K15634 | 0 AT5G22620.1 | 0 |
| 5 | | | | | |
| 6 | PTHR23029,P ⁻ KOG0235 | 3.1.3.63 | K15634 | 0 AT5G22620.1 | 0 |
| 7 | PTHR23315,P ⁻ | 0 6.3.2.19 | | 0 GO:0016567,C AT5G40140.1 | 0 |
| 8 | PTHR23315,P ⁻ | 0 6.3.2.19 | | 0 GO:0016567,C AT5G40140.1 | 0 |
| 9 | | | | | |
| 10 | PTHR23315,P ⁻ | 0 6.3.2.19 | | 0 GO:0016567,C AT5G40140.1 | 0 |
| 11 | PTHR23315,P ⁻ | 0 6.3.2.19 | | 0 GO:0016567,C AT5G40140.1 | 0 |
| 12 | PTHR23315,P ⁻ | 0 6.3.2.19 | | 0 GO:0016567,C AT5G40140.1 | 0 |
| 13 | | | | | |
| 14 | PTHR23315,P ⁻ | 0 6.3.2.19 | | 0 GO:0016567,C AT5G40140.1 | 0 |
| 15 | PTHR23315,P ⁻ | 0 6.3.2.19 | | 0 GO:0016567,C AT5G40140.1 | 0 |
| 16 | PTHR23315,P ⁻ | 0 6.3.2.19 | | 0 GO:0016567,C AT5G40140.1 | 0 |
| 17 | PTHR23315,P ⁻ | 0 6.3.2.19 | | 0 GO:0016567,C AT5G40140.1 | 0 |
| 18 | PTHR23315,P ⁻ | 0 6.3.2.19 | | 0 GO:0016567,C AT5G40140.1 | 0 |
| 19 | PTHR23315,P ⁻ | 0 6.3.2.19 | | 0 GO:0016567,C AT5G40140.1 | 0 |
| 20 | PTHR23315,P ⁻ | 0 6.3.2.19 | | 0 GO:0016567,C AT5G40140.1 | 0 |
| 21 | | | | | |
| 22 | PTHR23315,P ⁻ | 0 6.3.2.19 | | 0 GO:0016567,C AT5G40140.1 | 0 |
| 23 | | | | | |
| 24 | | | | | |
| 25 | | | | | |
| 26 | | | | | |
| 27 | | | | | |
| 28 | | | | | |
| 29 | | | | | |
| 30 | | | | | |
| 31 | | | | | |
| 32 | | | | | |
| 33 | | | | | |
| 34 | | | | | |
| 35 | | | | | |
| 36 | | | | | |
| 37 | | | | | |
| 38 | | | | | |
| 39 | | | | | |
| 40 | | | | | |
| 41 | | | | | |
| 42 | | | | | |
| 43 | | | | | |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

not distribute

| | arabi-defline | ID | Annot_defline | IDENTIFIER | NAME |
|----|-----------------------------------|----|---------------------------|----------------|----------------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 4 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 5 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 6 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 7 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 8 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 9 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 10 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 11 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 12 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 13 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 14 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 15 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 16 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 17 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 18 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 19 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 20 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 21 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 22 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 23 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 24 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 25 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 26 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 27 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 28 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 29 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 30 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 31 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 32 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 33 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 34 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 35 | Ankyrin-repeat containing protein | | Phvul.008G20PF13962 - Dor | Phvul.008G20 | not assigned.r |
| 36 | Ankyrin-repeat containing protein | | Phvul.008G20PF13962 - Dor | Phvul.008G20 | not assigned.r |
| 37 | Ankyrin-repeat containing protein | | Phvul.008G20PF13962 - Dor | Phvul.008G20 | not assigned.r |
| 38 | Ankyrin-repeat containing protein | | Phvul.008G20PF13962 - Dor | Phvul.008G20 | not assigned.r |
| 39 | Ankyrin-repeat containing protein | | Phvul.008G20PF13962 - Dor | Phvul.008G20 | not assigned.r |
| 40 | Ankyrin-repeat containing protein | | Phvul.008G20PF13962 - Dor | Phvul.008G20 | not assigned.r |
| 41 | Ankyrin-repeat containing protein | | Phvul.008G20PF13962 - Dor | Phvul.008G20 | not assigned.r |
| 42 | Ankyrin-repeat containing protein | | Phvul.008G20PF13962 - Dor | Phvul.008G20 | not assigned.r |
| 43 | Ankyrin-repeat containing protein | | Phvul.008G20PF13962 - Dor | Phvul.008G20 | not assigned.r |
| 44 | Ankyrin-repeat containing protein | | Phvul.008G20PF13962 - Dor | Phvul.008G20 | not assigned.r |
| 45 | Ankyrin-repeat containing protein | | Phvul.008G20PF13962 - Dor | Phvul.008G20 | not assigned.r |
| 46 | Ankyrin-repeat containing protein | | Phvul.008G20PF13962 - Dor | Phvul.008G20 | not assigned.r |
| 47 | Ankyrin-repeat containing protein | | Phvul.008G20PF13962 - Dor | Phvul.008G20 | not assigned.r |
| 48 | Ankyrin-repeat containing protein | | Phvul.008G20PF13962 - Dor | Phvul.008G20 | not assigned.r |
| 49 | Ankyrin-repeat containing protein | | Phvul.008G20PF13962 - Dor | Phvul.008G20 | not assigned.r |
| 50 | Ankyrin-repeat containing protein | | Phvul.008G20PF13962 - Dor | Phvul.008G20 | not assigned.r |
| 51 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 52 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 53 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 54 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 55 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 56 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 57 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 58 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 59 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |
| 60 | | 0 | 0 | 0 Phvul.003G16 | not assigned.r |

| | | | |
|----|-------------------------------|--------------------------|----------------------------|
| 1 | | | |
| 2 | | 0 | 0 |
| 3 | | 0 | 0 |
| 4 | | 0 | 0 |
| 5 | | 0 | 0 |
| 6 | | 0 | 0 |
| 7 | | 0 | 0 |
| 8 | | 0 | 0 |
| 9 | | 0 | 0 |
| 10 | | 0 | 0 |
| 11 | | 0 | 0 |
| 12 | | 0 | 0 |
| 13 | | 0 | 0 |
| 14 | | 0 | 0 |
| 15 | | 0 | 0 |
| 16 | | 0 | 0 |
| 17 | | 0 | 0 |
| 18 | | 0 | 0 |
| 19 | | 0 | 0 |
| 20 | | 0 | 0 |
| 21 | | 0 | 0 |
| 22 | | 0 | 0 |
| 23 | | 0 | 0 |
| 24 | | 0 | 0 |
| 25 | | 0 | 0 |
| 26 | | 0 | 0 |
| 27 | | 0 | 0 |
| 28 | MA3 domain-containing protein | Phvul.003G20PTHR12626:SI | Phvul.003G20Multi-process |
| 29 | MA3 domain-containing protein | Phvul.003G20PTHR12626:SI | Phvul.003G20Multi-process |
| 30 | MA3 domain-containing protein | Phvul.003G20PTHR12626:SI | Phvul.003G20Multi-process |
| 31 | MA3 domain-containing protein | Phvul.003G20PTHR12626:SI | Phvul.003G20Multi-process |
| 32 | MA3 domain-containing protein | Phvul.003G20PTHR12626:SI | Phvul.003G20Multi-process |
| 33 | MA3 domain-containing protein | Phvul.003G20PTHR12626:SI | Phvul.003G20Multi-process |
| 34 | MA3 domain-containing protein | Phvul.003G20PTHR12626:SI | Phvul.003G20Multi-process |
| 35 | MA3 domain-containing protein | Phvul.003G20PTHR12626:SI | Phvul.003G20Multi-process |
| 36 | MA3 domain-containing protein | Phvul.003G20PTHR12626:SI | Phvul.003G20Multi-process |
| 37 | MA3 domain-containing protein | Phvul.003G20PTHR12626:SI | Phvul.003G20Multi-process |
| 38 | MA3 domain-containing protein | Phvul.003G20PTHR12626:SI | Phvul.003G20Multi-process |
| 39 | MA3 domain-containing protein | Phvul.003G20PTHR12626:SI | Phvul.003G20Multi-process |
| 40 | MA3 domain-containing protein | Phvul.003G20PTHR12626:SI | Phvul.003G20Multi-process |
| 41 | MA3 domain-containing protein | Phvul.003G20PTHR12626:SI | Phvul.003G20Multi-process |
| 42 | MA3 domain-containing protein | Phvul.003G20PTHR12626:SI | Phvul.003G20Multi-process |
| 43 | nitrate transporter 1.1 | Phvul.003G21PTHR11654:SI | Phvul.003G21Solute transpc |
| 44 | nitrate transporter 1.1 | Phvul.003G21PTHR11654:SI | Phvul.003G21Solute transpc |
| 45 | nitrate transporter 1.1 | Phvul.003G21PTHR11654:SI | Phvul.003G21Solute transpc |
| 46 | nitrate transporter 1.1 | Phvul.003G21PTHR11654:SI | Phvul.003G21Solute transpc |
| 47 | nitrate transporter 1.1 | Phvul.003G21PTHR11654:SI | Phvul.003G21Solute transpc |
| 48 | nitrate transporter 1.1 | Phvul.003G21PTHR11654:SI | Phvul.003G21Solute transpc |
| 49 | nitrate transporter 1.1 | Phvul.003G21PTHR11654:SI | Phvul.003G21Solute transpc |
| 50 | nitrate transporter 1.1 | Phvul.003G21PTHR11654:SI | Phvul.003G21Solute transpc |
| 51 | nitrate transporter 1.1 | Phvul.003G21PTHR11654:SI | Phvul.003G21Solute transpc |
| 52 | nitrate transporter 1.1 | Phvul.003G21PTHR11654:SI | Phvul.003G21Solute transpc |
| 53 | nitrate transporter 1.1 | Phvul.003G21PTHR11654:SI | Phvul.003G21Solute transpc |
| 54 | nitrate transporter 1.1 | Phvul.003G21PTHR11654:SI | Phvul.003G21Solute transpc |
| 55 | nitrate transporter 1.1 | Phvul.003G21PTHR11654:SI | Phvul.003G21Solute transpc |
| 56 | nitrate transporter 1.1 | Phvul.003G21PTHR11654:SI | Phvul.003G21Solute transpc |
| 57 | nitrate transporter 1.1 | Phvul.003G21PTHR11654:SI | Phvul.003G21Solute transpc |
| 58 | nitrate transporter 1.1 | Phvul.003G21PTHR11654:SI | Phvul.003G21Solute transpc |
| 59 | nitrate transporter 1.1 | Phvul.003G21PTHR11654:SI | Phvul.003G21Solute transpc |
| 60 | nitrate transporter 1.1 | Phvul.003G21PTHR11654:SI | Phvul.003G21Solute transpc |

1 RNA-binding (RRM/RBD/RNP motifs) farPhvul.008G20PTHR24012:SlPhvul.008G20not assigned.a
2 RNA-binding (RRM/RBD/RNP motifs) farPhvul.008G20PTHR24012:SlPhvul.008G20not assigned.a
3 RNA-binding (RRM/RBD/RNP motifs) farPhvul.008G20PTHR24012:SlPhvul.008G20not assigned.a
4 RNA-binding (RRM/RBD/RNP motifs) farPhvul.008G20PTHR24012:SlPhvul.008G20not assigned.a
5 RNA-binding (RRM/RBD/RNP motifs) farPhvul.008G20PTHR24012:SlPhvul.008G20not assigned.a
6 RNA-binding (RRM/RBD/RNP motifs) farPhvul.008G20PTHR24012:SlPhvul.008G20not assigned.a
7 RNA-binding (RRM/RBD/RNP motifs) farPhvul.008G20PTHR24012:SlPhvul.008G20not assigned.a
8 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a
9 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a
10 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a
11 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a
12 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a
13 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a
14 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a
15 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a
16 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a
17 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a
18 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a
19 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a
20 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a
21 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a
22 Tetratricopeptide repeat (TPR)-like supePhvul.008G21PF01535//PF1Phvul.008G21not assigned.a
23 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home
24 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home
25 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home
26 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home
27 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home
28 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home
29 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home
30 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home
31 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home
32 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home
33 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home
34 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home
35 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home
36 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home
37 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home
38 Eukaryotic aspartyl protease family protPhvul.008G23PTHR13683:SlPhvul.008G23Protein home
39 0 0 0 Phvul.009G01not assigned.r
40 0 0 0 Phvul.009G01not assigned.r
41 0 0 0 Phvul.009G01not assigned.r
42 0 0 0 Phvul.009G01not assigned.r
43 0 0 0 Phvul.009G01not assigned.r
44 0 0 0 Phvul.009G01not assigned.r
45 0 0 0 Phvul.009G01not assigned.r
46 0 0 0 Phvul.009G01not assigned.r
47 0 0 0 Phvul.009G01not assigned.r
48 0 0 0 Phvul.009G01not assigned.r
49 0 0 0 Phvul.009G01not assigned.r
50 0 0 0 Phvul.009G01not assigned.r
51 0 0 0 Phvul.009G01not assigned.r
52 0 0 0 Phvul.009G01not assigned.r
53 0 0 0 Phvul.009G01not assigned.r
54
55 Transcription initiation factor IIF, beta slPhvul.009G01K03139 - tran:Phvul.009G01RNA biosynthe
56 Transcription initiation factor IIF, beta slPhvul.009G01K03139 - tran:Phvul.009G01RNA biosynthe
57 Transcription initiation factor IIF, beta slPhvul.009G01K03139 - tran:Phvul.009G01RNA biosynthe
58 Transcription initiation factor IIF, beta slPhvul.009G01K03139 - tran:Phvul.009G01RNA biosynthe
59 Transcription initiation factor IIF, beta slPhvul.009G01K03139 - tran:Phvul.009G01RNA biosynthe
60 Transcription initiation factor IIF, beta slPhvul.009G01K03139 - tran:Phvul.009G01RNA biosynthe

1 Tetratricopeptide repeat (TPR)-like supePhvul.001G09PF12854//PF1Phvul.001G09not assigned.a
2 Tetratricopeptide repeat (TPR)-like supePhvul.001G09PF12854//PF1Phvul.001G09not assigned.a
3 Tetratricopeptide repeat (TPR)-like supePhvul.001G09PF12854//PF1Phvul.001G09not assigned.a
4 Tetratricopeptide repeat (TPR)-like supePhvul.001G09PF12854//PF1Phvul.001G09not assigned.a
5 Tetratricopeptide repeat (TPR)-like supePhvul.001G09PF12854//PF1Phvul.001G09not assigned.a
6 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SfPhvul.001G19not assigned.a
7 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SfPhvul.001G19not assigned.a
8 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SfPhvul.001G19not assigned.a
9 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SfPhvul.001G19not assigned.a
10 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SfPhvul.001G19not assigned.a
11 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SfPhvul.001G19not assigned.a
12 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SfPhvul.001G19not assigned.a
13 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SfPhvul.001G19not assigned.a
14 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SfPhvul.001G19not assigned.a
15 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SfPhvul.001G19not assigned.a
16 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SfPhvul.001G19not assigned.a
17 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SfPhvul.001G19not assigned.a
18 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SfPhvul.001G19not assigned.a
19 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SfPhvul.001G19not assigned.a
20 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SfPhvul.001G19not assigned.a
21 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SfPhvul.001G19not assigned.a
22 Protein of unknown function, DUF593 Phvul.001G19PTHR31422:SfPhvul.001G19not assigned.a
23 FAR1-related sequence 5 Phvul.002G11PTHR31669:SfPhvul.002G11RNA biosynthe
24 FAR1-related sequence 5 Phvul.002G11PTHR31669:SfPhvul.002G11RNA biosynthe
25 FAR1-related sequence 5 Phvul.002G11PTHR31669:SfPhvul.002G11RNA biosynthe
26 FAR1-related sequence 5 Phvul.002G11PTHR31669:SfPhvul.002G11RNA biosynthe
27 FAR1-related sequence 5 Phvul.002G11PTHR31669:SfPhvul.002G11RNA biosynthe
28 FAR1-related sequence 5 Phvul.002G11PTHR31669:SfPhvul.002G11RNA biosynthe
29 FAR1-related sequence 5 Phvul.002G11PTHR31669:SfPhvul.002G11RNA biosynthe
30 FAR1-related sequence 5 Phvul.002G11PTHR31669:SfPhvul.002G11RNA biosynthe
31 FAR1-related sequence 5 Phvul.002G11PTHR31669:SfPhvul.002G11RNA biosynthe
32 FAR1-related sequence 5 Phvul.002G11PTHR31669:SfPhvul.002G11RNA biosynthe
33 FAR1-related sequence 5 Phvul.002G11PTHR31669:SfPhvul.002G11RNA biosynthe
34 FAR1-related sequence 5 Phvul.002G11PTHR31669:SfPhvul.002G11RNA biosynthe
35 FAR1-related sequence 5 Phvul.002G11PTHR31669:SfPhvul.002G11RNA biosynthe
36 FAR1-related sequence 5 Phvul.002G11PTHR31669:SfPhvul.002G11RNA biosynthe
37 FAR1-related sequence 5 Phvul.002G11PTHR31669:SfPhvul.002G11RNA biosynthe
38 FAR1-related sequence 5 Phvul.002G11PTHR31669:SfPhvul.002G11RNA biosynthe
39 RHO guanyl-nucleotide exchange factor Phvul.002G12PTHR33101:SfPhvul.002G12Multi-process
40 RHO guanyl-nucleotide exchange factor Phvul.002G12PTHR33101:SfPhvul.002G12Multi-process
41 Glutaredoxin family protein Phvul.002G32PTHR10168:SfPhvul.002G32not assigned.a
42 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a
43 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a
44 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a
45 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a
46 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a
47 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a
48 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a
49 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a
50 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a
51 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a
52 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a
53 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a
54 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a
55 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a
56 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a
57 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a
58 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a
59 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a
60 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a
CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SfPhvul.003G13not assigned.a

1 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a
2 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a
3 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a
4 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a
5 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a
6 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a
7 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a
8 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a
9 CRS1 / YhbY (CRM) domain-containing pPhvul.003G13PTHR31846:SlPhvul.003G13not assigned.a
10 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a
11 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a
12 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a
13 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a
14 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a
15 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a
16 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a
17 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a
18 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a
19 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a
20 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a
21 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a
22 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a
23 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a
24 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a
25 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a
26 Pentatricopeptide repeat (PPR) superfarPhvul.003G15PF01535//PF1Phvul.003G15not assigned.a
27 0 0 0 Phvul.003G19not assigned.r
28 0 0 0 Phvul.003G19not assigned.r
29 0 0 0 Phvul.003G19not assigned.r
30 0 0 0 Phvul.003G19not assigned.r
31 0 0 0 Phvul.003G19not assigned.r
32 0 0 0 Phvul.003G19not assigned.r
33 0 0 0 Phvul.003G19not assigned.r
34 0 0 0 Phvul.003G19not assigned.r
35 0 0 0 Phvul.003G19not assigned.r
36 0 0 0 Phvul.003G19not assigned.r
37 0 0 0 Phvul.003G19not assigned.r
38 0 0 0 Phvul.003G19not assigned.r
39 0 0 0 Phvul.003G19not assigned.r
40 0 0 0 Phvul.003G19not assigned.r
41 0 0 0 Phvul.003G19not assigned.r
42 0 0 0 Phvul.003G19not assigned.r
43 0 0 0 Phvul.003G19not assigned.r
44 0 0 0 Phvul.003G19not assigned.r
45 0 0 0 Phvul.003G19not assigned.r
46 0 0 0 Phvul.003G19not assigned.r
47 0 0 0 Phvul.003G19not assigned.r
48 0 0 0 Phvul.003G19not assigned.r
49 0 0 0 Phvul.003G19not assigned.r
50 0 0 0 Phvul.003G19not assigned.r
51 0 0 0 Phvul.003G19not assigned.r
52 0 0 0 Phvul.003G19not assigned.r
53 0 0 0 Phvul.003G19not assigned.r
54 0 0 0 Phvul.003G19not assigned.r
55 0 0 0 Phvul.003G19not assigned.r
56 0 0 0 Phvul.003G19not assigned.r
57 0 0 0 Phvul.003G19not assigned.r
58 S-adenosyl-L-methionine-dependent mePhvul.003G252.1.1.274 - SalPhvul.003G25Enzyme classifi
59 Tetratricopeptide repeat (TPR)-like supePhvul.003G29PF01535//PF1Phvul.003G29RNA processir
60 SPFH/Band 7/PHB domain-containing mPhvul.004G02PTHR10264//IPhvul.004G02not assigned.a

| | |
|----|--|
| 1 | |
| 2 | Aldolase-type TIM barrel family protein Phvul.008G00K00616 - tran:Phvul.008G00Carbohydrate |
| 3 | Aldolase-type TIM barrel family protein Phvul.008G00K00616 - tran:Phvul.008G00Carbohydrate |
| 4 | Aldolase-type TIM barrel family protein Phvul.008G00K00616 - tran:Phvul.008G00Carbohydrate |
| 5 | Aldolase-type TIM barrel family protein Phvul.008G00K00616 - tran:Phvul.008G00Carbohydrate |
| 6 | Aldolase-type TIM barrel family protein Phvul.008G00K00616 - tran:Phvul.008G00Carbohydrate |
| 7 | Auxin efflux carrier family protein Phvul.008G05PTHR31752:SlPhvul.008G05Solute transp |
| 8 | P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SlPhvul.008G16not assigned.a |
| 9 | P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SlPhvul.008G16not assigned.a |
| 10 | P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SlPhvul.008G16not assigned.a |
| 11 | P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SlPhvul.008G16not assigned.a |
| 12 | P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SlPhvul.008G16not assigned.a |
| 13 | P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SlPhvul.008G16not assigned.a |
| 14 | P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SlPhvul.008G16not assigned.a |
| 15 | P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SlPhvul.008G16not assigned.a |
| 16 | P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SlPhvul.008G16not assigned.a |
| 17 | P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SlPhvul.008G16not assigned.a |
| 18 | P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SlPhvul.008G16not assigned.a |
| 19 | P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SlPhvul.008G16not assigned.a |
| 20 | P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SlPhvul.008G16not assigned.a |
| 21 | P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SlPhvul.008G16not assigned.a |
| 22 | P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SlPhvul.008G16not assigned.a |
| 23 | P-loop containing nucleoside triphosphatPhvul.008G16PTHR10887:SlPhvul.008G16not assigned.a |
| 24 | RAD-like 6 Phvul.008G19PTHR24078:SlPhvul.008G19RNA biosynthe |
| 25 | RAD-like 6 Phvul.008G19PTHR24078:SlPhvul.008G19RNA biosynthe |
| 26 | RAD-like 6 Phvul.008G19PTHR24078:SlPhvul.008G19RNA biosynthe |
| 27 | RAD-like 6 Phvul.008G19PTHR24078:SlPhvul.008G19RNA biosynthe |
| 28 | RAD-like 6 Phvul.008G19PTHR24078:SlPhvul.008G19RNA biosynthe |
| 29 | RAD-like 6 Phvul.008G19PTHR24078:SlPhvul.008G19RNA biosynthe |
| 30 | RAD-like 6 Phvul.008G19PTHR24078:SlPhvul.008G19RNA biosynthe |
| 31 | RAD-like 6 Phvul.008G19PTHR24078:SlPhvul.008G19RNA biosynthe |
| 32 | RAD-like 6 Phvul.008G19PTHR24078:SlPhvul.008G19RNA biosynthe |
| 33 | RAD-like 6 Phvul.008G19PTHR24078:SlPhvul.008G19RNA biosynthe |
| 34 | RAD-like 6 Phvul.008G19PTHR24078:SlPhvul.008G19RNA biosynthe |
| 35 | RAD-like 6 Phvul.008G19PTHR24078:SlPhvul.008G19RNA biosynthe |
| 36 | RAD-like 6 Phvul.008G19PTHR24078:SlPhvul.008G19RNA biosynthe |
| 37 | RAD-like 6 Phvul.008G19PTHR24078:SlPhvul.008G19RNA biosynthe |
| 38 | RAD-like 6 Phvul.008G19PTHR24078:SlPhvul.008G19RNA biosynthe |
| 39 | RAD-like 6 Phvul.008G19PTHR24078:SlPhvul.008G19RNA biosynthe |
| 40 | Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SlPhvul.008G27Cell wall orgar |
| 41 | Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SlPhvul.008G27Cell wall orgar |
| 42 | Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SlPhvul.008G27Cell wall orgar |
| 43 | Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SlPhvul.008G27Cell wall orgar |
| 44 | Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SlPhvul.008G27Cell wall orgar |
| 45 | Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SlPhvul.008G27Cell wall orgar |
| 46 | Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SlPhvul.008G27Cell wall orgar |
| 47 | Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SlPhvul.008G27Cell wall orgar |
| 48 | Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SlPhvul.008G27Cell wall orgar |
| 49 | Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SlPhvul.008G27Cell wall orgar |
| 50 | Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SlPhvul.008G27Cell wall orgar |
| 51 | Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SlPhvul.008G27Cell wall orgar |
| 52 | Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SlPhvul.008G27Cell wall orgar |
| 53 | Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SlPhvul.008G27Cell wall orgar |
| 54 | Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SlPhvul.008G27Cell wall orgar |
| 55 | Pectin lyase-like superfamily protein Phvul.008G27PTHR31321:SlPhvul.008G27Cell wall orgar |
| 56 | Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli |
| 57 | Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli |
| 58 | Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli |
| 59 | Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli |
| 60 | Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli |

1 Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli
2 Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli
3 Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli
4 Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli
5 Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli
6 Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli
7 Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli
8 Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli
9 Neutral/alkaline non-lysosomal ceramidPhvul.008G28K12349 - neutPhvul.008G28Lipid metaboli
10
11 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
12 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
13 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
14 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
15 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
16 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
17 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
18 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
19 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
20 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
21 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
22 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
23 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
24 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
25 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
26 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
27 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
28 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
29 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
30 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
31 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
32 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
33 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
34 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
35 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
36 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
37 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
38 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
39 0 Phvul.009G08PF12776 - My Phvul.009G08not assigned.a
40 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc
41 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc
42 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc
43 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc
44 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc
45 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc
46 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc
47 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc
48 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc
49 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc
50 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc
51 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc
52 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc
53 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc
54 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc
55 AZA-guanine resistant1 Phvul.009G14K06901 - putaPhvul.009G14Solute transpc
56 cytochrome P450, family 88, subfamily 1Phvul.010G13PTHR24286:SFPhvul.010G13Enzyme classif
57 multidrug resistance-associated protein Phvul.010G14PTHR24223:SFPhvul.010G14Solute transpc
58 multidrug resistance-associated protein Phvul.010G14PTHR24223:SFPhvul.010G14Solute transpc
59 multidrug resistance-associated protein Phvul.010G14PTHR24223:SFPhvul.010G14Solute transpc
60 multidrug resistance-associated protein Phvul.010G14PTHR24223:SFPhvul.010G14Solute transpc

| | | |
|----|---------------------------------------|--|
| 1 | | |
| 2 | Late embryogenesis abundant (LEA) hyd | Phvul.005G10PF03168 - LatrPhvul.005G10not assigned.r |
| 3 | Late embryogenesis abundant (LEA) hyd | Phvul.005G10PF03168 - LatrPhvul.005G10not assigned.r |
| 4 | Late embryogenesis abundant (LEA) hyd | Phvul.005G10PF03168 - LatrPhvul.005G10not assigned.r |
| 5 | Late embryogenesis abundant (LEA) hyd | Phvul.005G10PF03168 - LatrPhvul.005G10not assigned.r |
| 6 | Late embryogenesis abundant (LEA) hyd | Phvul.005G10PF03168 - LatrPhvul.005G10not assigned.r |
| 7 | Late embryogenesis abundant (LEA) hyd | Phvul.005G10PF03168 - LatrPhvul.005G10not assigned.r |
| 8 | Late embryogenesis abundant (LEA) hyd | Phvul.005G10PF03168 - LatrPhvul.005G10not assigned.r |
| 9 | Late embryogenesis abundant (LEA) hyd | Phvul.005G10PF03168 - LatrPhvul.005G10not assigned.r |
| 10 | inositol transporter 4 | Phvul.006G14K08150 - MFS Phvul.006G14Solute transp |
| 11 | inositol transporter 4 | Phvul.006G14K08150 - MFS Phvul.006G14Solute transp |
| 12 | inositol transporter 4 | Phvul.006G14K08150 - MFS Phvul.006G14Solute transp |
| 13 | inositol transporter 4 | Phvul.006G14K08150 - MFS Phvul.006G14Solute transp |
| 14 | inositol transporter 4 | Phvul.006G14K08150 - MFS Phvul.006G14Solute transp |
| 15 | inositol transporter 4 | Phvul.006G14K08150 - MFS Phvul.006G14Solute transp |
| 16 | inositol transporter 4 | Phvul.006G14K08150 - MFS Phvul.006G14Solute transp |
| 17 | inositol transporter 4 | Phvul.006G14K08150 - MFS Phvul.006G14Solute transp |
| 18 | inositol transporter 4 | Phvul.006G14K08150 - MFS Phvul.006G14Solute transp |
| 19 | inositol transporter 4 | Phvul.006G14K08150 - MFS Phvul.006G14Solute transp |
| 20 | inositol transporter 4 | Phvul.006G14K08150 - MFS Phvul.006G14Solute transp |
| 21 | inositol transporter 4 | Phvul.006G14K08150 - MFS Phvul.006G14Solute transp |
| 22 | inositol transporter 4 | Phvul.006G14K08150 - MFS Phvul.006G14Solute transp |
| 23 | inositol transporter 4 | Phvul.006G14K08150 - MFS Phvul.006G14Solute transp |
| 24 | inositol transporter 4 | Phvul.006G14K08150 - MFS Phvul.006G14Solute transp |
| 25 | inositol transporter 4 | Phvul.006G14K08150 - MFS Phvul.006G14Solute transp |
| 26 | F-box/RNI-like superfamily protein | Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a |
| 27 | F-box/RNI-like superfamily protein | Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a |
| 28 | F-box/RNI-like superfamily protein | Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a |
| 29 | F-box/RNI-like superfamily protein | Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a |
| 30 | F-box/RNI-like superfamily protein | Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a |
| 31 | F-box/RNI-like superfamily protein | Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a |
| 32 | F-box/RNI-like superfamily protein | Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a |
| 33 | F-box/RNI-like superfamily protein | Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a |
| 34 | F-box/RNI-like superfamily protein | Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a |
| 35 | F-box/RNI-like superfamily protein | Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a |
| 36 | F-box/RNI-like superfamily protein | Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a |
| 37 | F-box/RNI-like superfamily protein | Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a |
| 38 | F-box/RNI-like superfamily protein | Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a |
| 39 | F-box/RNI-like superfamily protein | Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a |
| 40 | F-box/RNI-like superfamily protein | Phvul.006G15PTHR24006:SlPhvul.006G15not assigned.a |
| 41 | Protein of unknown function, DUF593 | Phvul.006G20PTHR31422:SlPhvul.006G20not assigned.r |
| 42 | carboxypeptidase D, putative | Phvul.007G083.4.17.22 - MεPhvul.007G08Protein home |
| 43 | carboxypeptidase D, putative | Phvul.007G083.4.17.22 - MεPhvul.007G08Protein home |
| 44 | carboxypeptidase D, putative | Phvul.007G083.4.17.22 - MεPhvul.007G08Protein home |
| 45 | Transducin/WD40 repeat-like superfami | Phvul.007G13PTHR22849//IPhvul.007G13External stimu |
| 46 | Transducin/WD40 repeat-like superfami | Phvul.007G13PTHR22849//IPhvul.007G13External stimu |
| 47 | Transducin/WD40 repeat-like superfami | Phvul.007G13PTHR22849//IPhvul.007G13External stimu |
| 48 | Transducin/WD40 repeat-like superfami | Phvul.007G13PTHR22849//IPhvul.007G13External stimu |
| 49 | Transducin/WD40 repeat-like superfami | Phvul.007G13PTHR22849//IPhvul.007G13External stimu |
| 50 | Transducin/WD40 repeat-like superfami | Phvul.007G13PTHR22849//IPhvul.007G13External stimu |
| 51 | Transducin/WD40 repeat-like superfami | Phvul.007G13PTHR22849//IPhvul.007G13External stimu |
| 52 | Transducin/WD40 repeat-like superfami | Phvul.007G13PTHR22849//IPhvul.007G13External stimu |
| 53 | Transducin/WD40 repeat-like superfami | Phvul.007G13PTHR22849//IPhvul.007G13External stimu |
| 54 | Transducin/WD40 repeat-like superfami | Phvul.007G13PTHR22849//IPhvul.007G13External stimu |
| 55 | Transducin/WD40 repeat-like superfami | Phvul.007G13PTHR22849//IPhvul.007G13External stimu |
| 56 | Transducin/WD40 repeat-like superfami | Phvul.007G13PTHR22849//IPhvul.007G13External stimu |
| 57 | Transducin/WD40 repeat-like superfami | Phvul.007G13PTHR22849//IPhvul.007G13External stimu |
| 58 | Transducin/WD40 repeat-like superfami | Phvul.007G13PTHR22849//IPhvul.007G13External stimu |
| 59 | Transducin/WD40 repeat-like superfami | Phvul.007G13PTHR22849//IPhvul.007G13External stimu |
| 60 | Beige/BEACH domain ;WD domain, G-βε | Phvul.007G17PTHR13743:SlPhvul.007G17not assigned.a |
| | Beige/BEACH domain ;WD domain, G-βε | Phvul.007G17PTHR13743:SlPhvul.007G17not assigned.a |

1 Beige/BEACH domain ;WD domain, G-bcPhvul.007G17PTHR13743:SfPhvul.007G17 not assigned.a
2 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe
3 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe
4 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe
5 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe
6 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe
7 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe
8 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe
9 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe
10 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe
11 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe
12 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe
13 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe
14 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe
15 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe
16 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe
17 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe
18 WRKY DNA-binding protein 21 Phvul.007G17PTHR31282:SfPhvul.007G17RNA biosynthe
19 0 Phvul.008G10PF03140 - PlaPhvul.008G10 not assigned.a
20 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a
21 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a
22 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a
23 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a
24 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a
25 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a
26 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a
27 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a
28 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a
29 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a
30 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a
31 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a
32 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a
33 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a
34 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a
35 P-loop containing nucleoside triphosphatPhvul.010G11PTHR24031:SfPhvul.010G11 not assigned.a
36 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe
37 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe
38 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe
39 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe
40 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe
41 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe
42 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe
43 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe
44 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe
45 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe
46 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe
47 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe
48 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe
49 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe
50 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe
51 ARID/BRIGHT DNA-binding domain-contPhvul.010G12PF01388 - ARI Phvul.010G12RNA biosynthe
52 Insulinase (Peptidase family M16) prote Phvul.010G143.4.24.64 - Mi Phvul.010G14 Protein modif
53 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SfPhvul.011G09Photosynthesi
54 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SfPhvul.011G09Photosynthesi
55 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SfPhvul.011G09Photosynthesi
56 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SfPhvul.011G09Photosynthesi
57 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SfPhvul.011G09Photosynthesi
58 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SfPhvul.011G09Photosynthesi
59 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SfPhvul.011G09Photosynthesi
60 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SfPhvul.011G09Photosynthesi

1 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SlPhvul.011G09Photosynthesi
2 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SlPhvul.011G09Photosynthesi
3 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SlPhvul.011G09Photosynthesi
4 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SlPhvul.011G09Photosynthesi
5 phosphoglycerate/bisphosphoglycerate Phvul.011G09PTHR23029:SlPhvul.011G09Photosynthesi
6 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home
7 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home
8 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home
9 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home
10 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home
11 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home
12 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home
13 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home
14 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home
15 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home
16 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home
17 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home
18 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home
19 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home
20 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home
21 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home
22 RING/U-box superfamily protein with AfPhvul.L00161(PTHR23315:SlPhvul.L00161(Protein home
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

not distribute

1
2 carboxy-D-arabinitol-1-phosphatase (CA1PP) (original description: pacid=37156982 transcript=Phv
3 carboxy-D-arabinitol-1-phosphatase (CA1PP) (original description: pacid=37156982 transcript=Phv
4 carboxy-D-arabinitol-1-phosphatase (CA1PP) (original description: pacid=37156982 transcript=Phv
5 carboxy-D-arabinitol-1-phosphatase (CA1PP) (original description: pacid=37156982 transcript=Phv
6 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F
7 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F
8 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F
9 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F
10 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F
11 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F
12 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F
13 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F
14 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F
15 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F
16 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F
17 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F
18 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F
19 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F
20 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F
21 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F
22 E3 ubiquitin ligase (PUB) (original description: pacid=37179033 transcript=Phvul.L001616.1 locus=F
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

not distribute

1 ul.011G090600.1 locus=Phvul.011G090600 ID=Phvul.011G090600.1.v2.1 annot-version=v2.1) &
2 ul.011G090600.1 locus=Phvul.011G090600 ID=Phvul.011G090600.1.v2.1 annot-version=v2.1) &
3 ul.011G090600.1 locus=Phvul.011G090600 ID=Phvul.011G090600.1.v2.1 annot-version=v2.1) &
4 ul.011G090600.1 locus=Phvul.011G090600 ID=Phvul.011G090600.1.v2.1 annot-version=v2.1) &
5 ul.011G090600.1 locus=Phvul.011G090600 ID=Phvul.011G090600.1.v2.1 annot-version=v2.1) &
6 Phvul.L001616 ID=Phvul.L001616.1.v2.1 annot-version=v2.1) &
7 Phvul.L001616 ID=Phvul.L001616.1.v2.1 annot-version=v2.1) &
8 Phvul.L001616 ID=Phvul.L001616.1.v2.1 annot-version=v2.1) &
9 Phvul.L001616 ID=Phvul.L001616.1.v2.1 annot-version=v2.1) &
10 Phvul.L001616 ID=Phvul.L001616.1.v2.1 annot-version=v2.1) &
11 Phvul.L001616 ID=Phvul.L001616.1.v2.1 annot-version=v2.1) &
12 Phvul.L001616 ID=Phvul.L001616.1.v2.1 annot-version=v2.1) &
13 Phvul.L001616 ID=Phvul.L001616.1.v2.1 annot-version=v2.1) &
14 Phvul.L001616 ID=Phvul.L001616.1.v2.1 annot-version=v2.1) &
15 Phvul.L001616 ID=Phvul.L001616.1.v2.1 annot-version=v2.1) &
16 Phvul.L001616 ID=Phvul.L001616.1.v2.1 annot-version=v2.1) &
17 Phvul.L001616 ID=Phvul.L001616.1.v2.1 annot-version=v2.1) &
18 Phvul.L001616 ID=Phvul.L001616.1.v2.1 annot-version=v2.1) &
19 Phvul.L001616 ID=Phvul.L001616.1.v2.1 annot-version=v2.1) &
20 Phvul.L001616 ID=Phvul.L001616.1.v2.1 annot-version=v2.1) &
21 Phvul.L001616 ID=Phvul.L001616.1.v2.1 annot-version=v2.1) &
22 Phvul.L001616 ID=Phvul.L001616.1.v2.1 annot-version=v2.1) &
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2 .) &
3 .) &
4 .) &
5 .) &
6 .) &
7 .) &
8 opsis thaliana (sp|o65607|msh3_arath : 82.0)
9 opsis thaliana (sp|o65607|msh3_arath : 82.0)
10 opsis thaliana (sp|o65607|msh3_arath : 82.0)
11 opsis thaliana (sp|o65607|msh3_arath : 82.0)
12 opsis thaliana (sp|o65607|msh3_arath : 82.0)
13 opsis thaliana (sp|o65607|msh3_arath : 82.0)
14 opsis thaliana (sp|o65607|msh3_arath : 82.0)
15 opsis thaliana (sp|o65607|msh3_arath : 82.0)
16 opsis thaliana (sp|o65607|msh3_arath : 82.0)
17 opsis thaliana (sp|o65607|msh3_arath : 82.0)
18 opsis thaliana (sp|o65607|msh3_arath : 82.0)
19 opsis thaliana (sp|o65607|msh3_arath : 82.0)
20 opsis thaliana (sp|o65607|msh3_arath : 82.0)
21 opsis thaliana (sp|o65607|msh3_arath : 82.0)
22 opsis thaliana (sp|o65607|msh3_arath : 82.0)
23 opsis thaliana (sp|o65607|msh3_arath : 82.0)
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39

40 l) &
41 l) &
42 l) &
43 l) &
44 l) &
45 l) &
46 l) &
47 l) &
48 l) &
49 l) &
50 l) &
51 l) &
52 l) &
53 l) &
54 l) &
55 l) &
56
57
58
59
60

not distribute

1
2
3
4
5
6
7
8
9
10
11 version=v2.1) &
12 version=v2.1) &
13 version=v2.1) &
14 version=v2.1) &
15 version=v2.1) &
16 version=v2.1) &
17 version=v2.1) &
18 version=v2.1) &
19 version=v2.1) &
20 version=v2.1) &
21 version=v2.1) &
22 version=v2.1) &
23 version=v2.1) &
24 version=v2.1) &
25) &
26) &
27) &
28) &
29) &
30) &
31) &
32) &
33) &
34) &
35) &
36) &
37) &
38) &
39) &
40) &
41) &
42) &
43) &
44) &
45) &
46) &
47) &
48) &
49) &
50) &
51) &
52) &
53) &
54) &
55) &
56) &
57) &
58) &
59) &
60) &
) &

Do not distribute

1
2 l) &
3 l) &
4 l) &
5 l) &
6 l) &
7 l) &
8 l) &
9 l) &
10 l) &
11 l) &

12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27

28 l) &
29 l) &
30 l) &
31 l) &
32 l) &
33 l) &
34 l) &
35 l) &
36 l) &
37 l) &
38 l) &
39 l) &
40 l) &
41 l) &
42 l) &
43 l) &

44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59

60 t-version=v2.1) &
t-version=v2.1) &

Do not distribute

1
2)t-version=v2.1) &
3)t-version=v2.1) &
4)t-version=v2.1) &
5)t-version=v2.1) &
6)t-version=v2.1) &
7)t-version=v2.1) &
8)t-version=v2.1) &
9)t-version=v2.1) &
10)t-version=v2.1) &
11)t-version=v2.1) &
12)t-version=v2.1) &
13)t-version=v2.1) &
14)t-version=v2.1) &
15 &
16 &
17 &
18 &
19 &
20 &
21 &
22 &
23 &
24 &
25 &
26 &
27 &
28 &
29 &
30 &
31 1g31430 OS=Arabidopsis thaliana (sp|q9c866|ppr65_arath : 668.0)
32 1g31430 OS=Arabidopsis thaliana (sp|q9c866|ppr65_arath : 668.0)
33 1g31430 OS=Arabidopsis thaliana (sp|q9c866|ppr65_arath : 668.0)
34 1g31430 OS=Arabidopsis thaliana (sp|q9c866|ppr65_arath : 668.0)
35 1g31430 OS=Arabidopsis thaliana (sp|q9c866|ppr65_arath : 668.0)
36 1g31430 OS=Arabidopsis thaliana (sp|q9c866|ppr65_arath : 668.0)
37 1g31430 OS=Arabidopsis thaliana (sp|q9c866|ppr65_arath : 668.0)
38 1g31430 OS=Arabidopsis thaliana (sp|q9c866|ppr65_arath : 668.0)
39 1g31430 OS=Arabidopsis thaliana (sp|q9c866|ppr65_arath : 668.0)
40 1g31430 OS=Arabidopsis thaliana (sp|q9c866|ppr65_arath : 668.0)
41 1g31430 OS=Arabidopsis thaliana (sp|q9c866|ppr65_arath : 668.0)
42 1g31430 OS=Arabidopsis thaliana (sp|q9c866|ppr65_arath : 668.0)
43 1g31430 OS=Arabidopsis thaliana (sp|q9c866|ppr65_arath : 668.0)
44 1g31430 OS=Arabidopsis thaliana (sp|q9c866|ppr65_arath : 668.0)
45 1g31430 OS=Arabidopsis thaliana (sp|q9c866|ppr65_arath : 668.0)
46 1g31430 OS=Arabidopsis thaliana (sp|q9c866|ppr65_arath : 668.0)
47 l) &
48 l) &
49 l) &
50 l) &
51 l) &
52 l) &
53 l) &
54 l) &
55 l) &
56 l) &
57 l) &
58 l) &
59 l) &
60 l) &

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

isis thaliana (sp|q9sth1|hsop3_arath : 85.1)
isis thaliana (sp|q9sth1|hsop3_arath : 85.1)
isis thaliana (sp|q9sth1|hsop3_arath : 85.1)
isis thaliana (sp|q9sth1|hsop3_arath : 85.1)
isis thaliana (sp|q9sth1|hsop3_arath : 85.1)
isis thaliana (sp|q9sth1|hsop3_arath : 85.1)
isis thaliana (sp|q9sth1|hsop3_arath : 85.1)
isis thaliana (sp|q9sth1|hsop3_arath : 85.1)
isis thaliana (sp|q9sth1|hsop3_arath : 85.1)
isis thaliana (sp|q9sth1|hsop3_arath : 85.1)
isis thaliana (sp|q9sth1|hsop3_arath : 85.1)
isis thaliana (sp|q9sth1|hsop3_arath : 85.1)
isis thaliana (sp|q9sth1|hsop3_arath : 85.1)
isis thaliana (sp|q9sth1|hsop3_arath : 85.1)
isis thaliana (sp|q9sth1|hsop3_arath : 85.1)
isis thaliana (sp|q9sth1|hsop3_arath : 85.1)

L) &
L) &
L) &
L) &
L) &
L) &
L) &
L) &
L) &
L) &
L) &

not distribute

- 1
- 2 l) &
- 3 l) &
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36 l) &
- 37 l) &
- 38 l) &
- 39 l) &
- 40 l) &
- 41 l) &
- 42 l) &
- 43 l) &
- 44 l) &
- 45 l) &
- 46 l) &
- 47 l) &
- 48 l) &
- 49 l) &
- 50 l) &
- 51 l) &
- 52 l) &
- 53 l) &
- 54 l) &
- 55 l) &
- 56 l) &
- 57 l) &
- 58 l) &
- 59 l) &
- 60 l) &

Do not distribute

- 1
- 2 L) &
- 3 L) &
- 4 L) &
- 5 L) &
- 6 L) &
- 7 L) &
- 8 L) &
- 9 L) &
- 10 L) &
- 11 L) &
- 12 L) &
- 13 L) &
- 14 L) &
- 15 L) &
- 16 L) &
- 17 L) &
- 18 L) &
- 19 L) &
- 20 L) &
- 21 L) &
- 22 L) &
- 23 L) &
- 24 L) &
- 25 L) &
- 26 L) &
- 27 L) &
- 28 L) &
- 29 L) &
- 30 L) &
- 31 L) &
- 32 L) &
- 33 L) &
- 34 L) &
- 35 L) &
- 36 L) &
- 37 L) &
- 38 L) &
- 39 L) &
- 40 L) &
- 41 L) &
- 42 L) &
- 43 L) &
- 44 L) &
- 45 L) &
- 46 L) &
- 47 L) &
- 48 L) &
- 49 L) &
- 50 L) &
- 51 L) &
- 52 L) &
- 53 L) &
- 54 L) &
- 55 L) &
- 56 L) &
- 57 L) &
- 58 L) &
- 59 L) &
- 60 L) &

Do not distribute

- 1
- 2 L) &
- 3 L) &
- 4 L) &
- 5 L) &
- 6 L) &
- 7 L) &
- 8 L) &
- 9 L) &
- 10 L) &
- 11 L) &
- 12 L) &
- 13 L) &
- 14 L) &
- 15 L) &
- 16 L) &
- 17 L) &
- 18 L) &
- 19 L) &
- 20 L) &
- 21 L) &
- 22 L) &
- 23 L) &
- 24 L) &
- 25 L) &
- 26 L) &
- 27 L) &
- 28 L) &
- 29 L) &
- 30 L) &
- 31 L) &
- 32 L) &
- 33 L) &
- 34 L) &
- 35 L) &
- 36 L) &
- 37 L) &
- 38 L) &
- 39 L) &
- 40 L) &
- 41 L) &
- 42 L) &
- 43 L) &
- 44 L) &
- 45 L) &
- 46 L) &
- 47 L) &
- 48 L) &
- 49 L) &
- 50 L) &
- 51 L) &
- 52 L) &
- 53 L) &
- 54 L) &
- 55 L) &
- 56 L) &
- 57
- 58
- 59
- 60

Do not distribute

- 1
- 2 L) &
- 3 L) &
- 4 L) &
- 5 L) &
- 6 L) &
- 7 L) &
- 8 L) &
- 9 L) &
- 10 L) &
- 11 L) &
- 12 L) &
- 13 L) &
- 14 L) &
- 15 L) &
- 16 L) &
- 17 L) &
- 18 L) &
- 19 L) &
- 20 L) &
- 21 L) &
- 22 L) &
- 23 L) &
- 24 L) &
- 25 L) &
- 26 L) &
- 27 L) &
- 28 L) &
- 29 L) &
- 30 L) &
- 31 L) &
- 32 L) &
- 33 L) &
- 34 L) &
- 35 L) &
- 36 L) &
- 37 L) &
- 38 L) &
- 39 L) &
- 40 L) &
- 41 L) &
- 42 L) &
- 43 L) &
- 44 L) &
- 45 L) &
- 46 L) &
- 47 L) &
- 48 L) &
- 49 L) &
- 50 L) &
- 51 L) &
- 52 L) &
- 53 L) &
- 54 L) &
- 55 L) &
- 56 L) &
- 57 L) &
- 58 L) &
- 59 L) &
- 60 L) &

Do not distribute

1 =Glycine max (sp|p24095|loxx_soybn : 884.0) (original description: pacid=37144293 transcript=Phv
2 =Glycine max (sp|p24095|loxx_soybn : 884.0) (original description: pacid=37144293 transcript=Phv
3 =Glycine max (sp|p24095|loxx_soybn : 884.0) (original description: pacid=37144293 transcript=Phv
4 =Glycine max (sp|p24095|loxx_soybn : 884.0) (original description: pacid=37144293 transcript=Phv
5 =Glycine max (sp|p24095|loxx_soybn : 884.0) (original description: pacid=37144293 transcript=Phv
6 =Glycine max (sp|p24095|loxx_soybn : 884.0) (original description: pacid=37144293 transcript=Phv
7 =Glycine max (sp|p24095|loxx_soybn : 884.0) (original description: pacid=37144293 transcript=Phv
8 =Glycine max (sp|p24095|loxx_soybn : 884.0) (original description: pacid=37144293 transcript=Phv
9 =Glycine max (sp|p24095|loxx_soybn : 884.0) (original description: pacid=37144293 transcript=Phv
10 =Glycine max (sp|p24095|loxx_soybn : 884.0) (original description: pacid=37144293 transcript=Phv
11 =Glycine max (sp|p24095|loxx_soybn : 884.0) (original description: pacid=37144293 transcript=Phv
12 =Glycine max (sp|p24095|loxx_soybn : 884.0) (original description: pacid=37144293 transcript=Phv
13 =Glycine max (sp|p24095|loxx_soybn : 884.0) (original description: pacid=37144293 transcript=Phv
14 =Glycine max (sp|p24095|loxx_soybn : 884.0) (original description: pacid=37144293 transcript=Phv
15 =Glycine max (sp|p24095|loxx_soybn : 884.0) (original description: pacid=37144293 transcript=Phv
16 =Glycine max (sp|p24095|loxx_soybn : 884.0) (original description: pacid=37144293 transcript=Phv
17 =Glycine max (sp|p24095|loxx_soybn : 884.0) (original description: pacid=37144293 transcript=Phv

18) &
19) &
20) &
21) &
22) &
23) &
24) &
25) &
26) &
27) &
28) &
29) &
30) &
31) &
32) &
33) &
34) &
35) &
36) &
37) &
38) &
39) &
40) &
41) &
42) &
43) &
44) &
45) &
46) &
47) &
48) &

49 400.1.v2.1 annot-version=v2.1) &
50 400.1.v2.1 annot-version=v2.1) &
51 400.1.v2.1 annot-version=v2.1) &
52 400.1.v2.1 annot-version=v2.1) &
53 400.1.v2.1 annot-version=v2.1) &
54 400.1.v2.1 annot-version=v2.1) &
55 400.1.v2.1 annot-version=v2.1) &
56 400.1.v2.1 annot-version=v2.1) &
57 400.1.v2.1 annot-version=v2.1) &
58 400.1.v2.1 annot-version=v2.1) &
59 400.1.v2.1 annot-version=v2.1) &
60 400.1.v2.1 annot-version=v2.1) &
400.1.v2.1 annot-version=v2.1) &

Do not distribute

1
2 400.1.v2.1 annot-version=v2.1) &
3 400.1.v2.1 annot-version=v2.1) &
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

2.1 annot-version=v2.1) &

) &
) &
) &
) &
) &
) &
) &
) &
) &
) &
) &
) &
) &
) &
) &
) &
) &
) &
) &
) &
) &
) &
) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26 rotein At3g11460, mitochondrial OS=Arabidopsis thaliana (sp|q9cay1|pp223_arath : 163.0)
27 rotein At3g11460, mitochondrial OS=Arabidopsis thaliana (sp|q9cay1|pp223_arath : 163.0)
28 rotein At3g11460, mitochondrial OS=Arabidopsis thaliana (sp|q9cay1|pp223_arath : 163.0)
29 rotein At3g11460, mitochondrial OS=Arabidopsis thaliana (sp|q9cay1|pp223_arath : 163.0)
30 rotein At3g11460, mitochondrial OS=Arabidopsis thaliana (sp|q9cay1|pp223_arath : 163.0)
31 rotein At3g11460, mitochondrial OS=Arabidopsis thaliana (sp|q9cay1|pp223_arath : 163.0)
32 rotein At3g11460, mitochondrial OS=Arabidopsis thaliana (sp|q9cay1|pp223_arath : 163.0)
33 rotein At3g11460, mitochondrial OS=Arabidopsis thaliana (sp|q9cay1|pp223_arath : 163.0)
34 rotein At3g11460, mitochondrial OS=Arabidopsis thaliana (sp|q9cay1|pp223_arath : 163.0)
35 rotein At3g11460, mitochondrial OS=Arabidopsis thaliana (sp|q9cay1|pp223_arath : 163.0)
36 rotein At3g11460, mitochondrial OS=Arabidopsis thaliana (sp|q9cay1|pp223_arath : 163.0)
37 rotein At3g11460, mitochondrial OS=Arabidopsis thaliana (sp|q9cay1|pp223_arath : 163.0)
38 rotein At3g11460, mitochondrial OS=Arabidopsis thaliana (sp|q9cay1|pp223_arath : 163.0)
39 rotein At3g11460, mitochondrial OS=Arabidopsis thaliana (sp|q9cay1|pp223_arath : 163.0)
40 rotein At3g11460, mitochondrial OS=Arabidopsis thaliana (sp|q9cay1|pp223_arath : 163.0)
41 scription: pacid=37166088 transcript=Phvul.007G212500.1 locus=Phvul.007G212500 ID=Phvul.007G
42 scription: pacid=37166088 transcript=Phvul.007G212500.1 locus=Phvul.007G212500 ID=Phvul.007G
43 scription: pacid=37166088 transcript=Phvul.007G212500.1 locus=Phvul.007G212500 ID=Phvul.007G
44 scription: pacid=37166088 transcript=Phvul.007G212500.1 locus=Phvul.007G212500 ID=Phvul.007G
45 scription: pacid=37166088 transcript=Phvul.007G212500.1 locus=Phvul.007G212500 ID=Phvul.007G
46 scription: pacid=37166088 transcript=Phvul.007G212500.1 locus=Phvul.007G212500 ID=Phvul.007G
47 scription: pacid=37166088 transcript=Phvul.007G212500.1 locus=Phvul.007G212500 ID=Phvul.007G
48 scription: pacid=37166088 transcript=Phvul.007G212500.1 locus=Phvul.007G212500 ID=Phvul.007G
49 scription: pacid=37166088 transcript=Phvul.007G212500.1 locus=Phvul.007G212500 ID=Phvul.007G
50 scription: pacid=37166088 transcript=Phvul.007G212500.1 locus=Phvul.007G212500 ID=Phvul.007G
51 scription: pacid=37166088 transcript=Phvul.007G212500.1 locus=Phvul.007G212500 ID=Phvul.007G
52 scription: pacid=37166088 transcript=Phvul.007G212500.1 locus=Phvul.007G212500 ID=Phvul.007G
53 scription: pacid=37166088 transcript=Phvul.007G212500.1 locus=Phvul.007G212500 ID=Phvul.007G
54 scription: pacid=37166088 transcript=Phvul.007G212500.1 locus=Phvul.007G212500 ID=Phvul.007G
55 scription: pacid=37166088 transcript=Phvul.007G212500.1 locus=Phvul.007G212500 ID=Phvul.007G
56 scription: pacid=37166088 transcript=Phvul.007G212500.1 locus=Phvul.007G212500 ID=Phvul.007G
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

id=37164693 transcript=Phvul.007G280800.1 locus=Phvul.007G280800 ID=Phvul.007G280800.1.v2.
id=37164693 transcript=Phvul.007G280800.1 locus=Phvul.007G280800 ID=Phvul.007G280800.1.v2.
id=37164693 transcript=Phvul.007G280800.1 locus=Phvul.007G280800 ID=Phvul.007G280800.1.v2.
id=37164693 transcript=Phvul.007G280800.1 locus=Phvul.007G280800 ID=Phvul.007G280800.1.v2.
id=37164693 transcript=Phvul.007G280800.1 locus=Phvul.007G280800 ID=Phvul.007G280800.1.v2.
id=37164693 transcript=Phvul.007G280800.1 locus=Phvul.007G280800 ID=Phvul.007G280800.1.v2.
id=37164693 transcript=Phvul.007G280800.1 locus=Phvul.007G280800 ID=Phvul.007G280800.1.v2.
id=37164693 transcript=Phvul.007G280800.1 locus=Phvul.007G280800 ID=Phvul.007G280800.1.v2.
id=37164693 transcript=Phvul.007G280800.1 locus=Phvul.007G280800 ID=Phvul.007G280800.1.v2.
id=37164693 transcript=Phvul.007G280800.1 locus=Phvul.007G280800 ID=Phvul.007G280800.1.v2.
id=37164693 transcript=Phvul.007G280800.1 locus=Phvul.007G280800 ID=Phvul.007G280800.1.v2.
id=37164693 transcript=Phvul.007G280800.1 locus=Phvul.007G280800 ID=Phvul.007G280800.1.v2.
id=37164693 transcript=Phvul.007G280800.1 locus=Phvul.007G280800 ID=Phvul.007G280800.1.v2.
OS=Arabidopsis thaliana (sp|o82484|drl23_arath : 219.0)
OS=Arabidopsis thaliana (sp|o82484|drl23_arath : 219.0)
OS=Arabidopsis thaliana (sp|o82484|drl23_arath : 219.0)
OS=Arabidopsis thaliana (sp|o82484|drl23_arath : 219.0)
OS=Arabidopsis thaliana (sp|o82484|drl23_arath : 219.0)
OS=Arabidopsis thaliana (sp|o82484|drl23_arath : 219.0)
OS=Arabidopsis thaliana (sp|o82484|drl23_arath : 219.0)
OS=Arabidopsis thaliana (sp|o82484|drl23_arath : 219.0)
OS=Arabidopsis thaliana (sp|o82484|drl23_arath : 219.0)
OS=Arabidopsis thaliana (sp|o82484|drl23_arath : 219.0)
OS=Arabidopsis thaliana (sp|o82484|drl23_arath : 219.0)
OS=Arabidopsis thaliana (sp|o82484|drl23_arath : 219.0)
OS=Arabidopsis thaliana (sp|o82484|drl23_arath : 219.0)
OS=Arabidopsis thaliana (sp|o82484|drl23_arath : 219.0)
OS=Arabidopsis thaliana (sp|o82484|drl23_arath : 219.0)
OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)

1 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
2 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
3 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
4 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
5 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
6 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
7 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
8 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
9 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
10 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
11 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
12 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
13 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
14 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
15 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
16 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
17 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
18 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
19 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
20 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
21 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
22 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
23 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
24 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
25 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
26 4g19890 OS=Arabidopsis thaliana (sp|p0c8q3|pp326_arath : 844.0)
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60

in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &
 in=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11 2g04860 OS=Arabidopsis thaliana (sp|q9sj73|pp148_arath : 728.0)
12 2g04860 OS=Arabidopsis thaliana (sp|q9sj73|pp148_arath : 728.0)
13 2g04860 OS=Arabidopsis thaliana (sp|q9sj73|pp148_arath : 728.0)
14 2g04860 OS=Arabidopsis thaliana (sp|q9sj73|pp148_arath : 728.0)
15 2g04860 OS=Arabidopsis thaliana (sp|q9sj73|pp148_arath : 728.0)
16 2g04860 OS=Arabidopsis thaliana (sp|q9sj73|pp148_arath : 728.0)
17 2g04860 OS=Arabidopsis thaliana (sp|q9sj73|pp148_arath : 728.0)
18 2g04860 OS=Arabidopsis thaliana (sp|q9sj73|pp148_arath : 728.0)
19 2g04860 OS=Arabidopsis thaliana (sp|q9sj73|pp148_arath : 728.0)
20 2g04860 OS=Arabidopsis thaliana (sp|q9sj73|pp148_arath : 728.0)
21 2g04860 OS=Arabidopsis thaliana (sp|q9sj73|pp148_arath : 728.0)
22 2g04860 OS=Arabidopsis thaliana (sp|q9sj73|pp148_arath : 728.0)
23 2g04860 OS=Arabidopsis thaliana (sp|q9sj73|pp148_arath : 728.0)
24 2g04860 OS=Arabidopsis thaliana (sp|q9sj73|pp148_arath : 728.0)
25
26 rsion=v2.1) &
27 rsion=v2.1) &
28 rsion=v2.1) &
29 rsion=v2.1) &
30 rsion=v2.1) &
31 rsion=v2.1) &
32 rsion=v2.1) &
33 rsion=v2.1) &
34 rsion=v2.1) &
35 rsion=v2.1) &
36 rsion=v2.1) &
37 rsion=v2.1) &
38 rsion=v2.1) &
39 rsion=v2.1) &
40 rsion=v2.1) &
41 rsion=v2.1) &
42 rsion=v2.1) &
43 rsion=v2.1) &
44 rsion=v2.1) &
45 rsion=v2.1) &
46 rsion=v2.1) &
47 rsion=v2.1) &
48 rsion=v2.1) &
49 rsion=v2.1) &
50 rsion=v2.1) &
51 rsion=v2.1) &
52 rsion=v2.1) &
53 rsion=v2.1) &
54 rsion=v2.1) &
55 rsion=v2.1) &
56 rsion=v2.1) &
57 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)
58 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)
59 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)
60 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

1 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

2 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

3 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

4 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

5 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

6 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

7 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

8 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

9 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

10 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

11 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

12 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

13 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

14 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

15 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

16 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

17 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

18 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

19 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

20 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

21 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

22 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

23 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

24 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

25 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

26 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

27 dopsis thaliana (sp|q944a6|snf4_arath : 499.0)

28 S=Glycine max (sp|p24095|loxx_soybn : 958.0) (original description: pacid=37143239 transcript=Pr

29 S=Glycine max (sp|p24095|loxx_soybn : 958.0) (original description: pacid=37144193 transcript=Pr

30

31

32

33

34

35

36

37

38

39

40

41

42

43

44

45

46

47

48

49

50

51

52

53

54

55

56

57

58

59

60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

-Arabidopsis thaliana (sp|q9lpr4|leu11_arath : 359.0)
-Arabidopsis thaliana (sp|q9lpr4|leu11_arath : 359.0)
-Arabidopsis thaliana (sp|q9lpr4|leu11_arath : 359.0)
-Arabidopsis thaliana (sp|q9lpr4|leu11_arath : 359.0)
-Arabidopsis thaliana (sp|q9lpr4|leu11_arath : 359.0)
-Arabidopsis thaliana (sp|q9lpr4|leu11_arath : 359.0)
-Arabidopsis thaliana (sp|q9lpr4|leu11_arath : 359.0)
-Arabidopsis thaliana (sp|q9lpr4|leu11_arath : 359.0)
-Arabidopsis thaliana (sp|q9lpr4|leu11_arath : 359.0)
-Arabidopsis thaliana (sp|q9lpr4|leu11_arath : 359.0)
-Arabidopsis thaliana (sp|q9lpr4|leu11_arath : 359.0)
ie max (sp|q39891|leu1_soybn : 313.0)
ie max (sp|q39891|leu1_soybn : 313.0)

1
2 ie max (sp|q39891|leu1_soybn : 313.0)
3 ie max (sp|q39891|leu1_soybn : 313.0)
4 ie max (sp|q39891|leu1_soybn : 313.0)
5 ie max (sp|q39891|leu1_soybn : 313.0)
6 ie max (sp|q39891|leu1_soybn : 313.0)
7 ie max (sp|q39891|leu1_soybn : 313.0)
8 ie max (sp|q39891|leu1_soybn : 313.0)
9 ie max (sp|q39891|leu1_soybn : 313.0)
10 ie max (sp|q39891|leu1_soybn : 313.0)
11 ie max (sp|q39891|leu1_soybn : 313.0)
12 ie max (sp|q39891|leu1_soybn : 313.0)
13 ie max (sp|q39891|leu1_soybn : 313.0)
14 ie max (sp|q39891|leu1_soybn : 313.0)
15 ie max (sp|q39891|leu1_soybn : 313.0)
16 ie max (sp|q39891|leu1_soybn : 313.0)
17 ie max (sp|q39891|leu1_soybn : 313.0)
18 ie max (sp|q39891|leu1_soybn : 313.0)
19 ie max (sp|q39891|leu1_soybn : 313.0)
20 ie max (sp|q39891|leu1_soybn : 313.0)
21 ie max (sp|q39891|leu1_soybn : 313.0)
22 ie max (sp|q39891|leu1_soybn : 313.0)
23 ie max (sp|q39891|leu1_soybn : 313.0)
24 ie max (sp|q39891|leu1_soybn : 313.0)
25 ie max (sp|q39891|leu1_soybn : 313.0)
26 ie max (sp|q39891|leu1_soybn : 313.0)
27 ie max (sp|q39891|leu1_soybn : 313.0)
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

opsis thaliana (sp|q9sl48|sly1_arath : 931.0)
opsis thaliana (sp|q9sl48|sly1_arath : 931.0)
opsis thaliana (sp|q9sl48|sly1_arath : 931.0)
opsis thaliana (sp|q9sl48|sly1_arath : 931.0)
opsis thaliana (sp|q9sl48|sly1_arath : 931.0)
opsis thaliana (sp|q9sl48|sly1_arath : 931.0)
opsis thaliana (sp|q9sl48|sly1_arath : 931.0)
opsis thaliana (sp|q9sl48|sly1_arath : 931.0)
opsis thaliana (sp|q9sl48|sly1_arath : 931.0)
opsis thaliana (sp|q9sl48|sly1_arath : 931.0)
opsis thaliana (sp|q9sl48|sly1_arath : 931.0)
opsis thaliana (sp|q9sl48|sly1_arath : 931.0)
&
&
&
&
&

1
2 | &
3 | &
4 | &
5 | &
6 | &
7 | &
8 | &
9 | &
10 | &
11 | &
12 | &
13 | &
14 | &
15 | &
16 | &
17 | &
18 | &
19 | &
20 | &
21 | &
22 | &
23 | &
24 | &
25 | &
26 | &
27 | 081|per42_arath : 526.0)
28 | 081|per42_arath : 526.0)
29 | 081|per42_arath : 526.0)
30 | 081|per42_arath : 526.0)
31 | 081|per42_arath : 526.0)
32 | 081|per42_arath : 526.0)
33 | 081|per42_arath : 526.0)
34 | 081|per42_arath : 526.0)
35 | 081|per42_arath : 526.0)
36 | 081|per42_arath : 526.0)
37 | 081|per42_arath : 526.0)
38 | 081|per42_arath : 526.0)
39 | 081|per42_arath : 526.0)
40 | 081|per42_arath : 526.0)
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

) &
) &
) &
) &
) &
) &
) &
) &
) &
) &
) &
) &

Do not distribute

1
2 fer protein SFH13 OS=Arabidopsis thaliana (sp|q501h5|sfh13_arath : 610.0)
3 fer protein SFH13 OS=Arabidopsis thaliana (sp|q501h5|sfh13_arath : 610.0)
4 it-version=v2.1) &
5 it-version=v2.1) &
6 it-version=v2.1) &
7 it-version=v2.1) &
8 it-version=v2.1) &
9 it-version=v2.1) &
10 it-version=v2.1) &
11 it-version=v2.1) &
12 it-version=v2.1) &
13 it-version=v2.1) &
14 it-version=v2.1) &
15 it-version=v2.1) &
16 it-version=v2.1) &
17 it-version=v2.1) &
18 it-version=v2.1) &
19 it-version=v2.1) &
20 it-version=v2.1) &
21 it-version=v2.1) &
22 it-version=v2.1) &
23 it-version=v2.1) &
24 it-version=v2.1) &
25 it-version=v2.1) &
26 it-version=v2.1) &
27 it-version=v2.1) &
28 it-version=v2.1) &
29 it-version=v2.1) &
30 it-version=v2.1) &
31 it-version=v2.1) &
32 it-version=v2.1) &
33 it-version=v2.1) &
34 it-version=v2.1) &
35 it-version=v2.1) &
36 it-version=v2.1) &
37 it-version=v2.1) &
38 it-version=v2.1) &
39 it-version=v2.1) &
40 it-version=v2.1) &
41 it-version=v2.1) &
42 it-version=v2.1) &
43 it-version=v2.1) &
44 it-version=v2.1) &
45 it-version=v2.1) &
46 it-version=v2.1) &
47 it-version=v2.1) &
48 it-version=v2.1) &
49 it-version=v2.1) &
50 it-version=v2.1) &
51 it-version=v2.1) &
52 2.1) &
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7 ·version=v2.1) &
8 ·version=v2.1) &
9 ·version=v2.1) &
10 ·version=v2.1) &
11 ·version=v2.1) &
12 ·version=v2.1) &
13 ·version=v2.1) &
14 ·version=v2.1) &
15 ·version=v2.1) &
16 ·version=v2.1) &
17 ·version=v2.1) &
18 ·version=v2.1) &
19 ·version=v2.1) &
20 ·version=v2.1) &
21 ·version=v2.1) &
22 ·version=v2.1) &
23 ·version=v2.1) &
24 ·version=v2.1) &
25 ·version=v2.1) &
26 ·version=v2.1) &
27 ·version=v2.1) &
28 ·version=v2.1) &
29 ·version=v2.1) &
30 ·version=v2.1) &
31 ·version=v2.1) &
32 ·version=v2.1) &
33 ·version=v2.1) &
34 ·version=v2.1) &
35 ·version=v2.1) &
36 ·version=v2.1) &
37 ·version=v2.1) &
38 ·version=v2.1) &

Do not distribute

39
40
41
42
43
44
45
46
47
48
49
50
51
52
53 ɹliana (sp|q9les2|uba2a_arath : 290.0)
54 ɹliana (sp|q9les2|uba2a_arath : 290.0)
55 ɹliana (sp|q9les2|uba2a_arath : 290.0)
56 ɹliana (sp|q9les2|uba2a_arath : 290.0)
57 ɹliana (sp|q9les2|uba2a_arath : 290.0)
58 ɹliana (sp|q9les2|uba2a_arath : 290.0)
59 ɹliana (sp|q9les2|uba2a_arath : 290.0)
60 ɹliana (sp|q9les2|uba2a_arath : 290.0)
ɹliana (sp|q9les2|uba2a_arath : 290.0)

1
2 thaliana (sp|q9les2|uba2a_arath : 290.0)
3 thaliana (sp|q9les2|uba2a_arath : 290.0)
4 thaliana (sp|q9les2|uba2a_arath : 290.0)
5 thaliana (sp|q9les2|uba2a_arath : 290.0)
6 thaliana (sp|q9les2|uba2a_arath : 290.0)
7 thaliana (sp|q9les2|uba2a_arath : 290.0)
8 3g02650, mitochondrial OS=Arabidopsis thaliana (sp|p0c896|pp209_arath : 462.0)
9 3g02650, mitochondrial OS=Arabidopsis thaliana (sp|p0c896|pp209_arath : 462.0)
10 3g02650, mitochondrial OS=Arabidopsis thaliana (sp|p0c896|pp209_arath : 462.0)
11 3g02650, mitochondrial OS=Arabidopsis thaliana (sp|p0c896|pp209_arath : 462.0)
12 3g02650, mitochondrial OS=Arabidopsis thaliana (sp|p0c896|pp209_arath : 462.0)
13 3g02650, mitochondrial OS=Arabidopsis thaliana (sp|p0c896|pp209_arath : 462.0)
14 3g02650, mitochondrial OS=Arabidopsis thaliana (sp|p0c896|pp209_arath : 462.0)
15 3g02650, mitochondrial OS=Arabidopsis thaliana (sp|p0c896|pp209_arath : 462.0)
16 3g02650, mitochondrial OS=Arabidopsis thaliana (sp|p0c896|pp209_arath : 462.0)
17 3g02650, mitochondrial OS=Arabidopsis thaliana (sp|p0c896|pp209_arath : 462.0)
18 3g02650, mitochondrial OS=Arabidopsis thaliana (sp|p0c896|pp209_arath : 462.0)
19 3g02650, mitochondrial OS=Arabidopsis thaliana (sp|p0c896|pp209_arath : 462.0)
20 3g02650, mitochondrial OS=Arabidopsis thaliana (sp|p0c896|pp209_arath : 462.0)
21 3g02650, mitochondrial OS=Arabidopsis thaliana (sp|p0c896|pp209_arath : 462.0)
22 3g02650, mitochondrial OS=Arabidopsis thaliana (sp|p0c896|pp209_arath : 462.0)
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55 /2.1) &
56 /2.1) &
57 /2.1) &
58 /2.1) &
59 /2.1) &
60 /2.1) &
/2.1) &

1 /2.1) &

2 /2.1) &

3 /2.1) &

4 /2.1) &

5 /2.1) &

6 /2.1) &

7 /2.1) &

8

9

10

11

12

13

14

15

16

17

18

19

20

21

22

23

24

25

26

27

28

29

30

31

32

33

34

35

36

37

38

39

40

41

42

43

44

45

46

47

48

49

50

51

52

53

54

55

56

57

58

59

60

lopsis thaliana (sp|q9ls48|sg1_arath : 158.0)

lopsis thaliana (sp|q9ls48|sg1_arath : 158.0)

lopsis thaliana (sp|q9ls48|sg1_arath : 158.0)

lopsis thaliana (sp|q9ls48|sg1_arath : 158.0)

lopsis thaliana (sp|q9ls48|sg1_arath : 158.0)

lopsis thaliana (sp|q9ls48|sg1_arath : 158.0)

lopsis thaliana (sp|q9ls48|sg1_arath : 158.0)

lopsis thaliana (sp|q9ls48|sg1_arath : 158.0)

lopsis thaliana (sp|q9ls48|sg1_arath : 158.0)

lopsis thaliana (sp|q9ls48|sg1_arath : 158.0)

lopsis thaliana (sp|q9ls48|sg1_arath : 158.0)

1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)

1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)

1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)

1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)

1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)

1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)

1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)

1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)

1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)

1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)

1 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
2 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
3 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
4 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
5 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
6 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
7 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
8 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
9 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
10 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
11 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
12 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
13 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
14 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
15 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
16 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
17 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
18 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
19 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
20 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
21 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
22 1g79540 OS=Arabidopsis thaliana (sp|q9saj5|pp133_arath : 509.0)
23 |p22195|per1_arahy : 366.0)
24 |p22195|per1_arahy : 366.0)
25 |p22195|per1_arahy : 366.0)
26 |p22195|per1_arahy : 366.0)
27 |p22195|per1_arahy : 366.0)
28 |p22195|per1_arahy : 366.0)
29 |p22195|per1_arahy : 366.0)
30 |p22195|per1_arahy : 366.0)
31 |p22195|per1_arahy : 366.0)
32 |p22195|per1_arahy : 366.0)
33 |p22195|per1_arahy : 366.0)
34 |p22195|per1_arahy : 366.0)
35 |p22195|per1_arahy : 366.0)
36 |p22195|per1_arahy : 366.0)
37 |p22195|per1_arahy : 366.0)
38 |p22195|per1_arahy : 366.0)
39 |p22195|per1_arahy : 327.0)
40 |p22195|per1_arahy : 327.0)
41 |p22195|per1_arahy : 327.0)
42 |p22195|per1_arahy : 327.0)
43 |p22195|per1_arahy : 327.0)
44 |p22195|per1_arahy : 327.0)
45 |p22195|per1_arahy : 327.0)
46 |p22195|per1_arahy : 327.0)
47 |p22195|per1_arahy : 327.0)
48 |p22195|per1_arahy : 327.0)
49 |p22195|per1_arahy : 327.0)
50 |p22195|per1_arahy : 327.0)
51 |p22195|per1_arahy : 327.0)
52 |p22195|per1_arahy : 327.0)
53 |p22195|per1_arahy : 327.0)
54 thaliana (sp|q9m041|bh140_arath : 644.0)
55 thaliana (sp|q9m041|bh140_arath : 644.0)
56 thaliana (sp|q9m041|bh140_arath : 644.0)
57 thaliana (sp|q9m041|bh140_arath : 644.0)
58 thaliana (sp|q9m041|bh140_arath : 644.0)
59 thaliana (sp|q9m041|bh140_arath : 644.0)
60 thaliana (sp|q9m041|bh140_arath : 644.0)

1
2 *haliana* (sp|q9m041|bh140_arath : 644.0)
3 *haliana* (sp|q9m041|bh140_arath : 644.0)
4 *haliana* (sp|q9m041|bh140_arath : 644.0)
5 *haliana* (sp|q9m041|bh140_arath : 644.0)
6 *haliana* (sp|q9m041|bh140_arath : 644.0)
7 *haliana* (sp|q9m041|bh140_arath : 644.0)
8 *haliana* (sp|q9m041|bh140_arath : 644.0)
9 *haliana* (sp|q9m041|bh140_arath : 644.0)
10 *haliana* (sp|q9m041|bh140_arath : 644.0)
11 *haliana* (sp|q9m041|bh140_arath : 644.0)
12 *haliana* (sp|q9m041|bh140_arath : 644.0)
13 *haliana* (sp|q9m041|bh140_arath : 644.0)
14 *haliana* (sp|q9m041|bh140_arath : 644.0)
15 *haliana* (sp|q9m041|bh140_arath : 644.0)
16 *haliana* (sp|q9m041|bh140_arath : 644.0)
17 *haliana* (sp|q9m041|bh140_arath : 644.0)
18 *haliana* (sp|q9m041|bh140_arath : 644.0)
19 *haliana* (sp|q9m041|bh140_arath : 644.0)
20 *haliana* (sp|q9m041|bh140_arath : 644.0)
21 *haliana* (sp|q9m041|bh140_arath : 644.0)
22 *haliana* (sp|q9m041|bh140_arath : 644.0)
23 *haliana* (sp|q9m041|bh140_arath : 644.0)
24 *haliana* (sp|q9m041|bh140_arath : 644.0)
25 *haliana* (sp|q9m041|bh140_arath : 644.0)
26 *haliana* (sp|q9m041|bh140_arath : 644.0)
27 *haliana* (sp|q9m041|bh140_arath : 644.0)
28 *haliana* (sp|q9m041|bh140_arath : 644.0)
29 *haliana* (sp|q9m041|bh140_arath : 644.0)
30 *haliana* (sp|q9m041|bh140_arath : 644.0)
31 *haliana* (sp|q9m041|bh140_arath : 644.0)
32 *haliana* (sp|q9m041|bh140_arath : 644.0)
33 *haliana* (sp|q9m041|bh140_arath : 644.0)
34 *haliana* (sp|q9m041|bh140_arath : 644.0)
35 *haliana* (sp|q9m041|bh140_arath : 644.0)
36 *haliana* (sp|q9m041|bh140_arath : 644.0)
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51

52 Phvul.011G112400 ID=Phvul.011G112400.1.v2.1 annot-version=v2.1) &
53 Phvul.011G112400 ID=Phvul.011G112400.1.v2.1 annot-version=v2.1) &
54 Phvul.011G112400 ID=Phvul.011G112400.1.v2.1 annot-version=v2.1) &
55 Phvul.011G112400 ID=Phvul.011G112400.1.v2.1 annot-version=v2.1) &
56 Phvul.011G112400 ID=Phvul.011G112400.1.v2.1 annot-version=v2.1) &
57 Phvul.011G112400 ID=Phvul.011G112400.1.v2.1 annot-version=v2.1) &
58 Phvul.011G112400 ID=Phvul.011G112400.1.v2.1 annot-version=v2.1) &
59 Phvul.011G112400 ID=Phvul.011G112400.1.v2.1 annot-version=v2.1) &
60 Phvul.011G112400 ID=Phvul.011G112400.1.v2.1 annot-version=v2.1) &
Phvul.011G112400 ID=Phvul.011G112400.1.v2.1 annot-version=v2.1) &

1 Phvul.011G112400 ID=Phvul.011G112400.1.v2.1 annot-version=v2.1) &
2 Phvul.011G112400 ID=Phvul.011G112400.1.v2.1 annot-version=v2.1) &
3 Phvul.011G112400 ID=Phvul.011G112400.1.v2.1 annot-version=v2.1) &
4 Phvul.011G112400 ID=Phvul.011G112400.1.v2.1 annot-version=v2.1) &
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21

22 original description: pacid=37169073 transcript=Phvul.001G024500.1 locus=Phvul.001G024500 ID=
23 original description: pacid=37169073 transcript=Phvul.001G024500.1 locus=Phvul.001G024500 ID=
24 original description: pacid=37169073 transcript=Phvul.001G024500.1 locus=Phvul.001G024500 ID=
25 original description: pacid=37169073 transcript=Phvul.001G024500.1 locus=Phvul.001G024500 ID=
26 original description: pacid=37169073 transcript=Phvul.001G024500.1 locus=Phvul.001G024500 ID=
27 original description: pacid=37169073 transcript=Phvul.001G024500.1 locus=Phvul.001G024500 ID=
28 original description: pacid=37169073 transcript=Phvul.001G024500.1 locus=Phvul.001G024500 ID=
29 original description: pacid=37169073 transcript=Phvul.001G024500.1 locus=Phvul.001G024500 ID=
30 original description: pacid=37169073 transcript=Phvul.001G024500.1 locus=Phvul.001G024500 ID=
31 original description: pacid=37169073 transcript=Phvul.001G024500.1 locus=Phvul.001G024500 ID=
32 original description: pacid=37169073 transcript=Phvul.001G024500.1 locus=Phvul.001G024500 ID=
33 original description: pacid=37169073 transcript=Phvul.001G024500.1 locus=Phvul.001G024500 ID=
34 original description: pacid=37169073 transcript=Phvul.001G024500.1 locus=Phvul.001G024500 ID=
35 original description: pacid=37169073 transcript=Phvul.001G024500.1 locus=Phvul.001G024500 ID=
36 original description: pacid=37169073 transcript=Phvul.001G024500.1 locus=Phvul.001G024500 ID=
37 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
38 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
39 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
40 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
41 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
42 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
43 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
44 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
45 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
46 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
47 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
48 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
49 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
50 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
51 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
52 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
53 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
54 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
55 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
56 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
57 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
58 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
59 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
60 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)

1 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
2 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
3 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
4 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
5 3g04130, mitochondrial OS=Arabidopsis thaliana (sp|q9m8w9|pp211_arath : 485.0)
6 ina (sp|q9fg14|myob7_arath : 382.0)
7 ina (sp|q9fg14|myob7_arath : 382.0)
8 ina (sp|q9fg14|myob7_arath : 382.0)
9 ina (sp|q9fg14|myob7_arath : 382.0)
10 ina (sp|q9fg14|myob7_arath : 382.0)
11 ina (sp|q9fg14|myob7_arath : 382.0)
12 ina (sp|q9fg14|myob7_arath : 382.0)
13 ina (sp|q9fg14|myob7_arath : 382.0)
14 ina (sp|q9fg14|myob7_arath : 382.0)
15 ina (sp|q9fg14|myob7_arath : 382.0)
16 ina (sp|q9fg14|myob7_arath : 382.0)
17 ina (sp|q9fg14|myob7_arath : 382.0)
18 ina (sp|q9fg14|myob7_arath : 382.0)
19 ina (sp|q9fg14|myob7_arath : 382.0)
20 ina (sp|q9fg14|myob7_arath : 382.0)
21 ina (sp|q9fg14|myob7_arath : 382.0)
22 ina (sp|q9fg14|myob7_arath : 382.0)
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39 i=v2.1) &
40 i=v2.1) &
41 oopsis thaliana (sp|q9fle8|y5986_arath : 127.0)
42 stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)
43 stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)
44 stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)
45 stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)
46 stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)
47 stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)
48 stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)
49 stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)
50 stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)
51 stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)
52 stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)
53 stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)
54 stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)
55 stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)
56 stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)
57 stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)
58 stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)
59 stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)
60 stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)
stic/mitochondrial OS=Oryza sativa subsp. japonica (sp|q2r1u8|cfm3_orysj : 477.0)

1
2 stic/mitochondrial OS=*Oryza sativa* subsp. *japonica* (sp|q2r1u8|cfm3_orysj : 477.0)
3 stic/mitochondrial OS=*Oryza sativa* subsp. *japonica* (sp|q2r1u8|cfm3_orysj : 477.0)
4 stic/mitochondrial OS=*Oryza sativa* subsp. *japonica* (sp|q2r1u8|cfm3_orysj : 477.0)
5 stic/mitochondrial OS=*Oryza sativa* subsp. *japonica* (sp|q2r1u8|cfm3_orysj : 477.0)
6 stic/mitochondrial OS=*Oryza sativa* subsp. *japonica* (sp|q2r1u8|cfm3_orysj : 477.0)
7 stic/mitochondrial OS=*Oryza sativa* subsp. *japonica* (sp|q2r1u8|cfm3_orysj : 477.0)
8 stic/mitochondrial OS=*Oryza sativa* subsp. *japonica* (sp|q2r1u8|cfm3_orysj : 477.0)
9 stic/mitochondrial OS=*Oryza sativa* subsp. *japonica* (sp|q2r1u8|cfm3_orysj : 477.0)
10 stic/mitochondrial OS=*Oryza sativa* subsp. *japonica* (sp|q2r1u8|cfm3_orysj : 477.0)
11 4g30700 OS=*Arabidopsis thaliana* (sp|q9suh6|pp341_arath : 1019.0)
12 4g30700 OS=*Arabidopsis thaliana* (sp|q9suh6|pp341_arath : 1019.0)
13 4g30700 OS=*Arabidopsis thaliana* (sp|q9suh6|pp341_arath : 1019.0)
14 4g30700 OS=*Arabidopsis thaliana* (sp|q9suh6|pp341_arath : 1019.0)
15 4g30700 OS=*Arabidopsis thaliana* (sp|q9suh6|pp341_arath : 1019.0)
16 4g30700 OS=*Arabidopsis thaliana* (sp|q9suh6|pp341_arath : 1019.0)
17 4g30700 OS=*Arabidopsis thaliana* (sp|q9suh6|pp341_arath : 1019.0)
18 4g30700 OS=*Arabidopsis thaliana* (sp|q9suh6|pp341_arath : 1019.0)
19 4g30700 OS=*Arabidopsis thaliana* (sp|q9suh6|pp341_arath : 1019.0)
20 4g30700 OS=*Arabidopsis thaliana* (sp|q9suh6|pp341_arath : 1019.0)
21 4g30700 OS=*Arabidopsis thaliana* (sp|q9suh6|pp341_arath : 1019.0)
22 4g30700 OS=*Arabidopsis thaliana* (sp|q9suh6|pp341_arath : 1019.0)
23 4g30700 OS=*Arabidopsis thaliana* (sp|q9suh6|pp341_arath : 1019.0)
24 4g30700 OS=*Arabidopsis thaliana* (sp|q9suh6|pp341_arath : 1019.0)
25 4g30700 OS=*Arabidopsis thaliana* (sp|q9suh6|pp341_arath : 1019.0)
26 4g30700 OS=*Arabidopsis thaliana* (sp|q9suh6|pp341_arath : 1019.0)
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57

58 original description: pacid=37147951 transcript=Phvul.003G255900.1 locus=Phvul.003G255900 ID=
59
60

Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)

1 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
2 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
3 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
4 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
5 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
6 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
7 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
8 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
9 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
10 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
11 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
12 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
13 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
14 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
15 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
16 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
17 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
18 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
19 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
20 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
21 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
22 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
23 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
24 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
25 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
26 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
27 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
28 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
29 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
30 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
31 Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

(50.2.7 : 376.0) (original description: pacid=37167361 transcript=Phvul.007G244900.1 locus=Phvul.l

1
2
3
4
5
6
7
8 is thaliana (sp|b6sfa4|maa3_arath : 916.0)
9 is thaliana (sp|b6sfa4|maa3_arath : 916.0)
10 is thaliana (sp|b6sfa4|maa3_arath : 916.0)
11 is thaliana (sp|b6sfa4|maa3_arath : 916.0)
12 is thaliana (sp|b6sfa4|maa3_arath : 916.0)
13 is thaliana (sp|b6sfa4|maa3_arath : 916.0)
14 is thaliana (sp|b6sfa4|maa3_arath : 916.0)
15 is thaliana (sp|b6sfa4|maa3_arath : 916.0)
16 is thaliana (sp|b6sfa4|maa3_arath : 916.0)
17 is thaliana (sp|b6sfa4|maa3_arath : 916.0)
18 is thaliana (sp|b6sfa4|maa3_arath : 916.0)
19 is thaliana (sp|b6sfa4|maa3_arath : 916.0)
20 is thaliana (sp|b6sfa4|maa3_arath : 916.0)
21 is thaliana (sp|b6sfa4|maa3_arath : 916.0)
22 is thaliana (sp|b6sfa4|maa3_arath : 916.0)
23 is thaliana (sp|b6sfa4|maa3_arath : 916.0)
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)
- | OS=Arabidopsis thaliana (sp|q9ffj8|limyb_arath : 115.0)

Arabidopsis thaliana (sp|o23051|kao1_arath : 137.0) (original description: pacid=37142514 transcr

1
2
3
4
5
6
7
8
9
10
11
12 S=Arabidopsis thaliana (sp|q8h1r2|ppa24_arath : 354.0)
13 S=Arabidopsis thaliana (sp|q8h1r2|ppa24_arath : 354.0)
14 S=Arabidopsis thaliana (sp|q8h1r2|ppa24_arath : 354.0)
15 S=Arabidopsis thaliana (sp|q8h1r2|ppa24_arath : 354.0)
16 S=Arabidopsis thaliana (sp|q8h1r2|ppa24_arath : 354.0)
17 S=Arabidopsis thaliana (sp|q8h1r2|ppa24_arath : 354.0)
18 S=Arabidopsis thaliana (sp|q8h1r2|ppa24_arath : 354.0)
19 S=Arabidopsis thaliana (sp|q8h1r2|ppa24_arath : 354.0)
20 S=Arabidopsis thaliana (sp|q8h1r2|ppa24_arath : 354.0)
21 S=Arabidopsis thaliana (sp|q8h1r2|ppa24_arath : 354.0)
22 S=Arabidopsis thaliana (sp|q8h1r2|ppa24_arath : 354.0)
23 S=Arabidopsis thaliana (sp|q8h1r2|ppa24_arath : 354.0)
24 S=Arabidopsis thaliana (sp|q8h1r2|ppa24_arath : 354.0)
25 S=Arabidopsis thaliana (sp|q8h1r2|ppa24_arath : 354.0)
26 S=Arabidopsis thaliana (sp|q8h1r2|ppa24_arath : 354.0)
27
28

29 :haliana (sp|q9zsp5|air3_arath : 490.0)
30 :haliana (sp|q9zsp5|air3_arath : 490.0)
31 :haliana (sp|q9zsp5|air3_arath : 490.0)
32 :haliana (sp|q9zsp5|air3_arath : 490.0)
33 :haliana (sp|q9zsp5|air3_arath : 490.0)
34 :haliana (sp|q9zsp5|air3_arath : 490.0)
35 :haliana (sp|q9zsp5|air3_arath : 490.0)
36 :haliana (sp|q9zsp5|air3_arath : 490.0)
37 :haliana (sp|q9zsp5|air3_arath : 490.0)
38 :haliana (sp|q9zsp5|air3_arath : 490.0)
39 :haliana (sp|q9zsp5|air3_arath : 490.0)
40 :haliana (sp|q9zsp5|air3_arath : 490.0)
41 :haliana (sp|q9zsp5|air3_arath : 490.0)
42 :haliana (sp|q9zsp5|air3_arath : 490.0)
43 :haliana (sp|q9zsp5|air3_arath : 490.0)
44 :haliana (sp|q9zsp5|air3_arath : 490.0)
45 :haliana (sp|q9zsp5|air3_arath : 490.0)
46 :haliana (sp|q9zsp5|air3_arath : 490.0)
47 :haliana (sp|q9zsp5|air3_arath : 490.0)
48 :haliana (sp|q9zsp5|air3_arath : 490.0)
49 :haliana (sp|q9zsp5|air3_arath : 490.0)
50 :haliana (sp|q9zsp5|air3_arath : 490.0)
51 :haliana (sp|q9zsp5|air3_arath : 490.0)
52 :haliana (sp|q9zsp5|air3_arath : 490.0)
53 :haliana (sp|q9zsp5|air3_arath : 490.0)
54 :haliana (sp|q9zsp5|air3_arath : 490.0)
55 :haliana (sp|q9zsp5|air3_arath : 490.0)
56 :haliana (sp|q9zsp5|air3_arath : 490.0)
57 :haliana (sp|q9zsp5|air3_arath : 490.0)
58 1 OS=Arabidopsis thaliana (sp|q947d2|praf1_arath : 772.0)
59 1 OS=Arabidopsis thaliana (sp|q947d2|praf1_arath : 772.0)
60 a (sp|q9fkm3|aatpk_arath : 775.0)

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

hzb2|bcha1_arath : 4995.0)

aliana (sp|q9sd53|y3720_arath : 87.0)
Arabidopsis thaliana (sp|q9ffq1|rh31_arath : 788.0)
Arabidopsis thaliana (sp|q9ffq1|rh31_arath : 788.0)
Arabidopsis thaliana (sp|q9ffq1|rh31_arath : 788.0)
Arabidopsis thaliana (sp|q9ffq1|rh31_arath : 788.0)
Arabidopsis thaliana (sp|q9ffq1|rh31_arath : 788.0)
Arabidopsis thaliana (sp|q9ffq1|rh31_arath : 788.0)
Arabidopsis thaliana (sp|q9ffq1|rh31_arath : 788.0)
Arabidopsis thaliana (sp|q9ffq1|rh31_arath : 788.0)
Arabidopsis thaliana (sp|q9ffq1|rh31_arath : 788.0)
Arabidopsis thaliana (sp|q9ffq1|rh31_arath : 788.0)
Arabidopsis thaliana (sp|q9ffq1|rh31_arath : 788.0)
Arabidopsis thaliana (sp|q9ffq1|rh31_arath : 788.0)
Arabidopsis thaliana (sp|q9ffq1|rh31_arath : 788.0)
Arabidopsis thaliana (sp|q9ffq1|rh31_arath : 788.0)

ot-version=v2.1) &

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2 *√*ul.010G135701.1 locus=Phvul.010G135701 ID=Phvul.010G135701.1.v2.1 annot-version=v2.1) &
3 *√*ul.010G135701.1 locus=Phvul.010G135701 ID=Phvul.010G135701.1.v2.1 annot-version=v2.1) &
4 *√*ul.010G135701.1 locus=Phvul.010G135701 ID=Phvul.010G135701.1.v2.1 annot-version=v2.1) &
5 *√*ul.010G135701.1 locus=Phvul.010G135701 ID=Phvul.010G135701.1.v2.1 annot-version=v2.1) &
6 *√*ul.010G135701.1 locus=Phvul.010G135701 ID=Phvul.010G135701.1.v2.1 annot-version=v2.1) &
7 *√*ul.010G135701.1 locus=Phvul.010G135701 ID=Phvul.010G135701.1.v2.1 annot-version=v2.1) &
8 *√*ul.010G135701.1 locus=Phvul.010G135701 ID=Phvul.010G135701.1.v2.1 annot-version=v2.1) &
9 *√*ul.010G135701.1 locus=Phvul.010G135701 ID=Phvul.010G135701.1.v2.1 annot-version=v2.1) &
10 *√*ul.010G135701.1 locus=Phvul.010G135701 ID=Phvul.010G135701.1.v2.1 annot-version=v2.1) &
11 *√*ul.010G135701.1 locus=Phvul.010G135701 ID=Phvul.010G135701.1.v2.1 annot-version=v2.1) &
12 *√*ul.010G135701.1 locus=Phvul.010G135701 ID=Phvul.010G135701.1.v2.1 annot-version=v2.1) &
13 *√*ul.010G135701.1 locus=Phvul.010G135701 ID=Phvul.010G135701.1.v2.1 annot-version=v2.1) &
14 *√*ul.010G135701.1 locus=Phvul.010G135701 ID=Phvul.010G135701.1.v2.1 annot-version=v2.1) &
15 *√*ul.010G135701.1 locus=Phvul.010G135701 ID=Phvul.010G135701.1.v2.1 annot-version=v2.1) &
16 *√*ul.010G135701.1 locus=Phvul.010G135701 ID=Phvul.010G135701.1.v2.1 annot-version=v2.1) &
17 *√*ul.010G135701.1 locus=Phvul.010G135701 ID=Phvul.010G135701.1.v2.1 annot-version=v2.1) &
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

.1 annot-version=v2.1) &
.1 annot-version=v2.1) &
.1 annot-version=v2.1) &
.1 annot-version=v2.1) &
.1 annot-version=v2.1) &
.1 annot-version=v2.1) &
.1 annot-version=v2.1) &
.1 annot-version=v2.1) &
.1 annot-version=v2.1) &
.1 annot-version=v2.1) &
.1 annot-version=v2.1) &
.1 annot-version=v2.1) &
.1 annot-version=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Phvul.010G135101.1 locus=Phvul.010G135101 ID=Phvul.010G135101.1.v2.1 annot-version=v2.1) &
Phvul.010G135151.1 locus=Phvul.010G135151 ID=Phvul.010G135151.1.v2.1 annot-version=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Phvul.003G240800.1.v2.1 annot-version=v2.1) &
Phvul.003G240800.1.v2.1 annot-version=v2.1) &
Phvul.003G240800.1.v2.1 annot-version=v2.1) &
Phvul.003G240800.1.v2.1 annot-version=v2.1) &
Phvul.003G240800.1.v2.1 annot-version=v2.1) &
Phvul.003G240800.1.v2.1 annot-version=v2.1) &
Phvul.003G240800.1.v2.1 annot-version=v2.1) &
Phvul.003G240800.1.v2.1 annot-version=v2.1) &
Phvul.003G240800.1.v2.1 annot-version=v2.1) &
Phvul.003G240800.1.v2.1 annot-version=v2.1) &
Phvul.003G240800.1.v2.1 annot-version=v2.1) &
Phvul.003G240800.1.v2.1 annot-version=v2.1) &
Phvul.003G240800.1.v2.1 annot-version=v2.1) &
Phvul.003G240800.1.v2.1 annot-version=v2.1) &
Phvul.003G240800.1.v2.1 annot-version=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

:Phvul.003G255900.1.v2.1 annot-version=v2.1) &

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

007G244900 ID=Phvul.007G244900.1.v2.1 annot-version=v2.1) &

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

ipt=Phvul.010G131100.2 locus=Phvul.010G131100 ID=Phvul.010G131100.2.v2.1 annot-version=v2.

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

.1) &

| miRNA_Acc. | Target_Acc. | Expectation | UPE\$ | miRNA_start | |
|------------|------------------------|--------------------|-------|-------------|---|
| 1 | | | | | |
| 2 | | | | | |
| 3 | ucuucccaauuccgcccauucc | Phvul.004G048000.1 | 0.5 | -1 | 1 |
| 4 | ucuucccuacaccucccauacc | Phvul.001G224800.1 | 2 | -1 | 1 |
| 5 | ucuucccuacaccucccauacc | Phvul.001G224800.2 | 2 | -1 | 1 |
| 6 | ucuucccuacaccucccauacc | Phvul.001G224800.1 | 2 | -1 | 1 |
| 7 | ucuucccuacaccucccauacc | Phvul.001G224800.2 | 2 | -1 | 1 |
| 8 | ucuucccuacaccucccauacc | Phvul.007G201700.1 | 2 | -1 | 1 |
| 9 | ucuucccuacaccucccauacc | Phvul.007G201700.1 | 2 | -1 | 1 |
| 10 | ucuucccuacaccucccauacc | Phvul.008G061300.2 | 2 | -1 | 1 |
| 11 | ucuucccuacaccucccauacc | Phvul.008G061300.1 | 2 | -1 | 1 |
| 12 | ucuucccuacaccucccauacc | Phvul.008G061300.2 | 2 | -1 | 1 |
| 13 | ucuucccuacaccucccauacc | Phvul.008G061300.1 | 2 | -1 | 1 |
| 14 | ucuucccuacaccucccauacc | Phvul.002G079200.1 | 2.5 | -1 | 1 |
| 15 | ucuucccaauuccgcccauucc | Phvul.001G217600.1 | 3 | -1 | 1 |
| 16 | ucuucccuacaccucccauacc | Phvul.002G001500.1 | 3 | -1 | 1 |
| 17 | ucuucccuacaccucccauacc | Phvul.002G001500.1 | 3 | -1 | 1 |
| 18 | ucuucccaauuccgcccauucc | Phvul.003G072500.1 | 3 | -1 | 1 |
| 19 | ucuucccaauuccgcccauucc | Phvul.003G244225.3 | 3 | -1 | 1 |
| 20 | ucuucccaauuccgcccauucc | Phvul.003G244225.2 | 3 | -1 | 1 |
| 21 | ucuucccaauuccgcccauucc | Phvul.003G244225.1 | 3 | -1 | 1 |
| 22 | ucuucccaauuccgcccauucc | Phvul.004G137300.1 | 3 | -1 | 1 |
| 23 | ucuucccaauuccgcccauucc | Phvul.005G029400.1 | 3 | -1 | 1 |
| 24 | ucuucccaauuccgcccauucc | Phvul.005G029400.3 | 3 | -1 | 1 |
| 25 | ucuucccaauuccgcccauucc | Phvul.005G029400.2 | 3 | -1 | 1 |
| 26 | ucuucccuacaccucccauacc | Phvul.007G210600.1 | 3 | -1 | 1 |
| 27 | ucuucccuacaccucccauacc | Phvul.007G210600.1 | 3 | -1 | 1 |
| 28 | ucuucccaauuccgcccauucc | Phvul.008G055500.1 | 3 | -1 | 1 |
| 29 | ucuucccuacaccucccauacc | Phvul.008G280900.1 | 3 | -1 | 1 |
| 30 | ucuucccuacaccucccauacc | Phvul.008G280900.1 | 3 | -1 | 1 |
| 31 | ucuucccaauuccgcccauucc | Phvul.010G064700.1 | 3 | -1 | 1 |
| 32 | ucuucccaauuccgcccauucc | Phvul.010G136700.1 | 3 | -1 | 1 |
| 33 | ucuucccaauuccgcccauucc | Phvul.011G149100.7 | 3 | -1 | 1 |
| 34 | ucuucccaauuccgcccauucc | Phvul.011G149100.6 | 3 | -1 | 1 |
| 35 | ucuucccaauuccgcccauucc | Phvul.011G149100.5 | 3 | -1 | 1 |
| 36 | ucuucccaauuccgcccauucc | Phvul.011G149100.2 | 3 | -1 | 1 |
| 37 | ucuucccaauuccgcccauucc | Phvul.011G149100.1 | 3 | -1 | 1 |
| 38 | ucuucccaauuccgcccauucc | Phvul.011G149100.4 | 3 | -1 | 1 |
| 39 | ucuucccaauuccgcccauucc | Phvul.011G149100.3 | 3 | -1 | 1 |
| 40 | ucuucccaauuccgcccauucc | Phvul.011G166100.1 | 3 | -1 | 1 |
| 41 | ucuucccaauuccgcccauucc | Phvul.001G128200.2 | 3.5 | -1 | 1 |
| 42 | ucuucccuacaccucccauacc | Phvul.001G134000.1 | 3.5 | -1 | 1 |
| 43 | ucuucccuacaccucccauacc | Phvul.001G134000.1 | 3.5 | -1 | 1 |
| 44 | ucuucccuacaccucccauacc | Phvul.001G243900.1 | 3.5 | -1 | 1 |
| 45 | ucuucccuacaccucccauacc | Phvul.001G243900.1 | 3.5 | -1 | 1 |
| 46 | ucuucccaauuccgcccauucc | Phvul.002G057300.2 | 3.5 | -1 | 1 |
| 47 | ucuucccaauuccgcccauucc | Phvul.002G057300.1 | 3.5 | -1 | 1 |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|------------------------|--------------------|-----|----|---|
| 1 | | | | | |
| 2 | ucuucccaauuccgcccauucc | Phvul.002G122200.1 | 3.5 | -1 | 1 |
| 3 | ucuucccaauuccgcccauucc | Phvul.002G187600.1 | 3.5 | -1 | 1 |
| 4 | ucuucccuacaccucccauacc | Phvul.002G261500.1 | 3.5 | -1 | 1 |
| 5 | ucuucccuacaccucccauacc | Phvul.002G261500.1 | 3.5 | -1 | 1 |
| 6 | ucuucccuacaccucccauacc | Phvul.003G101200.1 | 3.5 | -1 | 1 |
| 7 | ucuucccuacaccucccauacc | Phvul.003G101200.1 | 3.5 | -1 | 1 |
| 8 | ucuucccuacaccucccauacc | Phvul.003G202900.1 | 3.5 | -1 | 1 |
| 9 | ucuucccuacaccucccauacc | Phvul.003G202900.1 | 3.5 | -1 | 1 |
| 10 | ucuucccuacaccucccauacc | Phvul.004G026200.1 | 3.5 | -1 | 1 |
| 11 | ucuucccuacaccucccauacc | Phvul.004G140400.1 | 3.5 | -1 | 1 |
| 12 | ucuucccuacaccucccauacc | Phvul.004G140400.1 | 3.5 | -1 | 1 |
| 13 | ucuucccuacaccucccauacc | Phvul.005G038200.1 | 3.5 | -1 | 1 |
| 14 | ucuucccuacaccucccauacc | Phvul.005G038200.1 | 3.5 | -1 | 1 |
| 15 | ucuucccuacaccucccauacc | Phvul.005G087100.1 | 3.5 | -1 | 1 |
| 16 | ucuucccuacaccucccauacc | Phvul.005G087100.1 | 3.5 | -1 | 1 |
| 17 | ucuucccaauuccgcccauucc | Phvul.006G102700.1 | 3.5 | -1 | 1 |
| 18 | ucuucccuacaccucccauacc | Phvul.008G072300.2 | 3.5 | -1 | 1 |
| 19 | ucuucccuacaccucccauacc | Phvul.008G072300.1 | 3.5 | -1 | 1 |
| 20 | ucuucccuacaccucccauacc | Phvul.008G072300.2 | 3.5 | -1 | 1 |
| 21 | ucuucccuacaccucccauacc | Phvul.008G072300.1 | 3.5 | -1 | 1 |
| 22 | ucuucccaauuccgcccauucc | Phvul.008G202300.1 | 3.5 | -1 | 1 |
| 23 | ucuucccuacaccucccauacc | Phvul.008G259600.2 | 3.5 | -1 | 1 |
| 24 | ucuucccuacaccucccauacc | Phvul.008G259600.1 | 3.5 | -1 | 1 |
| 25 | ucuucccuacaccucccauacc | Phvul.008G259600.2 | 3.5 | -1 | 1 |
| 26 | ucuucccaauuccgcccauucc | Phvul.010G131650.1 | 3.5 | -1 | 1 |
| 27 | ucuucccaauuccgcccauucc | Phvul.010G132333.1 | 3.5 | -1 | 1 |
| 28 | ucuucccaauuccgcccauucc | Phvul.010G136800.1 | 3.5 | -1 | 1 |
| 29 | ucuucccuacaccucccauacc | Phvul.010G151400.6 | 3.5 | -1 | 1 |
| 30 | ucuucccuacaccucccauacc | Phvul.010G151400.4 | 3.5 | -1 | 1 |
| 31 | ucuucccuacaccucccauacc | Phvul.010G151400.6 | 3.5 | -1 | 1 |
| 32 | ucuucccuacaccucccauacc | Phvul.010G151400.4 | 3.5 | -1 | 1 |
| 33 | ucuucccaauuccgcccauucc | Phvul.011G140300.1 | 3.5 | -1 | 1 |
| 34 | ucuucccaauuccgcccauucc | Phvul.011G140400.1 | 3.5 | -1 | 1 |
| 35 | ucuucccaauuccgcccauucc | Phvul.011G151300.1 | 3.5 | -1 | 1 |
| 36 | ucuucccuacaccucccauacc | Phvul.011G181700.1 | 3.5 | -1 | 1 |
| 37 | ucuucccuacaccucccauacc | Phvul.011G181700.1 | 3.5 | -1 | 1 |
| 38 | ucuucccaauuccgcccauucc | Phvul.011G192400.1 | 3.5 | -1 | 1 |
| 39 | ucuucccaauuccgcccauucc | Phvul.011G192600.1 | 3.5 | -1 | 1 |
| 40 | ucuucccaauuccgcccauucc | Phvul.011G193100.1 | 3.5 | -1 | 1 |
| 41 | ucuucccaauuccgcccauucc | Phvul.011G193500.1 | 3.5 | -1 | 1 |
| 42 | ucuucccaauuccgcccauucc | Phvul.011G193600.1 | 3.5 | -1 | 1 |
| 43 | ucuucccaauuccgcccauucc | Phvul.011G194800.1 | 3.5 | -1 | 1 |
| 44 | ucuucccaauuccgcccauucc | Phvul.011G194900.1 | 3.5 | -1 | 1 |
| 45 | ucuucccaauuccgcccauucc | Phvul.011G195000.1 | 3.5 | -1 | 1 |
| 46 | ucuucccaauuccgcccauucc | Phvul.011G195200.1 | 3.5 | -1 | 1 |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|-----------------------|--------------------|-----|----|---|
| 1 | | | | | |
| 2 | ucuuccaauuccgcccauucc | Phvul.011G195400.1 | 3.5 | -1 | 1 |
| 3 | ucuuccaauuccgcccauucc | Phvul.011G195500.1 | 3.5 | -1 | 1 |
| 4 | ucuuccaauuccgcccauucc | Phvul.011G196000.1 | 3.5 | -1 | 1 |
| 5 | ucuuccaauuccgcccauucc | Phvul.011G196066.1 | 3.5 | -1 | 1 |
| 6 | ucuuccaauuccgcccauucc | Phvul.011G196066.1 | 3.5 | -1 | 1 |
| 7 | ucuuccuacaccucccauacc | Phvul.011G200820.1 | 3.5 | -1 | 1 |
| 8 | ucuuccuacaccucccauacc | Phvul.011G200820.1 | 3.5 | -1 | 1 |
| 9 | ucuuccuacaccucccauacc | Phvul.011G200820.1 | 3.5 | -1 | 1 |
| 10 | ucuuccuacaccucccauacc | Phvul.011G202100.1 | 3.5 | -1 | 1 |
| 11 | ucuuccuacaccucccauacc | Phvul.011G202100.1 | 3.5 | -1 | 1 |
| 12 | ucuuccuacaccucccauacc | Phvul.011G202300.1 | 3.5 | -1 | 1 |
| 13 | ucuuccuacaccucccauacc | Phvul.011G202300.1 | 3.5 | -1 | 1 |
| 14 | ucuuccuacaccucccauacc | Phvul.011G202300.1 | 3.5 | -1 | 1 |
| 15 | ucuuccuacaccucccauacc | Phvul.011G203100.1 | 3.5 | -1 | 1 |
| 16 | ucuuccuacaccucccauacc | Phvul.011G203100.1 | 3.5 | -1 | 1 |
| 17 | ucuuccuacaccucccauacc | Phvul.011G203100.1 | 3.5 | -1 | 1 |
| 18 | ucuuccuacaccucccauacc | Phvul.L002337.2 | 3.5 | -1 | 1 |
| 19 | ucuuccuacaccucccauacc | Phvul.L002337.1 | 3.5 | -1 | 1 |
| 20 | ucuuccuacaccucccauacc | Phvul.L002337.2 | 3.5 | -1 | 1 |
| 21 | ucuuccuacaccucccauacc | Phvul.L002337.2 | 3.5 | -1 | 1 |
| 22 | ucuuccuacaccucccauacc | Phvul.L002337.1 | 3.5 | -1 | 1 |
| 23 | ucuuccuacaccucccauacc | Phvul.001G015600.1 | 4 | -1 | 1 |
| 24 | ucuuccuacaccucccauacc | Phvul.001G015600.2 | 4 | -1 | 1 |
| 25 | ucuuccuacaccucccauacc | Phvul.001G015600.1 | 4 | -1 | 1 |
| 26 | ucuuccuacaccucccauacc | Phvul.001G015600.1 | 4 | -1 | 1 |
| 27 | ucuuccuacaccucccauacc | Phvul.001G015600.2 | 4 | -1 | 1 |
| 28 | ucuuccaauuccgcccauucc | Phvul.001G085500.2 | 4 | -1 | 1 |
| 29 | ucuuccaauuccgcccauucc | Phvul.001G085500.1 | 4 | -1 | 1 |
| 30 | ucuuccaauuccgcccauucc | Phvul.001G085500.1 | 4 | -1 | 1 |
| 31 | ucuuccuacaccucccauacc | Phvul.001G232600.1 | 4 | -1 | 1 |
| 32 | ucuuccuacaccucccauacc | Phvul.001G232600.1 | 4 | -1 | 1 |
| 33 | ucuuccaauuccgcccauucc | Phvul.002G041400.4 | 4 | -1 | 1 |
| 34 | ucuuccaauuccgcccauucc | Phvul.002G041400.4 | 4 | -1 | 1 |
| 35 | ucuuccaauuccgcccauucc | Phvul.002G041400.1 | 4 | -1 | 1 |
| 36 | ucuuccaauuccgcccauucc | Phvul.002G041400.2 | 4 | -1 | 1 |
| 37 | ucuuccaauuccgcccauucc | Phvul.002G041400.3 | 4 | -1 | 1 |
| 38 | ucuuccaauuccgcccauucc | Phvul.002G041400.3 | 4 | -1 | 1 |
| 39 | ucuuccaauuccgcccauucc | Phvul.002G298800.1 | 4 | -1 | 1 |
| 40 | ucuuccuacaccucccauacc | Phvul.003G010900.1 | 4 | -1 | 1 |
| 41 | ucuuccuacaccucccauacc | Phvul.003G010900.1 | 4 | -1 | 1 |
| 42 | ucuuccuacaccucccauacc | Phvul.003G010900.1 | 4 | -1 | 1 |
| 43 | ucuuccaauuccgcccauucc | Phvul.003G195800.2 | 4 | -1 | 1 |
| 44 | ucuuccaauuccgcccauucc | Phvul.003G195800.1 | 4 | -1 | 1 |
| 45 | ucuuccuacaccucccauacc | Phvul.003G252400.1 | 4 | -1 | 1 |
| 46 | ucuuccuacaccucccauacc | Phvul.003G252400.1 | 4 | -1 | 1 |
| 47 | ucuuccuacaccucccauacc | Phvul.003G252400.1 | 4 | -1 | 1 |
| 48 | ucuuccaauuccgcccauucc | Phvul.003G295800.4 | 4 | -1 | 1 |
| 49 | ucuuccaauuccgcccauucc | Phvul.003G295800.3 | 4 | -1 | 1 |
| 50 | ucuuccaauuccgcccauucc | Phvul.003G295800.3 | 4 | -1 | 1 |
| 51 | ucuuccaauuccgcccauucc | Phvul.003G295800.2 | 4 | -1 | 1 |
| 52 | ucuuccuacaccucccauacc | Phvul.004G032300.4 | 4 | -1 | 1 |
| 53 | ucuuccuacaccucccauacc | Phvul.004G032300.2 | 4 | -1 | 1 |
| 54 | ucuuccuacaccucccauacc | Phvul.004G032300.3 | 4 | -1 | 1 |
| 55 | ucuuccuacaccucccauacc | Phvul.004G032300.3 | 4 | -1 | 1 |
| 56 | ucuuccuacaccucccauacc | Phvul.004G032300.1 | 4 | -1 | 1 |
| 57 | ucuuccuacaccucccauacc | Phvul.004G032300.4 | 4 | -1 | 1 |
| 58 | ucuuccuacaccucccauacc | Phvul.004G032300.4 | 4 | -1 | 1 |
| 59 | ucuuccuacaccucccauacc | Phvul.004G032300.2 | 4 | -1 | 1 |
| 60 | ucuuccuacaccucccauacc | Phvul.004G032300.3 | 4 | -1 | 1 |
| | ucuuccuacaccucccauacc | Phvul.004G032300.1 | 4 | -1 | 1 |

| | | | | | |
|----|------------------------|--------------------|---|----|---|
| 1 | | | | | |
| 2 | ucuuccuacaccucccauacc | Phvul.004G048000.1 | 4 | -1 | 1 |
| 3 | ucuuccuacaccucccauacc | Phvul.004G048000.1 | 4 | -1 | 1 |
| 4 | ucuuccuacaccucccauacc | Phvul.004G106800.2 | 4 | -1 | 1 |
| 5 | ucuuccuacaccucccauacc | Phvul.004G106800.2 | 4 | -1 | 1 |
| 6 | ucuuccuacaccucccauacc | Phvul.004G106800.2 | 4 | -1 | 1 |
| 7 | ucuucccaauuccgcccauucc | Phvul.004G133100.1 | 4 | -1 | 1 |
| 8 | ucuuccuacaccucccauacc | Phvul.005G165800.1 | 4 | -1 | 1 |
| 9 | ucuuccuacaccucccauacc | Phvul.005G165800.1 | 4 | -1 | 1 |
| 10 | ucuuccuacaccucccauacc | Phvul.005G165800.1 | 4 | -1 | 1 |
| 11 | ucuucccaauuccgcccauucc | Phvul.006G066800.1 | 4 | -1 | 1 |
| 12 | ucuucccaauuccgcccauucc | Phvul.006G086800.1 | 4 | -1 | 1 |
| 13 | ucuucccaauuccgcccauucc | Phvul.006G148800.1 | 4 | -1 | 1 |
| 14 | ucuucccaauuccgcccauucc | Phvul.006G148800.1 | 4 | -1 | 1 |
| 15 | ucuuccuacaccucccauacc | Phvul.006G180900.1 | 4 | -1 | 1 |
| 16 | ucuuccuacaccucccauacc | Phvul.006G180900.1 | 4 | -1 | 1 |
| 17 | ucuuccuacaccucccauacc | Phvul.006G180900.1 | 4 | -1 | 1 |
| 18 | ucuucccaauuccgcccauucc | Phvul.007G027400.1 | 4 | -1 | 1 |
| 19 | ucuucccaauuccgcccauucc | Phvul.007G096800.1 | 4 | -1 | 1 |
| 20 | ucuucccaauuccgcccauucc | Phvul.008G158100.1 | 4 | -1 | 1 |
| 21 | ucuucccaauuccgcccauucc | Phvul.008G158100.1 | 4 | -1 | 1 |
| 22 | ucuuccuacaccucccauacc | Phvul.009G020000.1 | 4 | -1 | 1 |
| 23 | ucuuccuacaccucccauacc | Phvul.009G020000.1 | 4 | -1 | 1 |
| 24 | ucuuccuacaccucccauacc | Phvul.009G065500.1 | 4 | -1 | 1 |
| 25 | ucuuccuacaccucccauacc | Phvul.009G065500.2 | 4 | -1 | 1 |
| 26 | ucuuccuacaccucccauacc | Phvul.009G065500.2 | 4 | -1 | 1 |
| 27 | ucuuccuacaccucccauacc | Phvul.009G065500.1 | 4 | -1 | 1 |
| 28 | ucuuccuacaccucccauacc | Phvul.009G065500.2 | 4 | -1 | 1 |
| 29 | ucuuccuacaccucccauacc | Phvul.009G065500.2 | 4 | -1 | 1 |
| 30 | ucuucccaauuccgcccauucc | Phvul.009G213300.1 | 4 | -1 | 1 |
| 31 | ucuuccuacaccucccauacc | Phvul.009G226300.2 | 4 | -1 | 1 |
| 32 | ucuuccuacaccucccauacc | Phvul.009G226300.1 | 4 | -1 | 1 |
| 33 | ucuuccuacaccucccauacc | Phvul.009G226300.2 | 4 | -1 | 1 |
| 34 | ucuuccuacaccucccauacc | Phvul.009G226300.2 | 4 | -1 | 1 |
| 35 | ucuuccuacaccucccauacc | Phvul.009G226300.1 | 4 | -1 | 1 |
| 36 | ucuucccaauuccgcccauucc | Phvul.009G233700.1 | 4 | -1 | 1 |
| 37 | ucuuccuacaccucccauacc | Phvul.009G233700.1 | 4 | -1 | 1 |
| 38 | ucuuccuacaccucccauacc | Phvul.009G233700.1 | 4 | -1 | 1 |
| 39 | ucuuccuacaccucccauacc | Phvul.009G233700.1 | 4 | -1 | 1 |
| 40 | ucuucccaauuccgcccauucc | Phvul.010G008700.2 | 4 | -1 | 1 |
| 41 | ucuucccaauuccgcccauucc | Phvul.010G008700.1 | 4 | -1 | 1 |
| 42 | ucuucccaauuccgcccauucc | Phvul.010G008700.1 | 4 | -1 | 1 |
| 43 | ucuuccuacaccucccauacc | Phvul.010G056500.1 | 4 | -1 | 1 |
| 44 | ucuuccuacaccucccauacc | Phvul.010G056500.1 | 4 | -1 | 1 |
| 45 | ucuucccaauuccgcccauucc | Phvul.010G063100.1 | 4 | -1 | 1 |
| 46 | ucuucccaauuccgcccauucc | Phvul.010G063100.1 | 4 | -1 | 1 |
| 47 | ucuucccaauuccgcccauucc | Phvul.010G070584.1 | 4 | -1 | 1 |
| 48 | ucuucccaauuccgcccauucc | Phvul.010G146900.6 | 4 | -1 | 1 |
| 49 | ucuucccaauuccgcccauucc | Phvul.010G146900.2 | 4 | -1 | 1 |
| 50 | ucuucccaauuccgcccauucc | Phvul.010G146900.2 | 4 | -1 | 1 |
| 51 | ucuucccaauuccgcccauucc | Phvul.010G146900.3 | 4 | -1 | 1 |
| 52 | ucuucccaauuccgcccauucc | Phvul.010G146900.1 | 4 | -1 | 1 |
| 53 | ucuucccaauuccgcccauucc | Phvul.010G146900.4 | 4 | -1 | 1 |
| 54 | ucuucccaauuccgcccauucc | Phvul.010G146900.4 | 4 | -1 | 1 |
| 55 | ucuucccaauuccgcccauucc | Phvul.010G146900.5 | 4 | -1 | 1 |
| 56 | ucuucccaauuccgcccauucc | Phvul.011G014500.2 | 4 | -1 | 1 |
| 57 | ucuuccuacaccucccauacc | Phvul.011G014500.2 | 4 | -1 | 1 |
| 58 | ucuuccuacaccucccauacc | Phvul.011G014500.2 | 4 | -1 | 1 |
| 59 | ucuuccuacaccucccauacc | Phvul.011G014500.2 | 4 | -1 | 1 |
| 60 | ucuucccaauuccgcccauucc | Phvul.011G082700.3 | 4 | -1 | 1 |
| | ucuucccaauuccgcccauucc | Phvul.011G082700.2 | 4 | -1 | 1 |

| | | | | | |
|----|-------------------------------|---------------------------|----------|-----------|----------|
| 1 | | | | | |
| 2 | ucuucccaauuccgcccauucc | Phvul.011G082700.1 | 4 | -1 | 1 |
| 3 | ucuucccuacaccucccauacc | Phvul.011G149400.1 | 4 | -1 | 1 |
| 4 | ucuucccuacaccucccauacc | Phvul.011G149400.1 | 4 | -1 | 1 |
| 5 | ucuucccaauuccgcccauucc | Phvul.011G181500.1 | 4 | -1 | 1 |
| 6 | ucuucccuacaccucccauacc | Phvul.011G182900.1 | 4 | -1 | 1 |
| 7 | ucuucccuacaccucccauacc | Phvul.011G182900.1 | 4 | -1 | 1 |
| 8 | ucuucccuacaccucccauacc | Phvul.011G182900.1 | 4 | -1 | 1 |
| 9 | ucuucccaauuccgcccauucc | Phvul.011G191600.1 | 4 | -1 | 1 |
| 10 | ucuucccaauuccgcccauucc | Phvul.011G191600.1 | 4 | -1 | 1 |
| 11 | ucuucccaauuccgcccauucc | Phvul.011G191800.1 | 4 | -1 | 1 |
| 12 | ucuucccaauuccgcccauucc | Phvul.011G192200.1 | 4 | -1 | 1 |
| 13 | ucuucccuacaccucccauacc | Phvul.011G192900.1 | 4 | -1 | 1 |
| 14 | ucuucccuacaccucccauacc | Phvul.011G192900.1 | 4 | -1 | 1 |
| 15 | ucuucccuacaccucccauacc | Phvul.011G192900.1 | 4 | -1 | 1 |
| 16 | ucuucccaauuccgcccauucc | Phvul.011G195751.1 | 4 | -1 | 1 |
| 17 | ucuucccaauuccgcccauucc | Phvul.011G198400.1 | 4 | -1 | 1 |
| 18 | ucuucccaauuccgcccauucc | Phvul.011G198400.1 | 4 | -1 | 1 |
| 19 | ucuucccaauuccgcccauucc | Phvul.011G201000.1 | 4 | -1 | 1 |
| 20 | ucuucccaauuccgcccauucc | Phvul.011G201101.1 | 4 | -1 | 1 |
| 21 | ucuucccaauuccgcccauucc | Phvul.011G201101.1 | 4 | -1 | 1 |
| 22 | ucuucccaauuccgcccauucc | Phvul.001G027100.1 | 4.5 | -1 | 1 |
| 23 | ucuucccaauuccgcccauucc | Phvul.001G123000.2 | 4.5 | -1 | 1 |
| 24 | ucuucccuacaccucccauacc | Phvul.001G132516.1 | 4.5 | -1 | 1 |
| 25 | ucuucccuacaccucccauacc | Phvul.001G132516.1 | 4.5 | -1 | 1 |
| 26 | ucuucccuacaccucccauacc | Phvul.001G132516.1 | 4.5 | -1 | 1 |
| 27 | ucuucccuacaccucccauacc | Phvul.001G132701.1 | 4.5 | -1 | 1 |
| 28 | ucuucccuacaccucccauacc | Phvul.001G132701.1 | 4.5 | -1 | 1 |
| 29 | ucuucccuacaccucccauacc | Phvul.001G132701.1 | 4.5 | -1 | 1 |
| 30 | ucuucccuacaccucccauacc | Phvul.001G132800.1 | 4.5 | -1 | 1 |
| 31 | ucuucccuacaccucccauacc | Phvul.001G132800.1 | 4.5 | -1 | 1 |
| 32 | ucuucccuacaccucccauacc | Phvul.001G132864.1 | 4.5 | -1 | 1 |
| 33 | ucuucccuacaccucccauacc | Phvul.001G132864.1 | 4.5 | -1 | 1 |
| 34 | ucuucccuacaccucccauacc | Phvul.001G132864.1 | 4.5 | -1 | 1 |
| 35 | ucuucccuacaccucccauacc | Phvul.001G133100.1 | 4.5 | -1 | 1 |
| 36 | ucuucccuacaccucccauacc | Phvul.001G133100.1 | 4.5 | -1 | 1 |
| 37 | ucuucccuacaccucccauacc | Phvul.001G133101.1 | 4.5 | -1 | 1 |
| 38 | ucuucccuacaccucccauacc | Phvul.001G133101.1 | 4.5 | -1 | 1 |
| 39 | ucuucccuacaccucccauacc | Phvul.001G133101.1 | 4.5 | -1 | 1 |
| 40 | ucuucccuacaccucccauacc | Phvul.001G185400.1 | 4.5 | -1 | 1 |
| 41 | ucuucccuacaccucccauacc | Phvul.001G185400.1 | 4.5 | -1 | 1 |
| 42 | ucuucccuacaccucccauacc | Phvul.001G185400.1 | 4.5 | -1 | 1 |
| 43 | ucuucccaauuccgcccauucc | Phvul.001G217800.1 | 4.5 | -1 | 1 |
| 44 | ucuucccuacaccucccauacc | Phvul.002G063500.1 | 4.5 | -1 | 1 |
| 45 | ucuucccuacaccucccauacc | Phvul.002G063500.1 | 4.5 | -1 | 1 |
| 46 | ucuucccuacaccucccauacc | Phvul.002G063500.1 | 4.5 | -1 | 1 |
| 47 | ucuucccuacaccucccauacc | Phvul.002G104200.1 | 4.5 | -1 | 1 |
| 48 | ucuucccuacaccucccauacc | Phvul.002G104200.1 | 4.5 | -1 | 1 |
| 49 | ucuucccaauuccgcccauucc | Phvul.002G279500.1 | 4.5 | -1 | 1 |
| 50 | ucuucccaauuccgcccauucc | Phvul.002G279500.1 | 4.5 | -1 | 1 |
| 51 | ucuucccaauuccgcccauucc | Phvul.003G050200.2 | 4.5 | -1 | 1 |
| 52 | ucuucccaauuccgcccauucc | Phvul.003G050200.1 | 4.5 | -1 | 1 |
| 53 | ucuucccuacaccucccauacc | Phvul.003G076900.1 | 4.5 | -1 | 1 |
| 54 | ucuucccuacaccucccauacc | Phvul.003G076900.1 | 4.5 | -1 | 1 |
| 55 | ucuucccuacaccucccauacc | Phvul.003G076900.1 | 4.5 | -1 | 1 |
| 56 | ucuucccuacaccucccauacc | Phvul.003G104900.1 | 4.5 | -1 | 1 |
| 57 | ucuucccuacaccucccauacc | Phvul.003G104900.1 | 4.5 | -1 | 1 |
| 58 | ucuucccuacaccucccauacc | Phvul.003G104900.1 | 4.5 | -1 | 1 |
| 59 | ucuucccaauuccgcccauucc | Phvul.003G157600.1 | 4.5 | -1 | 1 |
| 60 | ucuucccuacaccucccauacc | Phvul.003G158700.1 | 4.5 | -1 | 1 |
| | ucuucccuacaccucccauacc | Phvul.003G158700.1 | 4.5 | -1 | 1 |

| | | | | | |
|----|------------------------|--------------------|-----|----|---|
| 1 | | | | | |
| 2 | ucuucccaauuccgcccauucc | Phvul.003G162300.1 | 4.5 | -1 | 1 |
| 3 | ucuucccaauuccgcccauucc | Phvul.003G209600.2 | 4.5 | -1 | 1 |
| 4 | ucuucccaauuccgcccauucc | Phvul.003G209600.1 | 4.5 | -1 | 1 |
| 5 | ucuucccaauuccgcccauucc | Phvul.003G209600.1 | 4.5 | -1 | 1 |
| 6 | ucuucccuacaccucccauacc | Phvul.003G288300.1 | 4.5 | -1 | 1 |
| 7 | ucuucccuacaccucccauacc | Phvul.003G288300.1 | 4.5 | -1 | 1 |
| 8 | ucuucccaauuccgcccauucc | Phvul.004G011400.1 | 4.5 | -1 | 1 |
| 9 | ucuucccaauuccgcccauucc | Phvul.004G011400.1 | 4.5 | -1 | 1 |
| 10 | ucuucccuacaccucccauacc | Phvul.004G064300.1 | 4.5 | -1 | 1 |
| 11 | ucuucccuacaccucccauacc | Phvul.004G064300.1 | 4.5 | -1 | 1 |
| 12 | ucuucccuacaccucccauacc | Phvul.004G131300.1 | 4.5 | -1 | 1 |
| 13 | ucuucccuacaccucccauacc | Phvul.004G131300.1 | 4.5 | -1 | 1 |
| 14 | ucuucccuacaccucccauacc | Phvul.004G131300.1 | 4.5 | -1 | 1 |
| 15 | ucuucccaauuccgcccauucc | Phvul.005G031200.1 | 4.5 | -1 | 1 |
| 16 | ucuucccuacaccucccauacc | Phvul.005G071300.1 | 4.5 | -1 | 1 |
| 17 | ucuucccuacaccucccauacc | Phvul.005G071300.1 | 4.5 | -1 | 1 |
| 18 | ucuucccuacaccucccauacc | Phvul.005G071300.1 | 4.5 | -1 | 1 |
| 19 | ucuucccaauuccgcccauucc | Phvul.006G057000.1 | 4.5 | -1 | 1 |
| 20 | ucuucccaauuccgcccauucc | Phvul.006G057100.5 | 4.5 | -1 | 1 |
| 21 | ucuucccaauuccgcccauucc | Phvul.006G057100.4 | 4.5 | -1 | 1 |
| 22 | ucuucccaauuccgcccauucc | Phvul.006G057100.4 | 4.5 | -1 | 1 |
| 23 | ucuucccaauuccgcccauucc | Phvul.006G057700.2 | 4.5 | -1 | 1 |
| 24 | ucuucccuacaccucccauacc | Phvul.006G066800.1 | 4.5 | -1 | 1 |
| 25 | ucuucccuacaccucccauacc | Phvul.006G066800.1 | 4.5 | -1 | 1 |
| 26 | ucuucccuacaccucccauacc | Phvul.006G066800.1 | 4.5 | -1 | 1 |
| 27 | ucuucccaauuccgcccauucc | Phvul.007G086300.2 | 4.5 | -1 | 1 |
| 28 | ucuucccaauuccgcccauucc | Phvul.007G086300.1 | 4.5 | -1 | 1 |
| 29 | ucuucccuacaccucccauacc | Phvul.008G014700.1 | 4.5 | -1 | 1 |
| 30 | ucuucccuacaccucccauacc | Phvul.008G014700.1 | 4.5 | -1 | 1 |
| 31 | ucuucccuacaccucccauacc | Phvul.008G014700.1 | 4.5 | -1 | 1 |
| 32 | ucuucccuacaccucccauacc | Phvul.008G072032.1 | 4.5 | -1 | 1 |
| 33 | ucuucccuacaccucccauacc | Phvul.008G072032.1 | 4.5 | -1 | 1 |
| 34 | ucuucccuacaccucccauacc | Phvul.008G072032.1 | 4.5 | -1 | 1 |
| 35 | ucuucccaauuccgcccauucc | Phvul.008G168300.2 | 4.5 | -1 | 1 |
| 36 | ucuucccaauuccgcccauucc | Phvul.008G168300.1 | 4.5 | -1 | 1 |
| 37 | ucuucccaauuccgcccauucc | Phvul.009G039200.1 | 4.5 | -1 | 1 |
| 38 | ucuucccaauuccgcccauucc | Phvul.009G039200.1 | 4.5 | -1 | 1 |
| 39 | ucuucccuacaccucccauacc | Phvul.009G079700.1 | 4.5 | -1 | 1 |
| 40 | ucuucccuacaccucccauacc | Phvul.009G079700.1 | 4.5 | -1 | 1 |
| 41 | ucuucccuacaccucccauacc | Phvul.009G180800.1 | 4.5 | -1 | 1 |
| 42 | ucuucccuacaccucccauacc | Phvul.009G180800.1 | 4.5 | -1 | 1 |
| 43 | ucuucccuacaccucccauacc | Phvul.009G180800.2 | 4.5 | -1 | 1 |
| 44 | ucuucccuacaccucccauacc | Phvul.009G180800.1 | 4.5 | -1 | 1 |
| 45 | ucuucccuacaccucccauacc | Phvul.009G180800.2 | 4.5 | -1 | 1 |
| 46 | ucuucccuacaccucccauacc | Phvul.009G180800.2 | 4.5 | -1 | 1 |
| 47 | ucuucccaauuccgcccauucc | Phvul.009G249500.1 | 4.5 | -1 | 1 |
| 48 | ucuucccaauuccgcccauucc | Phvul.010G025000.1 | 4.5 | -1 | 1 |
| 49 | ucuucccaauuccgcccauucc | Phvul.010G025700.1 | 4.5 | -1 | 1 |
| 50 | ucuucccaauuccgcccauucc | Phvul.010G025700.1 | 4.5 | -1 | 1 |
| 51 | ucuucccaauuccgcccauucc | Phvul.010G063700.2 | 4.5 | -1 | 1 |
| 52 | ucuucccaauuccgcccauucc | Phvul.010G101700.1 | 4.5 | -1 | 1 |
| 53 | ucuucccaauuccgcccauucc | Phvul.010G101700.1 | 4.5 | -1 | 1 |
| 54 | ucuucccaauuccgcccauucc | Phvul.010G141400.1 | 4.5 | -1 | 1 |
| 55 | ucuucccuacaccucccauacc | Phvul.010G149500.1 | 4.5 | -1 | 1 |
| 56 | ucuucccuacaccucccauacc | Phvul.010G149500.1 | 4.5 | -1 | 1 |
| 57 | ucuucccaauuccgcccauucc | Phvul.011G015000.1 | 4.5 | -1 | 1 |
| 58 | ucuucccuacaccucccauacc | Phvul.011G181500.1 | 4.5 | -1 | 1 |
| 59 | ucuucccuacaccucccauacc | Phvul.011G181500.1 | 4.5 | -1 | 1 |
| 60 | ucuucccuacaccucccauacc | Phvul.011G181500.1 | 4.5 | -1 | 1 |
| | ucuucccuacaccucccauacc | Phvul.011G198000.1 | 4.5 | -1 | 1 |

| | | | | | |
|----|------------------------|--------------------|-----|----|---|
| 1 | | | | | |
| 2 | ucuucccuacaccucccauacc | Phvul.011G198000.1 | 4.5 | -1 | 1 |
| 3 | ucuucccaauuccgcccauucc | Phvul.011G200880.2 | 4.5 | -1 | 1 |
| 4 | ucuucccaauuccgcccauucc | Phvul.011G200880.1 | 4.5 | -1 | 1 |
| 5 | ucuucccuacaccucccauacc | Phvul.011G201000.1 | 4.5 | -1 | 1 |
| 6 | ucuucccuacaccucccauacc | Phvul.011G201000.1 | 4.5 | -1 | 1 |
| 7 | ucuucccuacaccucccauacc | Phvul.011G201101.1 | 4.5 | -1 | 1 |
| 8 | ucuucccuacaccucccauacc | Phvul.011G201101.1 | 4.5 | -1 | 1 |
| 9 | ucuucccuacaccucccauacc | Phvul.011G201101.1 | 4.5 | -1 | 1 |
| 10 | ucuucccuacaccucccauacc | Phvul.011G201101.1 | 4.5 | -1 | 1 |
| 11 | ucuucccuacaccucccauacc | Phvul.011G202366.1 | 4.5 | -1 | 1 |
| 12 | ucuucccuacaccucccauacc | Phvul.011G202366.1 | 4.5 | -1 | 1 |
| 13 | ucuucccuacaccucccauacc | Phvul.L004500.1 | 4.5 | -1 | 1 |
| 14 | ucuucccuacaccucccauacc | Phvul.L004500.1 | 4.5 | -1 | 1 |
| 15 | ucuucccuacaccucccauacc | Phvul.L004500.1 | 4.5 | -1 | 1 |
| 16 | ucuucccaauuccgcccauucc | Phvul.001G183400.2 | 5 | -1 | 1 |
| 17 | ucuucccaauuccgcccauucc | Phvul.001G183400.3 | 5 | -1 | 1 |
| 18 | ucuucccaauuccgcccauucc | Phvul.001G183400.4 | 5 | -1 | 1 |
| 19 | ucuucccaauuccgcccauucc | Phvul.001G183400.1 | 5 | -1 | 1 |
| 20 | ucuucccaauuccgcccauucc | Phvul.001G183400.1 | 5 | -1 | 1 |
| 21 | ucuucccaauuccgcccauucc | Phvul.001G183400.1 | 5 | -1 | 1 |
| 22 | ucuucccuacaccucccauacc | Phvul.002G089800.1 | 5 | -1 | 1 |
| 23 | ucuucccuacaccucccauacc | Phvul.002G089800.1 | 5 | -1 | 1 |
| 24 | ucuucccaauuccgcccauucc | Phvul.002G171400.1 | 5 | -1 | 1 |
| 25 | ucuucccuacaccucccauacc | Phvul.002G244900.1 | 5 | -1 | 1 |
| 26 | ucuucccuacaccucccauacc | Phvul.002G244900.1 | 5 | -1 | 1 |
| 27 | ucuucccuacaccucccauacc | Phvul.002G244900.1 | 5 | -1 | 1 |
| 28 | ucuucccuacaccucccauacc | Phvul.002G245000.5 | 5 | -1 | 1 |
| 29 | ucuucccuacaccucccauacc | Phvul.002G245000.4 | 5 | -1 | 1 |
| 30 | ucuucccuacaccucccauacc | Phvul.002G245000.4 | 5 | -1 | 1 |
| 31 | ucuucccuacaccucccauacc | Phvul.002G245000.3 | 5 | -1 | 1 |
| 32 | ucuucccuacaccucccauacc | Phvul.002G245000.1 | 5 | -1 | 1 |
| 33 | ucuucccuacaccucccauacc | Phvul.002G245000.2 | 5 | -1 | 1 |
| 34 | ucuucccuacaccucccauacc | Phvul.002G245000.2 | 5 | -1 | 1 |
| 35 | ucuucccuacaccucccauacc | Phvul.002G245000.5 | 5 | -1 | 1 |
| 36 | ucuucccuacaccucccauacc | Phvul.002G245000.4 | 5 | -1 | 1 |
| 37 | ucuucccuacaccucccauacc | Phvul.002G245000.3 | 5 | -1 | 1 |
| 38 | ucuucccuacaccucccauacc | Phvul.002G245000.3 | 5 | -1 | 1 |
| 39 | ucuucccuacaccucccauacc | Phvul.002G245000.1 | 5 | -1 | 1 |
| 40 | ucuucccuacaccucccauacc | Phvul.002G245000.2 | 5 | -1 | 1 |
| 41 | ucuucccuacaccucccauacc | Phvul.003G002200.5 | 5 | -1 | 1 |
| 42 | ucuucccuacaccucccauacc | Phvul.003G002200.4 | 5 | -1 | 1 |
| 43 | ucuucccuacaccucccauacc | Phvul.003G002200.4 | 5 | -1 | 1 |
| 44 | ucuucccuacaccucccauacc | Phvul.003G002200.3 | 5 | -1 | 1 |
| 45 | ucuucccuacaccucccauacc | Phvul.003G002200.5 | 5 | -1 | 1 |
| 46 | ucuucccuacaccucccauacc | Phvul.003G002200.5 | 5 | -1 | 1 |
| 47 | ucuucccuacaccucccauacc | Phvul.003G002200.4 | 5 | -1 | 1 |
| 48 | ucuucccuacaccucccauacc | Phvul.003G002200.3 | 5 | -1 | 1 |
| 49 | ucuucccaauuccgcccauucc | Phvul.003G050200.2 | 5 | -1 | 1 |
| 50 | ucuucccaauuccgcccauucc | Phvul.003G050200.2 | 5 | -1 | 1 |
| 51 | ucuucccaauuccgcccauucc | Phvul.003G050200.1 | 5 | -1 | 1 |
| 52 | ucuucccaauuccgcccauucc | Phvul.003G244225.3 | 5 | -1 | 1 |
| 53 | ucuucccaauuccgcccauucc | Phvul.003G244225.2 | 5 | -1 | 1 |
| 54 | ucuucccaauuccgcccauucc | Phvul.003G244225.1 | 5 | -1 | 1 |
| 55 | ucuucccaauuccgcccauucc | Phvul.003G244225.1 | 5 | -1 | 1 |
| 56 | ucuucccaauuccgcccauucc | Phvul.003G282200.3 | 5 | -1 | 1 |
| 57 | ucuucccaauuccgcccauucc | Phvul.003G282200.2 | 5 | -1 | 1 |
| 58 | ucuucccaauuccgcccauucc | Phvul.003G282200.2 | 5 | -1 | 1 |
| 59 | ucuucccaauuccgcccauucc | Phvul.003G282250.1 | 5 | -1 | 1 |
| 60 | ucuucccaauuccgcccauucc | Phvul.004G011100.1 | 5 | -1 | 1 |
| | ucuucccaauuccgcccauucc | Phvul.004G086300.2 | 5 | -1 | 1 |

| | | | | | |
|----|------------------------|--------------------|---|----|---|
| 1 | | | | | |
| 2 | ucuucccaauuccgcccauucc | Phvul.004G086300.1 | 5 | -1 | 1 |
| 3 | ucuucccuacaccucccauacc | Phvul.005G041300.1 | 5 | -1 | 1 |
| 4 | ucuucccuacaccucccauacc | Phvul.005G041300.1 | 5 | -1 | 1 |
| 5 | ucuucccuacaccucccauacc | Phvul.005G069700.1 | 5 | -1 | 1 |
| 6 | ucuucccuacaccucccauacc | Phvul.005G069700.1 | 5 | -1 | 1 |
| 7 | ucuucccuacaccucccauacc | Phvul.005G072000.1 | 5 | -1 | 1 |
| 8 | ucuucccaauuccgcccauucc | Phvul.005G072000.1 | 5 | -1 | 1 |
| 9 | ucuucccuacaccucccauacc | Phvul.006G027500.1 | 5 | -1 | 1 |
| 10 | ucuucccuacaccucccauacc | Phvul.006G027500.1 | 5 | -1 | 1 |
| 11 | ucuucccuacaccucccauacc | Phvul.006G100600.1 | 5 | -1 | 1 |
| 12 | ucuucccaauuccgcccauucc | Phvul.006G100600.1 | 5 | -1 | 1 |
| 13 | ucuucccuacaccucccauacc | Phvul.006G126400.1 | 5 | -1 | 1 |
| 14 | ucuucccuacaccucccauacc | Phvul.006G126400.1 | 5 | -1 | 1 |
| 15 | ucuucccuacaccucccauacc | Phvul.006G126400.1 | 5 | -1 | 1 |
| 16 | ucuucccaauuccgcccauucc | Phvul.006G170700.1 | 5 | -1 | 1 |
| 17 | ucuucccuacaccucccauacc | Phvul.008G107400.1 | 5 | -1 | 1 |
| 18 | ucuucccuacaccucccauacc | Phvul.008G107400.1 | 5 | -1 | 1 |
| 19 | ucuucccuacaccucccauacc | Phvul.008G206300.1 | 5 | -1 | 1 |
| 20 | ucuucccaauuccgcccauucc | Phvul.008G206300.1 | 5 | -1 | 1 |
| 21 | ucuucccaauuccgcccauucc | Phvul.009G103100.1 | 5 | -1 | 1 |
| 22 | ucuucccaauuccgcccauucc | Phvul.010G008500.1 | 5 | -1 | 1 |
| 23 | ucuucccaauuccgcccauucc | Phvul.010G013500.1 | 5 | -1 | 1 |
| 24 | ucuucccaauuccgcccauucc | Phvul.010G013500.1 | 5 | -1 | 1 |
| 25 | ucuucccuacaccucccauacc | Phvul.010G044000.3 | 5 | -1 | 1 |
| 26 | ucuucccuacaccucccauacc | Phvul.010G044000.3 | 5 | -1 | 1 |
| 27 | ucuucccuacaccucccauacc | Phvul.010G044000.3 | 5 | -1 | 1 |
| 28 | ucuucccuacaccucccauacc | Phvul.010G044000.2 | 5 | -1 | 1 |
| 29 | ucuucccuacaccucccauacc | Phvul.010G044000.2 | 5 | -1 | 1 |
| 30 | ucuucccuacaccucccauacc | Phvul.010G044000.2 | 5 | -1 | 1 |
| 31 | ucuucccuacaccucccauacc | Phvul.010G044000.3 | 5 | -1 | 1 |
| 32 | ucuucccuacaccucccauacc | Phvul.010G044000.3 | 5 | -1 | 1 |
| 33 | ucuucccuacaccucccauacc | Phvul.010G044000.2 | 5 | -1 | 1 |
| 34 | ucuucccuacaccucccauacc | Phvul.010G044000.2 | 5 | -1 | 1 |
| 35 | ucuucccuacaccucccauacc | Phvul.010G044000.2 | 5 | -1 | 1 |
| 36 | ucuucccaauuccgcccauucc | Phvul.010G145600.1 | 5 | -1 | 1 |
| 37 | ucuucccaauuccgcccauucc | Phvul.011G181700.1 | 5 | -1 | 1 |
| 38 | ucuucccaauuccgcccauucc | Phvul.011G181700.1 | 5 | -1 | 1 |
| 39 | ucuucccaauuccgcccauucc | Phvul.011G200820.1 | 5 | -1 | 1 |
| 40 | ucuucccaauuccgcccauucc | Phvul.011G202100.1 | 5 | -1 | 1 |
| 41 | ucuucccaauuccgcccauucc | Phvul.011G202300.1 | 5 | -1 | 1 |
| 42 | ucuucccaauuccgcccauucc | Phvul.011G202300.1 | 5 | -1 | 1 |
| 43 | ucuucccaauuccgcccauucc | Phvul.011G203100.1 | 5 | -1 | 1 |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| miRNA_end | Target_start | Target_end | miRNA_align | alignment | Target_align | Inhibition |
|-----------|--------------|------------|-------------|-----------|--------------|-------------|
| 22 | 667 | 688 | UCUUCCCAAL | | GGAAUGGGC | Cleavage |
| 22 | 1158 | 1179 | UCUUCCCUAC | | UAUAUGGCG | Cleavage |
| 22 | 993 | 1014 | UCUUCCCUAC | | UAUAUGGCG | Cleavage |
| 22 | 1158 | 1179 | UCUUCCCUAC | | UAUAUGGCG | Cleavage |
| 22 | 993 | 1014 | UCUUCCCUAC | | UAUAUGGCG | Cleavage |
| 22 | 1110 | 1131 | UCUUCCCUAC | | UAUAUGGCG | Cleavage |
| 22 | 1110 | 1131 | UCUUCCCUAC | | UAUAUGGCG | Cleavage |
| 22 | 1023 | 1044 | UCUUCCCUAC | | GGUAUGGGG | Cleavage |
| 22 | 1520 | 1541 | UCUUCCCUAC | | GGUAUGGGG | Cleavage |
| 22 | 1023 | 1044 | UCUUCCCUAC | | GGUAUGGGG | Cleavage |
| 22 | 1520 | 1541 | UCUUCCCUAC | | GGUAUGGGG | Cleavage |
| 22 | 863 | 884 | UCUUCCCAAL | | GGAAUGGGU | Cleavage |
| 22 | 104 | 125 | UCUUCCCAAL | | UGUGUGGUU | Cleavage |
| 22 | 2120 | 2141 | UCUUCCCUAC | | AUUGUGGGA | Cleavage |
| 22 | 2120 | 2141 | UCUUCCCUAC | | AUUGUGGGA | Cleavage |
| 22 | 782 | 803 | UCUUCCCAAL | | GGGAUGGGU | Cleavage |
| 22 | 2213 | 2234 | UCUUCCCAAL | | CAGAUGGGG | Cleavage |
| 22 | 2213 | 2234 | UCUUCCCAAL | | CAGAUGGGG | Cleavage |
| 22 | 2209 | 2230 | UCUUCCCAAL | | CAGAUGGGG | Cleavage |
| 22 | 763 | 784 | UCUUCCCAAL | | GGAAUAGGU | Cleavage |
| 22 | 986 | 1007 | UCUUCCCAAL | | GAGGUGGGU | Cleavage |
| 22 | 1081 | 1102 | UCUUCCCAAL | | GAGGUGGGU | Cleavage |
| 22 | 1155 | 1176 | UCUUCCCAAL | | GAGGUGGGU | Cleavage |
| 22 | 516 | 537 | UCUUCCCUAC | | GAUUUGAGG | Cleavage |
| 22 | 516 | 537 | UCUUCCCUAC | | GAUUUGAGG | Cleavage |
| 22 | 78 | 99 | UCUUCCCAAL | | UGCGUGUGU | Cleavage |
| 22 | 864 | 885 | UCUUCCCUAC | | AAGAUUGGA | Cleavage |
| 22 | 864 | 885 | UCUUCCCUAC | | AAGAUUGGA | Cleavage |
| 22 | 571 | 592 | UCUUCCCAAL | | GGCAUGGGU | Cleavage |
| 22 | 811 | 832 | UCUUCCCAAL | | GGUAUGGGU | Cleavage |
| 22 | 781 | 802 | UCUUCCCAAL | | GAGGAGGGU | Cleavage |
| 22 | 781 | 802 | UCUUCCCAAL | | GAGGAGGGU | Cleavage |
| 22 | 781 | 802 | UCUUCCCAAL | | GAGGAGGGU | Cleavage |
| 22 | 781 | 802 | UCUUCCCAAL | | GAGGAGGGU | Cleavage |
| 22 | 781 | 802 | UCUUCCCAAL | | GAGGAGGGU | Cleavage |
| 22 | 781 | 802 | UCUUCCCAAL | | GAGGAGGGU | Cleavage |
| 22 | 517 | 538 | UCUUCCCAAL | | GGUAUGGGC | Cleavage |
| 22 | 746 | 767 | UCUUCCCAAL | | GGCAUGGGU | Translation |
| 22 | 709 | 730 | UCUUCCCUAC | | GGGAUGGGA | Translation |
| 22 | 709 | 730 | UCUUCCCUAC | | GGGAUGGGA | Translation |
| 22 | 1008 | 1029 | UCUUCCCUAC | | GACGUGGAG | Cleavage |
| 22 | 1008 | 1029 | UCUUCCCUAC | | GACGUGGAG | Cleavage |
| 22 | 513 | 534 | UCUUCCCAAL | | AGGAUGGGU | Cleavage |
| 22 | 613 | 634 | UCUUCCCAAL | | AGGAUGGGU | Cleavage |

| | | | | |
|----|----|------|-----------------|-----------------------------------|
| 1 | | | | |
| 2 | 22 | 1221 | 1242 UCUUCCCAAL | :: :: : ::::: AUAAGGGUCI Cleavage |
| 3 | 22 | 493 | 514 UCUUCCCAAL | ::: ::::: CCUACUGGUC Cleavage |
| 4 | 22 | 138 | 159 UCUUCCCUAC | ::: ::::: UGGCAGGGA Cleavage |
| 5 | 22 | 138 | 159 UCUUCCCUAC | ::: ::::: UGGCAGGGA Cleavage |
| 6 | 22 | 126 | 147 UCUUCCCUAC | ::: ::::: GAGGUGGAA Cleavage |
| 7 | 22 | 126 | 147 UCUUCCCUAC | ::: ::::: GAGGUGGAA Cleavage |
| 8 | 22 | 2611 | 2632 UCUUCCCUAC | ::: : ::::: GCUAUGUCAI Cleavage |
| 9 | 22 | 2611 | 2632 UCUUCCCUAC | ::: : ::::: GCUAUGUCAI Cleavage |
| 10 | 22 | 487 | 508 UCUUCCCAAL | ::: ::::: UUAGCGGGC Cleavage |
| 11 | 22 | 661 | 682 UCUUCCCUAC | ::: ::::: GGAAUGGGC Cleavage |
| 12 | 22 | 661 | 682 UCUUCCCUAC | ::: ::::: GGAAUGGGC Cleavage |
| 13 | 22 | 844 | 865 UCUUCCCUAC | ::: ::::: UGUUUGGGA Translation |
| 14 | 22 | 844 | 865 UCUUCCCUAC | ::: ::::: UGUUUGGGA Translation |
| 15 | 22 | 508 | 529 UCUUCCCUAC | ::: ::::: GGCAUGGGA Translation |
| 16 | 22 | 508 | 529 UCUUCCCUAC | ::: ::::: GGCAUGGGA Translation |
| 17 | 22 | 2091 | 2112 UCUUCCCAAL | ::: ::::: GGGGUUGGC Translation |
| 18 | 22 | 550 | 571 UCUUCCCUAC | ::: ::::: GGGGUUGGA Cleavage |
| 19 | 22 | 550 | 571 UCUUCCCUAC | ::: ::::: GGGGUUGGA Cleavage |
| 20 | 22 | 550 | 571 UCUUCCCUAC | ::: ::::: GGGGUUGGA Cleavage |
| 21 | 22 | 550 | 571 UCUUCCCUAC | ::: ::::: GGGGUUGGA Cleavage |
| 22 | 22 | 1939 | 1960 UCUUCCCAAL | ::: ::::: AUAGUAGGC Cleavage |
| 23 | 22 | 113 | 134 UCUUCCCUAC | ::: ::::: AUUUUGAGG Cleavage |
| 24 | 22 | 113 | 134 UCUUCCCUAC | ::: ::::: AUUUUGAGG Cleavage |
| 25 | 22 | 113 | 134 UCUUCCCUAC | ::: ::::: AUUUUGAGG Cleavage |
| 26 | 22 | 113 | 134 UCUUCCCUAC | ::: ::::: AUUUUGAGG Cleavage |
| 27 | 22 | 750 | 771 UCUUCCCAAL | ::: ::::: GGCAUGGGU Translation |
| 28 | 22 | 747 | 768 UCUUCCCAAL | ::: ::::: GGCAUGGGU Translation |
| 29 | 22 | 802 | 823 UCUUCCCAAL | ::: ::::: GGUAUGGGG Cleavage |
| 30 | 22 | 59 | 80 UCUUCCCUAC | ::: ::::: UUAUUGGUA Cleavage |
| 31 | 22 | 59 | 80 UCUUCCCUAC | ::: ::::: UUAUUGGUA Cleavage |
| 32 | 22 | 59 | 80 UCUUCCCUAC | ::: ::::: UUAUUGGUA Cleavage |
| 33 | 22 | 59 | 80 UCUUCCCUAC | ::: ::::: UUAUUGGUA Cleavage |
| 34 | 22 | 680 | 701 UCUUCCCAAL | ::: ::::: GGGAUUGGU Cleavage |
| 35 | 22 | 720 | 741 UCUUCCCAAL | ::: ::::: GGGAUUGGU Cleavage |
| 36 | 22 | 586 | 607 UCUUCCCAAL | ::: ::::: GGUAUGGGC Cleavage |
| 37 | 22 | 658 | 679 UCUUCCCUAC | ::: ::::: GGAAUGGGA Translation |
| 38 | 22 | 658 | 679 UCUUCCCUAC | ::: ::::: GGAAUGGGA Translation |
| 39 | 22 | 793 | 814 UCUUCCCAAL | ::: ::::: GGUAUGGGC Cleavage |
| 40 | 22 | 589 | 610 UCUUCCCAAL | ::: ::::: GGUAUGGGC Cleavage |
| 41 | 22 | 703 | 724 UCUUCCCAAL | ::: ::::: GGUAUGGGC Cleavage |
| 42 | 22 | 798 | 819 UCUUCCCAAL | ::: ::::: GGUAUGGGC Cleavage |
| 43 | 22 | 723 | 744 UCUUCCCAAL | ::: ::::: GGUAUGGGC Cleavage |
| 44 | 22 | 532 | 553 UCUUCCCAAL | ::: ::::: GGUAUGGGC Cleavage |
| 45 | 22 | 589 | 610 UCUUCCCAAL | ::: ::::: GGUAUGGGC Cleavage |
| 46 | 22 | 656 | 677 UCUUCCCAAL | ::: ::::: GGUAUGGGC Cleavage |
| 47 | 22 | 636 | 657 UCUUCCCAAL | ::: ::::: GGCAUGGGC Cleavage |
| 48 | | | | |
| 49 | | | | |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

| | | | |
|----|----|------|---|
| 1 | | | |
| 2 | 22 | 589 | 610 UCUUCCCAAL:: : : : :GGUAUGGGC Cleavage |
| 3 | 22 | 589 | 610 UCUUCCCAAL : : : : :GCUAUGGGC Cleavage |
| 4 | 22 | 842 | 863 UCUUCCCAAL:: : : : :GGUAUGGGC Cleavage |
| 5 | 22 | 39 | 60 UCUUCCCAAL:: : : : :GGGAUGGGC Cleavage |
| 6 | 22 | 716 | 737 UCUUCCCUAC:: : : : :GGAAUGGGA Translation |
| 7 | 22 | 716 | 737 UCUUCCCUAC:: : : : :GGAAUGGGA Translation |
| 8 | 22 | 601 | 622 UCUUCCCUAC:: : : : :GGAAUGGGA Translation |
| 9 | 22 | 601 | 622 UCUUCCCUAC:: : : : :GGAAUGGGA Translation |
| 10 | 22 | 604 | 625 UCUUCCCUAC:: : : : :GGAAUGGGA Translation |
| 11 | 22 | 604 | 625 UCUUCCCUAC:: : : : :GGAAUGGGA Translation |
| 12 | 22 | 604 | 625 UCUUCCCUAC:: : : : :GGAAUGGGA Translation |
| 13 | 22 | 604 | 625 UCUUCCCUAC:: : : : :GGAAUGGGA Translation |
| 14 | 22 | 752 | 773 UCUUCCCUAC:: : : : :GGAAUGGGA Translation |
| 15 | 22 | 752 | 773 UCUUCCCUAC:: : : : :GGAAUGGGA Translation |
| 16 | 22 | 211 | 232 UCUUCCCUAC: : : : :GUUGUGGAA Cleavage |
| 17 | 22 | 516 | 537 UCUUCCCUAC: : : : :GUUGUGGAA Cleavage |
| 18 | 22 | 211 | 232 UCUUCCCUAC: : : : :GUUGUGGAA Cleavage |
| 19 | 22 | 516 | 537 UCUUCCCUAC: : : : :GUUGUGGAA Cleavage |
| 20 | 22 | 1599 | 1620 UCUUCCCUAC:: : : : :GGAAUUAGG Cleavage |
| 21 | 22 | 1681 | 1702 UCUUCCCUAC:: : : : :GGAAUUAGG Cleavage |
| 22 | 22 | 1599 | 1620 UCUUCCCUAC:: : : : :GGAAUUAGG Cleavage |
| 23 | 22 | 1681 | 1702 UCUUCCCUAC:: : : : :GGAAUUAGG Cleavage |
| 24 | 22 | 757 | 778 UCUUCCCAAL:: : : : :GGAAGGGGA Cleavage |
| 25 | 22 | 757 | 778 UCUUCCCAAL:: : : : :GGAAGGGGA Cleavage |
| 26 | 22 | 647 | 668 UCUUCCCUAC : : : : :AACGUGGGA Cleavage |
| 27 | 22 | 647 | 668 UCUUCCCUAC : : : : :AACGUGGGA Cleavage |
| 28 | 22 | 414 | 435 UCUUCCCAAL : : : : :CAGAUGGGU Cleavage |
| 29 | 22 | 724 | 745 UCUUCCCAAL : : : : :CAGAUGGGU Cleavage |
| 30 | 22 | 720 | 741 UCUUCCCAAL : : : : :CAGAUGGGU Cleavage |
| 31 | 22 | 801 | 822 UCUUCCCAAL : : : : :CAGAUGGGU Cleavage |
| 32 | 22 | 1183 | 1204 UCUUCCCAAL : : : : :UUGAUGGGU Translation |
| 33 | 22 | 2066 | 2087 UCUUCCCUAC : : : : :CUUGUGGAA Cleavage |
| 34 | 22 | 2066 | 2087 UCUUCCCUAC : : : : :CUUGUGGAA Cleavage |
| 35 | 22 | 804 | 825 UCUUCCCAAL: : : : :GGGGUGGGU Cleavage |
| 36 | 22 | 804 | 825 UCUUCCCAAL: : : : :GGGGUGGGU Cleavage |
| 37 | 22 | 505 | 526 UCUUCCCUAC : : : : :AUUAUUGGA Cleavage |
| 38 | 22 | 505 | 526 UCUUCCCUAC : : : : :AUUAUUGGA Cleavage |
| 39 | 22 | 83 | 104 UCUUCCCAAL : : : : :AAAUGGGGA Cleavage |
| 40 | 22 | 83 | 104 UCUUCCCAAL : : : : :AAAUGGGGA Cleavage |
| 41 | 22 | 83 | 104 UCUUCCCAAL : : : : :AAAUGGGGA Cleavage |
| 42 | 22 | 1325 | 1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation |
| 43 | 22 | 1325 | 1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation |
| 44 | 22 | 1325 | 1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation |
| 45 | 22 | 1325 | 1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation |
| 46 | 22 | 1325 | 1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation |
| 47 | 22 | 1325 | 1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation |
| 48 | 22 | 1325 | 1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation |
| 49 | 22 | 1325 | 1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation |
| 50 | 22 | 1325 | 1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation |
| 51 | 22 | 1325 | 1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation |
| 52 | 22 | 1325 | 1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation |
| 53 | 22 | 1325 | 1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation |
| 54 | 22 | 1325 | 1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation |
| 55 | 22 | 1325 | 1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation |
| 56 | 22 | 1325 | 1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation |
| 57 | 22 | 1325 | 1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation |
| 58 | 22 | 1325 | 1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation |
| 59 | 22 | 1325 | 1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation |
| 60 | 22 | 1325 | 1346 UCUUCCCUAC : : : : :CCGAUGGGAI Translation |

| | | | |
|----|----|------|--|
| 1 | | | |
| 2 | 22 | 667 | 688 UCUUCCCUAC:: : : : :GGAAUGGGC(Translation |
| 3 | 22 | 667 | 688 UCUUCCCUAC:: : : : :GGAAUGGGC(Translation |
| 4 | 22 | 326 | 347 UCUUCCCUAC:: : : : :GGCAAGGGC(Cleavage |
| 5 | 22 | 326 | 347 UCUUCCCUAC:: : : : :GGCAAGGGC(Cleavage |
| 6 | 22 | 326 | 347 UCUUCCCUAC:: : : : :GGCAAGGGC(Cleavage |
| 7 | 22 | 791 | 812 UCUUCCCAAL : : : : :UGAGUGGGC(Cleavage |
| 8 | 22 | 837 | 858 UCUUCCCUAC : : : : :UGUAUGGGU(Cleavage |
| 9 | 22 | 837 | 858 UCUUCCCUAC : : : : :UGUAUGGGU(Cleavage |
| 10 | 22 | 837 | 858 UCUUCCCUAC : : : : :UGUAUGGGU(Cleavage |
| 11 | 22 | 634 | 655 UCUUCCCAAL : : : : :GGAAUGGGU(Cleavage |
| 12 | 22 | 666 | 687 UCUUCCCAAL : : : : :AAUGUGGGU(Cleavage |
| 13 | 22 | 1615 | 1636 UCUUCCCAAL : : : : :GGCAUGGGU(Cleavage |
| 14 | 22 | 619 | 640 UCUUCCCUAC : : : : :GGCAAAGGA(Cleavage |
| 15 | 22 | 619 | 640 UCUUCCCUAC : : : : :GGCAAAGGA(Cleavage |
| 16 | 22 | 619 | 640 UCUUCCCUAC : : : : :GGCAAAGGA(Cleavage |
| 17 | 22 | 265 | 287 UCUUCCCAAL : : : : :GUGAUGGGU(Cleavage |
| 18 | 22 | 265 | 287 UCUUCCCAAL : : : : :GUGAUGGGU(Cleavage |
| 19 | 22 | 312 | 333 UCUUCCCAAL : : : : :GGGAAAGGA(Cleavage |
| 20 | 22 | 1781 | 1802 UCUUCCCAAL : : : : :GGAAUAGGU(Cleavage |
| 21 | 22 | 1891 | 1912 UCUUCCCUAC : : : : :CGUGUGGGA(Cleavage |
| 22 | 22 | 1891 | 1912 UCUUCCCUAC : : : : :CGUGUGGGA(Cleavage |
| 23 | 22 | 1891 | 1912 UCUUCCCUAC : : : : :CGUGUGGGA(Cleavage |
| 24 | 22 | 404 | 425 UCUUCCCUAC : : : : :ACCAUGGGAC(Translation |
| 25 | 22 | 479 | 500 UCUUCCCUAC : : : : :ACCAUGGGAC(Translation |
| 26 | 22 | 479 | 500 UCUUCCCUAC : : : : :ACCAUGGGAC(Translation |
| 27 | 22 | 404 | 425 UCUUCCCUAC : : : : :ACCAUGGGAC(Translation |
| 28 | 22 | 479 | 500 UCUUCCCUAC : : : : :ACCAUGGGAC(Translation |
| 29 | 22 | 479 | 500 UCUUCCCUAC : : : : :ACCAUGGGAC(Translation |
| 30 | 22 | 1415 | 1436 UCUUCCCAAL : : : : :AAGCAGGGU(Cleavage |
| 31 | 22 | 715 | 736 UCUUCCCUAC : : : : :GAUGUGGAA(Cleavage |
| 32 | 22 | 728 | 749 UCUUCCCUAC : : : : :GAUGUGGAA(Cleavage |
| 33 | 22 | 728 | 749 UCUUCCCUAC : : : : :GAUGUGGAA(Cleavage |
| 34 | 22 | 715 | 736 UCUUCCCUAC : : : : :GAUGUGGAA(Cleavage |
| 35 | 22 | 728 | 749 UCUUCCCUAC : : : : :GAUGUGGAA(Cleavage |
| 36 | 22 | 811 | 832 UCUUCCCAAL : : : : :GGGAUGGGG(Translation |
| 37 | 22 | 811 | 832 UCUUCCCUAC : : : : :GGGAUGGGG(Translation |
| 38 | 22 | 811 | 832 UCUUCCCUAC : : : : :GGGAUGGGG(Translation |
| 39 | 22 | 811 | 832 UCUUCCCUAC : : : : :GGGAUGGGG(Translation |
| 40 | 22 | 1673 | 1694 UCUUCCCAAL : : : : :GGGAUGGGGA(Cleavage |
| 41 | 22 | 1698 | 1719 UCUUCCCAAL : : : : :GGGAUGGGGA(Cleavage |
| 42 | 22 | 1698 | 1719 UCUUCCCAAL : : : : :GGGAUGGGGA(Cleavage |
| 43 | 22 | 1135 | 1156 UCUUCCCUAC : : : : :UGAAUGGGGA(Cleavage |
| 44 | 22 | 1135 | 1156 UCUUCCCUAC : : : : :UGAAUGGGGA(Cleavage |
| 45 | 22 | 596 | 617 UCUUCCCAAL : : : : :GGCAUGGGC(Cleavage |
| 46 | 22 | 596 | 617 UCUUCCCAAL : : : : :GGCAUGGGC(Cleavage |
| 47 | 22 | 2364 | 2385 UCUUCCCAAL : : : : :AAAUGGGGA(Cleavage |
| 48 | 22 | 409 | 430 UCUUCCCAAL : : : : :GCAAUGGCUI(Cleavage |
| 49 | 22 | 719 | 740 UCUUCCCAAL : : : : :GCAAUGGCUI(Cleavage |
| 50 | 22 | 719 | 740 UCUUCCCAAL : : : : :GCAAUGGCUI(Cleavage |
| 51 | 22 | 722 | 743 UCUUCCCAAL : : : : :GCAAUGGCUI(Cleavage |
| 52 | 22 | 722 | 743 UCUUCCCAAL : : : : :GCAAUGGCUI(Cleavage |
| 53 | 22 | 719 | 740 UCUUCCCAAL : : : : :GCAAUGGCUI(Cleavage |
| 54 | 22 | 719 | 740 UCUUCCCAAL : : : : :GCAAUGGCUI(Cleavage |
| 55 | 22 | 770 | 791 UCUUCCCAAL : : : : :GCAAUGGCUI(Cleavage |
| 56 | 22 | 568 | 589 UCUUCCCAAL : : : : :GGCAUGGGG(Translation |
| 57 | 22 | 568 | 589 UCUUCCCUAC : : : : :GGCAUGGGG(Translation |
| 58 | 22 | 568 | 589 UCUUCCCUAC : : : : :GGCAUGGGG(Translation |
| 59 | 22 | 568 | 589 UCUUCCCUAC : : : : :GGCAUGGGG(Translation |
| 60 | 22 | 180 | 201 UCUUCCCAAL : : : : :GCGAUGGGC(Cleavage |
| | 22 | 159 | 180 UCUUCCCAAL : : : : :GCGAUGGGC(Cleavage |

| | | | |
|----|----|------|---|
| 1 | | | |
| 2 | 22 | 180 | 201 UCUUCCCAAL : :::::: .. : ::::::GCGAUGGGC(Cleavage |
| 3 | 22 | 618 | 639 UCUUCCCUAC : :: :: : ::::::: :GGAAUGGCC(Cleavage |
| 4 | 22 | 618 | 639 UCUUCCCUAC : :: :: : ::::::: :GGAAUGGCC(Cleavage |
| 5 | 22 | 817 | 838 UCUUCCCAAL : ::::::: : : :: ::GGAAUGGGU Cleavage |
| 6 | 22 | 444 | 465 UCUUCCCUAC : :: :: : :::::::AAUAUGAGA(Translation |
| 7 | 22 | 444 | 465 UCUUCCCUAC : :: :: : :::::::AAUAUGAGA(Translation |
| 8 | 22 | 592 | 613 UCUUCCCAAL : ::::::: : : :: ::GGUAUGGGU Cleavage |
| 9 | 22 | 640 | 661 UCUUCCCAAL : ::::::: : : :: ::GGUAUGGGU Cleavage |
| 10 | 22 | 529 | 550 UCUUCCCAAL : ::::::: : : :: ::GGUAUGGGU Cleavage |
| 11 | 22 | 667 | 688 UCUUCCCUAC : ::::::: : : :: ::GGUAUGGGC Translation |
| 12 | 22 | 667 | 688 UCUUCCCUAC : ::::::: : : :: ::GGUAUGGGC Translation |
| 13 | 22 | 589 | 610 UCUUCCCAAL : ::::::: : : :: ::GGUAUGGGU Cleavage |
| 14 | 22 | 779 | 800 UCUUCCCAAL : ::::::: : : :: ::GGUAUGGGU Cleavage |
| 15 | 22 | 634 | 655 UCUUCCCAAL : ::::::: : : :: ::GGAAUGGGU Cleavage |
| 16 | 22 | 640 | 661 UCUUCCCAAL : ::::::: : : :: ::GGCAUGGGU Cleavage |
| 17 | 22 | 823 | 844 UCUUCCCAAL .. : ::::::: : AUGGUUGGU Cleavage |
| 18 | 22 | 1538 | 1559 UCUUCCCAAL : ::::::: : AGCUCUGGU(Cleavage |
| 19 | 22 | 651 | 672 UCUUCCCUAC : :: :: : :::::::GGUAUUGGA Translation |
| 20 | 22 | 651 | 672 UCUUCCCUAC : :: :: : :::::::GGUAUUGGA Translation |
| 21 | 22 | 64 | 85 UCUUCCCUAC : :: :: : :::::::GGUAUUGGA Translation |
| 22 | 22 | 64 | 85 UCUUCCCUAC : :: :: : :::::::GGUAUUGGA Translation |
| 23 | 22 | 615 | 636 UCUUCCCUAC : :: :: : :::::::GGUAUUGGA Translation |
| 24 | 22 | 615 | 636 UCUUCCCUAC : :: :: : :::::::GGUAUUGGA Translation |
| 25 | 22 | 916 | 937 UCUUCCCUAC : :: :: : :::::::GGUAUUGGA Translation |
| 26 | 22 | 916 | 937 UCUUCCCUAC : :: :: : :::::::GGUAUUGGA Translation |
| 27 | 22 | 651 | 672 UCUUCCCUAC : :: :: : :::::::GGUAUUGGA Translation |
| 28 | 22 | 651 | 672 UCUUCCCUAC : :: :: : :::::::GGUAUUGGA Translation |
| 29 | 22 | 635 | 656 UCUUCCCUAC : :: :: : :::::::GGUAUUGGA Translation |
| 30 | 22 | 635 | 656 UCUUCCCUAC : :: :: : :::::::GGUAUUGGA Translation |
| 31 | 22 | 1429 | 1450 UCUUCCCUAC : :: : : ::::::: UACAUGGAC(Cleavage |
| 32 | 22 | 1429 | 1450 UCUUCCCUAC : :: : : ::::::: UACAUGGAC(Cleavage |
| 33 | 22 | 653 | 674 UCUUCCCAAL : ::::::: : : :: ::CAAUGGGU(Cleavage |
| 34 | 22 | 963 | 984 UCUUCCCUAC : : :::::: : ::::::AGUUUGGGA Translation |
| 35 | 22 | 963 | 984 UCUUCCCUAC : : :::::: : ::::::AGUUUGGGA Translation |
| 36 | 22 | 932 | 953 UCUUCCCUAC : : : : :::::: :GGCACGGGA/ Cleavage |
| 37 | 22 | 932 | 953 UCUUCCCUAC : : : : :::::: :GGCACGGGA/ Cleavage |
| 38 | 22 | 591 | 612 UCUUCCCAAL : : ::::::: : : AGCAUGGGU(Cleavage |
| 39 | 22 | 1313 | 1334 UCUUCCCAAL : : : : : : :: ::UUCAUGAGA(Cleavage |
| 40 | 22 | 1335 | 1356 UCUUCCCAAL : : : : : : :: ::UUCAUGAGA(Cleavage |
| 41 | 22 | 1014 | 1035 UCUUCCCUAC : :: . : :::::::AUUGUGGAG Cleavage |
| 42 | 22 | 1014 | 1035 UCUUCCCUAC : :: . : :::::::AUUGUGGAG Cleavage |
| 43 | 22 | 29 | 50 UCUUCCCUAC : :: : :::::: : ::::::UGUGUGUGA Cleavage |
| 44 | 22 | 29 | 50 UCUUCCCUAC : :: : :::::: : ::::::UGUGUGUGA Cleavage |
| 45 | 22 | 2018 | 2039 UCUUCCCAAL : :::::: : : :::::::GGGAUGGAA(Cleavage |
| 46 | 22 | 2000 | 2021 UCUUCCCUAC : :::::: : : :::::::CAUAUGGGU(Cleavage |
| 47 | 22 | 2000 | 2021 UCUUCCCUAC : :::::: : : :::::::CAUAUGGGU(Cleavage |

| | | | |
|----|----|------|--|
| 1 | | | |
| 2 | 22 | 816 | 837 UCUUCCCAAL::: : :::: :GGGAUCGCU Cleavage |
| 3 | 22 | 449 | 470 UCUUCCCAAL::: : :::: :GGGUUGGGU Cleavage |
| 4 | 22 | 449 | 470 UCUUCCCAAL::: : :::: :GGGUUGGGU Cleavage |
| 5 | 22 | 1711 | 1732 UCUUCCCUAC :::: : :::: :UUUAUGGGU Cleavage |
| 6 | 22 | 1711 | 1732 UCUUCCCUAC :::: : :::: :UUUAUGGGU Cleavage |
| 7 | 22 | 529 | 550 UCUUCCCAAL :::: : :::: :CUACAGGGC/ Cleavage |
| 8 | 22 | 525 | 546 UCUUCCCUAC :::: : :::: :AAUAUGGGC/ Cleavage |
| 9 | 22 | 525 | 546 UCUUCCCUAC :::: : :::: :AAUAUGGGC/ Cleavage |
| 10 | 22 | 843 | 864 UCUUCCCUAC::: : :::: :GGUUUGGUG Cleavage |
| 11 | 22 | 843 | 864 UCUUCCCUAC::: : :::: :GGUUUGGUG Cleavage |
| 12 | 22 | 822 | 843 UCUUCCCAAL::: : :::: :GGAAUGGGA Cleavage |
| 13 | 22 | 248 | 269 UCUUCCCUAC::: : :::: :GGAGUGGCA Cleavage |
| 14 | 22 | 248 | 269 UCUUCCCUAC::: : :::: :GGAGUGGCA Cleavage |
| 15 | 22 | 1667 | 1688 UCUUCCCAAL :::: : :::: :UGGGUGGAU Cleavage |
| 16 | 22 | 1756 | 1777 UCUUCCCAAL :::: : :::: :UGGGUGGAU Cleavage |
| 17 | 22 | 1759 | 1780 UCUUCCCAAL :::: : :::: :UGGGUGGAU Cleavage |
| 18 | 22 | 181 | 202 UCUUCCCAAL: :::: : :::: :GAAUUGGAU Cleavage |
| 19 | 22 | 634 | 655 UCUUCCCUAC::: : :::: :GGAAUGGGU Translation |
| 20 | 22 | 634 | 655 UCUUCCCUAC::: : :::: :GGAAUGGGU Translation |
| 21 | 22 | 704 | 725 UCUUCCCAAL: :::: : :::: :GGCAUGGGU Cleavage |
| 22 | 22 | 704 | 725 UCUUCCCAAL: :::: : :::: :GGCAUGGGU Cleavage |
| 23 | 22 | 732 | 753 UCUUCCCUAC::: : :::: :GGUAUGGGU Translation |
| 24 | 22 | 732 | 753 UCUUCCCUAC::: : :::: :GGUAUGGGU Translation |
| 25 | 22 | 544 | 565 UCUUCCCUAC::: : :::: :GGUGUUGGU Cleavage |
| 26 | 22 | 544 | 565 UCUUCCCUAC::: : :::: :GGUGUUGGU Cleavage |
| 27 | 22 | 494 | 516 UCUUC-CCAAL :::: : :::: :CUUGUGGGU Cleavage |
| 28 | 22 | 750 | 772 UCUUC-CCAAL :::: : :::: :CUUGUGGGU Cleavage |
| 29 | 22 | 620 | 641 UCUUCCCAAL::: : :::: :GGAGAGGGU Cleavage |
| 30 | 22 | 271 | 292 UCUUCCCUAC :::: : :::: :GGAUGGGGA Cleavage |
| 31 | 22 | 271 | 292 UCUUCCCUAC :::: : :::: :GGAUGGGGA Cleavage |
| 32 | 22 | 226 | 247 UCUUCCCUAC :::: : :::: :GGGGACGGA Cleavage |
| 33 | 22 | 226 | 247 UCUUCCCUAC :::: : :::: :GGGGACGGA Cleavage |
| 34 | 22 | 226 | 247 UCUUCCCUAC :::: : :::: :GGGGACGGA Cleavage |
| 35 | 22 | 226 | 247 UCUUCCCUAC :::: : :::: :GGGGACGGA Cleavage |
| 36 | 22 | 244 | 265 UCUUCCCAAL: :::: : :::: :GGUAUGAGC Cleavage |
| 37 | 22 | 673 | 694 UCUUCCCAAL::: : :::: :GGAAUGGGA Cleavage |
| 38 | 22 | 646 | 667 UCUUCCCAAL::: : :::: :GGAAUGGGA Cleavage |
| 39 | 22 | 566 | 587 UCUUCCCAAL: :::: : :::: :GGCAUGGGU Cleavage |
| 40 | 22 | 286 | 306 UCUUCCCAAL: :::: : :::: :GAAUUGGGU Cleavage |
| 41 | 22 | 1001 | 1022 UCUUCCCAAL :::: : :::: :AAAUUGGGU Translation |
| 42 | 22 | 468 | 489 UCUUCCCUAC: :::: : :::: :GUUAUGGGU Cleavage |
| 43 | 22 | 468 | 489 UCUUCCCUAC: :::: : :::: :GUUAUGGGU Cleavage |
| 44 | 22 | 1083 | 1104 UCUUCCCAAL :::: : :::: :UGAAUUGGC Cleavage |
| 45 | 22 | 817 | 838 UCUUCCCUAC::: : :::: :GGAAUGGGU Translation |
| 46 | 22 | 817 | 838 UCUUCCCUAC::: : :::: :GGAAUGGGU Translation |
| 47 | 22 | 716 | 737 UCUUCCCUAC::: : :::: :GGGAUGGGC Translation |

| | | | |
|----|----|------|---|
| 1 | | | |
| 2 | 22 | 716 | 737 UCUUCCCUAC:: : : : :GGGAUGGGC Translation |
| 3 | 22 | 1231 | 1252 UCUUCCCAAL:: : : : :GGAAUGGGA Cleavage |
| 4 | 22 | 1231 | 1252 UCUUCCCAAL:: : : : :GGAAUGGGA Cleavage |
| 5 | 22 | 634 | 655 UCUUCCCUAC:: : : : :GGAAUGGGU Translation |
| 6 | 22 | 634 | 655 UCUUCCCUAC:: : : : :GGAAUGGGU Translation |
| 7 | 22 | 634 | 655 UCUUCCCUAC:: : : : :GGAAUGGGU Translation |
| 8 | 22 | 640 | 661 UCUUCCCUAC:: : : : :GGCAUGGGU Translation |
| 9 | 22 | 640 | 661 UCUUCCCUAC:: : : : :GGCAUGGGU Translation |
| 10 | 22 | 640 | 661 UCUUCCCUAC:: : : : :GGCAUGGGU Translation |
| 11 | 22 | 238 | 259 UCUUCCCUAC:: : : : :GGAAUGCGA Translation |
| 12 | 22 | 238 | 259 UCUUCCCUAC:: : : : :GGAAUGCGA Translation |
| 13 | 22 | 1714 | 1735 UCUUCCCUAC:: : : : :GGGAUGAGA Cleavage |
| 14 | 22 | 1714 | 1735 UCUUCCCUAC:: : : : :GGGAUGAGA Cleavage |
| 15 | 22 | 318 | 339 UCUUCCCAAL : : : : :AGGGUGGGU Cleavage |
| 16 | 22 | 394 | 415 UCUUCCCAAL : : : : :AGGGUGGGU Cleavage |
| 17 | 22 | 394 | 415 UCUUCCCAAL : : : : :AGGGUGGGU Cleavage |
| 18 | 22 | 394 | 415 UCUUCCCAAL : : : : :AGGGUGGGU Cleavage |
| 19 | 22 | 394 | 415 UCUUCCCAAL : : : : :AGGGUGGGU Cleavage |
| 20 | 22 | 334 | 355 UCUUCCCUAC : : : : :CGUUUGGGG Translation |
| 21 | 22 | 334 | 355 UCUUCCCUAC : : : : :CGUUUGGGG Translation |
| 22 | 22 | 334 | 355 UCUUCCCUAC : : : : :CGUUUGGGG Translation |
| 23 | 22 | 838 | 859 UCUUCCCAAL:: : : : :GGAAUCGGG Cleavage |
| 24 | 22 | 321 | 342 UCUUCCCUAC : : : : :ACUGUGGGA Cleavage |
| 25 | 22 | 321 | 342 UCUUCCCUAC : : : : :ACUGUGGGA Cleavage |
| 26 | 22 | 321 | 342 UCUUCCCUAC : : : : :ACUGUGGGA Cleavage |
| 27 | 22 | 383 | 404 UCUUCCCUAC : : : : :ACUGUGGGA Cleavage |
| 28 | 22 | 434 | 455 UCUUCCCUAC : : : : :ACUGUGGGA Cleavage |
| 29 | 22 | 434 | 455 UCUUCCCUAC : : : : :ACUGUGGGA Cleavage |
| 30 | 22 | 434 | 455 UCUUCCCUAC : : : : :ACUGUGGGA Cleavage |
| 31 | 22 | 434 | 455 UCUUCCCUAC : : : : :ACUGUGGGA Cleavage |
| 32 | 22 | 434 | 455 UCUUCCCUAC : : : : :ACUGUGGGA Cleavage |
| 33 | 22 | 434 | 455 UCUUCCCUAC : : : : :ACUGUGGGA Cleavage |
| 34 | 22 | 434 | 455 UCUUCCCUAC : : : : :ACUGUGGGA Cleavage |
| 35 | 22 | 383 | 404 UCUUCCCUAC : : : : :ACUGUGGGA Cleavage |
| 36 | 22 | 434 | 455 UCUUCCCUAC : : : : :ACUGUGGGA Cleavage |
| 37 | 22 | 434 | 455 UCUUCCCUAC : : : : :ACUGUGGGA Cleavage |
| 38 | 22 | 434 | 455 UCUUCCCUAC : : : : :ACUGUGGGA Cleavage |
| 39 | 22 | 434 | 455 UCUUCCCUAC : : : : :ACUGUGGGA Cleavage |
| 40 | 22 | 434 | 455 UCUUCCCUAC : : : : :ACUGUGGGA Cleavage |
| 41 | 22 | 1054 | 1075 UCUUCCCUAC:: : : : :GGUGAGAGU Cleavage |
| 42 | 22 | 1360 | 1381 UCUUCCCUAC:: : : : :GGUGAGAGU Cleavage |
| 43 | 22 | 1452 | 1473 UCUUCCCUAC:: : : : :GGUGAGAGU Cleavage |
| 44 | 22 | 1054 | 1075 UCUUCCCUAC:: : : : :GGUGAGAGU Cleavage |
| 45 | 22 | 1360 | 1381 UCUUCCCUAC:: : : : :GGUGAGAGU Cleavage |
| 46 | 22 | 1452 | 1473 UCUUCCCUAC:: : : : :GGUGAGAGU Cleavage |
| 47 | 22 | 923 | 944 UCUUCCCAAL:: : : : :GGAGUGGUC Cleavage |
| 48 | 22 | 945 | 966 UCUUCCCAAL:: : : : :GGAGUGGUC Cleavage |
| 49 | 22 | 5224 | 5245 UCUUCCCAAL : : : : :GAAGUGCGU Cleavage |
| 50 | 22 | 5224 | 5245 UCUUCCCAAL : : : : :GAAGUGCGU Cleavage |
| 51 | 22 | 5220 | 5241 UCUUCCCAAL : : : : :GAAGUGCGU Cleavage |
| 52 | 22 | 1887 | 1908 UCUUCCCAAL : : : : :AAGAUGGGC Cleavage |
| 53 | 22 | 1887 | 1908 UCUUCCCAAL : : : : :AAGAUGGGC Cleavage |
| 54 | 22 | 1887 | 1908 UCUUCCCAAL : : : : :AAGAUGGGC Cleavage |
| 55 | 22 | 3331 | 3352 UCUUCCCAAL : : : : :AAGAUGGGC Cleavage |
| 56 | 22 | 623 | 644 UCUUCCCAAL:: : : : :GGAAUGGUU Cleavage |
| 57 | 22 | 733 | 754 UCUUCCCAAL:: : : : :GGAAGGGGU Translation |
| 58 | | | |
| 59 | | | |
| 60 | | | |

| | | | |
|----|----|------|--|
| 1 | | | |
| 2 | 22 | 1265 | 1286 UCUUCCCAAL:::: ::::: ::::: :::::GGAAGGGGU Translation |
| 3 | 22 | 1508 | 1528 UCUUCCCUAC ::::: ::::: :::::UGUAUGCGA\ Cleavage |
| 4 | 22 | 1508 | 1528 UCUUCCCUAC ::::: ::::: :::::UGUAUGCGA\ Cleavage |
| 5 | | | |
| 6 | 22 | 11 | 30 UCUUCCCUAC::::: ::::: :::::GGUAUGG-AC\ Cleavage |
| 7 | 22 | 11 | 30 UCUUCCCUAC::::: ::::: :::::GGUAUGG-AC\ Cleavage |
| 8 | | | |
| 9 | 22 | 519 | 540 UCUUCCCAAL::: : : ::::: GGGGUUGGG Cleavage |
| 10 | 22 | 525 | 546 UCUUCCCUAC ::::: ::::: ::::: UUCAUGGGA\ Cleavage |
| 11 | 22 | 525 | 546 UCUUCCCUAC ::::: ::::: ::::: UUCAUGGGA\ Cleavage |
| 12 | | | |
| 13 | 22 | 81 | 102 UCUUCCCAAL ::::: : : ::::: UGAAUGGGG Cleavage |
| 14 | 22 | 46 | 67 UCUUCCCUAC ::::: ::::: ::::: CUAGUGGGA\ Cleavage |
| 15 | 22 | 46 | 67 UCUUCCCUAC ::::: ::::: ::::: CUAGUGGGA\ Cleavage |
| 16 | | | |
| 17 | 22 | 81 | 102 UCUUCCCAAL ::::: ::::: :::::UGAGUGGGG Cleavage |
| 18 | 22 | 845 | 866 UCUUCCCUAC ::::: ::::: :::::AGUGUGGGA Translation |
| 19 | 22 | 845 | 866 UCUUCCCUAC ::::: ::::: :::::AGUGUGGGA Translation |
| 20 | | | |
| 21 | 22 | 419 | 440 UCUUCCCAAL::: : : ::::: GGAGUUGGG Cleavage |
| 22 | 22 | 1622 | 1643 UCUUCCCAAL::: : : ::::: GGAAGGGU Cleavage |
| 23 | 22 | 1951 | 1974 UCUUCCCAAL::::: ::::: :::::GGAUGGGA\ Cleavage |
| 24 | 22 | 716 | 737 UCUUCCCAAL ::::: ::::: ::::: CCAGUGGGA\ Cleavage |
| 25 | | | |
| 26 | 22 | 1608 | 1629 UCUUCCCUAC ::::: ::::: :::::AGUAUUGGG Cleavage |
| 27 | 22 | 643 | 664 UCUUCCCUAC : ::::: : : :::::UGAGUGGGA Translation |
| 28 | 22 | 1537 | 1558 UCUUCCCUAC ::::: ::::: :::::AGUAUUGGG Cleavage |
| 29 | | | |
| 30 | 22 | 688 | 709 UCUUCCCUAC : ::::: : : :::::UGAGUGGGA Translation |
| 31 | 22 | 1608 | 1629 UCUUCCCUAC ::::: ::::: :::::AGUAUUGGG Cleavage |
| 32 | 22 | 643 | 664 UCUUCCCUAC : ::::: : : :::::UGAGUGGGA Translation |
| 33 | | | |
| 34 | 22 | 1537 | 1558 UCUUCCCUAC ::::: ::::: :::::AGUAUUGGG Cleavage |
| 35 | 22 | 688 | 709 UCUUCCCUAC : ::::: : : :::::UGAGUGGGA Translation |
| 36 | 22 | 3093 | 3114 UCUUCCCAAL::: : : :::::GGAGUUAGU Cleavage |
| 37 | 22 | 658 | 679 UCUUCCCAAL::::: ::::: :::::GGAUGGGA\ Cleavage |
| 38 | | | |
| 39 | 22 | 716 | 737 UCUUCCCAAL::::: ::::: :::::GGAUGGGA\ Cleavage |
| 40 | 22 | 601 | 622 UCUUCCCAAL::::: ::::: :::::GGAUGGGA\ Cleavage |
| 41 | | | |
| 42 | 22 | 604 | 625 UCUUCCCAAL::::: ::::: :::::GGAUGGGA\ Cleavage |
| 43 | 22 | 752 | 773 UCUUCCCAAL::::: ::::: :::::GGAUGGGA\ Cleavage |
| 44 | | | |
| 45 | | | |
| 46 | | | |
| 47 | | | |
| 48 | | | |
| 49 | | | |
| 50 | | | |
| 51 | | | |
| 52 | | | |
| 53 | | | |
| 54 | | | |
| 55 | | | |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

| | Target_Desc. | Multiplicity | Target_Acc. | ID | locusName | Pfam |
|----|--------------|--------------|--------------------|------------------|--------------|--------------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | pacid=371636 | 1 | Phvul.004G048000.1 | Phvul.004G048000 | Phvul.004G04 | PF00931 |
| 4 | pacid=371689 | 1 | Phvul.001G224800.1 | Phvul.001G224800 | Phvul.001G22 | PF01344,PF13 |
| 5 | pacid=371689 | 1 | Phvul.001G224800.2 | Phvul.001G224800 | Phvul.001G22 | PF01344,PF13 |
| 6 | pacid=371689 | 1 | Phvul.001G224800.1 | Phvul.001G224800 | Phvul.001G22 | PF01344,PF13 |
| 7 | pacid=371689 | 1 | Phvul.001G224800.2 | Phvul.001G224800 | Phvul.001G22 | PF01344,PF13 |
| 8 | pacid=371689 | 1 | Phvul.001G224800.2 | Phvul.001G224800 | Phvul.001G22 | PF01344,PF13 |
| 9 | pacid=371656 | 1 | Phvul.007G201700.1 | Phvul.007G201700 | Phvul.007G20 | PF01344,PF13 |
| 10 | pacid=371656 | 1 | Phvul.007G201700.1 | Phvul.007G201700 | Phvul.007G20 | PF01344,PF13 |
| 11 | pacid=371606 | 1 | Phvul.008G061300.2 | Phvul.008G061300 | Phvul.008G06 | PF13855,PF00 |
| 12 | pacid=371606 | 1 | Phvul.008G061300.1 | Phvul.008G061300 | Phvul.008G06 | PF13855,PF00 |
| 13 | pacid=371606 | 1 | Phvul.008G061300.2 | Phvul.008G061300 | Phvul.008G06 | PF13855,PF00 |
| 14 | pacid=371606 | 1 | Phvul.008G061300.1 | Phvul.008G061300 | Phvul.008G06 | PF13855,PF00 |
| 15 | pacid=371606 | 1 | Phvul.008G061300.2 | Phvul.008G061300 | Phvul.008G06 | PF13855,PF00 |
| 16 | pacid=371606 | 1 | Phvul.008G061300.1 | Phvul.008G061300 | Phvul.008G06 | PF13855,PF00 |
| 17 | pacid=371779 | 1 | Phvul.002G079200.1 | Phvul.002G079200 | Phvul.002G07 | PF05729,PF13 |
| 18 | pacid=371683 | 1 | Phvul.001G217600.1 | Phvul.001G217600 | Phvul.001G21 | 0 |
| 19 | pacid=371775 | 1 | Phvul.002G001500.1 | Phvul.002G001500 | Phvul.002G00 | PF13919,PF00 |
| 20 | pacid=371775 | 1 | Phvul.002G001500.1 | Phvul.002G001500 | Phvul.002G00 | PF13919,PF00 |
| 21 | pacid=371775 | 1 | Phvul.002G001500.1 | Phvul.002G001500 | Phvul.002G00 | PF13919,PF00 |
| 22 | pacid=371469 | 1 | Phvul.003G072500.1 | Phvul.003G072500 | Phvul.003G07 | PF13676,PF00 |
| 23 | pacid=371456 | 2 | Phvul.003G244225.3 | Phvul.003G244225 | Phvul.003G24 | 0 |
| 24 | pacid=371456 | 2 | Phvul.003G244225.2 | Phvul.003G244225 | Phvul.003G24 | 0 |
| 25 | pacid=371456 | 2 | Phvul.003G244225.1 | Phvul.003G244225 | Phvul.003G24 | 0 |
| 26 | pacid=371456 | 2 | Phvul.003G244225.1 | Phvul.003G244225 | Phvul.003G24 | 0 |
| 27 | pacid=371634 | 1 | Phvul.004G137300.1 | Phvul.004G137300 | Phvul.004G13 | PF13676,PF00 |
| 28 | pacid=371543 | 1 | Phvul.005G029400.1 | Phvul.005G029400 | Phvul.005G02 | PF03145 |
| 29 | pacid=371543 | 1 | Phvul.005G029400.3 | Phvul.005G029400 | Phvul.005G02 | PF03145 |
| 30 | pacid=371543 | 1 | Phvul.005G029400.2 | Phvul.005G029400 | Phvul.005G02 | PF03145 |
| 31 | pacid=371662 | 1 | Phvul.007G210600.1 | Phvul.007G210600 | Phvul.007G21 | PF03110 |
| 32 | pacid=371662 | 1 | Phvul.007G210600.1 | Phvul.007G210600 | Phvul.007G21 | PF03110 |
| 33 | pacid=371662 | 1 | Phvul.007G210600.1 | Phvul.007G210600 | Phvul.007G21 | PF03110 |
| 34 | pacid=371662 | 1 | Phvul.007G210600.1 | Phvul.007G210600 | Phvul.007G21 | PF03110 |
| 35 | pacid=371605 | 1 | Phvul.008G055500.1 | Phvul.008G055500 | Phvul.008G05 | PF00005 |
| 36 | pacid=371577 | 1 | Phvul.008G280900.1 | Phvul.008G280900 | Phvul.008G28 | PF01594 |
| 37 | pacid=371577 | 1 | Phvul.008G280900.1 | Phvul.008G280900 | Phvul.008G28 | PF01594 |
| 38 | pacid=371577 | 1 | Phvul.008G280900.1 | Phvul.008G280900 | Phvul.008G28 | PF01594 |
| 39 | pacid=371428 | 1 | Phvul.010G064700.1 | Phvul.010G064700 | Phvul.010G06 | PF00931 |
| 40 | pacid=371428 | 1 | Phvul.010G064700.1 | Phvul.010G064700 | Phvul.010G06 | PF00931 |
| 41 | pacid=371426 | 1 | Phvul.010G136700.1 | Phvul.010G136700 | Phvul.010G13 | PF07725,PF13 |
| 42 | pacid=371426 | 1 | Phvul.010G136700.1 | Phvul.010G136700 | Phvul.010G13 | PF07725,PF13 |
| 43 | pacid=371549 | 1 | Phvul.011G149100.7 | Phvul.011G149100 | Phvul.011G14 | 0 |
| 44 | pacid=371549 | 1 | Phvul.011G149100.6 | Phvul.011G149100 | Phvul.011G14 | 0 |
| 45 | pacid=371549 | 1 | Phvul.011G149100.5 | Phvul.011G149100 | Phvul.011G14 | 0 |
| 46 | pacid=371549 | 1 | Phvul.011G149100.5 | Phvul.011G149100 | Phvul.011G14 | 0 |
| 47 | pacid=371549 | 1 | Phvul.011G149100.2 | Phvul.011G149100 | Phvul.011G14 | 0 |
| 48 | pacid=371549 | 1 | Phvul.011G149100.1 | Phvul.011G149100 | Phvul.011G14 | 0 |
| 49 | pacid=371549 | 1 | Phvul.011G149100.1 | Phvul.011G149100 | Phvul.011G14 | 0 |
| 50 | pacid=371549 | 1 | Phvul.011G149100.4 | Phvul.011G149100 | Phvul.011G14 | 0 |
| 51 | pacid=371549 | 1 | Phvul.011G149100.3 | Phvul.011G149100 | Phvul.011G14 | 0 |
| 52 | pacid=371549 | 1 | Phvul.011G149100.3 | Phvul.011G149100 | Phvul.011G14 | 0 |
| 53 | pacid=371569 | 1 | Phvul.011G166100.1 | Phvul.011G166100 | Phvul.011G16 | PF00931 |
| 54 | pacid=371711 | 1 | Phvul.001G128200.2 | Phvul.001G128200 | Phvul.001G12 | PF07725,PF13 |
| 55 | pacid=371696 | 1 | Phvul.001G134000.1 | Phvul.001G134000 | Phvul.001G13 | PF13855,PF00 |
| 56 | pacid=371696 | 1 | Phvul.001G134000.1 | Phvul.001G134000 | Phvul.001G13 | PF13855,PF00 |
| 57 | pacid=371696 | 1 | Phvul.001G134000.1 | Phvul.001G134000 | Phvul.001G13 | PF13855,PF00 |
| 58 | pacid=371708 | 1 | Phvul.001G243900.1 | Phvul.001G243900 | Phvul.001G24 | PF02861,PF07 |
| 59 | pacid=371708 | 1 | Phvul.001G243900.1 | Phvul.001G243900 | Phvul.001G24 | PF02861,PF07 |
| 60 | pacid=371772 | 1 | Phvul.002G057300.2 | Phvul.002G057300 | Phvul.002G05 | PF08458,PF05 |
| 61 | pacid=371772 | 1 | Phvul.002G057300.1 | Phvul.002G057300 | Phvul.002G05 | PF08458,PF05 |

| | | | | | |
|----|--------------|----------------------|------------------|---------------------------|---|
| 1 | | | | | |
| 2 | pacid=371769 | 1 Phvul.002G122200.1 | Phvul.002G122200 | Phvul.002G12 PF00067 | |
| 3 | pacid=371750 | 1 Phvul.002G187600.1 | Phvul.002G187600 | Phvul.002G18 | 0 |
| 4 | pacid=371773 | 1 Phvul.002G261500.1 | Phvul.002G261500 | Phvul.002G26 PF00076 | |
| 5 | pacid=371773 | 1 Phvul.002G261500.1 | Phvul.002G261500 | Phvul.002G26 PF00076 | |
| 6 | pacid=371475 | 1 Phvul.003G101200.1 | Phvul.003G101200 | Phvul.003G10 PF04535 | |
| 7 | pacid=371475 | 1 Phvul.003G101200.1 | Phvul.003G101200 | Phvul.003G10 PF04535 | |
| 8 | pacid=371460 | 1 Phvul.003G202900.1 | Phvul.003G202900 | Phvul.003G20 PF02657,PF02 | |
| 9 | pacid=371460 | 1 Phvul.003G202900.1 | Phvul.003G202900 | Phvul.003G20 PF02657,PF02 | |
| 10 | pacid=371627 | 1 Phvul.004G026200.1 | Phvul.004G026200 | Phvul.004G02 PF00505,PF08 | |
| 11 | pacid=371631 | 1 Phvul.004G140400.1 | Phvul.004G140400 | Phvul.004G14 PF05729,PF13 | |
| 12 | pacid=371631 | 1 Phvul.004G140400.1 | Phvul.004G140400 | Phvul.004G14 PF05729,PF13 | |
| 13 | pacid=371524 | 1 Phvul.005G038200.1 | Phvul.005G038200 | Phvul.005G03 PF00590 | |
| 14 | pacid=371524 | 1 Phvul.005G038200.1 | Phvul.005G038200 | Phvul.005G03 PF00590 | |
| 15 | pacid=371534 | 1 Phvul.005G087100.1 | Phvul.005G087100 | Phvul.005G08 PF13855,PF00 | |
| 16 | pacid=371534 | 1 Phvul.005G087100.1 | Phvul.005G087100 | Phvul.005G08 PF13855,PF00 | |
| 17 | pacid=371730 | 1 Phvul.006G102700.1 | Phvul.006G102700 | Phvul.006G10 PF11721,PF00 | |
| 18 | pacid=371579 | 1 Phvul.008G072300.2 | Phvul.008G072300 | Phvul.008G07 PF00931 | |
| 19 | pacid=371579 | 1 Phvul.008G072300.1 | Phvul.008G072300 | Phvul.008G07 PF00931 | |
| 20 | pacid=371579 | 1 Phvul.008G072300.2 | Phvul.008G072300 | Phvul.008G07 PF00931 | |
| 21 | pacid=371579 | 1 Phvul.008G072300.1 | Phvul.008G072300 | Phvul.008G07 PF00931 | |
| 22 | pacid=371579 | 1 Phvul.008G202300.1 | Phvul.008G202300 | Phvul.008G20 PF04031 | |
| 23 | pacid=371595 | 1 Phvul.008G259600.2 | Phvul.008G259600 | Phvul.008G25 PF02705 | |
| 24 | pacid=371595 | 1 Phvul.008G259600.1 | Phvul.008G259600 | Phvul.008G25 PF02705 | |
| 25 | pacid=371595 | 1 Phvul.008G259600.2 | Phvul.008G259600 | Phvul.008G25 PF02705 | |
| 26 | pacid=371595 | 1 Phvul.008G259600.1 | Phvul.008G259600 | Phvul.008G25 PF02705 | |
| 27 | pacid=371424 | 1 Phvul.010G131650.1 | Phvul.010G131650 | Phvul.010G13 PF07725,PF13 | |
| 28 | pacid=371433 | 1 Phvul.010G132333.1 | Phvul.010G132333 | Phvul.010G13 PF07725 | |
| 29 | pacid=371436 | 1 Phvul.010G136800.1 | Phvul.010G136800 | Phvul.010G13 PF07725,PF13 | |
| 30 | pacid=371426 | 1 Phvul.010G151400.6 | Phvul.010G151400 | Phvul.010G15 PF16994 | |
| 31 | pacid=371426 | 1 Phvul.010G151400.4 | Phvul.010G151400 | Phvul.010G15 PF16994 | |
| 32 | pacid=371426 | 1 Phvul.010G151400.6 | Phvul.010G151400 | Phvul.010G15 PF16994 | |
| 33 | pacid=371426 | 1 Phvul.010G151400.4 | Phvul.010G151400 | Phvul.010G15 PF16994 | |
| 34 | pacid=371547 | 1 Phvul.011G140300.1 | Phvul.011G140300 | Phvul.011G14 PF07725,PF13 | |
| 35 | pacid=371561 | 1 Phvul.011G140400.1 | Phvul.011G140400 | Phvul.011G14 PF13676,PF13 | |
| 36 | pacid=371574 | 1 Phvul.011G151300.1 | Phvul.011G151300 | Phvul.011G15 PF00931 | |
| 37 | pacid=371561 | 1 Phvul.011G181700.1 | Phvul.011G181700 | Phvul.011G18 PF00931 | |
| 38 | pacid=371561 | 1 Phvul.011G181700.1 | Phvul.011G181700 | Phvul.011G18 PF00931 | |
| 39 | pacid=371570 | 1 Phvul.011G192400.1 | Phvul.011G192400 | Phvul.011G19 PF00931 | |
| 40 | pacid=371555 | 1 Phvul.011G192600.1 | Phvul.011G192600 | Phvul.011G19 PF13855,PF00 | |
| 41 | pacid=371558 | 1 Phvul.011G193100.1 | Phvul.011G193100 | Phvul.011G19 PF00931 | |
| 42 | pacid=371551 | 1 Phvul.011G193500.1 | Phvul.011G193500 | Phvul.011G19 PF13855,PF00 | |
| 43 | pacid=371558 | 1 Phvul.011G193600.1 | Phvul.011G193600 | Phvul.011G19 PF13855,PF00 | |
| 44 | pacid=371550 | 1 Phvul.011G194800.1 | Phvul.011G194800 | Phvul.011G19 PF00931 | |
| 45 | pacid=371546 | 1 Phvul.011G194900.1 | Phvul.011G194900 | Phvul.011G19 PF00931 | |
| 46 | pacid=371570 | 1 Phvul.011G195000.1 | Phvul.011G195000 | Phvul.011G19 PF00931 | |
| 47 | pacid=371563 | 1 Phvul.011G195200.1 | Phvul.011G195200 | Phvul.011G19 PF00931 | |

| | | | | |
|----|--------------|----------------------|------------------|----------------------------|
| 1 | | | | |
| 2 | pacid=371572 | 1 Phvul.011G195400.1 | Phvul.011G195400 | Phvul.011G19 PF00931 |
| 3 | pacid=371554 | 1 Phvul.011G195500.1 | Phvul.011G195500 | Phvul.011G19 PF00931 |
| 4 | pacid=371565 | 1 Phvul.011G196000.1 | Phvul.011G196000 | Phvul.011G19PF13855,PF00 |
| 5 | | | | |
| 6 | pacid=371571 | 1 Phvul.011G196066.1 | Phvul.011G196066 | Phvul.011G19 PF00931 |
| 7 | pacid=371573 | 1 Phvul.011G200820.1 | Phvul.011G200820 | Phvul.011G20 PF00931 |
| 8 | pacid=371573 | 1 Phvul.011G200820.1 | Phvul.011G200820 | Phvul.011G20 PF00931 |
| 9 | | | | |
| 10 | pacid=371560 | 1 Phvul.011G202100.1 | Phvul.011G202100 | Phvul.011G20 PF00931 |
| 11 | pacid=371560 | 1 Phvul.011G202100.1 | Phvul.011G202100 | Phvul.011G20 PF00931 |
| 12 | pacid=371555 | 1 Phvul.011G202300.1 | Phvul.011G202300 | Phvul.011G20 PF00931 |
| 13 | | | | |
| 14 | pacid=371555 | 1 Phvul.011G202300.1 | Phvul.011G202300 | Phvul.011G20 PF00931 |
| 15 | pacid=371563 | 1 Phvul.011G203100.1 | Phvul.011G203100 | Phvul.011G20 PF00931 |
| 16 | pacid=371563 | 1 Phvul.011G203100.1 | Phvul.011G203100 | Phvul.011G20 PF00931 |
| 17 | | | | |
| 18 | pacid=371575 | 1 Phvul.L002337.2 | Phvul.L002337 | Phvul.L002337:PF00107,PF08 |
| 19 | pacid=371575 | 1 Phvul.L002337.1 | Phvul.L002337 | Phvul.L002337:PF00107,PF08 |
| 20 | pacid=371575 | 1 Phvul.L002337.2 | Phvul.L002337 | Phvul.L002337:PF00107,PF08 |
| 21 | | | | |
| 22 | pacid=371575 | 1 Phvul.L002337.1 | Phvul.L002337 | Phvul.L002337:PF00107,PF08 |
| 23 | pacid=371699 | 1 Phvul.001G015600.1 | Phvul.001G015600 | Phvul.001G01 PF01553 |
| 24 | pacid=371699 | 1 Phvul.001G015600.2 | Phvul.001G015600 | Phvul.001G01 PF01553 |
| 25 | | | | |
| 26 | pacid=371699 | 1 Phvul.001G015600.1 | Phvul.001G015600 | Phvul.001G01 PF01553 |
| 27 | pacid=371699 | 1 Phvul.001G015600.2 | Phvul.001G015600 | Phvul.001G01 PF01553 |
| 28 | pacid=371677 | 1 Phvul.001G085500.2 | Phvul.001G085500 | Phvul.001G08 PF00010 |
| 29 | pacid=371677 | 1 Phvul.001G085500.1 | Phvul.001G085500 | Phvul.001G08 PF00010 |
| 30 | | | | |
| 31 | pacid=371685 | 1 Phvul.001G232600.1 | Phvul.001G232600 | Phvul.001G23 PF03330,PF01 |
| 32 | pacid=371685 | 1 Phvul.001G232600.1 | Phvul.001G232600 | Phvul.001G23 PF03330,PF01 |
| 33 | pacid=371756 | 1 Phvul.002G041400.4 | Phvul.002G041400 | Phvul.002G04 PF04640 |
| 34 | | | | |
| 35 | pacid=371756 | 1 Phvul.002G041400.1 | Phvul.002G041400 | Phvul.002G04 PF04640 |
| 36 | pacid=371756 | 1 Phvul.002G041400.2 | Phvul.002G041400 | Phvul.002G04 PF04640 |
| 37 | pacid=371756 | 1 Phvul.002G041400.3 | Phvul.002G041400 | Phvul.002G04 PF04640 |
| 38 | | | | |
| 39 | pacid=371778 | 1 Phvul.002G298800.1 | Phvul.002G298800 | Phvul.002G29 PF01764 |
| 40 | pacid=371450 | 1 Phvul.003G010900.1 | Phvul.003G010900 | Phvul.003G01 PF00503 |
| 41 | pacid=371450 | 1 Phvul.003G010900.1 | Phvul.003G010900 | Phvul.003G01 PF00503 |
| 42 | | | | |
| 43 | pacid=371453 | 1 Phvul.003G195800.2 | Phvul.003G195800 | Phvul.003G19PF01535,PF13 |
| 44 | pacid=371453 | 1 Phvul.003G195800.1 | Phvul.003G195800 | Phvul.003G19PF01535,PF13 |
| 45 | pacid=371455 | 1 Phvul.003G252400.1 | Phvul.003G252400 | Phvul.003G25 PF12171 |
| 46 | | | | |
| 47 | pacid=371455 | 1 Phvul.003G252400.1 | Phvul.003G252400 | Phvul.003G25 PF12171 |
| 48 | pacid=371465 | 1 Phvul.003G295800.4 | Phvul.003G295800 | Phvul.003G29PF12624,PF09 |
| 49 | pacid=371465 | 1 Phvul.003G295800.3 | Phvul.003G295800 | Phvul.003G29PF12624,PF09 |
| 50 | | | | |
| 51 | pacid=371465 | 1 Phvul.003G295800.2 | Phvul.003G295800 | Phvul.003G29PF12624,PF09 |
| 52 | pacid=371636 | 1 Phvul.004G032300.4 | Phvul.004G032300 | Phvul.004G03 PF14008,PF16 |
| 53 | pacid=371636 | 1 Phvul.004G032300.2 | Phvul.004G032300 | Phvul.004G03 PF14008,PF16 |
| 54 | | | | |
| 55 | pacid=371636 | 1 Phvul.004G032300.3 | Phvul.004G032300 | Phvul.004G03 PF14008,PF16 |
| 56 | pacid=371636 | 1 Phvul.004G032300.1 | Phvul.004G032300 | Phvul.004G03 PF14008,PF16 |
| 57 | pacid=371636 | 1 Phvul.004G032300.4 | Phvul.004G032300 | Phvul.004G03 PF14008,PF16 |
| 58 | pacid=371636 | 1 Phvul.004G032300.2 | Phvul.004G032300 | Phvul.004G03 PF14008,PF16 |
| 59 | pacid=371636 | 1 Phvul.004G032300.3 | Phvul.004G032300 | Phvul.004G03 PF14008,PF16 |
| 60 | pacid=371636 | 1 Phvul.004G032300.1 | Phvul.004G032300 | Phvul.004G03 PF14008,PF16 |

| | | | | | |
|----|--------------|----------------------|------------------|--------------|--------------|
| 1 | | | | | |
| 2 | pacid=371636 | 1 Phvul.004G048000.1 | Phvul.004G048000 | Phvul.004G04 | PF00931 |
| 3 | pacid=371636 | 1 Phvul.004G048000.1 | Phvul.004G048000 | Phvul.004G04 | PF00931 |
| 4 | pacid=371625 | 1 Phvul.004G106800.2 | Phvul.004G106800 | Phvul.004G10 | PF01656 |
| 5 | pacid=371625 | 1 Phvul.004G106800.2 | Phvul.004G106800 | Phvul.004G10 | PF01656 |
| 6 | pacid=371628 | 1 Phvul.004G133100.1 | Phvul.004G133100 | Phvul.004G13 | PF12695 |
| 7 | pacid=371545 | 1 Phvul.005G165800.1 | Phvul.005G165800 | Phvul.005G16 | PF01535,PF12 |
| 8 | pacid=371545 | 1 Phvul.005G165800.1 | Phvul.005G165800 | Phvul.005G16 | PF01535,PF12 |
| 9 | pacid=371714 | 1 Phvul.006G066800.1 | Phvul.006G066800 | Phvul.006G06 | PF00931 |
| 10 | pacid=371738 | 1 Phvul.006G086800.1 | Phvul.006G086800 | Phvul.006G08 | PF03330,PF01 |
| 11 | pacid=371723 | 1 Phvul.006G148800.1 | Phvul.006G148800 | Phvul.006G14 | 0 |
| 12 | pacid=371734 | 1 Phvul.006G180900.1 | Phvul.006G180900 | Phvul.006G18 | PF08100,PF00 |
| 13 | pacid=371734 | 1 Phvul.006G180900.1 | Phvul.006G180900 | Phvul.006G18 | PF08100,PF00 |
| 14 | pacid=371673 | 1 Phvul.007G027400.1 | Phvul.007G027400 | Phvul.007G02 | 0 |
| 15 | pacid=371669 | 1 Phvul.007G096800.1 | Phvul.007G096800 | Phvul.007G09 | PF01656 |
| 16 | pacid=371591 | 1 Phvul.008G158100.1 | Phvul.008G158100 | Phvul.008G15 | PF08263,PF13 |
| 17 | pacid=371493 | 1 Phvul.009G020000.1 | Phvul.009G020000 | Phvul.009G02 | PF08241,PF08 |
| 18 | pacid=371493 | 1 Phvul.009G020000.1 | Phvul.009G020000 | Phvul.009G02 | PF08241,PF08 |
| 19 | pacid=371498 | 1 Phvul.009G065500.1 | Phvul.009G065500 | Phvul.009G06 | PF00170 |
| 20 | pacid=371498 | 1 Phvul.009G065500.2 | Phvul.009G065500 | Phvul.009G06 | PF00170 |
| 21 | pacid=371498 | 1 Phvul.009G065500.1 | Phvul.009G065500 | Phvul.009G06 | PF00170 |
| 22 | pacid=371498 | 1 Phvul.009G065500.2 | Phvul.009G065500 | Phvul.009G06 | PF00170 |
| 23 | pacid=371487 | 1 Phvul.009G213300.1 | Phvul.009G213300 | Phvul.009G21 | PF13812,PF01 |
| 24 | pacid=371497 | 1 Phvul.009G226300.2 | Phvul.009G226300 | Phvul.009G22 | PF14416,PF13 |
| 25 | pacid=371497 | 1 Phvul.009G226300.1 | Phvul.009G226300 | Phvul.009G22 | PF14416,PF13 |
| 26 | pacid=371497 | 1 Phvul.009G226300.2 | Phvul.009G226300 | Phvul.009G22 | PF14416,PF13 |
| 27 | pacid=371497 | 1 Phvul.009G226300.1 | Phvul.009G226300 | Phvul.009G22 | PF14416,PF13 |
| 28 | pacid=371517 | 1 Phvul.009G233700.1 | Phvul.009G233700 | Phvul.009G23 | PF00931 |
| 29 | pacid=371517 | 1 Phvul.009G233700.1 | Phvul.009G233700 | Phvul.009G23 | PF00931 |
| 30 | pacid=371517 | 1 Phvul.009G233700.1 | Phvul.009G233700 | Phvul.009G23 | PF00931 |
| 31 | pacid=371439 | 1 Phvul.010G008700.2 | Phvul.010G008700 | Phvul.010G00 | PF00931 |
| 32 | pacid=371439 | 1 Phvul.010G008700.1 | Phvul.010G008700 | Phvul.010G00 | PF00931 |
| 33 | pacid=371428 | 1 Phvul.010G056500.1 | Phvul.010G056500 | Phvul.010G05 | PF13041 |
| 34 | pacid=371428 | 1 Phvul.010G056500.1 | Phvul.010G056500 | Phvul.010G05 | PF13041 |
| 35 | pacid=371423 | 1 Phvul.010G063100.1 | Phvul.010G063100 | Phvul.010G06 | PF00931 |
| 36 | pacid=371428 | 1 Phvul.010G070584.1 | Phvul.010G070584 | Phvul.010G07 | PF00890,PF05 |
| 37 | pacid=371439 | 1 Phvul.010G146900.6 | Phvul.010G146900 | Phvul.010G14 | PF07766 |
| 38 | pacid=371439 | 1 Phvul.010G146900.2 | Phvul.010G146900 | Phvul.010G14 | PF07766 |
| 39 | pacid=371439 | 1 Phvul.010G146900.3 | Phvul.010G146900 | Phvul.010G14 | PF07766 |
| 40 | pacid=371438 | 1 Phvul.010G146900.1 | Phvul.010G146900 | Phvul.010G14 | PF07766 |
| 41 | pacid=371438 | 1 Phvul.010G146900.4 | Phvul.010G146900 | Phvul.010G14 | PF07766 |
| 42 | pacid=371439 | 1 Phvul.010G146900.5 | Phvul.010G146900 | Phvul.010G14 | PF07766 |
| 43 | pacid=371563 | 1 Phvul.011G014500.2 | Phvul.011G014500 | Phvul.011G01 | PF00931 |
| 44 | pacid=371563 | 1 Phvul.011G014500.2 | Phvul.011G014500 | Phvul.011G01 | PF00931 |
| 45 | pacid=371563 | 1 Phvul.011G014500.2 | Phvul.011G014500 | Phvul.011G01 | PF00931 |
| 46 | pacid=371573 | 1 Phvul.011G082700.3 | Phvul.011G082700 | Phvul.011G08 | 0 |
| 47 | pacid=371573 | 1 Phvul.011G082700.2 | Phvul.011G082700 | Phvul.011G08 | 0 |

| | | | | | |
|----|--------------|----------------------|------------------|---------------------------|---|
| 1 | | | | | |
| 2 | pacid=371573 | 1 Phvul.011G082700.1 | Phvul.011G082700 | Phvul.011G08 | 0 |
| 3 | pacid=371549 | 1 Phvul.011G149400.1 | Phvul.011G149400 | Phvul.011G14 PF00931 | |
| 4 | pacid=371549 | 1 Phvul.011G149400.1 | Phvul.011G149400 | Phvul.011G14 PF00931 | |
| 5 | pacid=371566 | 1 Phvul.011G181500.1 | Phvul.011G181500 | Phvul.011G18 PF00931 | |
| 6 | pacid=371546 | 1 Phvul.011G182900.1 | Phvul.011G182900 | Phvul.011G18 PF00407 | |
| 7 | pacid=371546 | 1 Phvul.011G182900.1 | Phvul.011G182900 | Phvul.011G18 PF00407 | |
| 8 | pacid=371551 | 1 Phvul.011G191600.1 | Phvul.011G191600 | Phvul.011G19PF13191,PF13 | |
| 9 | pacid=371571 | 1 Phvul.011G191800.1 | Phvul.011G191800 | Phvul.011G19 PF00931 | |
| 10 | pacid=371553 | 1 Phvul.011G192200.1 | Phvul.011G192200 | Phvul.011G19 PF00931 | |
| 11 | pacid=371553 | 1 Phvul.011G192900.1 | Phvul.011G192900 | Phvul.011G19 PF00931 | |
| 12 | pacid=371553 | 1 Phvul.011G192900.1 | Phvul.011G192900 | Phvul.011G19 PF00931 | |
| 13 | pacid=371552 | 1 Phvul.011G195751.1 | Phvul.011G195751 | Phvul.011G19 PF00931 | |
| 14 | pacid=371555 | 1 Phvul.011G198400.1 | Phvul.011G198400 | Phvul.011G19PF13855,PF00 | |
| 15 | pacid=371548 | 1 Phvul.011G201000.1 | Phvul.011G201000 | Phvul.011G20 PF00931 | |
| 16 | pacid=371569 | 1 Phvul.011G201101.1 | Phvul.011G201101 | Phvul.011G20 PF00931 | |
| 17 | pacid=371680 | 1 Phvul.001G027100.1 | Phvul.001G027100 | Phvul.001G02 PF00646 | |
| 18 | pacid=371711 | 1 Phvul.001G123000.2 | Phvul.001G123000 | Phvul.001G12 PF01055 | |
| 19 | pacid=371712 | 1 Phvul.001G132516.1 | Phvul.001G132516 | Phvul.001G13 PF00931 | |
| 20 | pacid=371712 | 1 Phvul.001G132516.1 | Phvul.001G132516 | Phvul.001G13 PF00931 | |
| 21 | pacid=371694 | 1 Phvul.001G132701.1 | Phvul.001G132701 | Phvul.001G13 PF13855,PF00 | |
| 22 | pacid=371694 | 1 Phvul.001G132701.1 | Phvul.001G132701 | Phvul.001G13 PF13855,PF00 | |
| 23 | pacid=371700 | 1 Phvul.001G132800.1 | Phvul.001G132800 | Phvul.001G13 PF13855,PF00 | |
| 24 | pacid=371700 | 1 Phvul.001G132800.1 | Phvul.001G132800 | Phvul.001G13 PF13855,PF00 | |
| 25 | pacid=371678 | 1 Phvul.001G132864.1 | Phvul.001G132864 | Phvul.001G13 PF13855,PF00 | |
| 26 | pacid=371678 | 1 Phvul.001G132864.1 | Phvul.001G132864 | Phvul.001G13 PF13855,PF00 | |
| 27 | pacid=371687 | 1 Phvul.001G133100.1 | Phvul.001G133100 | Phvul.001G13 PF13855,PF00 | |
| 28 | pacid=371687 | 1 Phvul.001G133100.1 | Phvul.001G133100 | Phvul.001G13 PF13855,PF00 | |
| 29 | pacid=371684 | 1 Phvul.001G133101.1 | Phvul.001G133101 | Phvul.001G13 PF13855,PF00 | |
| 30 | pacid=371684 | 1 Phvul.001G133101.1 | Phvul.001G133101 | Phvul.001G13 PF13855,PF00 | |
| 31 | pacid=371712 | 1 Phvul.001G185400.1 | Phvul.001G185400 | Phvul.001G18PF08263,PF00 | |
| 32 | pacid=371712 | 1 Phvul.001G185400.1 | Phvul.001G185400 | Phvul.001G18PF08263,PF00 | |
| 33 | pacid=371700 | 1 Phvul.001G217800.1 | Phvul.001G217800 | Phvul.001G21 PF07885 | |
| 34 | pacid=371778 | 1 Phvul.002G063500.1 | Phvul.002G063500 | Phvul.002G06 PF00295 | |
| 35 | pacid=371778 | 1 Phvul.002G063500.1 | Phvul.002G063500 | Phvul.002G06 PF00295 | |
| 36 | pacid=371754 | 1 Phvul.002G104200.1 | Phvul.002G104200 | Phvul.002G10PF00614,PF00 | |
| 37 | pacid=371754 | 1 Phvul.002G104200.1 | Phvul.002G104200 | Phvul.002G10PF00614,PF00 | |
| 38 | pacid=371780 | 1 Phvul.002G279500.1 | Phvul.002G279500 | Phvul.002G27PF03470,PF03 | |
| 39 | pacid=371464 | 2 Phvul.003G050200.2 | Phvul.003G050200 | Phvul.003G05 | 0 |
| 40 | pacid=371464 | 2 Phvul.003G050200.1 | Phvul.003G050200 | Phvul.003G05 | 0 |
| 41 | pacid=371478 | 1 Phvul.003G076900.1 | Phvul.003G076900 | Phvul.003G07 PF00067 | |
| 42 | pacid=371478 | 1 Phvul.003G076900.1 | Phvul.003G076900 | Phvul.003G07 PF00067 | |
| 43 | pacid=371447 | 1 Phvul.003G104900.1 | Phvul.003G104900 | Phvul.003G10 PF00403 | |
| 44 | pacid=371447 | 1 Phvul.003G104900.1 | Phvul.003G104900 | Phvul.003G10 PF00403 | |
| 45 | pacid=371471 | 1 Phvul.003G157600.1 | Phvul.003G157600 | Phvul.003G15 PF05182 | |
| 46 | pacid=371466 | 1 Phvul.003G158700.1 | Phvul.003G158700 | Phvul.003G15PF07714,PF00 | |
| 47 | pacid=371466 | 1 Phvul.003G158700.1 | Phvul.003G158700 | Phvul.003G15PF07714,PF00 | |

| | | | | |
|----|--------------|----------------------|------------------|---------------------------|
| 1 | | | | |
| 2 | pacid=371463 | 1 Phvul.003G162300.1 | Phvul.003G162300 | Phvul.003G16PF12854,PF14 |
| 3 | pacid=371483 | 1 Phvul.003G209600.2 | Phvul.003G209600 | Phvul.003G20PF07521,PF00 |
| 4 | pacid=371483 | 1 Phvul.003G209600.1 | Phvul.003G209600 | Phvul.003G20PF07521,PF00 |
| 5 | | | | |
| 6 | pacid=371483 | 1 Phvul.003G288300.1 | Phvul.003G288300 | Phvul.003G28 PF00069 |
| 7 | pacid=371483 | 1 Phvul.003G288300.1 | Phvul.003G288300 | Phvul.003G28 PF00069 |
| 8 | pacid=371628 | 1 Phvul.004G011400.1 | Phvul.004G011400 | Phvul.004G01 PF13921 |
| 9 | | | | |
| 10 | pacid=371621 | 1 Phvul.004G064300.1 | Phvul.004G064300 | Phvul.004G06 PF00415 |
| 11 | pacid=371621 | 1 Phvul.004G064300.1 | Phvul.004G064300 | Phvul.004G06 PF00415 |
| 12 | pacid=371634 | 1 Phvul.004G131300.1 | Phvul.004G131300 | Phvul.004G13 PF01535,PF12 |
| 13 | | | | |
| 14 | pacid=371634 | 1 Phvul.004G131300.1 | Phvul.004G131300 | Phvul.004G13 PF01535,PF12 |
| 15 | pacid=371542 | 1 Phvul.005G031200.1 | Phvul.005G031200 | Phvul.005G03 PF00931 |
| 16 | pacid=371542 | 1 Phvul.005G071300.1 | Phvul.005G071300 | Phvul.005G07 PF00304 |
| 17 | | | | |
| 18 | pacid=371542 | 1 Phvul.005G071300.1 | Phvul.005G071300 | Phvul.005G07 PF00304 |
| 19 | pacid=371723 | 1 Phvul.006G057000.1 | Phvul.006G057000 | Phvul.006G05 PF00076 |
| 20 | pacid=371721 | 1 Phvul.006G057100.5 | Phvul.006G057100 | Phvul.006G05 PF00076 |
| 21 | | | | |
| 22 | pacid=371721 | 1 Phvul.006G057100.4 | Phvul.006G057100 | Phvul.006G05 PF00076 |
| 23 | pacid=371716 | 1 Phvul.006G057700.2 | Phvul.006G057700 | Phvul.006G05 PF02146 |
| 24 | pacid=371714 | 1 Phvul.006G066800.1 | Phvul.006G066800 | Phvul.006G06 PF00931 |
| 25 | | | | |
| 26 | pacid=371714 | 1 Phvul.006G066800.1 | Phvul.006G066800 | Phvul.006G06 PF00931 |
| 27 | pacid=371653 | 1 Phvul.007G086300.2 | Phvul.007G086300 | Phvul.007G08 PF00931 |
| 28 | pacid=371653 | 1 Phvul.007G086300.1 | Phvul.007G086300 | Phvul.007G08 PF00931 |
| 29 | | | | |
| 30 | pacid=371596 | 1 Phvul.008G014700.1 | Phvul.008G014700 | Phvul.008G01 PF00931 |
| 31 | pacid=371596 | 1 Phvul.008G014700.1 | Phvul.008G014700 | Phvul.008G01 PF00931 |
| 32 | pacid=371582 | 1 Phvul.008G072032.1 | Phvul.008G072032 | Phvul.008G07 PF13855,PF00 |
| 33 | | | | |
| 34 | pacid=371582 | 1 Phvul.008G072032.1 | Phvul.008G072032 | Phvul.008G07 PF13855,PF00 |
| 35 | pacid=371605 | 1 Phvul.008G168300.2 | Phvul.008G168300 | Phvul.008G16 0 |
| 36 | pacid=371604 | 1 Phvul.008G168300.1 | Phvul.008G168300 | Phvul.008G16 0 |
| 37 | | | | |
| 38 | pacid=371505 | 1 Phvul.009G039200.1 | Phvul.009G039200 | Phvul.009G03 PF00892 |
| 39 | pacid=371497 | 1 Phvul.009G079700.1 | Phvul.009G079700 | Phvul.009G07 PF00433,PF07 |
| 40 | pacid=371497 | 1 Phvul.009G079700.1 | Phvul.009G079700 | Phvul.009G07 PF00433,PF07 |
| 41 | | | | |
| 42 | pacid=371486 | 1 Phvul.009G180800.1 | Phvul.009G180800 | Phvul.009G18 PF08477 |
| 43 | pacid=371486 | 1 Phvul.009G180800.2 | Phvul.009G180800 | Phvul.009G18 PF08477 |
| 44 | pacid=371486 | 1 Phvul.009G180800.1 | Phvul.009G180800 | Phvul.009G18 PF08477 |
| 45 | pacid=371486 | 1 Phvul.009G180800.2 | Phvul.009G180800 | Phvul.009G18 PF08477 |
| 46 | | | | |
| 47 | pacid=371520 | 1 Phvul.009G249500.1 | Phvul.009G249500 | Phvul.009G24 PF03242 |
| 48 | pacid=371428 | 1 Phvul.010G025000.1 | Phvul.010G025000 | Phvul.010G02 PF13676,PF00 |
| 49 | pacid=371440 | 1 Phvul.010G025700.1 | Phvul.010G025700 | Phvul.010G02 PF13676,PF00 |
| 50 | | | | |
| 51 | pacid=371426 | 1 Phvul.010G063700.2 | Phvul.010G063700 | Phvul.010G06 PF00931 |
| 52 | pacid=371437 | 1 Phvul.010G101700.1 | Phvul.010G101700 | Phvul.010G10 0 |
| 53 | pacid=371429 | 1 Phvul.010G141400.1 | Phvul.010G141400 | Phvul.010G14 PF02701 |
| 54 | | | | |
| 55 | pacid=371432 | 1 Phvul.010G149500.1 | Phvul.010G149500 | Phvul.010G14 PF13307,PF06 |
| 56 | pacid=371432 | 1 Phvul.010G149500.1 | Phvul.010G149500 | Phvul.010G14 PF13307,PF06 |
| 57 | | | | |
| 58 | pacid=371571 | 1 Phvul.011G015000.1 | Phvul.011G015000 | Phvul.011G01 PF03514 |
| 59 | pacid=371566 | 1 Phvul.011G181500.1 | Phvul.011G181500 | Phvul.011G18 PF00931 |
| 60 | pacid=371566 | 1 Phvul.011G181500.1 | Phvul.011G181500 | Phvul.011G18 PF00931 |
| | pacid=371548 | 1 Phvul.011G198000.1 | Phvul.011G198000 | Phvul.011G19 PF00931 |

| | | | | | |
|----|--------------|----------------------|------------------|---------------|--------------|
| 1 | | | | | |
| 2 | pacid=371548 | 1 Phvul.011G198000.1 | Phvul.011G198000 | Phvul.011G19 | PF00931 |
| 3 | pacid=371547 | 1 Phvul.011G200880.2 | Phvul.011G200880 | Phvul.011G20 | PF00931 |
| 4 | pacid=371547 | 1 Phvul.011G200880.1 | Phvul.011G200880 | Phvul.011G20 | PF00931 |
| 5 | | | | | |
| 6 | pacid=371548 | 1 Phvul.011G201000.1 | Phvul.011G201000 | Phvul.011G20 | PF00931 |
| 7 | pacid=371548 | 1 Phvul.011G201000.1 | Phvul.011G201000 | Phvul.011G20 | PF00931 |
| 8 | pacid=371569 | 1 Phvul.011G201101.1 | Phvul.011G201101 | Phvul.011G20 | PF00931 |
| 9 | | | | | |
| 10 | pacid=371569 | 1 Phvul.011G201101.1 | Phvul.011G201101 | Phvul.011G20 | PF00931 |
| 11 | pacid=371566 | 1 Phvul.011G202366.1 | Phvul.011G202366 | Phvul.011G20 | PF13191 |
| 12 | pacid=371566 | 1 Phvul.011G202366.1 | Phvul.011G202366 | Phvul.011G20 | PF13191 |
| 13 | | | | | |
| 14 | pacid=371639 | 1 Phvul.L004500.1 | Phvul.L004500 | Phvul.L004500 | (PF00332 |
| 15 | pacid=371639 | 1 Phvul.L004500.1 | Phvul.L004500 | Phvul.L004500 | (PF00332 |
| 16 | pacid=371683 | 1 Phvul.001G183400.2 | Phvul.001G183400 | Phvul.001G18 | PF04640 |
| 17 | pacid=371683 | 1 Phvul.001G183400.3 | Phvul.001G183400 | Phvul.001G18 | PF04640 |
| 18 | pacid=371683 | 1 Phvul.001G183400.4 | Phvul.001G183400 | Phvul.001G18 | PF04640 |
| 19 | pacid=371683 | 1 Phvul.001G183400.1 | Phvul.001G183400 | Phvul.001G18 | PF04640 |
| 20 | | | | | |
| 21 | pacid=371768 | 1 Phvul.002G089800.1 | Phvul.002G089800 | Phvul.002G08 | PF08536 |
| 22 | pacid=371768 | 1 Phvul.002G089800.1 | Phvul.002G089800 | Phvul.002G08 | PF08536 |
| 23 | pacid=371777 | 1 Phvul.002G171400.1 | Phvul.002G171400 | Phvul.002G17 | PF13676,PF13 |
| 24 | pacid=371778 | 1 Phvul.002G244900.1 | Phvul.002G244900 | Phvul.002G24 | PF01925 |
| 25 | pacid=371778 | 1 Phvul.002G244900.1 | Phvul.002G244900 | Phvul.002G24 | PF01925 |
| 26 | pacid=371757 | 1 Phvul.002G245000.5 | Phvul.002G245000 | Phvul.002G24 | PF01925 |
| 27 | pacid=371757 | 1 Phvul.002G245000.4 | Phvul.002G245000 | Phvul.002G24 | PF01925 |
| 28 | pacid=371757 | 1 Phvul.002G245000.3 | Phvul.002G245000 | Phvul.002G24 | PF01925 |
| 29 | pacid=371757 | 1 Phvul.002G245000.1 | Phvul.002G245000 | Phvul.002G24 | PF01925 |
| 30 | pacid=371757 | 1 Phvul.002G245000.2 | Phvul.002G245000 | Phvul.002G24 | PF01925 |
| 31 | pacid=371757 | 1 Phvul.002G245000.5 | Phvul.002G245000 | Phvul.002G24 | PF01925 |
| 32 | pacid=371757 | 1 Phvul.002G245000.4 | Phvul.002G245000 | Phvul.002G24 | PF01925 |
| 33 | pacid=371757 | 1 Phvul.002G245000.3 | Phvul.002G245000 | Phvul.002G24 | PF01925 |
| 34 | pacid=371757 | 1 Phvul.002G245000.1 | Phvul.002G245000 | Phvul.002G24 | PF01925 |
| 35 | pacid=371757 | 1 Phvul.002G245000.2 | Phvul.002G245000 | Phvul.002G24 | PF01925 |
| 36 | pacid=371757 | 1 Phvul.002G245000.5 | Phvul.002G245000 | Phvul.002G24 | PF01925 |
| 37 | pacid=371757 | 1 Phvul.002G245000.4 | Phvul.002G245000 | Phvul.002G24 | PF01925 |
| 38 | pacid=371757 | 1 Phvul.002G245000.3 | Phvul.002G245000 | Phvul.002G24 | PF01925 |
| 39 | pacid=371757 | 1 Phvul.002G245000.1 | Phvul.002G245000 | Phvul.002G24 | PF01925 |
| 40 | pacid=371757 | 1 Phvul.002G245000.2 | Phvul.002G245000 | Phvul.002G24 | PF01925 |
| 41 | pacid=371449 | 1 Phvul.003G002200.5 | Phvul.003G002200 | Phvul.003G00 | PF00612,PF00 |
| 42 | pacid=371449 | 1 Phvul.003G002200.4 | Phvul.003G002200 | Phvul.003G00 | PF00612,PF00 |
| 43 | pacid=371449 | 1 Phvul.003G002200.3 | Phvul.003G002200 | Phvul.003G00 | PF00612,PF00 |
| 44 | pacid=371449 | 1 Phvul.003G002200.5 | Phvul.003G002200 | Phvul.003G00 | PF00612,PF00 |
| 45 | pacid=371449 | 1 Phvul.003G002200.4 | Phvul.003G002200 | Phvul.003G00 | PF00612,PF00 |
| 46 | pacid=371449 | 1 Phvul.003G002200.3 | Phvul.003G002200 | Phvul.003G00 | PF00612,PF00 |
| 47 | pacid=371464 | 2 Phvul.003G050200.2 | Phvul.003G050200 | Phvul.003G05 | 0 |
| 48 | pacid=371464 | 2 Phvul.003G050200.1 | Phvul.003G050200 | Phvul.003G05 | 0 |
| 49 | pacid=371456 | 2 Phvul.003G244225.3 | Phvul.003G244225 | Phvul.003G24 | 0 |
| 50 | pacid=371456 | 2 Phvul.003G244225.2 | Phvul.003G244225 | Phvul.003G24 | 0 |
| 51 | pacid=371456 | 2 Phvul.003G244225.1 | Phvul.003G244225 | Phvul.003G24 | 0 |
| 52 | pacid=371459 | 1 Phvul.003G282200.3 | Phvul.003G282200 | Phvul.003G28 | PF00856,PF05 |
| 53 | pacid=371459 | 1 Phvul.003G282200.2 | Phvul.003G282200 | Phvul.003G28 | PF00856,PF05 |
| 54 | pacid=371464 | 1 Phvul.003G282250.1 | Phvul.003G282250 | Phvul.003G28 | PF01535,PF13 |
| 55 | pacid=371615 | 1 Phvul.004G011100.1 | Phvul.004G011100 | Phvul.004G01 | PF03726,PF00 |
| 56 | pacid=371618 | 1 Phvul.004G086300.2 | Phvul.004G086300 | Phvul.004G08 | PF00069 |

| | | | | | |
|----|--------------|---|--------------------|------------------|---------------------------|
| 1 | | | | | |
| 2 | pacid=371618 | 1 | Phvul.004G086300.1 | Phvul.004G086300 | Phvul.004G08 PF00069 |
| 3 | pacid=371544 | 1 | Phvul.005G041300.1 | Phvul.005G041300 | Phvul.005G04 PF13041,PF01 |
| 4 | pacid=371544 | 1 | Phvul.005G041300.1 | Phvul.005G041300 | Phvul.005G04 PF13041,PF01 |
| 5 | | | | | |
| 6 | pacid=371528 | 1 | Phvul.005G069700.1 | Phvul.005G069700 | Phvul.005G06 0 |
| 7 | pacid=371528 | 1 | Phvul.005G069700.1 | Phvul.005G069700 | Phvul.005G06 0 |
| 8 | pacid=371525 | 1 | Phvul.005G072000.1 | Phvul.005G072000 | Phvul.005G07 PF04765 |
| 9 | | | | | |
| 10 | pacid=371724 | 1 | Phvul.006G027500.1 | Phvul.006G027500 | Phvul.006G02 PF00400 |
| 11 | pacid=371724 | 1 | Phvul.006G027500.1 | Phvul.006G027500 | Phvul.006G02 PF00400 |
| 12 | pacid=371735 | 1 | Phvul.006G100600.1 | Phvul.006G100600 | Phvul.006G10 PF06026 |
| 13 | | | | | |
| 14 | pacid=371715 | 1 | Phvul.006G126400.1 | Phvul.006G126400 | Phvul.006G12 0 |
| 15 | pacid=371715 | 1 | Phvul.006G126400.1 | Phvul.006G126400 | Phvul.006G12 0 |
| 16 | pacid=371718 | 1 | Phvul.006G170700.1 | Phvul.006G170700 | Phvul.006G17 PF12796,PF13 |
| 17 | | | | | |
| 18 | pacid=371615 | 1 | Phvul.008G107400.1 | Phvul.008G107400 | Phvul.008G10 PF01535,PF12 |
| 19 | pacid=371615 | 1 | Phvul.008G107400.1 | Phvul.008G107400 | Phvul.008G10 PF01535,PF12 |
| 20 | pacid=371598 | 1 | Phvul.008G206300.1 | Phvul.008G206300 | Phvul.008G20 PF05383 |
| 21 | | | | | |
| 22 | pacid=371492 | 1 | Phvul.009G103100.1 | Phvul.009G103100 | Phvul.009G10 PF13855,PF08 |
| 23 | pacid=371436 | 1 | Phvul.010G008500.1 | Phvul.010G008500 | Phvul.010G00 PF05340 |
| 24 | pacid=371429 | 1 | Phvul.010G013500.1 | Phvul.010G013500 | Phvul.010G01 PF02701 |
| 25 | | | | | |
| 26 | pacid=371430 | 2 | Phvul.010G044000.3 | Phvul.010G044000 | Phvul.010G04 PF02493 |
| 27 | pacid=371430 | 2 | Phvul.010G044000.3 | Phvul.010G044000 | Phvul.010G04 PF02493 |
| 28 | pacid=371430 | 2 | Phvul.010G044000.2 | Phvul.010G044000 | Phvul.010G04 PF02493 |
| 29 | pacid=371430 | 2 | Phvul.010G044000.2 | Phvul.010G044000 | Phvul.010G04 PF02493 |
| 30 | pacid=371430 | 2 | Phvul.010G044000.3 | Phvul.010G044000 | Phvul.010G04 PF02493 |
| 31 | pacid=371430 | 2 | Phvul.010G044000.3 | Phvul.010G044000 | Phvul.010G04 PF02493 |
| 32 | pacid=371430 | 2 | Phvul.010G044000.3 | Phvul.010G044000 | Phvul.010G04 PF02493 |
| 33 | pacid=371430 | 2 | Phvul.010G044000.2 | Phvul.010G044000 | Phvul.010G04 PF02493 |
| 34 | pacid=371430 | 2 | Phvul.010G044000.2 | Phvul.010G044000 | Phvul.010G04 PF02493 |
| 35 | pacid=371430 | 2 | Phvul.010G044000.2 | Phvul.010G044000 | Phvul.010G04 PF02493 |
| 36 | pacid=371432 | 1 | Phvul.010G145600.1 | Phvul.010G145600 | Phvul.010G14 PF14510,PF08 |
| 37 | pacid=371561 | 1 | Phvul.011G181700.1 | Phvul.011G181700 | Phvul.011G18 PF00931 |
| 38 | | | | | |
| 39 | pacid=371573 | 1 | Phvul.011G200820.1 | Phvul.011G200820 | Phvul.011G20 PF00931 |
| 40 | pacid=371560 | 1 | Phvul.011G202100.1 | Phvul.011G202100 | Phvul.011G20 PF00931 |
| 41 | pacid=371555 | 1 | Phvul.011G202300.1 | Phvul.011G202300 | Phvul.011G20 PF00931 |
| 42 | | | | | |
| 43 | pacid=371563 | 1 | Phvul.011G203100.1 | Phvul.011G203100 | Phvul.011G20 PF00931 |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| 1 | Panther | KOG | KEGG | KOG | GO | Best-hit-arabi-arabi-symbol | |
|----|----------------------------------|----------|------------|----------|----------------|-----------------------------|---|
| 2 | PTHR23155,P ⁻ | | 0 | 0 | 0 GO:0043531 | AT4G27220.1 | 0 |
| 3 | PTHR23244,P ⁻ | | 0 | 0 | 0 GO:0005515 | AT1G74150.1 | 0 |
| 4 | PTHR23244,P ⁻ | | 0 | 0 | 0 GO:0005515 | AT1G74150.1 | 0 |
| 5 | PTHR23244,P ⁻ | | 0 | 0 | 0 GO:0005515 | AT1G74150.1 | 0 |
| 6 | PTHR23244,P ⁻ | | 0 | 0 | 0 GO:0005515 | AT1G74150.1 | 0 |
| 7 | PTHR23244,P ⁻ | | 0 | 0 | 0 GO:0005515 | AT1G74150.1 | 0 |
| 8 | PTHR23244,P ⁻ | | 0 | 0 | 0 GO:0005515 | AT1G74150.1 | 0 |
| 9 | PTHR23244,P ⁻ | | 0 | 0 | 0 GO:0005515 | AT1G74150.1 | 0 |
| 10 | PTHR23244,P ⁻ KOG4693 | | | 0 | 0 GO:0005515 | AT1G74150.1 | 0 |
| 11 | PTHR23244,P ⁻ KOG4693 | | | 0 | 0 GO:0005515 | AT1G74150.1 | 0 |
| 12 | PTHR23155,P ⁻ | | 0 | 0 K13459 | GO:0005515,(| AT5G63020.1 | 0 |
| 13 | PTHR23155,P ⁻ | | 0 | 0 K13459 | GO:0005515,(| AT5G63020.1 | 0 |
| 14 | PTHR23155,P ⁻ | | 0 | 0 K13459 | GO:0005515,(| AT5G63020.1 | 0 |
| 15 | PTHR23155,P ⁻ | | 0 | 0 K13459 | GO:0005515,(| AT5G63020.1 | 0 |
| 16 | PTHR23155,P ⁻ | | 0 | 0 K13459 | GO:0005515,(| AT5G63020.1 | 0 |
| 17 | PTHR11017,P ⁻ KOG4658 | | | 0 | 0 GO:0007165,(| AT1G27170.1 | 0 |
| 18 | PTHR24078,P ⁻ | | 0 | 0 | 0 | 0 AT1G75250.1 ATRL6,RL6,RSI | |
| 19 | PTHR10071,P ⁻ | | 0 | 0 | 0 GO:0043565,(| AT4G17570.3 GATA26 | |
| 20 | PTHR10071,P ⁻ | | 0 | 0 | 0 GO:0043565,(| AT4G17570.3 GATA26 | |
| 21 | PTHR10071,P ⁻ | | 0 | 0 | 0 GO:0043565,(| AT4G17570.3 GATA26 | |
| 22 | PTHR10071,P ⁻ | | 0 | 0 | 0 GO:0043565,(| AT4G17570.3 GATA26 | |
| 23 | PTHR11017,P ⁻ KOG4658 | | | 0 | 0 GO:0007165,(| AT1G27170.1 | 0 |
| 24 | PTHR32093,P ⁻ | | 0 | 0 | 0 | 0 AT3G50370.1 | 0 |
| 25 | PTHR32093,P ⁻ | | 0 | 0 | 0 | 0 AT3G50370.1 | 0 |
| 26 | PTHR32093,P ⁻ | | 0 | 0 | 0 | 0 AT3G50370.1 | 0 |
| 27 | PTHR32093,P ⁻ | | 0 | 0 | 0 | 0 AT3G50370.1 | 0 |
| 28 | PTHR11017,P ⁻ KOG4658 | | | 0 | 0 GO:0007165,(| AT5G36930.2 | 0 |
| 29 | PTHR10315,P ⁻ KOG3002 | 6.3.2.19 | | K04506 | GO:0007275,(| AT3G61790.1 | 0 |
| 30 | PTHR10315,P ⁻ KOG3002 | 6.3.2.19 | | K04506 | GO:0007275,(| AT3G61790.1 | 0 |
| 31 | PTHR10315,P ⁻ KOG3002 | 6.3.2.19 | | K04506 | GO:0007275,(| AT3G61790.1 | 0 |
| 32 | PTHR10315,P ⁻ KOG3002 | 6.3.2.19 | | K04506 | GO:0007275,(| AT3G61790.1 | 0 |
| 33 | PTHR31251,P ⁻ | | 0 | 0 | 0 GO:0005634,(| AT2G47070.1 SPL1 | |
| 34 | PTHR31251,P ⁻ | | 0 | 0 | 0 GO:0005634,(| AT2G47070.1 SPL1 | |
| 35 | PTHR31251,P ⁻ | | 0 | 0 | 0 GO:0005634,(| AT2G47070.1 SPL1 | |
| 36 | PTHR24220,P ⁻ | | 0 3.6.3.25 | | 0 GO:0016887,(| AT1G65410.1 ATNAP11,NAF | |
| 37 | PTHR21716,P ⁻ KOG2365 | | | 0 | 0 | 0 AT5G55960.1 | 0 |
| 38 | PTHR21716,P ⁻ KOG2365 | | | 0 | 0 | 0 AT5G55960.1 | 0 |
| 39 | PTHR21716,P ⁻ KOG2365 | | | 0 | 0 | 0 AT5G55960.1 | 0 |
| 40 | PTHR23155,P ⁻ KOG4658 | | | 0 | 0 GO:0043531 | AT3G14470.1 | 0 |
| 41 | PTHR11017,P ⁻ | | 0 | 0 | 0 GO:0007165,(| AT5G17680.1 | 0 |
| 42 | PTHR11017,P ⁻ | | 0 | 0 | 0 GO:0007165,(| AT5G17680.1 | 0 |
| 43 | PTHR14221,P ⁻ | | 0 | 0 | 0 | 0 AT5G54200.1 | 0 |
| 44 | PTHR14221,P ⁻ | | 0 | 0 | 0 | 0 AT5G54200.1 | 0 |
| 45 | PTHR14221,P ⁻ | | 0 | 0 | 0 | 0 AT5G54200.1 | 0 |
| 46 | PTHR14221,P ⁻ | | 0 | 0 | 0 | 0 AT5G54200.1 | 0 |
| 47 | PTHR14221,P ⁻ | | 0 | 0 | 0 | 0 AT5G54200.1 | 0 |
| 48 | PTHR14221,P ⁻ | | 0 | 0 | 0 | 0 AT5G54200.1 | 0 |
| 49 | PTHR14221,P ⁻ | | 0 | 0 | 0 | 0 AT5G54200.1 | 0 |
| 50 | PTHR14221,P ⁻ | | 0 | 0 | 0 | 0 AT5G54200.1 | 0 |
| 51 | PTHR14221,P ⁻ | | 0 | 0 | 0 | 0 AT5G54200.1 | 0 |
| 52 | PTHR23155,P ⁻ KOG4658 | | | 0 | 0 GO:0043531 | AT3G14470.1 | 0 |
| 53 | PTHR11017,P ⁻ KOG0472 | | | 0 | 0 | 0 AT5G17680.1 | 0 |
| 54 | PTHR11017,P ⁻ KOG0472 | | | 0 | 0 | 0 AT5G17680.1 | 0 |
| 55 | PTHR23155,P ⁻ KOG4658 | | | 0 | 0 GO:0005515,(| AT3G14470.1 | 0 |
| 56 | PTHR23155,P ⁻ KOG4658 | | | 0 | 0 GO:0005515,(| AT3G14470.1 | 0 |
| 57 | PTHR11638,P ⁻ KOG1051 | | | 0 | 0 GO:0019538,(| AT2G40130.2 | 0 |
| 58 | PTHR11638,P ⁻ KOG1051 | | | 0 | 0 GO:0019538,(| AT2G40130.2 | 0 |
| 59 | PTHR11638,P ⁻ KOG1051 | | | 0 | 0 GO:0019538,(| AT2G40130.2 | 0 |
| 60 | PTHR31351,P ⁻ | | 0 | 0 | 0 | 0 AT4G17350.1 | 0 |
| | PTHR31351,P ⁻ | | 0 | 0 | 0 | 0 AT4G17350.1 | 0 |

| | | | | | |
|----|----------------------------------|------------|----------|--------------------------------------|---|
| 1 | | | | | |
| 2 | PTHR24286,P ⁻ KOG0157 | 1.14.13.93 | | 0 GO:0055114,(AT4G19230.1 CYP707A1 | |
| 3 | PTHR36320,P ⁻ | 0 | 0 | 0 AT1G30880.1 | 0 |
| 4 | PTHR24012,P ⁻ KOG4209 | | 0 K14396 | GO:0003676 AT5G10350.1 | 0 |
| 5 | PTHR24012,P ⁻ KOG4209 | | 0 K14396 | GO:0003676 AT5G10350.1 | 0 |
| 6 | PTHR11615,P ⁻ | 0 | 0 | 0 AT4G15630.1 | 0 |
| 7 | PTHR11615,P ⁻ | 0 | 0 | 0 AT4G15630.1 | 0 |
| 8 | PTHR30573,P ⁻ | 0 2.5.1.72 | K03517 | GO:0051539,(AT5G50210.1 OLD5,QS,SUFF | |
| 9 | PTHR30573,P ⁻ | 0 2.5.1.72 | K03517 | GO:0051539,(AT5G50210.1 OLD5,QS,SUFF | |
| 10 | PTHR13711,P ⁻ | 0 | 0 K09272 | 0 AT3G28730.1 ATHMG,HMG, | |
| 11 | PTHR11017,P ⁻ | 0 | 0 | 0 GO:0007165,(AT5G17680.1 | 0 |
| 12 | PTHR11017,P ⁻ | 0 | 0 | 0 GO:0007165,(AT5G17680.1 | 0 |
| 13 | PTHR21091,P ⁻ KOG1527 | | 0 | 0 GO:0008168,(AT5G40850.1 UPM1 | |
| 14 | PTHR21091,P ⁻ KOG1527 | | 0 | 0 GO:0008168,(AT5G40850.1 UPM1 | |
| 15 | PTHR23155,P ⁻ KOG4658 | | 0 K13459 | GO:0005515,(AT4G27220.1 | 0 |
| 16 | PTHR23155,P ⁻ KOG4658 | | 0 K13459 | GO:0005515,(AT4G27220.1 | 0 |
| 17 | PTHR27003,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT3G04690.1 ANX1 | |
| 18 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT1G63350.1 | 0 |
| 19 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT1G63350.1 | 0 |
| 20 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT1G63350.1 | 0 |
| 21 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT1G63350.1 | 0 |
| 22 | PTHR15002 KOG2425 | | 0 K16912 | 0 AT5G12220.1 | 0 |
| 23 | PTHR30540,P ⁻ | 0 | 0 | 0 GO:0071805,(AT2G30070.1 ATK1,ATK1F | |
| 24 | PTHR30540,P ⁻ | 0 | 0 | 0 GO:0071805,(AT2G30070.1 ATK1,ATK1F | |
| 25 | PTHR30540,P ⁻ | 0 | 0 | 0 GO:0071805,(AT2G30070.1 ATK1,ATK1F | |
| 26 | PTHR30540,P ⁻ | 0 | 0 | 0 GO:0071805,(AT2G30070.1 ATK1,ATK1F | |
| 27 | PTHR11017,P ⁻ KOG4658 | | 0 | 0 GO:0007165,(AT5G41750.1 | 0 |
| 28 | PTHR11017,P ⁻ KOG0617 | | 0 | 0 AT5G41750.2 | 0 |
| 29 | PTHR11017,P ⁻ KOG4658 | | 0 | 0 GO:0007165,(AT5G17680.1 | 0 |
| 30 | PTHR12526,P ⁻ KOG0853 | | 0 | 0 AT3G15940.2 | 0 |
| 31 | PTHR12526,P ⁻ KOG0853 | | 0 | 0 AT3G15940.2 | 0 |
| 32 | PTHR12526,P ⁻ KOG0853 | | 0 | 0 AT3G15940.2 | 0 |
| 33 | PTHR12526,P ⁻ KOG0853 | | 0 | 0 AT3G15940.2 | 0 |
| 34 | PTHR11017,P ⁻ KOG4658 | | 0 | 0 GO:0007165,(AT5G17680.1 | 0 |
| 35 | PTHR11017,P ⁻ KOG4658 | | 0 | 0 GO:0007165,(AT5G17680.1 | 0 |
| 36 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |
| 37 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |
| 38 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |
| 39 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |
| 40 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |
| 41 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0005515,(AT3G14470.1 | 0 |
| 42 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |
| 43 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0005515,(AT3G14470.1 | 0 |
| 44 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0005515,(AT3G14470.1 | 0 |
| 45 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0005515,(AT3G14470.1 | 0 |
| 46 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14460.1 | 0 |
| 47 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |
| 48 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |
| 49 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |
| 50 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |
| 51 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |
| 52 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |
| 53 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |
| 54 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |
| 55 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |
| 56 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |
| 57 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |
| 58 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |
| 59 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |
| 60 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 AT3G14470.1 | 0 |

| | | | | | | |
|----|----------------------------------|-----------------|----------|----------------|----------------------------|---|
| 1 | | | | | | |
| 2 | PTHR23155,P ⁻ | 0 | 0 | 0 GO:0043531 | AT3G14460.1 | 0 |
| 3 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14470.1 | 0 |
| 4 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0005515,(| AT3G14470.1 | 0 |
| 5 | | | | | | |
| 6 | PTHR23155,P ⁻ | 0 | 0 | 0 GO:0043531 | AT3G14470.1 | 0 |
| 7 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14470.1 | 0 |
| 8 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14470.1 | 0 |
| 9 | | | | | | |
| 10 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14460.1 | 0 |
| 11 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14460.1 | 0 |
| 12 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14470.1 | 0 |
| 13 | | | | | | |
| 14 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14470.1 | 0 |
| 15 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14460.1 | 0 |
| 16 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14460.1 | 0 |
| 17 | | | | | | |
| 18 | PTHR11695,P ⁻ KOG0022 | 1.1.1.1 | | 0 GO:0055114,(| AT5G42250.1 | 0 |
| 19 | PTHR11695,P ⁻ KOG0022 | 1.1.1.1 | | 0 GO:0055114,(| AT5G42250.1 | 0 |
| 20 | PTHR11695,P ⁻ KOG0022 | 1.1.1.1 | | 0 GO:0055114,(| AT5G42250.1 | 0 |
| 21 | | | | | | |
| 22 | PTHR11695,P ⁻ KOG0022 | 1.1.1.1 | | 0 GO:0055114,(| AT5G42250.1 | 0 |
| 23 | PTHR23063,P ⁻ KOG4666 | 2.3.1.25 | K13510 | GO:0016746,(| AT1G80950.1 | 0 |
| 24 | PTHR23063,P ⁻ KOG4666 | 2.3.1.25 | K13510 | GO:0016746,(| AT1G80950.1 | 0 |
| 25 | PTHR23063,P ⁻ KOG4666 | 2.3.1.25 | K13510 | GO:0016746,(| AT1G80950.1 | 0 |
| 26 | | | | | | |
| 27 | PTHR23063,P ⁻ KOG4666 | 2.3.1.25 | K13510 | GO:0016746,(| AT1G80950.1 | 0 |
| 28 | | | | | | |
| 29 | PTHR31945,P ⁻ | 0 | 0 | 0 GO:0046983 | AT3G26744.1 ATICE1,ICE1,S | |
| 30 | PTHR31945,P ⁻ | 0 | 0 | 0 GO:0046983 | AT3G26744.1 ATICE1,ICE1,S | |
| 31 | PTHR31867,P ⁻ | 0 | 0 | 0 | 0 AT2G39700.1 ATEXP4,ATEXI | |
| 32 | PTHR31867,P ⁻ | 0 | 0 | 0 | 0 AT2G39700.1 ATEXP4,ATEXI | |
| 33 | | | | | | |
| 34 | PTHR31065,P ⁻ | 0 | 0 | 0 | 0 AT1G32700.1 | 0 |
| 35 | PTHR31065,P ⁻ | 0 | 0 | 0 | 0 AT1G32700.1 | 0 |
| 36 | PTHR31065,P ⁻ | 0 | 0 | 0 | 0 AT1G32700.1 | 0 |
| 37 | PTHR31065,P ⁻ | 0 | 0 | 0 | 0 AT1G32700.1 | 0 |
| 38 | | | | | | |
| 39 | PTHR31479,P ⁻ | 0 | 0 | 0 GO:0006629 | AT4G10955.1 | 0 |
| 40 | PTHR10218,P ⁻ KOG0082 | | 0 | 0 GO:0031683,(| AT2G23460.1 ATXLG1,XLG1 | |
| 41 | PTHR10218,P ⁻ KOG0082 | | 0 | 0 GO:0031683,(| AT2G23460.1 ATXLG1,XLG1 | |
| 42 | | | | | | |
| 43 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G74850.1 PTAC2 | |
| 44 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G74850.1 PTAC2 | |
| 45 | PTHR10593,P ⁻ | 0 | 0 | 0 | 0 AT5G66730.1 | 0 |
| 46 | PTHR10593,P ⁻ | 0 | 0 | 0 | 0 AT5G66730.1 | 0 |
| 47 | | | | | | |
| 48 | PTHR13190,P ⁻ KOG2993 | | 0 K17906 | GO:0006914 | AT3G19190.1 ATATG2,ATG2 | |
| 49 | PTHR13190,P ⁻ KOG2993 | | 0 K17906 | GO:0006914 | AT3G19190.1 ATATG2,ATG2 | |
| 50 | | | | | | |
| 51 | PTHR13190,P ⁻ KOG2993 | | 0 K17906 | GO:0006914 | AT3G19190.1 ATATG2,ATG2 | |
| 52 | PTHR22953,P ⁻ KOG1378 | 3.6.1.7,3.1.3.2 | | 0 GO:0016787 | AT4G13700.1 ATPAP23,PAP. | |
| 53 | PTHR22953,P ⁻ KOG1378 | 3.6.1.7,3.1.3.2 | | 0 GO:0016787 | AT4G13700.1 ATPAP23,PAP. | |
| 54 | PTHR22953,P ⁻ KOG1378 | 3.6.1.7,3.1.3.2 | | 0 GO:0016787 | AT4G13700.1 ATPAP23,PAP. | |
| 55 | PTHR22953,P ⁻ KOG1378 | 3.6.1.7,3.1.3.2 | | 0 GO:0016787 | AT4G13700.1 ATPAP23,PAP. | |
| 56 | PTHR22953,P ⁻ KOG1378 | 3.6.1.7,3.1.3.2 | | 0 GO:0016787 | AT4G13700.1 ATPAP23,PAP. | |
| 57 | PTHR22953,P ⁻ KOG1378 | 3.6.1.7,3.1.3.2 | | 0 GO:0016787 | AT4G13700.1 ATPAP23,PAP. | |
| 58 | PTHR22953,P ⁻ KOG1378 | 3.6.1.7,3.1.3.2 | | 0 GO:0016787 | AT4G13700.1 ATPAP23,PAP. | |
| 59 | PTHR22953,P ⁻ KOG1378 | 3.6.1.7,3.1.3.2 | | 0 GO:0016787 | AT4G13700.1 ATPAP23,PAP. | |
| 60 | PTHR22953,P ⁻ KOG1378 | 3.6.1.7,3.1.3.2 | | 0 GO:0016787 | AT4G13700.1 ATPAP23,PAP. | |
| | PTHR22953,P ⁻ KOG1378 | 3.6.1.7,3.1.3.2 | | 0 GO:0016787 | AT4G13700.1 ATPAP23,PAP. | |

| | | | | | | | | |
|----|----------------------------------|----------------|--------|--------|--------------|--------------|--------------|---------------|
| 1 | | | | | | | | |
| 2 | PTHR23155,P ⁻ | 0 | 0 | 0 | GO:0043531 | AT4G27220.1 | 0 | |
| 3 | PTHR23155,P ⁻ | 0 | 0 | 0 | GO:0043531 | AT4G27220.1 | 0 | |
| 4 | PTHR13696,P ⁻ KOG3022 | | 0 | K03609 | 0 | AT5G24020.1 | ARC11,ATMIN | |
| 5 | | | | | | | | |
| 6 | PTHR13696,P ⁻ KOG3022 | | 0 | K03609 | 0 | AT5G24020.1 | ARC11,ATMIN | |
| 7 | PTHR23024,P ⁻ KOG1515 | 3.1.1.1 | | | 0 | 0 | AT5G23530.1 | AtCXE18,CXE1 |
| 8 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G49730.1 | 0 |
| 9 | | | | | | | | |
| 10 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G49730.1 | 0 |
| 11 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 | AT3G14470.1 | 0 | |
| 12 | PTHR31867,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G03220.1 | AATEXP13,ATE) |
| 13 | | | | | | | | |
| 14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 15 | PTHR11746,P ⁻ KOG3178 | | 0 | 0 | GO:0046983,(| AT4G35160.1 | 0 | |
| 16 | PTHR11746,P ⁻ KOG3178 | | 0 | 0 | GO:0046983,(| AT4G35160.1 | 0 | |
| 17 | | | | | | | | |
| 18 | 0 | 0 | 0 | 0 | 0 | 0 | AT1G68500.1 | 0 |
| 19 | PTHR10803 KOG2825 | 3.6.3.16 | K01551 | | GO:0016887,(| AT3G10350.1 | 0 | |
| 20 | PTHR27008,P ⁻ KOG1187 | 2.7.11.1 | | | 0 | GO:0005515,(| AT5G35390.1 | 0 |
| 21 | | | | | | | | |
| 22 | PTHR10108,P ⁻ KOG1269 | 2.1.1.143,2.1. | K08242 | | GO:0008168,(| AT1G20330.1 | CVP1,FRL1,SV | |
| 23 | PTHR10108,P ⁻ KOG1269 | 2.1.1.143,2.1. | K08242 | | GO:0008168,(| AT1G20330.1 | CVP1,FRL1,SV | |
| 24 | PTHR22952,P ⁻ | 0 | 0 | K14432 | GO:0043565,(| AT1G45249.1 | ABF2,AREB1,A | |
| 25 | PTHR22952,P ⁻ | 0 | 0 | K14432 | GO:0043565,(| AT1G45249.1 | ABF2,AREB1,A | |
| 26 | PTHR22952,P ⁻ | 0 | 0 | K14432 | GO:0043565,(| AT1G45249.1 | ABF2,AREB1,A | |
| 27 | PTHR22952,P ⁻ | 0 | 0 | K14432 | GO:0043565,(| AT1G45249.1 | ABF2,AREB1,A | |
| 28 | PTHR22952,P ⁻ | 0 | 0 | K14432 | GO:0043565,(| AT1G45249.1 | ABF2,AREB1,A | |
| 29 | | | | | | | | |
| 30 | PTHR24015,P ⁻ | 0 | 0 | K17964 | 0 | 0 | AT1G19290.1 | 0 |
| 31 | PTHR13533,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT5G20680.1 | TBL16 |
| 32 | PTHR13533,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT5G20680.1 | TBL16 |
| 33 | PTHR13533,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT5G20680.1 | TBL16 |
| 34 | PTHR13533,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT5G20680.1 | TBL16 |
| 35 | PTHR13533,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT5G20680.1 | TBL16 |
| 36 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 | AT1G50180.1 | 0 | |
| 37 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 | AT1G50180.1 | 0 | |
| 38 | | | | | | | | |
| 39 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 | AT1G50180.1 | 0 | |
| 40 | PTHR11017,P ⁻ | 0 | 0 | 0 | GO:0043531 | AT5G36930.2 | 0 | |
| 41 | PTHR11017,P ⁻ | 0 | 0 | 0 | GO:0043531 | AT5G36930.2 | 0 | |
| 42 | | | | | | | | |
| 43 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT2G17670.1 | 0 |
| 44 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT2G17670.1 | 0 |
| 45 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 | AT3G14460.1 | 0 | |
| 46 | | | | | | | | |
| 47 | PTHR10668,P ⁻ KOG1238 | 1.1.3.20 | K17756 | | GO:0055114,(| AT3G23410.1 | ATFAO3,FAO3 | |
| 48 | PTHR14009,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G11560.2 | 0 |
| 49 | PTHR14009,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G11560.2 | 0 |
| 50 | | | | | | | | |
| 51 | PTHR14009,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G11560.2 | 0 |
| 52 | PTHR14009,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G11560.2 | 0 |
| 53 | PTHR14009,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G11560.2 | 0 |
| 54 | PTHR14009,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G11560.2 | 0 |
| 55 | PTHR14009,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT3G11560.2 | 0 |
| 56 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 | AT3G46530.1 | RPP13 | |
| 57 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 | AT3G46530.1 | RPP13 | |
| 58 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 | AT3G46530.1 | RPP13 | |
| 59 | | | | | | | | |
| 60 | PTHR33477,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT5G60760.1 | 0 |
| | PTHR33477,P ⁻ | 0 | 0 | 0 | 0 | 0 | AT5G60760.1 | 0 |

| | | | | | | |
|----|----------------------------------|----------|----------|----------|-------------------------------------|----------|
| 1 | | | | | | |
| 2 | PTHR33477,P⁻ | 0 | 0 | 0 | 0 AT5G60760.1 | 0 |
| 3 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT4G26090.1 RPS2 | |
| 4 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT4G26090.1 RPS2 | |
| 5 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G14470.1 | 0 |
| 6 | PTHR31907,P ⁻ | 0 | 0 | 0 | GO:0009607,(AT1G70890.1 MLP43 | |
| 7 | PTHR31907,P ⁻ | 0 | 0 | 0 | GO:0009607,(AT1G70890.1 MLP43 | |
| 8 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0005515 AT3G14470.1 | 0 |
| 9 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G14470.1 | 0 |
| 10 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G14460.1 | 0 |
| 11 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G14460.1 | 0 |
| 12 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G14460.1 | 0 |
| 13 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G14470.1 | 0 |
| 14 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0005515,(AT3G14470.1 | 0 |
| 15 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G14460.1 | 0 |
| 16 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G14470.1 | 0 |
| 17 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0005515,(AT3G14470.1 | 0 |
| 18 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G14460.1 | 0 |
| 19 | PTHR23155,P ⁻ | 0 | 0 | 0 | GO:0043531 AT3G14470.1 | 0 |
| 20 | PTHR32133,P ⁻ | 0 | 0 | 0 | GO:0005515 AT5G43190.1 | 0 |
| 21 | PTHR22762,P ⁻ | 0 | 3.2.1.20 | 0 | GO:0005975,(AT5G63840.1 PSL5,RSW3 | |
| 22 | PTHR23155,P ⁻ | 0 | 0 | 0 | GO:0043531 AT3G14470.1 | 0 |
| 23 | PTHR23155,P ⁻ | 0 | 0 | 0 | GO:0043531 AT3G14470.1 | 0 |
| 24 | PTHR23155,P ⁻ KOG0617 | | 0 | 0 | GO:0005515,(AT3G14470.1 | 0 |
| 25 | PTHR23155,P ⁻ KOG0617 | | 0 | 0 | GO:0005515,(AT3G14470.1 | 0 |
| 26 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0005515,(AT3G14470.1 | 0 |
| 27 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0005515,(AT3G14470.1 | 0 |
| 28 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0005515,(AT3G14470.1 | 0 |
| 29 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0005515,(AT3G14470.1 | 0 |
| 30 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0005515,(AT3G14470.1 | 0 |
| 31 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0005515,(AT3G14470.1 | 0 |
| 32 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0005515,(AT3G14470.1 | 0 |
| 33 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0005515,(AT3G14470.1 | 0 |
| 34 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0005515,(AT3G14470.1 | 0 |
| 35 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0005515,(AT3G14470.1 | 0 |
| 36 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0005515,(AT3G14470.1 | 0 |
| 37 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0005515,(AT3G14470.1 | 0 |
| 38 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0005515,(AT3G14470.1 | 0 |
| 39 | PTHR27008,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT2G36570.1 | 0 |
| 40 | PTHR27008,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT2G36570.1 | 0 |
| 41 | PTHR11003,P ⁻ | 0 | 0 | K05389 | 0 AT4G01840.1 ATKCO5,ATTP | |
| 42 | PTHR31375,P ⁻ | 0 | 3.2.1.15 | K01213 | GO:0005975,(AT3G26610.1 | 0 |
| 43 | PTHR31375,P ⁻ | 0 | 3.2.1.15 | K01213 | GO:0005975,(AT3G26610.1 | 0 |
| 44 | PTHR18896,P ⁻ | 0 | 3.1.4.4 | K01115 | GO:0003824,(AT4G35790.2 ATPLDELTA,I | |
| 45 | PTHR18896,P ⁻ | 0 | 3.1.4.4 | K01115 | GO:0003824,(AT4G35790.2 ATPLDELTA,I | |
| 46 | PTHR21596,P ⁻ | 0 | 0 | 0 | GO:0031047 AT5G23570.1 ATSGS3,SGS3 | |
| 47 | PTHR37076,P ⁻ | 0 | 0 | 0 | 0 | 0 |
| 48 | PTHR37076,P ⁻ | 0 | 0 | 0 | 0 | 0 |
| 49 | PTHR24298,P ⁻ KOG0156 | | 0 | 0 | GO:0055114,(AT1G11600.1 CYP77B1 | |
| 50 | PTHR24298,P ⁻ KOG0156 | | 0 | 0 | GO:0055114,(AT1G11600.1 CYP77B1 | |
| 51 | PTHR22814,P ⁻ KOG1603 | | 0 | 0 | GO:0046872,(AT5G27690.1 | 0 |
| 52 | PTHR22814,P ⁻ KOG1603 | | 0 | 0 | GO:0046872,(AT5G27690.1 | 0 |
| 53 | PTHR36884 | 0 | 0 | 0 | 0 AT5G58040.1 ATFIP1[V],ATF | |
| 54 | PTHR27002,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT4G23180.1 CRK10,RLK4 | |
| 55 | PTHR27002,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT4G23180.1 CRK10,RLK4 | |

| | | | | | |
|----|----------------------------------|------------|----------|-------------------------|---|
| 1 | | | | | |
| 2 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G08070.1 OTP82 |
| 3 | PTHR11203,P ⁻ KOG1137 | 3.5.2.6 | | 0 | GO:0046872,(AT5G63420.1 emb2746 |
| 4 | PTHR11203,P ⁻ KOG1137 | 3.5.2.6 | | 0 | GO:0046872,(AT5G63420.1 emb2746 |
| 5 | | | | | |
| 6 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT5G10520.1 RBK1 |
| 7 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT5G10520.1 RBK1 |
| 8 | PTHR10641,P ⁻ | 0 | 0 | 0 | 0 AT3G27785.1 ATMYB118,M |
| 9 | | | | | |
| 10 | PTHR22870,P ⁻ KOG1427 | | 0 | 0 | 0 AT5G16040.1 |
| 11 | PTHR22870,P ⁻ KOG1427 | | 0 | 0 | 0 AT5G16040.1 |
| 12 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G12775.1 |
| 13 | | | | | |
| 14 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G12775.1 |
| 15 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G14460.1 |
| 16 | PTHR33147 | 0 | 0 | 0 | 0 AT2G02130.1 LCR68,PDF2.3 |
| 17 | | | | | |
| 18 | PTHR33147 | 0 | 0 | 0 | 0 AT2G02130.1 LCR68,PDF2.3 |
| 19 | PTHR24012,P ⁻ | 0 | 0 K14398 | GO:0003676 | AT5G55670.1 |
| 20 | PTHR24012,P ⁻ | 0 | 0 K14398 | GO:0003676 | AT5G55670.1 |
| 21 | | | | | |
| 22 | PTHR24012,P ⁻ | 0 | 0 K14398 | GO:0003676 | AT5G55670.1 |
| 23 | PTHR11085,P ⁻ KOG1905 | | 0 K11416 | GO:0070403 | AT5G55760.1 SRT1 |
| 24 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G14470.1 |
| 25 | | | | | |
| 26 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G14470.1 |
| 27 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G14460.1 |
| 28 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G14460.1 |
| 29 | | | | | |
| 30 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G46530.1 RPP13 |
| 31 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G46530.1 RPP13 |
| 32 | PTHR23155,P ⁻ | 0 | 0 | 0 | GO:0005515,(AT4G27190.1 |
| 33 | | | | | |
| 34 | PTHR23155,P ⁻ | 0 | 0 | 0 | GO:0005515,(AT4G27190.1 |
| 35 | PTHR34112,P ⁻ | 0 | 0 | 0 | 0 AT1G36990.1 |
| 36 | PTHR34112,P ⁻ | 0 | 0 | 0 | 0 AT1G36990.1 |
| 37 | | | | | |
| 38 | PTHR31218,P ⁻ | 0 | 0 | 0 | GO:0016021,(AT1G09380.1 |
| 39 | PTHR24356,P ⁻ | 0 2.7.11.1 | | 0 | GO:0006468,(AT4G33080.2 |
| 40 | PTHR24356,P ⁻ | 0 2.7.11.1 | | 0 | GO:0006468,(AT4G33080.2 |
| 41 | | | | | |
| 42 | PTHR24072,P ⁻ KOG0393 | 3.6.5.2 | K04392 | GO:0007264,(AT3G48040.1 | ARAC8,ATRAC |
| 43 | PTHR24072,P ⁻ KOG0393 | 3.6.5.2 | K04392 | GO:0007264,(AT3G48040.1 | ARAC8,ATRAC |
| 44 | PTHR24072,P ⁻ KOG0393 | 3.6.5.2 | K04392 | GO:0007264,(AT3G48040.1 | ARAC8,ATRAC |
| 45 | PTHR24072,P ⁻ KOG0393 | 3.6.5.2 | K04392 | GO:0007264,(AT3G48040.1 | ARAC8,ATRAC |
| 46 | | | | | |
| 47 | PTHR33509,P ⁻ | 0 | 0 | 0 | GO:0006950 AT4G15910.1 ATDI21,DI21 |
| 48 | PTHR11017,P ⁻ | 0 | 0 | 0 | GO:0007165,(AT5G36930.2 |
| 49 | PTHR11017,P ⁻ | 0 | 0 | 0 | GO:0007165,(AT5G36930.2 |
| 50 | | | | | |
| 51 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G14460.1 |
| 52 | PTHR31016,P ⁻ | 0 | 0 | 0 | 0 AT2G30530.1 |
| 53 | PTHR31992,P⁻ | 0 | 0 | 0 | GO:0006355,(AT1G51700.1 ADOF1,DOF1 |
| 54 | | | | | |
| 55 | PTHR11472,P ⁻ | 0 3.6.4.13 | K11273 | GO:0016818,(AT1G79890.1 | |
| 56 | PTHR11472,P ⁻ | 0 3.6.4.13 | K11273 | GO:0016818,(AT1G79890.1 | |
| 57 | PTHR31636,P ⁻ | 0 | 0 | 0 | 0 AT1G50420.1 SCL-3,SCL3 |
| 58 | | | | | |
| 59 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G14470.1 |
| 60 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G14470.1 |
| | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 AT3G14470.1 |

| | | | | | | | | |
|----|----------------------------------|-----------------|----------|--------|--------------|--------------|--------------|---|
| 1 | | | | | | | | |
| 2 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 | AT3G14470.1 | 0 | |
| 3 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 | AT3G14460.1 | 0 | |
| 4 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 | AT3G14460.1 | 0 | |
| 5 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 | AT3G14460.1 | 0 | |
| 6 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 | AT3G14460.1 | 0 | |
| 7 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 | GO:0043531 | AT3G14460.1 | 0 | |
| 8 | PTHR23155,P ⁻ | 0 | 0 | 0 | GO:0043531 | AT3G14470.1 | 0 | |
| 9 | PTHR23155,P ⁻ | 0 | 0 | 0 | GO:0043531 | AT3G14470.1 | 0 | |
| 10 | PTHR23155,P ⁻ | 0 | 0 | 0 | GO:0043531 | AT3G14470.1 | 0 | |
| 11 | PTHR23155,P ⁻ | 0 | 0 | 0 | 0 | AT3G14470.1 | 0 | |
| 12 | PTHR23155,P ⁻ | 0 | 0 | 0 | 0 | AT3G14470.1 | 0 | |
| 13 | PTHR23155,P ⁻ | 0 | 0 | 0 | 0 | AT3G14470.1 | 0 | |
| 14 | PTHR32227,P ⁻ | 0 | 3.2.1.39 | 0 | GO:0005975,C | AT1G32860.1 | 0 | |
| 15 | PTHR32227,P ⁻ | 0 | 3.2.1.39 | 0 | GO:0005975,C | AT1G32860.1 | 0 | |
| 16 | PTHR31065,P ⁻ | 0 | 0 | 0 | 0 | AT2G27930.1 | 0 | |
| 17 | PTHR31065,P ⁻ | 0 | 0 | 0 | 0 | AT2G27930.1 | 0 | |
| 18 | PTHR31065,P ⁻ | 0 | 0 | 0 | 0 | AT2G27930.1 | 0 | |
| 19 | PTHR31065,P ⁻ | 0 | 0 | 0 | 0 | AT2G27930.1 | 0 | |
| 20 | PTHR31065,P ⁻ | 0 | 0 | 0 | 0 | AT2G27930.1 | 0 | |
| 21 | PTHR31065,P ⁻ | 0 | 0 | 0 | 0 | AT2G27930.1 | 0 | |
| 22 | PTHR31745,P ⁻ | 0 | 0 | 0 | 0 | AT1G14410.1 | ATWHY1,PTAC | |
| 23 | PTHR31745,P ⁻ | 0 | 0 | 0 | 0 | AT1G14410.1 | ATWHY1,PTAC | |
| 24 | PTHR11017,P ⁻ KOG0617 | | 0 | 0 | GO:0007165,C | AT5G17680.1 | 0 | |
| 25 | PTHR14255,P ⁻ | 0 | 0 | 0 | GO:0016021 | AT2G25737.1 | 0 | |
| 26 | PTHR14255,P ⁻ | 0 | 0 | 0 | GO:0016021 | AT2G25737.1 | 0 | |
| 27 | PTHR14255,P ⁻ | 0 | 0 | 0 | GO:0016021 | AT2G25737.1 | 0 | |
| 28 | PTHR14255,P ⁻ | 0 | 0 | 0 | GO:0016021 | AT2G25737.1 | 0 | |
| 29 | PTHR14255,P ⁻ | 0 | 0 | 0 | GO:0016021 | AT2G25737.1 | 0 | |
| 30 | PTHR14255,P ⁻ | 0 | 0 | 0 | GO:0016021 | AT2G25737.1 | 0 | |
| 31 | PTHR14255,P ⁻ | 0 | 0 | 0 | GO:0016021 | AT2G25737.1 | 0 | |
| 32 | PTHR14255,P ⁻ | 0 | 0 | 0 | GO:0016021 | AT2G25737.1 | 0 | |
| 33 | PTHR14255,P ⁻ | 0 | 0 | 0 | GO:0016021 | AT2G25737.1 | 0 | |
| 34 | PTHR14255,P ⁻ | 0 | 0 | 0 | GO:0016021 | AT2G25737.1 | 0 | |
| 35 | PTHR14255,P ⁻ | 0 | 0 | 0 | GO:0016021 | AT2G25737.1 | 0 | |
| 36 | PTHR14255,P ⁻ | 0 | 0 | 0 | GO:0016021 | AT2G25737.1 | 0 | |
| 37 | PTHR14255,P ⁻ | 0 | 0 | 0 | GO:0016021 | AT2G25737.1 | 0 | |
| 38 | PTHR14255,P ⁻ | 0 | 0 | 0 | GO:0016021 | AT2G25737.1 | 0 | |
| 39 | PTHR14255,P ⁻ | 0 | 0 | 0 | GO:0016021 | AT2G25737.1 | 0 | |
| 40 | PTHR14255,P ⁻ | 0 | 0 | 0 | GO:0016021 | AT2G25737.1 | 0 | |
| 41 | PTHR13140,P ⁻ | 0 | 3.6.4.1 | 0 | GO:0005515,C | AT3G19960.1 | ATM1 | |
| 42 | PTHR13140,P ⁻ | 0 | 3.6.4.1 | 0 | GO:0005515,C | AT3G19960.1 | ATM1 | |
| 43 | PTHR13140,P ⁻ | 0 | 3.6.4.1 | 0 | GO:0005515,C | AT3G19960.1 | ATM1 | |
| 44 | PTHR13140,P ⁻ | 0 | 3.6.4.1 | 0 | GO:0005515,C | AT3G19960.1 | ATM1 | |
| 45 | PTHR13140,P ⁻ | 0 | 3.6.4.1 | 0 | GO:0005515,C | AT3G19960.1 | ATM1 | |
| 46 | PTHR13140,P ⁻ | 0 | 3.6.4.1 | 0 | GO:0005515,C | AT3G19960.1 | ATM1 | |
| 47 | PTHR13140,P ⁻ | 0 | 3.6.4.1 | 0 | GO:0005515,C | AT3G19960.1 | ATM1 | |
| 48 | PTHR13140,P ⁻ | 0 | 3.6.4.1 | 0 | GO:0005515,C | AT3G19960.1 | ATM1 | |
| 49 | PTHR37076,P ⁻ | 0 | 0 | 0 | 0 | 0 | 0 | |
| 50 | PTHR37076,P ⁻ | 0 | 0 | 0 | 0 | 0 | 0 | |
| 51 | PTHR37076,P ⁻ | 0 | 0 | 0 | 0 | 0 | 0 | |
| 52 | PTHR32093,P ⁻ | 0 | 0 | 0 | 0 | AT3G50370.1 | 0 | |
| 53 | PTHR32093,P ⁻ | 0 | 0 | 0 | 0 | AT3G50370.1 | 0 | |
| 54 | PTHR32093,P ⁻ | 0 | 0 | 0 | 0 | AT3G50370.1 | 0 | |
| 55 | PTHR32093,P ⁻ | 0 | 0 | 0 | 0 | AT3G50370.1 | 0 | |
| 56 | PTHR22884,P ⁻ KOG1082 | 2.1.1.43 | K11420 | 0 | GO:0005515,C | AT4G13460.1 | SDG22,SET22, | |
| 57 | PTHR22884,P ⁻ KOG1082 | 2.1.1.43 | K11420 | 0 | GO:0005515,C | AT4G13460.1 | SDG22,SET22, | |
| 58 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | AT2G03380.1 | 0 | |
| 59 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 | AT2G03380.1 | 0 | |
| 60 | PTHR11252,P ⁻ | 0 | 2.7.7.8 | K00962 | 0 | GO:0006396,C | AT5G14580.1 | 0 |
| | PTHR27001,P ⁻ KOG1187 | 2.7.11.1,2.7.10 | | 0 | GO:0006468,C | AT1G71830.1 | ATSERK1,SERK | |

| | | | | | | |
|----|----------------------------------|-----------------|----------|----------------|--------------------------|---|
| 1 | | | | | | |
| 2 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1,2.7.11 | | 0 GO:0006468,C | AT1G71830.1 ATSERK1,SERK | |
| 3 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G03510.1 | 0 |
| 4 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G03510.1 | 0 |
| 5 | | | | | | |
| 6 | PTHR23198,P ⁻ | 0 | 0 K14297 | | 0 AT1G10390.2 | 0 |
| 7 | PTHR23198,P ⁻ | 0 | 0 K14297 | | 0 AT1G10390.2 | 0 |
| 8 | PTHR12956,P ⁻ | 0 | 0 | 0 | 0 AT1G53040.1 | 0 |
| 9 | | | | | | |
| 10 | PTHR22838,P ⁻ | 0 | 0 | 0 GO:0005515 | AT5G08560.1 | 0 |
| 11 | PTHR22838,P ⁻ | 0 | 0 | 0 GO:0005515 | AT5G08560.1 | 0 |
| 12 | PTHR11934,P ⁻ KOG3075 | 5.3.1.6 | K01807 | GO:0009052,C | AT3G04790.1 | 0 |
| 13 | | | | | | |
| 14 | PTHR31656,P ⁻ | 0 2.4.1.10 | | 0 | 0 AT3G19430.1 | 0 |
| 15 | PTHR31656,P ⁻ | 0 2.4.1.10 | | 0 | 0 AT3G19430.1 | 0 |
| 16 | PTHR24177,P ⁻ KOG4412 | 2.7.11.1 | | 0 | 0 AT3G18670.1 | 0 |
| 17 | | | | | | |
| 18 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G09060.1 | 0 |
| 19 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT3G09060.1 | 0 |
| 20 | PTHR22792,P ⁻ KOG2590 | | 0 K18757 | | 0 AT5G21160.3 | 0 |
| 21 | | | | | | |
| 22 | PTHR27008,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0005515,C | AT5G35390.1 | 0 |
| 23 | PTHR31659,P ⁻ | 0 | 0 | 0 | 0 AT3G09070.1 | 0 |
| 24 | PTHR31992,P ⁻ | 0 | 0 | 0 GO:0006355,C | AT3G55370.2 OBP3 | |
| 25 | | | | | | |
| 26 | PTHR23084,P ⁻ | 0 2.7.1.68 | | 0 | 0 AT4G17080.1 | 0 |
| 27 | PTHR23084,P ⁻ | 0 2.7.1.68 | | 0 | 0 AT4G17080.1 | 0 |
| 28 | PTHR23084,P ⁻ | 0 2.7.1.68 | | 0 | 0 AT4G17080.1 | 0 |
| 29 | PTHR23084,P ⁻ | 0 2.7.1.68 | | 0 | 0 AT4G17080.1 | 0 |
| 30 | PTHR23084,P ⁻ | 0 2.7.1.68 | | 0 | 0 AT4G17080.1 | 0 |
| 31 | PTHR23084,P ⁻ | 0 2.7.1.68 | | 0 | 0 AT4G17080.1 | 0 |
| 32 | PTHR23084,P ⁻ | 0 2.7.1.68 | | 0 | 0 AT4G17080.1 | 0 |
| 33 | PTHR23084,P ⁻ | 0 2.7.1.68 | | 0 | 0 AT4G17080.1 | 0 |
| 34 | PTHR23084,P ⁻ | 0 2.7.1.68 | | 0 | 0 AT4G17080.1 | 0 |
| 35 | PTHR23084,P ⁻ | 0 2.7.1.68 | | 0 | 0 AT4G17080.1 | 0 |
| 36 | PTHR19241,P ⁻ | 0 3.6.3.25 | | 0 GO:0016887,C | AT1G59870.1 ABCG36,ATAB | |
| 37 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14470.1 | 0 |
| 38 | | | | | | |
| 39 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14470.1 | 0 |
| 40 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14460.1 | 0 |
| 41 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14470.1 | 0 |
| 42 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14460.1 | 0 |
| 43 | PTHR23155,P ⁻ KOG4658 | | 0 | 0 GO:0043531 | AT3G14460.1 | 0 |
| 44 | | | | | | |
| 45 | | | | | | |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| arabi-defline | ID | Annot_defline | IDENTIFIER |
|--|---------------------|--------------------|---------------------------|
| NB-ARC domain-containing disease resistance protein | Phvul.004G04 | PTHR23155//I | Phvul.004G04 |
| Galactose oxidase/kelch repeat superfamily protein | Phvul.001G22 | PTHR23244//I | Phvul.001G22 |
| Galactose oxidase/kelch repeat superfamily protein | Phvul.001G22 | PTHR23244//I | Phvul.001G22 |
| Galactose oxidase/kelch repeat superfamily protein | Phvul.001G22 | PTHR23244//I | Phvul.001G22 |
| Galactose oxidase/kelch repeat superfamily protein | Phvul.001G22 | PTHR23244//I | Phvul.001G22 |
| Galactose oxidase/kelch repeat superfamily protein | Phvul.007G20 | PTHR23244//I | Phvul.007G20 |
| Galactose oxidase/kelch repeat superfamily protein | Phvul.007G20 | PTHR23244//I | Phvul.007G20 |
| Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G06 | PTHR23155:S | Phvul.008G06 |
| Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G06 | PTHR23155:S | Phvul.008G06 |
| Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G06 | PTHR23155:S | Phvul.008G06 |
| Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G06 | PTHR23155:S | Phvul.008G06 |
| transmembrane receptors;ATP binding | Phvul.002G07 | PTHR11017:S | Phvul.002G07 |
| RAD-like 6 | Phvul.001G21 | PTHR24078:S | Phvul.001G21 |
| GATA transcription factor 26 | Phvul.002G00 | PTHR10071:S | Phvul.002G00 |
| GATA transcription factor 26 | Phvul.002G00 | PTHR10071:S | Phvul.002G00 |
| transmembrane receptors;ATP binding | Phvul.003G07 | PTHR11017:S | Phvul.003G07 |
| | 0 | 0 | 0 Phvul.003G24 |
| | 0 | 0 | 0 Phvul.003G24 |
| | 0 | 0 | 0 Phvul.003G24 |
| Disease resistance protein (TIR-NBS-LRR class) family | Phvul.004G13 | PTHR11017//I | Phvul.004G13 |
| Protein with RING/U-box and TRAF-like domains | Phvul.005G02 | PTHR10315//I | Phvul.005G02 |
| Protein with RING/U-box and TRAF-like domains | Phvul.005G02 | PTHR10315//I | Phvul.005G02 |
| Protein with RING/U-box and TRAF-like domains | Phvul.005G02 | PTHR10315//I | Phvul.005G02 |
| squamosa promoter binding protein-like 1 | Phvul.007G21 | PTHR31251:S | Phvul.007G21 |
| squamosa promoter binding protein-like 1 | Phvul.007G21 | PTHR31251:S | Phvul.007G21 |
| non-intrinsic ABC protein 11 | Phvul.008G05 | PTHR24220:S | Phvul.008G05 |
| | 0 | Phvul.008G28 | PTHR21716 - `Phvul.008G28 |
| | 0 | Phvul.008G28 | PTHR21716 - `Phvul.008G28 |
| NB-ARC domain-containing disease resistance protein | Phvul.010G06 | PTHR23155//I | Phvul.010G06 |
| disease resistance protein (TIR-NBS-LRR class), putative | Phvul.010G13 | PTHR11017//I | Phvul.010G13 |
| Transducin/WD40 repeat-like superfamily protein | Phvul.011G14 | PTHR14221:S | Phvul.011G14 |
| Transducin/WD40 repeat-like superfamily protein | Phvul.011G14 | PTHR14221:S | Phvul.011G14 |
| Transducin/WD40 repeat-like superfamily protein | Phvul.011G14 | PTHR14221:S | Phvul.011G14 |
| Transducin/WD40 repeat-like superfamily protein | Phvul.011G14 | PTHR14221:S | Phvul.011G14 |
| Transducin/WD40 repeat-like superfamily protein | Phvul.011G14 | PTHR14221:S | Phvul.011G14 |
| Transducin/WD40 repeat-like superfamily protein | Phvul.011G14 | PTHR14221:S | Phvul.011G14 |
| Transducin/WD40 repeat-like superfamily protein | Phvul.011G14 | PTHR14221:S | Phvul.011G14 |
| NB-ARC domain-containing disease resistance protein | Phvul.011G16 | PTHR23155//I | Phvul.011G16 |
| disease resistance protein (TIR-NBS-LRR class), putative | Phvul.001G12 | PF07725//PF1 | Phvul.001G12 |
| NB-ARC domain-containing disease resistance protein | Phvul.001G13 | PTHR23155//I | Phvul.001G13 |
| NB-ARC domain-containing disease resistance protein | Phvul.001G13 | PTHR23155//I | Phvul.001G13 |
| Double Clp-N motif-containing P-loop nucleoside triphosphate | Phvul.001G24 | PTHR11638:S | Phvul.001G24 |
| Double Clp-N motif-containing P-loop nucleoside triphosphate | Phvul.001G24 | PTHR11638:S | Phvul.001G24 |
| Plant protein of unknown function (DUF828) with | Phvul.002G05 | PF05703 - Au | Phvul.002G05 |
| Plant protein of unknown function (DUF828) with | Phvul.002G05 | PF05703 - Au | Phvul.002G05 |

| | | | |
|----|--|-----------------------------------|---------------------|
| 1 | | | |
| 2 | cytochrome P450, family 707, subfamily A, polypeptide | Phvul.002G12PTHR24286:SI | Phvul.002G12 |
| 3 | | 0 | 0 |
| 4 | | | 0 Phvul.002G18 |
| 5 | RNA-binding (RRM/RBD/RNP motifs) family protein | Phvul.002G26K14396 - poly: | Phvul.002G26 |
| 6 | RNA-binding (RRM/RBD/RNP motifs) family protein | Phvul.002G26K14396 - poly: | Phvul.002G26 |
| 7 | Uncharacterised protein family (UPF0497) | Phvul.003G10PTHR11615://I | Phvul.003G10 |
| 8 | Uncharacterised protein family (UPF0497) | Phvul.003G10PTHR11615://I | Phvul.003G10 |
| 9 | quinolinate synthase | Phvul.003G20K03517 - quin | Phvul.003G20 |
| 10 | quinolinate synthase | Phvul.003G20K03517 - quin | Phvul.003G20 |
| 11 | high mobility group | Phvul.004G02K09272 - struc | Phvul.004G02 |
| 12 | disease resistance protein (TIR-NBS-LRR class), putative | Phvul.004G14PF05729//PF1 | Phvul.004G14 |
| 13 | disease resistance protein (TIR-NBS-LRR class), putative | Phvul.004G14PF05729//PF1 | Phvul.004G14 |
| 14 | uroporphyrin methylase 1 | Phvul.005G03PTHR21091:SI | Phvul.005G03 |
| 15 | uroporphyrin methylase 1 | Phvul.005G03PTHR21091:SI | Phvul.005G03 |
| 16 | NB-ARC domain-containing disease resistance protein | Phvul.005G08PTHR23155:SI | Phvul.005G08 |
| 17 | NB-ARC domain-containing disease resistance protein | Phvul.005G08PTHR23155:SI | Phvul.005G08 |
| 18 | Malectin/receptor-like protein kinase family protein | Phvul.006G10PTHR27003:SI | Phvul.006G10 |
| 19 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155://I | Phvul.008G07 |
| 20 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155://I | Phvul.008G07 |
| 21 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155://I | Phvul.008G07 |
| 22 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155://I | Phvul.008G07 |
| 23 | las1-like family protein | Phvul.008G20K16912 - ribosome | Phvul.008G20 |
| 24 | potassium transporter 1 | Phvul.008G25PTHR30540:SI | Phvul.008G25 |
| 25 | potassium transporter 1 | Phvul.008G25PTHR30540:SI | Phvul.008G25 |
| 26 | potassium transporter 1 | Phvul.008G25PTHR30540:SI | Phvul.008G25 |
| 27 | potassium transporter 1 | Phvul.008G25PTHR30540:SI | Phvul.008G25 |
| 28 | Disease resistance protein (TIR-NBS-LRR class) family | Phvul.010G13PF00931//PFC | Phvul.010G13 |
| 29 | Disease resistance protein (TIR-NBS-LRR class) family | Phvul.010G13PF07725 - Leu | Phvul.010G13 |
| 30 | disease resistance protein (TIR-NBS-LRR class), putative | Phvul.010G13PTHR11017://I | Phvul.010G13 |
| 31 | UDP-Glycosyltransferase superfamily protein | Phvul.010G15PTHR12526://I | Phvul.010G15 |
| 32 | UDP-Glycosyltransferase superfamily protein | Phvul.010G15PTHR12526://I | Phvul.010G15 |
| 33 | UDP-Glycosyltransferase superfamily protein | Phvul.010G15PTHR12526://I | Phvul.010G15 |
| 34 | UDP-Glycosyltransferase superfamily protein | Phvul.010G15PTHR12526://I | Phvul.010G15 |
| 35 | disease resistance protein (TIR-NBS-LRR class), putative | Phvul.011G14PF00931//PFC | Phvul.011G14 |
| 36 | disease resistance protein (TIR-NBS-LRR class), putative | Phvul.011G14PF00931//PF1 | Phvul.011G14 |
| 37 | NB-ARC domain-containing disease resistance protein | Phvul.011G15PTHR23155://I | Phvul.011G15 |
| 38 | NB-ARC domain-containing disease resistance protein | Phvul.011G18PTHR23155://I | Phvul.011G18 |
| 39 | NB-ARC domain-containing disease resistance protein | Phvul.011G18PTHR23155://I | Phvul.011G18 |
| 40 | NB-ARC domain-containing disease resistance protein | Phvul.011G19PTHR23155://I | Phvul.011G19 |
| 41 | NB-ARC domain-containing disease resistance protein | Phvul.011G19PF00931//PF1 | Phvul.011G19 |
| 42 | NB-ARC domain-containing disease resistance protein | Phvul.011G19PTHR23155://I | Phvul.011G19 |
| 43 | NB-ARC domain-containing disease resistance protein | Phvul.011G19PF00931//PF1 | Phvul.011G19 |
| 44 | NB-ARC domain-containing disease resistance protein | Phvul.011G19PF00931//PF1 | Phvul.011G19 |
| 45 | LRR and NB-ARC domains-containing disease resistance | Phvul.011G19PTHR23155://I | Phvul.011G19 |
| 46 | NB-ARC domain-containing disease resistance protein | Phvul.011G19PTHR23155://I | Phvul.011G19 |
| 47 | LRR and NB-ARC domains-containing disease resistance | Phvul.011G19PTHR23155://I | Phvul.011G19 |
| 48 | NB-ARC domain-containing disease resistance protein | Phvul.011G19PTHR23155://I | Phvul.011G19 |
| 49 | NB-ARC domain-containing disease resistance protein | Phvul.011G19PTHR23155://I | Phvul.011G19 |
| 50 | NB-ARC domain-containing disease resistance protein | Phvul.011G19PTHR23155://I | Phvul.011G19 |
| 51 | NB-ARC domain-containing disease resistance protein | Phvul.011G19PTHR23155://I | Phvul.011G19 |
| 52 | NB-ARC domain-containing disease resistance protein | Phvul.011G19PTHR23155://I | Phvul.011G19 |
| 53 | NB-ARC domain-containing disease resistance protein | Phvul.011G19PTHR23155://I | Phvul.011G19 |
| 54 | NB-ARC domain-containing disease resistance protein | Phvul.011G19PTHR23155://I | Phvul.011G19 |
| 55 | NB-ARC domain-containing disease resistance protein | Phvul.011G19PTHR23155://I | Phvul.011G19 |
| 56 | NB-ARC domain-containing disease resistance protein | Phvul.011G19PTHR23155://I | Phvul.011G19 |
| 57 | NB-ARC domain-containing disease resistance protein | Phvul.011G19PTHR23155://I | Phvul.011G19 |
| 58 | NB-ARC domain-containing disease resistance protein | Phvul.011G19PTHR23155://I | Phvul.011G19 |
| 59 | NB-ARC domain-containing disease resistance protein | Phvul.011G19PTHR23155://I | Phvul.011G19 |
| 60 | NB-ARC domain-containing disease resistance protein | Phvul.011G19PTHR23155://I | Phvul.011G19 |

1 LRR and NB-ARC domains-containing disease resis Phvul.011G19PTHR23155//IPhvul.011G19
 2 NB-ARC domain-containing disease resistance pro Phvul.011G19PTHR23155//IPhvul.011G19
 3 NB-ARC domain-containing disease resistance pro Phvul.011G19PF00931//PF1Phvul.011G19
 4 NB-ARC domain-containing disease resistance pro Phvul.011G19PTHR23155//IPhvul.011G19
 5 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//IPhvul.011G20
 6 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//IPhvul.011G20
 7 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvul.011G20
 8 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvul.011G20
 9 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//IPhvul.011G20
 10 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//IPhvul.011G20
 11 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvul.011G20
 12 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvul.011G20
 13 Zinc-binding alcohol dehydrogenase family proteirPhvul.L00233:PTHR11695:SIPhvul.L00233:
 14 Zinc-binding alcohol dehydrogenase family proteirPhvul.L00233:PTHR11695:SIPhvul.L00233:
 15 Zinc-binding alcohol dehydrogenase family proteirPhvul.L00233:PTHR11695:SIPhvul.L00233:
 16 Zinc-binding alcohol dehydrogenase family proteirPhvul.L00233:PTHR11695:SIPhvul.L00233:
 17 Phospholipid/glycerol acyltransferase family protePhvul.001G01K13510 - lysořPhvul.001G01
 18 Phospholipid/glycerol acyltransferase family protePhvul.001G01K13510 - lysořPhvul.001G01
 19 Phospholipid/glycerol acyltransferase family protePhvul.001G01K13510 - lysořPhvul.001G01
 20 Phospholipid/glycerol acyltransferase family protePhvul.001G01K13510 - lysořPhvul.001G01
 21 basic helix-loop-helix (bHLH) DNA-binding superfa Phvul.001G08PTHR31945:SIPhvul.001G08
 22 basic helix-loop-helix (bHLH) DNA-binding superfa Phvul.001G08PTHR31945:SIPhvul.001G08
 23 expansin A4 Phvul.001G23PTHR31867:SIPhvul.001G23
 24 expansin A4 Phvul.001G23PTHR31867:SIPhvul.001G23
 25 PLATZ transcription factor family protein Phvul.002G04PF04640 - PLAPhvul.002G04
 26 PLATZ transcription factor family protein Phvul.002G04PF04640 - PLAPhvul.002G04
 27 PLATZ transcription factor family protein Phvul.002G04PF04640 - PLAPhvul.002G04
 28 PLATZ transcription factor family protein Phvul.002G04PF04640 - PLAPhvul.002G04
 29 alpha/beta-Hydrolases superfamily protein Phvul.002G29PTHR31479:SIPhvul.002G29
 30 extra-large G-protein 1 Phvul.003G01PTHR10218:SIPhvul.003G01
 31 extra-large G-protein 1 Phvul.003G01PTHR10218:SIPhvul.003G01
 32 plastid transcriptionally active 2 Phvul.003G19PF01535//PF1Phvul.003G19
 33 plastid transcriptionally active 2 Phvul.003G19PF01535//PF1Phvul.003G19
 34 C2H2-like zinc finger protein Phvul.003G25PTHR10593:SIPhvul.003G25
 35 C2H2-like zinc finger protein Phvul.003G25PTHR10593:SIPhvul.003G25
 36 **autophagy 2 Phvul.003G29K17906 - autoPhvul.003G29**
 37 **autophagy 2 Phvul.003G29K17906 - autoPhvul.003G29**
 38 **autophagy 2 Phvul.003G29K17906 - autoPhvul.003G29**
 39 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 40 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 41 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 42 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 43 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 44 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 45 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 46 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 47 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 48 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 49 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 50 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 51 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 52 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 53 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 54 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 55 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 56 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 57 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 58 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 59 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03
 60 purple acid phosphatase 23 Phvul.004G033.1.3.2//3.1.3 Phvul.004G03

| | |
|----|---|
| 1 | |
| 2 | NB-ARC domain-containing disease resistance pro Phvul.004G04PTHR23155//IPhvul.004G04 |
| 3 | NB-ARC domain-containing disease resistance pro Phvul.004G04PTHR23155//IPhvul.004G04 |
| 4 | septum site-determining protein (MIND) Phvul.004G10K03609 - sept Phvul.004G10 |
| 5 | septum site-determining protein (MIND) Phvul.004G10K03609 - sept Phvul.004G10 |
| 6 | septum site-determining protein (MIND) Phvul.004G10K03609 - sept Phvul.004G10 |
| 7 | carboxyesterase 18 Phvul.004G13PTHR23024//IPhvul.004G13 |
| 8 | Tetratricopeptide repeat (TPR)-like superfamily pr Phvul.005G16PF01535//PF1Phvul.005G16 |
| 9 | Tetratricopeptide repeat (TPR)-like superfamily pr Phvul.005G16PF01535//PF1Phvul.005G16 |
| 10 | Tetratricopeptide repeat (TPR)-like superfamily pr Phvul.005G16PF01535//PF1Phvul.005G16 |
| 11 | NB-ARC domain-containing disease resistance pro Phvul.006G06PTHR23155//IPhvul.006G06 |
| 12 | expansin A13 Phvul.006G08PTHR31867:SIPhvul.006G08 |
| 13 | |
| 14 | 0 0 0 Phvul.006G14 |
| 15 | O-methyltransferase family protein Phvul.006G18PTHR11746//IPhvul.006G18 |
| 16 | O-methyltransferase family protein Phvul.006G18PTHR11746//IPhvul.006G18 |
| 17 | O-methyltransferase family protein Phvul.006G18PTHR11746//IPhvul.006G18 |
| 18 | 0 0 0 Phvul.007G02 |
| 19 | P-loop containing nucleoside triphosphate hydrolase Phvul.007G093.6.3.16 - ArsePhvul.007G09 |
| 20 | Leucine-rich repeat protein kinase family protein Phvul.008G15PF07714//PFCPhvul.008G15 |
| 21 | sterol methyltransferase 2 Phvul.009G022.1.1.142 - CyPhvul.009G02 |
| 22 | sterol methyltransferase 2 Phvul.009G022.1.1.142 - CyPhvul.009G02 |
| 23 | sterol methyltransferase 2 Phvul.009G022.1.1.142 - CyPhvul.009G02 |
| 24 | abscisic acid responsive elements-binding factor 2 Phvul.009G06PTHR22952//IPhvul.009G06 |
| 25 | abscisic acid responsive elements-binding factor 2 Phvul.009G06PTHR22952//IPhvul.009G06 |
| 26 | abscisic acid responsive elements-binding factor 2 Phvul.009G06PTHR22952//IPhvul.009G06 |
| 27 | abscisic acid responsive elements-binding factor 2 Phvul.009G06PTHR22952//IPhvul.009G06 |
| 28 | abscisic acid responsive elements-binding factor 2 Phvul.009G06PTHR22952//IPhvul.009G06 |
| 29 | abscisic acid responsive elements-binding factor 2 Phvul.009G06PTHR22952//IPhvul.009G06 |
| 30 | Pentatricopeptide repeat (PPR) superfamily protein Phvul.009G21K17964 - leuciPhvul.009G21 |
| 31 | TRICHOME BIREFRINGENCE-LIKE 16 Phvul.009G22PF14416 - PM Phvul.009G22 |
| 32 | TRICHOME BIREFRINGENCE-LIKE 16 Phvul.009G22PF14416 - PM Phvul.009G22 |
| 33 | TRICHOME BIREFRINGENCE-LIKE 16 Phvul.009G22PF14416 - PM Phvul.009G22 |
| 34 | TRICHOME BIREFRINGENCE-LIKE 16 Phvul.009G22PF14416 - PM Phvul.009G22 |
| 35 | TRICHOME BIREFRINGENCE-LIKE 16 Phvul.009G22PF14416 - PM Phvul.009G22 |
| 36 | NB-ARC domain-containing disease resistance pro Phvul.009G23PTHR23155:SIPhvul.009G23 |
| 37 | NB-ARC domain-containing disease resistance pro Phvul.009G23PTHR23155:SIPhvul.009G23 |
| 38 | NB-ARC domain-containing disease resistance pro Phvul.009G23PTHR23155:SIPhvul.009G23 |
| 39 | NB-ARC domain-containing disease resistance pro Phvul.009G23PTHR23155:SIPhvul.009G23 |
| 40 | Disease resistance protein (TIR-NBS-LRR class) far Phvul.010G00PF00931//PF1Phvul.010G00 |
| 41 | Disease resistance protein (TIR-NBS-LRR class) far Phvul.010G00PF00931//PF1Phvul.010G00 |
| 42 | Disease resistance protein (TIR-NBS-LRR class) far Phvul.010G00PF00931//PF1Phvul.010G00 |
| 43 | Tetratricopeptide repeat (TPR)-like superfamily pr Phvul.010G05PF13041 - PPFPhvul.010G05 |
| 44 | Tetratricopeptide repeat (TPR)-like superfamily pr Phvul.010G05PF13041 - PPFPhvul.010G05 |
| 45 | Tetratricopeptide repeat (TPR)-like superfamily pr Phvul.010G05PF13041 - PPFPhvul.010G05 |
| 46 | LRR and NB-ARC domains-containing disease resistance Phvul.010G06PTHR23155//IPhvul.010G06 |
| 47 | fatty alcohol oxidase 3 Phvul.010G07K17756 - long Phvul.010G07 |
| 48 | LETM1-like protein Phvul.010G14PTHR14009//IPhvul.010G14 |
| 49 | LETM1-like protein Phvul.010G14PTHR14009//IPhvul.010G14 |
| 50 | LETM1-like protein Phvul.010G14PTHR14009//IPhvul.010G14 |
| 51 | LETM1-like protein Phvul.010G14PTHR14009//IPhvul.010G14 |
| 52 | LETM1-like protein Phvul.010G14PTHR14009//IPhvul.010G14 |
| 53 | LETM1-like protein Phvul.010G14PTHR14009//IPhvul.010G14 |
| 54 | LETM1-like protein Phvul.010G14PTHR14009//IPhvul.010G14 |
| 55 | LETM1-like protein Phvul.010G14PTHR14009//IPhvul.010G14 |
| 56 | NB-ARC domain-containing disease resistance pro Phvul.011G01PTHR23155:SIPhvul.011G01 |
| 57 | NB-ARC domain-containing disease resistance pro Phvul.011G01PTHR23155:SIPhvul.011G01 |
| 58 | NB-ARC domain-containing disease resistance pro Phvul.011G01PTHR23155:SIPhvul.011G01 |
| 59 | NB-ARC domain-containing disease resistance pro Phvul.011G01PTHR23155:SIPhvul.011G01 |
| 60 | P-loop containing nucleoside triphosphate hydrolase Phvul.011G08PTHR33477:SIPhvul.011G08 |
| | P-loop containing nucleoside triphosphate hydrolase Phvul.011G08PTHR33477:SIPhvul.011G08 |

P-loop containing nucleoside triphosphate hydrolase Phvul.011G08PTHR33477:SI Phvul.011G08
 NB-ARC domain-containing disease resistance pro Phvul.011G14PTHR23155//IPhvu.011G14
 NB-ARC domain-containing disease resistance pro Phvul.011G14PTHR23155//IPhvu.011G14
 NB-ARC domain-containing disease resistance pro Phvul.011G18PTHR23155//IPhvu.011G18
 MLP-like protein 43 Phvul.011G18PF00407 - Pat Phvul.011G18
 MLP-like protein 43 Phvul.011G18PF00407 - Pat Phvul.011G18
 NB-ARC domain-containing disease resistance pro Phvul.011G19PF13191//PF1Phvu.011G19
 NB-ARC domain-containing disease resistance pro Phvul.011G19PTHR23155//IPhvu.011G19
 LRR and NB-ARC domains-containing disease resis Phvul.011G19PTHR23155//IPhvu.011G19
 LRR and NB-ARC domains-containing disease resis Phvul.011G19PTHR23155//IPhvu.011G19
 LRR and NB-ARC domains-containing disease resis Phvul.011G19PTHR23155//IPhvu.011G19
 NB-ARC domain-containing disease resistance pro Phvul.011G19PTHR23155//IPhvu.011G19
 NB-ARC domain-containing disease resistance pro Phvul.011G19PF00931//PF1Phvu.011G19
 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvu.011G20
 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//IPhvu.011G20
 Galactose oxidase/kelch repeat superfamily protei Phvul.001G02PF00646 - F-b Phvul.001G02
 Glycosyl hydrolases family 31 protein Phvul.001G12PTHR22762//IPhvu.001G12
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvu.001G13
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvu.001G13
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvu.001G13
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvu.001G13
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvu.001G13
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvu.001G13
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvu.001G13
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvu.001G13
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvu.001G13
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvu.001G13
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvu.001G13
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvu.001G13
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvu.001G13
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvu.001G13
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvu.001G13
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvu.001G13
 NB-ARC domain-containing disease resistance pro Phvul.001G13PTHR23155//IPhvu.001G13
 Leucine-rich repeat protein kinase family protein Phvul.001G18PF00069//PF1Phvu.001G18
 Leucine-rich repeat protein kinase family protein Phvul.001G18PF00069//PF1Phvu.001G18
 Ca²⁺ activated outward rectifying K⁺ channel 5 Phvul.001G21PTHR11003:SI Phvul.001G21
 Pectin lyase-like superfamily protein Phvul.002G06PTHR31375:SI Phvul.002G06
 Pectin lyase-like superfamily protein Phvul.002G06PTHR31375:SI Phvul.002G06
 phospholipase D delta Phvul.002G10PTHR18896:SI Phvul.002G10
 phospholipase D delta Phvul.002G10PTHR18896:SI Phvul.002G10
 XS domain-containing protein / XS zinc finger dom Phvul.002G27PTHR21596:SI Phvul.002G27
 0 0 0 Phvul.003G05
 0 0 0 Phvul.003G05
 cytochrome P450, family 77, subfamily B, polypep Phvul.003G07PTHR24298:SI Phvul.003G07
 cytochrome P450, family 77, subfamily B, polypep Phvul.003G07PTHR24298:SI Phvul.003G07
 Heavy metal transport/detoxification superfamily Phvul.003G10PTHR22814//IPhvu.003G10
 Heavy metal transport/detoxification superfamily Phvul.003G10PTHR22814//IPhvu.003G10
 homolog of yeast FIP1 [V] Phvul.003G15PF05182 - Fip: Phvul.003G15
 cysteine-rich RLK (RECEPTOR-like protein kinase) 1 Phvul.003G15PF00704//PF1Phvu.003G15
 cysteine-rich RLK (RECEPTOR-like protein kinase) 1 Phvul.003G15PF00704//PF1Phvu.003G15

| | | | | |
|----|--|----------------------------------|---------------------|----------------|
| 1 | | | | |
| 2 | Tetratricopeptide repeat (TPR)-like superfamily pr | Phvul.003G16PF01535//PF1 | Phvul.003G16 | |
| 3 | RNA-metabolising metallo-beta-lactamase family | Phvul.003G203.5.2.6 - Beta- | Phvul.003G20 | |
| 4 | RNA-metabolising metallo-beta-lactamase family | Phvul.003G203.5.2.6 - Beta- | Phvul.003G20 | |
| 5 | | | | |
| 6 | ROP binding protein kinases 1 | Phvul.003G28PTHR27001:SI | Phvul.003G28 | |
| 7 | ROP binding protein kinases 1 | Phvul.003G28PTHR27001:SI | Phvul.003G28 | |
| 8 | myb domain protein 118 | Phvul.004G01PTHR10641:SI | Phvul.004G01 | |
| 9 | | | | |
| 10 | Regulator of chromosome condensation (RCC1) fa | Phvul.004G06PTHR22870//I | Phvul.004G06 | |
| 11 | Regulator of chromosome condensation (RCC1) fa | Phvul.004G06PTHR22870//I | Phvul.004G06 | |
| 12 | Pentatricopeptide repeat (PPR) superfamily protei | Phvul.004G13PTHR24015:SI | Phvul.004G13 | |
| 13 | Pentatricopeptide repeat (PPR) superfamily protei | Phvul.004G13PTHR24015:SI | Phvul.004G13 | |
| 14 | | | | |
| 15 | LRR and NB-ARC domains-containing disease resis | Phvul.005G03PTHR23155//I | Phvul.005G03 | |
| 16 | low-molecular-weight cysteine-rich 68 | Phvul.005G07PF00304 - Gar | Phvul.005G07 | |
| 17 | low-molecular-weight cysteine-rich 68 | Phvul.005G07PF00304 - Gar | Phvul.005G07 | |
| 18 | | | | |
| 19 | RNA-binding (RRM/RBD/RNP motifs) family protei | Phvul.006G05K14398 - clea | Phvul.006G05 | |
| 20 | RNA-binding (RRM/RBD/RNP motifs) family protei | Phvul.006G05K14398 - clea | Phvul.006G05 | |
| 21 | | | | |
| 22 | RNA-binding (RRM/RBD/RNP motifs) family protei | Phvul.006G05K14398 - clea | Phvul.006G05 | |
| 23 | sirtuin 1 | Phvul.006G05K11416 - mon | Phvul.006G05 | |
| 24 | NB-ARC domain-containing disease resistance pro | Phvul.006G06PTHR23155//I | Phvul.006G06 | |
| 25 | NB-ARC domain-containing disease resistance pro | Phvul.006G06PTHR23155//I | Phvul.006G06 | |
| 26 | | | | |
| 27 | LRR and NB-ARC domains-containing disease resis | Phvul.007G08PTHR23155//I | Phvul.007G08 | |
| 28 | LRR and NB-ARC domains-containing disease resis | Phvul.007G08PTHR23155//I | Phvul.007G08 | |
| 29 | | | | |
| 30 | NB-ARC domain-containing disease resistance pro | Phvul.008G01PTHR23155:SI | Phvul.008G01 | |
| 31 | NB-ARC domain-containing disease resistance pro | Phvul.008G01PTHR23155:SI | Phvul.008G01 | |
| 32 | NB-ARC domain-containing disease resistance pro | Phvul.008G07PTHR23155//I | Phvul.008G07 | |
| 33 | NB-ARC domain-containing disease resistance pro | Phvul.008G07PTHR23155//I | Phvul.008G07 | |
| 34 | | | | |
| 35 | | 0 | 0 | 0 Phvul.008G16 |
| 36 | | 0 | 0 | 0 Phvul.008G16 |
| 37 | | | | |
| 38 | nodulin MtN21 /EamA-like transporter family prot | Phvul.009G03PF00892 - Ean | Phvul.009G03 | |
| 39 | AGC (cAMP-dependent, cGMP-dependent and prc | Phvul.009G07PTHR24356:SI | Phvul.009G07 | |
| 40 | AGC (cAMP-dependent, cGMP-dependent and prc | Phvul.009G07PTHR24356:SI | Phvul.009G07 | |
| 41 | | | | |
| 42 | RHO-related protein from plants 10 | Phvul.009G18PTHR24072:SI | Phvul.009G18 | |
| 43 | RHO-related protein from plants 10 | Phvul.009G18PTHR24072:SI | Phvul.009G18 | |
| 44 | RHO-related protein from plants 10 | Phvul.009G18PTHR24072:SI | Phvul.009G18 | |
| 45 | RHO-related protein from plants 10 | Phvul.009G18PTHR24072:SI | Phvul.009G18 | |
| 46 | | | | |
| 47 | drought-induced 21 | Phvul.009G24PTHR33509:SI | Phvul.009G24 | |
| 48 | Disease resistance protein (TIR-NBS-LRR class) far | Phvul.010G02PF00931//PF1 | Phvul.010G02 | |
| 49 | Disease resistance protein (TIR-NBS-LRR class) far | Phvul.010G02PF00931//PF1 | Phvul.010G02 | |
| 50 | | | | |
| 51 | LRR and NB-ARC domains-containing disease resis | Phvul.010G06PTHR23155//I | Phvul.010G06 | |
| 52 | | 0 | 0 | 0 Phvul.010G10 |
| 53 | DOF zinc finger protein 1 | Phvul.010G14PF02701 - Dof | Phvul.010G14 | |
| 54 | | | | |
| 55 | RAD3-like DNA-binding helicase protein | Phvul.010G14K11273 - chro | Phvul.010G14 | |
| 56 | RAD3-like DNA-binding helicase protein | Phvul.010G14K11273 - chro | Phvul.010G14 | |
| 57 | scarecrow-like 3 | Phvul.011G01PF03514 - GR | Phvul.011G01 | |
| 58 | | | | |
| 59 | NB-ARC domain-containing disease resistance pro | Phvul.011G18PTHR23155//I | Phvul.011G18 | |
| 60 | NB-ARC domain-containing disease resistance pro | Phvul.011G18PTHR23155//I | Phvul.011G18 | |
| | NB-ARC domain-containing disease resistance pro | Phvul.011G19PTHR23155//I | Phvul.011G19 | |

1 NB-ARC domain-containing disease resistance pro Phvul.011G19PTHR23155//IPhvul.011G19
 2 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvul.011G20
 3 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvul.011G20
 4 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvul.011G20
 5 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvul.011G20
 6 LRR and NB-ARC domains-containing disease resis Phvul.011G20PTHR23155//IPhvul.011G20
 7 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//IPhvul.011G20
 8 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//IPhvul.011G20
 9 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//IPhvul.011G20
 10 NB-ARC domain-containing disease resistance pro Phvul.011G20PF13191 - AA/Phvul.011G20
 11 NB-ARC domain-containing disease resistance pro Phvul.011G20PF13191 - AA/Phvul.011G20
 12 Glycosyl hydrolase superfamily protein Phvul.L00450(PTHR32227:SfPhvul.L00450(
 13 Glycosyl hydrolase superfamily protein Phvul.L00450(PTHR32227:SfPhvul.L00450(
 14 PLATZ transcription factor family protein Phvul.001G18PTHR31065:SfPhvul.001G18
 15 PLATZ transcription factor family protein Phvul.001G18PTHR31065:SfPhvul.001G18
 16 PLATZ transcription factor family protein Phvul.001G18PTHR31065:SfPhvul.001G18
 17 PLATZ transcription factor family protein Phvul.001G18PTHR31065:SfPhvul.001G18
 18 ssDNA-binding transcriptional regulator Phvul.002G08PTHR31745:SfPhvul.002G08
 19 ssDNA-binding transcriptional regulator Phvul.002G08PTHR31745:SfPhvul.002G08
 20 disease resistance protein (TIR-NBS-LRR class), put Phvul.002G17PF00931//PF1Phvul.002G17
 21 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 22 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 23 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 24 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 25 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 26 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 27 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 28 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 29 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 30 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 31 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 32 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 33 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 34 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 35 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 36 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 37 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 38 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 39 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 40 Sulfite exporter TauE/SafE family protein Phvul.002G24PTHR14255//IPhvul.002G24
 41 myosin 1 Phvul.003G00PTHR13140:SfPhvul.003G00
 42 myosin 1 Phvul.003G00PTHR13140:SfPhvul.003G00
 43 myosin 1 Phvul.003G00PTHR13140:SfPhvul.003G00
 44 myosin 1 Phvul.003G00PTHR13140:SfPhvul.003G00
 45 myosin 1 Phvul.003G00PTHR13140:SfPhvul.003G00
 46 myosin 1 Phvul.003G00PTHR13140:SfPhvul.003G00
 47 myosin 1 Phvul.003G00PTHR13140:SfPhvul.003G00
 48 myosin 1 Phvul.003G00PTHR13140:SfPhvul.003G00
 49 0 0 0 Phvul.003G05
 50 0 0 0 Phvul.003G05
 51 0 0 0 Phvul.003G24
 52 0 0 0 Phvul.003G24
 53 0 0 0 Phvul.003G24
 54 0 0 0 Phvul.003G24
 55 SU(VAR)3-9 homolog 9 Phvul.003G28PTHR22884:SfPhvul.003G28
 56 SU(VAR)3-9 homolog 9 Phvul.003G28PTHR22884:SfPhvul.003G28
 57 Pentatricopeptide repeat (PPR) superfamily proteiPhvul.003G28PF01535//PF1Phvul.003G28
 58 polyribonucleotide nucleotidyltransferase, putativPhvul.004G012.7.7.8 - Polyr Phvul.004G01
 59 somatic embryogenesis receptor-like kinase 1 Phvul.004G08K13418 - som:Phvul.004G08

1 somatic embryogenesis receptor-like kinase 1 Phvul.004G08K13418 - som:Phvul.004G08
2
3 Tetratricopeptide repeat (TPR)-like superfamily pr Phvul.005G04PF01535//PF1Phvul.005G04
4
5 Tetratricopeptide repeat (TPR)-like superfamily pr Phvul.005G04PF01535//PF1Phvul.005G04
6
6 Nucleoporin autopeptidase Phvul.005G06K14297 - nucl:Phvul.005G06
7
7 Nucleoporin autopeptidase Phvul.005G06K14297 - nucl:Phvul.005G06
8
8 Protein of unknown function (DUF616) Phvul.005G07PTHR12956//I Phvul.005G07
9
9 transducin family protein / WD-40 repeat family p Phvul.006G02PTHR22838:SI Phvul.006G02
10
10 transducin family protein / WD-40 repeat family p Phvul.006G02PTHR22838:SI Phvul.006G02
11
11 Ribose 5-phosphate isomerase, type A protein Phvul.006G10PTHR11934:SI Phvul.006G10
12
12 late embryogenesis abundant protein-related / LE:Phvul.006G122.4.1.10 - Lev:Phvul.006G12
13
13 late embryogenesis abundant protein-related / LE:Phvul.006G122.4.1.10 - Lev:Phvul.006G12
14
14 Ankyrin repeat family protein Phvul.006G17PF12796//PF1 Phvul.006G17
15
15 Pentatricopeptide repeat (PPR) superfamily protei Phvul.008G10PF01535//PF1 Phvul.008G10
16
16 Pentatricopeptide repeat (PPR) superfamily protei Phvul.008G10PF01535//PF1 Phvul.008G10
17
17 LA RNA-binding protein Phvul.008G20PTHR22792:SI Phvul.008G20
18
18 Leucine-rich repeat protein kinase family protein Phvul.009G10PF07714//PFC Phvul.009G10
19
19 Protein of unknown function (DUF740) Phvul.010G00PF05340 - Pro Phvul.010G00
20
20 OBF-binding protein 3 Phvul.010G01PF02701 - Dof Phvul.010G01
21
21 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04
22
22 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04
23
23 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04
24
24 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04
25
25 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04
26
26 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04
27
27 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04
28
28 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04
29
29 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04
30
30 Histone H3 K4-specific methyltransferase SET7/9 f Phvul.010G04PTHR23084:SI Phvul.010G04
31
31 ABC-2 and Plant PDR ABC-type transporter family Phvul.010G14PTHR19241:SI Phvul.010G14
32
32 NB-ARC domain-containing disease resistance pro Phvul.011G18PTHR23155//I Phvul.011G18
33
33 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//I Phvul.011G20
34
34 LRR and NB-ARC domains-containing disease resis: Phvul.011G20PTHR23155//I Phvul.011G20
35
35 NB-ARC domain-containing disease resistance pro Phvul.011G20PTHR23155//I Phvul.011G20
36
36 LRR and NB-ARC domains-containing disease resis: Phvul.011G20PTHR23155//I Phvul.011G20
37
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| 1 | NAME | DESCRIPTION |
|----|----------------|---|
| 2 | | |
| 3 | not assigned.ε | (original description: pacid=37163660 transcript=Phvul.004G048000.1 locus=Phvul.C |
| 4 | not assigned.ε | (original description: pacid=37168996 transcript=Phvul.001G224800.2 locus=Phvul.C |
| 5 | not assigned.ε | (original description: pacid=37168996 transcript=Phvul.001G224800.2 locus=Phvul.C |
| 6 | not assigned.ε | (original description: pacid=37168996 transcript=Phvul.001G224800.2 locus=Phvul.C |
| 7 | not assigned.ε | (original description: pacid=37168996 transcript=Phvul.001G224800.2 locus=Phvul.C |
| 8 | not assigned.ε | (original description: pacid=37168996 transcript=Phvul.001G224800.2 locus=Phvul.C |
| 9 | not assigned.ε | (original description: pacid=37168996 transcript=Phvul.001G224800.2 locus=Phvul.C |
| 10 | not assigned.ε | (original description: pacid=37165645 transcript=Phvul.007G201700.1 locus=Phvul.C |
| 11 | not assigned.ε | (original description: pacid=37165645 transcript=Phvul.007G201700.1 locus=Phvul.C |
| 12 | not assigned.ε | (original description: pacid=37165645 transcript=Phvul.007G201700.1 locus=Phvul.C |
| 13 | not assigned.ε | (original description: pacid=37160667 transcript=Phvul.008G061300.2 locus=Phvul.C |
| 14 | not assigned.ε | (original description: pacid=37160667 transcript=Phvul.008G061300.2 locus=Phvul.C |
| 15 | not assigned.ε | (original description: pacid=37160667 transcript=Phvul.008G061300.2 locus=Phvul.C |
| 16 | not assigned.ε | (original description: pacid=37160667 transcript=Phvul.008G061300.2 locus=Phvul.C |
| 17 | not assigned.ε | (original description: pacid=37160667 transcript=Phvul.008G061300.2 locus=Phvul.C |
| 18 | External stimu | effector receptor (NLR) (original description: pacid=37177951 transcript=Phvul.002G |
| 19 | RNA biosynth | transcription factor (MYB-related) (original description: pacid=37168368 transcript=F |
| 20 | RNA biosynth | transcription factor (GATA) (original description: pacid=37177588 transcript=Phvul.0 |
| 21 | RNA biosynth | transcription factor (GATA) (original description: pacid=37177588 transcript=Phvul.0 |
| 22 | RNA biosynth | transcription factor (GATA) (original description: pacid=37177588 transcript=Phvul.0 |
| 23 | External stimu | effector receptor (NLR) (original description: pacid=37146968 transcript=Phvul.003G |
| 24 | not assigned.r | no hits & (original description: pacid=37145696 transcript=Phvul.003G244225.3 locu |
| 25 | not assigned.r | no hits & (original description: pacid=37145696 transcript=Phvul.003G244225.3 locu |
| 26 | not assigned.r | no hits & (original description: pacid=37145696 transcript=Phvul.003G244225.3 locu |
| 27 | not assigned.r | no hits & (original description: pacid=37145696 transcript=Phvul.003G244225.3 locu |
| 28 | External stimu | effector receptor (NLR) (original description: pacid=37163438 transcript=Phvul.004G |
| 29 | Protein home | SINA-class E3 ligase (original description: pacid=37154353 transcript=Phvul.005G029 |
| 30 | Protein home | SINA-class E3 ligase (original description: pacid=37154353 transcript=Phvul.005G029 |
| 31 | Protein home | SINA-class E3 ligase (original description: pacid=37154353 transcript=Phvul.005G029 |
| 32 | Protein home | SINA-class E3 ligase (original description: pacid=37154353 transcript=Phvul.005G029 |
| 33 | RNA biosynth | transcription factor (SBP) (original description: pacid=37166230 transcript=Phvul.007 |
| 34 | RNA biosynth | transcription factor (SBP) (original description: pacid=37166230 transcript=Phvul.007 |
| 35 | RNA biosynth | transcription factor (SBP) (original description: pacid=37166230 transcript=Phvul.007 |
| 36 | Lipid metaboli | ATPase component TGD3 of TGD lipid importer complex (original description: pacid= |
| 37 | not assigned.r | no hits & (original description: pacid=37157769 transcript=Phvul.008G280900.1 locu |
| 38 | not assigned.r | no hits & (original description: pacid=37157769 transcript=Phvul.008G280900.1 locu |
| 39 | not assigned.r | no hits & (original description: pacid=37157769 transcript=Phvul.008G280900.1 locu |
| 40 | not assigned.ε | (original description: pacid=37142899 transcript=Phvul.010G064700.1 locus=Phvul.C |
| 41 | External stimu | effector receptor (NLR) (original description: pacid=37142699 transcript=Phvul.010G |
| 42 | External stimu | effector receptor (NLR) (original description: pacid=37142699 transcript=Phvul.010G |
| 43 | not assigned.r | no hits & (original description: pacid=37154984 transcript=Phvul.011G149100.7 locu |
| 44 | not assigned.r | no hits & (original description: pacid=37154984 transcript=Phvul.011G149100.7 locu |
| 45 | not assigned.r | no hits & (original description: pacid=37154984 transcript=Phvul.011G149100.7 locu |
| 46 | not assigned.r | no hits & (original description: pacid=37154984 transcript=Phvul.011G149100.7 locu |
| 47 | not assigned.r | no hits & (original description: pacid=37154984 transcript=Phvul.011G149100.7 locu |
| 48 | not assigned.r | no hits & (original description: pacid=37154984 transcript=Phvul.011G149100.7 locu |
| 49 | not assigned.r | no hits & (original description: pacid=37154984 transcript=Phvul.011G149100.7 locu |
| 50 | not assigned.r | no hits & (original description: pacid=37154984 transcript=Phvul.011G149100.7 locu |
| 51 | not assigned.r | no hits & (original description: pacid=37154984 transcript=Phvul.011G149100.7 locu |
| 52 | not assigned.ε | (original description: pacid=37156909 transcript=Phvul.011G166100.1 locus=Phvul.C |
| 53 | not assigned.ε | (original description: pacid=37171124 transcript=Phvul.001G128200.2 locus=Phvul.C |
| 54 | not assigned.ε | (original description: pacid=37171124 transcript=Phvul.001G128200.2 locus=Phvul.C |
| 55 | not assigned.ε | (original description: pacid=37169603 transcript=Phvul.001G134000.1 locus=Phvul.C |
| 56 | not assigned.ε | (original description: pacid=37169603 transcript=Phvul.001G134000.1 locus=Phvul.C |
| 57 | Phytohormon | SMXL strigolactone signal transducer (original description: pacid=37170890 transcrip |
| 58 | Phytohormon | SMXL strigolactone signal transducer (original description: pacid=37170890 transcrip |
| 59 | Phytohormon | SMXL strigolactone signal transducer (original description: pacid=37170890 transcrip |
| 60 | not assigned.r | no hits & (original description: pacid=37177208 transcript=Phvul.002G057300.2 locu |
| | not assigned.r | no hits & (original description: pacid=37177208 transcript=Phvul.002G057300.2 locu |

1 Phytohormon abscisic acid hydroxylase (original description: pacid=37176949 transcript=Phvul.002
2 not assigned.r no hits & (original description: pacid=37175068 transcript=Phvul.002G187600.1 locu
3 **RNA processir poly(A) RNA polymerase regulatory protein (original description: pacid=37177379 tra**
4 **RNA processir poly(A) RNA polymerase regulatory protein (original description: pacid=37177379 tra**
5 not assigned.ε (original description: pacid=37147525 transcript=Phvul.003G101200.1 locus=Phvul.C
6 not assigned.ε (original description: pacid=37147525 transcript=Phvul.003G101200.1 locus=Phvul.C
7 Coenzyme me component SUF-E2/-E3 of plastidial SUF system assembly phase (original description
8 Coenzyme me component SUF-E2/-E3 of plastidial SUF system assembly phase (original description
9 Chromatin org component SSRP of FACT histone chaperone complex (original description: pacid=37
10 External stimu effector receptor (NLR) (original description: pacid=37163195 transcript=Phvul.004G
11 External stimu effector receptor (NLR) (original description: pacid=37163195 transcript=Phvul.004G
12 Coenzyme me uroporphyrinogen III methyltransferase (original description: pacid=37152438 transc
13 Coenzyme me uroporphyrinogen III methyltransferase (original description: pacid=37152438 transc
14 not assigned.ε (original description: pacid=37153472 transcript=Phvul.005G087100.1 locus=Phvul.C
15 not assigned.ε (original description: pacid=37153472 transcript=Phvul.005G087100.1 locus=Phvul.C
16 Protein modif protein kinase (CrIRLK1) (original description: pacid=37173044 transcript=Phvul.006C
17 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
18 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
19 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
20 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
21 Protein biosyr LAS1 pre-rRNA cleavage factor involved in ITS2 rRNA removal (original description: p
22 Solute transp potassium cation transporter (HAK/KUP/KT) (original description: pacid=37159589 tr
23 Solute transp potassium cation transporter (HAK/KUP/KT) (original description: pacid=37159589 tr
24 Solute transp potassium cation transporter (HAK/KUP/KT) (original description: pacid=37159589 tr
25 Solute transp potassium cation transporter (HAK/KUP/KT) (original description: pacid=37159589 tr
26 External stimu effector receptor (NLR) (original description: pacid=37142428 transcript=Phvul.010G
27 not assigned.ε (original description: pacid=37143313 transcript=Phvul.010G132333.3 locus=Phvul.C
28 External stimu effector receptor (NLR) (original description: pacid=37143628 transcript=Phvul.010G
29 not assigned.r no hits & (original description: pacid=37142610 transcript=Phvul.010G151400.6 locu
30 not assigned.r no hits & (original description: pacid=37142610 transcript=Phvul.010G151400.6 locu
31 not assigned.r no hits & (original description: pacid=37142610 transcript=Phvul.010G151400.6 locu
32 not assigned.r no hits & (original description: pacid=37142610 transcript=Phvul.010G151400.6 locu
33 External stimu effector receptor (NLR) (original description: pacid=37154763 transcript=Phvul.011G
34 External stimu effector receptor (NLR) (original description: pacid=37156164 transcript=Phvul.011G
35 not assigned.ε (original description: pacid=37157447 transcript=Phvul.011G151300.1 locus=Phvul.C
36 not assigned.ε (original description: pacid=37156104 transcript=Phvul.011G181700.1 locus=Phvul.C
37 not assigned.ε (original description: pacid=37156104 transcript=Phvul.011G181700.1 locus=Phvul.C
38 not assigned.ε (original description: pacid=37157092 transcript=Phvul.011G192400.1 locus=Phvul.C
39 not assigned.ε (original description: pacid=37155577 transcript=Phvul.011G192600.1 locus=Phvul.C
40 not assigned.ε (original description: pacid=37155824 transcript=Phvul.011G193100.1 locus=Phvul.C
41 not assigned.ε (original description: pacid=37155134 transcript=Phvul.011G193500.1 locus=Phvul.C
42 not assigned.ε (original description: pacid=37155823 transcript=Phvul.011G193600.1 locus=Phvul.C
43 not assigned.ε (original description: pacid=37155090 transcript=Phvul.011G194800.1 locus=Phvul.C
44 not assigned.ε (original description: pacid=37154689 transcript=Phvul.011G194900.1 locus=Phvul.C
45 not assigned.ε (original description: pacid=37157033 transcript=Phvul.011G195000.1 locus=Phvul.C
46 not assigned.ε (original description: pacid=37156343 transcript=Phvul.011G195200.1 locus=Phvul.C

1 not assigned.ε (original description: pacid=37157211 transcript=Phvul.011G195400.2 locus=Phvul.C
2 not assigned.ε (original description: pacid=37155487 transcript=Phvul.011G195500.1 locus=Phvul.C
3 not assigned.ε (original description: pacid=37156565 transcript=Phvul.011G196000.1 locus=Phvul.C
4 not assigned.ε (original description: pacid=37157155 transcript=Phvul.011G196066.1 locus=Phvul.C
5 not assigned.ε (original description: pacid=37157395 transcript=Phvul.011G200820.1 locus=Phvul.C
6 not assigned.ε (original description: pacid=37157395 transcript=Phvul.011G200820.1 locus=Phvul.C
7 not assigned.ε (original description: pacid=37156073 transcript=Phvul.011G202100.1 locus=Phvul.C
8 not assigned.ε (original description: pacid=37156073 transcript=Phvul.011G202100.1 locus=Phvul.C
9 not assigned.ε (original description: pacid=37155566 transcript=Phvul.011G202300.1 locus=Phvul.C
10 not assigned.ε (original description: pacid=37155566 transcript=Phvul.011G202300.1 locus=Phvul.C
11 not assigned.ε (original description: pacid=37155566 transcript=Phvul.011G202300.1 locus=Phvul.C
12 not assigned.ε (original description: pacid=37155566 transcript=Phvul.011G202300.1 locus=Phvul.C
13 not assigned.ε (original description: pacid=37156337 transcript=Phvul.011G203100.1 locus=Phvul.C
14 not assigned.ε (original description: pacid=37156337 transcript=Phvul.011G203100.1 locus=Phvul.C
15 not assigned.ε (original description: pacid=37156337 transcript=Phvul.011G203100.1 locus=Phvul.C
16 not assigned.ε (original description: pacid=37156337 transcript=Phvul.011G203100.1 locus=Phvul.C
17 not assigned.ε (original description: pacid=37157542 transcript=Phvul.L002337.2 locus=Phvul.L002:
18 not assigned.ε (original description: pacid=37157542 transcript=Phvul.L002337.2 locus=Phvul.L002:
19 not assigned.ε (original description: pacid=37157542 transcript=Phvul.L002337.2 locus=Phvul.L002:
20 not assigned.ε (original description: pacid=37157542 transcript=Phvul.L002337.2 locus=Phvul.L002:
21 not assigned.ε (original description: pacid=37157542 transcript=Phvul.L002337.2 locus=Phvul.L002:
22 not assigned.ε (original description: pacid=37157542 transcript=Phvul.L002337.2 locus=Phvul.L002:
23 not assigned.ε (original description: pacid=37169910 transcript=Phvul.001G015600.3 locus=Phvul.C
24 not assigned.ε (original description: pacid=37169910 transcript=Phvul.001G015600.3 locus=Phvul.C
25 not assigned.ε (original description: pacid=37169910 transcript=Phvul.001G015600.3 locus=Phvul.C
26 not assigned.ε (original description: pacid=37169910 transcript=Phvul.001G015600.3 locus=Phvul.C
27 External stimu transcription factor (ICE1|2) (original description: pacid=37167713 transcript=Phvul.(
28 External stimu transcription factor (ICE1|2) (original description: pacid=37167713 transcript=Phvul.(
29 Cell wall orgar alpha-class expansin (original description: pacid=37168526 transcript=Phvul.001G23:
30 Cell wall orgar alpha-class expansin (original description: pacid=37168526 transcript=Phvul.001G23:
31 RNA biosynth transcription factor (PLATZ) (original description: pacid=37175648 transcript=Phvul.0
32 RNA biosynth transcription factor (PLATZ) (original description: pacid=37175648 transcript=Phvul.0
33 RNA biosynth transcription factor (PLATZ) (original description: pacid=37175648 transcript=Phvul.0
34 RNA biosynth transcription factor (PLATZ) (original description: pacid=37175648 transcript=Phvul.0
35 not assigned.ε (original description: pacid=37177875 transcript=Phvul.002G298800.1 locus=Phvul.C
36 External stimu G-alpha component XLG of non-canonical heterotrimeric G-protein complex (original
37 External stimu G-alpha component XLG of non-canonical heterotrimeric G-protein complex (original
38 RNA biosynth PAP2/TAC2 cofactor of plastid-encoded RNA polymerase (original description: pacid=
39 RNA biosynth PAP2/TAC2 cofactor of plastid-encoded RNA polymerase (original description: pacid=
40 RNA biosynth C2H2 zinc finger transcription factor (original description: pacid=37145501 transcript
41 RNA biosynth C2H2 zinc finger transcription factor (original description: pacid=37145501 transcript
42 **Protein home component ATG2 of autophagosome ATG9-2-18 membrane shuttling complex (origir**
43 **Protein home component ATG2 of autophagosome ATG9-2-18 membrane shuttling complex (origir**
44 **Protein home component ATG2 of autophagosome ATG9-2-18 membrane shuttling complex (origir**
45 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C
46 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C
47 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C
48 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C
49 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C
50 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C
51 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C
52 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C
53 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C
54 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C
55 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C
56 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C
57 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C
58 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C
59 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C
60 not assigned.ε (original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.C

1 not assigned.ε (original description: pacid=37163660 transcript=Phvul.004G048000.1 locus=Phvul.C
2 not assigned.ε (original description: pacid=37163660 transcript=Phvul.004G048000.1 locus=Phvul.C
3 not assigned.ε (original description: pacid=37162532 transcript=Phvul.004G048000.1 locus=Phvul.C
4 Cell cycle orgaMinD plastid division FtsZ assembly factor (original description: pacid=37162532 tra
5 Cell cycle orgaMinD plastid division FtsZ assembly factor (original description: pacid=37162532 tra
6 not assigned.ε (original description: pacid=37162837 transcript=Phvul.004G133100.1 locus=Phvul.C
7 not assigned.ε (original description: pacid=37154568 transcript=Phvul.005G165800.1 locus=Phvul.C
8 not assigned.ε (original description: pacid=37154568 transcript=Phvul.005G165800.1 locus=Phvul.C
9 not assigned.ε (original description: pacid=37154568 transcript=Phvul.005G165800.1 locus=Phvul.C
10 not assigned.ε (original description: pacid=37171447 transcript=Phvul.006G066800.1 locus=Phvul.C
11 Cell wall orgar alpha-class expansin (original description: pacid=37173891 transcript=Phvul.006G08
12 not assigned.r no hits & (original description: pacid=37172393 transcript=Phvul.006G148800.1 locu
13 Enzyme classiiTrans-resveratrol di-O-methyltransferase OS=Vitis vinifera (sp|b6vjs4|romt_vitvi : 34
14 Enzyme classiiTrans-resveratrol di-O-methyltransferase OS=Vitis vinifera (sp|b6vjs4|romt_vitvi : 34
15 not assigned.r no hits & (original description: pacid=37167355 transcript=Phvul.007G027400.1 locu
16 Enzyme classiiATPase ARSA1 OS=Chlamydomonas reinhardtii (sp|a8jgb0|asna1_chlre : 369.0) & En
17 Protein modif protein kinase (LRR-III) (original description: pacid=37159143 transcript=Phvul.008G1
18 Lipid metabolisterol C-24 methyltransferase (original description: pacid=37149363 transcript=Phvu
19 Lipid metabolisterol C-24 methyltransferase (original description: pacid=37149363 transcript=Phvu
20 RNA biosynthtranscription factor (bZIP) (original description: pacid=37149873 transcript=Phvul.00
21 RNA biosynthtranscription factor (bZIP) (original description: pacid=37149873 transcript=Phvul.00
22 RNA biosynthtranscription factor (bZIP) (original description: pacid=37149873 transcript=Phvul.00
23 RNA biosynthtranscription factor (bZIP) (original description: pacid=37149873 transcript=Phvul.00
24 not assigned.ε (original description: pacid=37148715 transcript=Phvul.009G213300.1 locus=Phvul.C
25 not assigned.ε (original description: pacid=37149744 transcript=Phvul.009G226300.2 locus=Phvul.C
26 not assigned.ε (original description: pacid=37149744 transcript=Phvul.009G226300.2 locus=Phvul.C
27 not assigned.ε (original description: pacid=37149744 transcript=Phvul.009G226300.2 locus=Phvul.C
28 not assigned.ε (original description: pacid=37149744 transcript=Phvul.009G226300.2 locus=Phvul.C
29 not assigned.ε (original description: pacid=37151719 transcript=Phvul.009G233700.1 locus=Phvul.C
30 not assigned.ε (original description: pacid=37151719 transcript=Phvul.009G233700.1 locus=Phvul.C
31 not assigned.ε (original description: pacid=37151719 transcript=Phvul.009G233700.1 locus=Phvul.C
32 not assigned.ε (original description: pacid=37143979 transcript=Phvul.010G008700.2 locus=Phvul.C
33 not assigned.ε (original description: pacid=37143979 transcript=Phvul.010G008700.2 locus=Phvul.C
34 not assigned.ε (original description: pacid=37142864 transcript=Phvul.010G056500.1 locus=Phvul.C
35 not assigned.ε (original description: pacid=37142864 transcript=Phvul.010G056500.1 locus=Phvul.C
36 not assigned.ε (original description: pacid=37142368 transcript=Phvul.010G063100.1 locus=Phvul.C
37 not assigned.ε (original description: pacid=37142879 transcript=Phvul.010G070584.1 locus=Phvul.C
38 not assigned.r no hits & (original description: pacid=37143904 transcript=Phvul.010G146900.7 locu
39 not assigned.r no hits & (original description: pacid=37143904 transcript=Phvul.010G146900.7 locu
40 not assigned.r no hits & (original description: pacid=37143904 transcript=Phvul.010G146900.7 locu
41 not assigned.r no hits & (original description: pacid=37143904 transcript=Phvul.010G146900.7 locu
42 not assigned.r no hits & (original description: pacid=37143904 transcript=Phvul.010G146900.7 locu
43 not assigned.ε (original description: pacid=37156367 transcript=Phvul.011G014500.2 locus=Phvul.C
44 not assigned.ε (original description: pacid=37156367 transcript=Phvul.011G014500.2 locus=Phvul.C
45 not assigned.ε (original description: pacid=37156367 transcript=Phvul.011G014500.2 locus=Phvul.C
46 not assigned.ε (original description: pacid=37157349 transcript=Phvul.011G082700.3 locus=Phvul.C
47 not assigned.ε (original description: pacid=37157349 transcript=Phvul.011G082700.3 locus=Phvul.C
48 not assigned.ε (original description: pacid=37157349 transcript=Phvul.011G082700.3 locus=Phvul.C
49 not assigned.ε (original description: pacid=37157349 transcript=Phvul.011G082700.3 locus=Phvul.C
50 not assigned.ε (original description: pacid=37157349 transcript=Phvul.011G082700.3 locus=Phvul.C
51 not assigned.ε (original description: pacid=37157349 transcript=Phvul.011G082700.3 locus=Phvul.C
52 not assigned.ε (original description: pacid=37157349 transcript=Phvul.011G082700.3 locus=Phvul.C
53 not assigned.ε (original description: pacid=37157349 transcript=Phvul.011G082700.3 locus=Phvul.C
54 not assigned.ε (original description: pacid=37157349 transcript=Phvul.011G082700.3 locus=Phvul.C
55 not assigned.ε (original description: pacid=37157349 transcript=Phvul.011G082700.3 locus=Phvul.C
56 not assigned.ε (original description: pacid=37157349 transcript=Phvul.011G082700.3 locus=Phvul.C
57 not assigned.ε (original description: pacid=37157349 transcript=Phvul.011G082700.3 locus=Phvul.C
58 not assigned.ε (original description: pacid=37157349 transcript=Phvul.011G082700.3 locus=Phvul.C
59 not assigned.ε (original description: pacid=37157349 transcript=Phvul.011G082700.3 locus=Phvul.C
60 not assigned.ε (original description: pacid=37157349 transcript=Phvul.011G082700.3 locus=Phvul.C

1 not assigned.ε (original description: pacid=37157349 transcript=Phvul.011G082700.3 locus=Phvul.C
2 not assigned.ε (original description: pacid=37154977 transcript=Phvul.011G149400.1 locus=Phvul.C
3 not assigned.ε (original description: pacid=37154977 transcript=Phvul.011G149400.1 locus=Phvul.C
4 not assigned.ε (original description: pacid=37156674 transcript=Phvul.011G181500.1 locus=Phvul.C
5 not assigned.r no hits & (original description: pacid=37154681 transcript=Phvul.011G182900.1 locu
6 not assigned.r no hits & (original description: pacid=37154681 transcript=Phvul.011G182900.1 locu
7 not assigned.ε (original description: pacid=37155164 transcript=Phvul.011G191600.1 locus=Phvul.C
8 not assigned.ε (original description: pacid=37157159 transcript=Phvul.011G191800.1 locus=Phvul.C
9 not assigned.ε (original description: pacid=37155368 transcript=Phvul.011G192200.1 locus=Phvul.C
10 not assigned.ε (original description: pacid=37155339 transcript=Phvul.011G192900.1 locus=Phvul.C
11 not assigned.ε (original description: pacid=37155339 transcript=Phvul.011G192900.1 locus=Phvul.C
12 not assigned.ε (original description: pacid=37155272 transcript=Phvul.011G195751.1 locus=Phvul.C
13 not assigned.ε (original description: pacid=37155563 transcript=Phvul.011G198400.1 locus=Phvul.C
14 not assigned.ε (original description: pacid=37154846 transcript=Phvul.011G201000.1 locus=Phvul.C
15 not assigned.ε (original description: pacid=37156971 transcript=Phvul.011G201101.1 locus=Phvul.C
16 not assigned.ε (original description: pacid=37168061 transcript=Phvul.001G027100.1 locus=Phvul.C
17 not assigned.ε (original description: pacid=37171176 transcript=Phvul.001G123000.2 locus=Phvul.C
18 not assigned.ε (original description: pacid=37171258 transcript=Phvul.001G132516.1 locus=Phvul.C
19 not assigned.ε (original description: pacid=37171258 transcript=Phvul.001G132516.1 locus=Phvul.C
20 not assigned.ε (original description: pacid=37169452 transcript=Phvul.001G132701.1 locus=Phvul.C
21 not assigned.ε (original description: pacid=37169452 transcript=Phvul.001G132701.1 locus=Phvul.C
22 not assigned.ε (original description: pacid=37170073 transcript=Phvul.001G132800.1 locus=Phvul.C
23 not assigned.ε (original description: pacid=37170073 transcript=Phvul.001G132800.1 locus=Phvul.C
24 not assigned.ε (original description: pacid=37167899 transcript=Phvul.001G132864.1 locus=Phvul.C
25 not assigned.ε (original description: pacid=37167899 transcript=Phvul.001G132864.1 locus=Phvul.C
26 not assigned.ε (original description: pacid=37168771 transcript=Phvul.001G133100.1 locus=Phvul.C
27 not assigned.ε (original description: pacid=37168771 transcript=Phvul.001G133100.1 locus=Phvul.C
28 not assigned.ε (original description: pacid=37168444 transcript=Phvul.001G133101.1 locus=Phvul.C
29 not assigned.ε (original description: pacid=37168444 transcript=Phvul.001G133101.1 locus=Phvul.C
30 Protein modif protein kinase (LRR-III) (original description: pacid=37171243 transcript=Phvul.001G1
31 Protein modif protein kinase (LRR-III) (original description: pacid=37171243 transcript=Phvul.001G1
32 Solute transpcvoltage-gated potassium cation channel (TPK/KCO) (original description: pacid=37171
33 Cell wall orgar polygalacturonase (PGX1) (original description: pacid=37177802 transcript=Phvul.00
34 Cell wall orgar polygalacturonase (PGX1) (original description: pacid=37177802 transcript=Phvul.00
35 Lipid metaboliphospholipase D (PLD-delta) (original description: pacid=37175497 transcript=Phvul.
36 Lipid metaboliphospholipase D (PLD-delta) (original description: pacid=37175497 transcript=Phvul.
37 Chromatin orgSGS3 stabilization factor of DNA methylation pathway (original description: pacid=37
38 not assigned.r no hits & (original description: pacid=37146447 transcript=Phvul.003G050200.2 locu
39 not assigned.r no hits & (original description: pacid=37146447 transcript=Phvul.003G050200.2 locu
40 Enzyme classiiCytochrome P450 77A1 (Fragment) OS=Solanum melongena (sp|p37123|c77a1_soln
41 Enzyme classiiCytochrome P450 77A1 (Fragment) OS=Solanum melongena (sp|p37123|c77a1_soln
42 not assigned.ε (original description: pacid=37144721 transcript=Phvul.003G104900.1 locus=Phvul.C
43 not assigned.ε (original description: pacid=37144721 transcript=Phvul.003G104900.1 locus=Phvul.C
44 RNA processir component Fip1 of Cleavage and Polyadenylation Specificity Factor (CPSF) complex (r
45 Protein modif protein kinase (SD-1) (original description: pacid=37146603 transcript=Phvul.003G15
46 Protein modif protein kinase (SD-1) (original description: pacid=37146603 transcript=Phvul.003G15

1 RNA processir RNA editing factor (OTP82) (original description: pacid=37146356 transcript=Phvul.01
2 RNA processir exo-/endoribonuclease (RNase J) (original description: pacid=37148378 transcript=Phvul.01
3 RNA processir exo-/endoribonuclease (RNase J) (original description: pacid=37148378 transcript=Phvul.01
4 Multi-process GTPase interactive protein kinase (RBK/RRK) (original description: pacid=37148383 transcript=Phvul.01
5 Multi-process GTPase interactive protein kinase (RBK/RRK) (original description: pacid=37148383 transcript=Phvul.01
6 RNA biosynthe transcription factor (MYB) (original description: pacid=37162815 transcript=Phvul.00
7 not assigned.ε (original description: pacid=37162157 transcript=Phvul.004G064300.1 locus=Phvul.C
8 not assigned.ε (original description: pacid=37162157 transcript=Phvul.004G064300.1 locus=Phvul.C
9 not assigned.ε (original description: pacid=37163473 transcript=Phvul.004G131300.1 locus=Phvul.C
10 not assigned.ε (original description: pacid=37163473 transcript=Phvul.004G131300.1 locus=Phvul.C
11 not assigned.ε (original description: pacid=37154207 transcript=Phvul.005G031200.1 locus=Phvul.C
12 External stimu defensin (PDF1) (original description: pacid=37154287 transcript=Phvul.005G071300
13 External stimu defensin (PDF1) (original description: pacid=37154287 transcript=Phvul.005G071300
14 RNA processir component CPFS6/CFIm68 of Cleavage Factor I (CF-Im) complex (original description:
15 RNA processir component CPFS6/CFIm68 of Cleavage Factor I (CF-Im) complex (original description:
16 RNA processir component CPFS6/CFIm68 of Cleavage Factor I (CF-Im) complex (original description:
17 Chromatin org histone deacetylase (SRT) (original description: pacid=37171603 transcript=Phvul.006
18 not assigned.ε (original description: pacid=37171447 transcript=Phvul.006G066800.1 locus=Phvul.C
19 not assigned.ε (original description: pacid=37171447 transcript=Phvul.006G066800.1 locus=Phvul.C
20 not assigned.ε (original description: pacid=37165347 transcript=Phvul.007G086300.2 locus=Phvul.C
21 not assigned.ε (original description: pacid=37165347 transcript=Phvul.007G086300.2 locus=Phvul.C
22 not assigned.ε (original description: pacid=37159623 transcript=Phvul.008G014700.1 locus=Phvul.C
23 not assigned.ε (original description: pacid=37159623 transcript=Phvul.008G014700.1 locus=Phvul.C
24 not assigned.ε (original description: pacid=37158229 transcript=Phvul.008G072032.1 locus=Phvul.C
25 not assigned.ε (original description: pacid=37158229 transcript=Phvul.008G072032.1 locus=Phvul.C
26 not assigned.r no hits & (original description: pacid=37160500 transcript=Phvul.008G168300.2 locu
27 not assigned.r no hits & (original description: pacid=37160500 transcript=Phvul.008G168300.2 locu
28 Solute transp solute transporter (UmamiT) (original description: pacid=37150535 transcript=Phvul.
29 Protein modif protein kinase (AGC-VII/NDR) (original description: pacid=37149778 transcript=Phvul
30 Protein modif protein kinase (AGC-VII/NDR) (original description: pacid=37149778 transcript=Phvul
31 Multi-process small GTPase (ROP) (original description: pacid=37148638 transcript=Phvul.009G180
32 Multi-process small GTPase (ROP) (original description: pacid=37148638 transcript=Phvul.009G180
33 Multi-process small GTPase (ROP) (original description: pacid=37148638 transcript=Phvul.009G180
34 Multi-process small GTPase (ROP) (original description: pacid=37148638 transcript=Phvul.009G180
35 not assigned.r no hits & (original description: pacid=37152061 transcript=Phvul.009G249500.1 locu
36 External stimu effector receptor (NLR) (original description: pacid=37142827 transcript=Phvul.010G
37 External stimu effector receptor (NLR) (original description: pacid=37144038 transcript=Phvul.010G
38 not assigned.ε (original description: pacid=37142695 transcript=Phvul.010G063700.2 locus=Phvul.C
39 not assigned.r no hits & (original description: pacid=37143741 transcript=Phvul.010G101700.1 locu
40 **RNA biosynthe transcription factor (DOF) (original description: pacid=37142901 transcript=Phvul.011**
41 not assigned.ε (original description: pacid=37143246 transcript=Phvul.010G149500.1 locus=Phvul.C
42 not assigned.ε (original description: pacid=37143246 transcript=Phvul.010G149500.1 locus=Phvul.C
43 RNA biosynthe transcription factor (GRAS) (original description: pacid=37157104 transcript=Phvul.011
44 not assigned.ε (original description: pacid=37156674 transcript=Phvul.011G181500.1 locus=Phvul.C
45 not assigned.ε (original description: pacid=37156674 transcript=Phvul.011G181500.1 locus=Phvul.C
46 not assigned.ε (original description: pacid=37154890 transcript=Phvul.011G198000.1 locus=Phvul.C

1 not assigned.ε (original description: pacid=37154890 transcript=Phvul.011G198000.1 locus=Phvul.C
2 not assigned.ε (original description: pacid=37154739 transcript=Phvul.011G200880.2 locus=Phvul.C
3 not assigned.ε (original description: pacid=37154739 transcript=Phvul.011G200880.2 locus=Phvul.C
4 not assigned.ε (original description: pacid=37154846 transcript=Phvul.011G201000.1 locus=Phvul.C
5 not assigned.ε (original description: pacid=37154846 transcript=Phvul.011G201000.1 locus=Phvul.C
6 not assigned.ε (original description: pacid=37156971 transcript=Phvul.011G201101.1 locus=Phvul.C
7 not assigned.ε (original description: pacid=37156971 transcript=Phvul.011G201101.1 locus=Phvul.C
8 not assigned.ε (original description: pacid=37156646 transcript=Phvul.011G202366.1 locus=Phvul.C
9 not assigned.ε (original description: pacid=37156646 transcript=Phvul.011G202366.1 locus=Phvul.C
10 not assigned.ε (original description: pacid=37156646 transcript=Phvul.011G202366.1 locus=Phvul.C
11 Enzyme classiiGlucan endo-1,3-beta-glucosidase 11 OS=Arabidopsis thaliana (sp|q8l868|e1311_ar
12 Enzyme classiiGlucan endo-1,3-beta-glucosidase 11 OS=Arabidopsis thaliana (sp|q8l868|e1311_ar
13 RNA biosynthetranscription factor (PLATZ) (original description: pacid=37168365 transcript=Phvul.0
14 RNA biosynthetranscription factor (PLATZ) (original description: pacid=37168365 transcript=Phvul.0
15 RNA biosynthetranscription factor (PLATZ) (original description: pacid=37168365 transcript=Phvul.0
16 RNA biosynthetranscription factor (PLATZ) (original description: pacid=37168365 transcript=Phvul.0
17 RNA processirWhirly-type plastidial RNA splicing factor (original description: pacid=37176882 trans
18 RNA processirWhirly-type plastidial RNA splicing factor (original description: pacid=37176882 trans
19 External stimuleffector receptor (NLR) (original description: pacid=37177710 transcript=Phvul.002G
20 Solute transpctransport protein (TSUP) (original description: pacid=37177847 transcript=Phvul.002
21 Solute transpctransport protein (TSUP) (original description: pacid=37177847 transcript=Phvul.002
22 Solute transpctransport protein (TSUP) (original description: pacid=37175732 transcript=Phvul.002
23 Solute transpctransport protein (TSUP) (original description: pacid=37175732 transcript=Phvul.002
24 Solute transpctransport protein (TSUP) (original description: pacid=37175732 transcript=Phvul.002
25 Solute transpctransport protein (TSUP) (original description: pacid=37175732 transcript=Phvul.002
26 Solute transpctransport protein (TSUP) (original description: pacid=37175732 transcript=Phvul.002
27 Solute transpctransport protein (TSUP) (original description: pacid=37175732 transcript=Phvul.002
28 Solute transpctransport protein (TSUP) (original description: pacid=37175732 transcript=Phvul.002
29 Solute transpctransport protein (TSUP) (original description: pacid=37175732 transcript=Phvul.002
30 Cytoskeleton class VIII myosin microfilament-based motor protein (original description: pacid=371
31 Cytoskeleton class VIII myosin microfilament-based motor protein (original description: pacid=371
32 Cytoskeleton class VIII myosin microfilament-based motor protein (original description: pacid=371
33 Cytoskeleton class VIII myosin microfilament-based motor protein (original description: pacid=371
34 Cytoskeleton class VIII myosin microfilament-based motor protein (original description: pacid=371
35 Cytoskeleton class VIII myosin microfilament-based motor protein (original description: pacid=371
36 not assigned.r no hits & (original description: pacid=37146447 transcript=Phvul.003G050200.2 locu
37 not assigned.r no hits & (original description: pacid=37146447 transcript=Phvul.003G050200.2 locu
38 not assigned.r no hits & (original description: pacid=37145696 transcript=Phvul.003G244225.3 locu
39 not assigned.r no hits & (original description: pacid=37145696 transcript=Phvul.003G244225.3 locu
40 not assigned.r no hits & (original description: pacid=37145696 transcript=Phvul.003G244225.3 locu
41 Chromatin orgSUVH2/9 methyl-DNA-binding factor of DNA methylation pathway (original descripti
42 Chromatin orgSUVH2/9 methyl-DNA-binding factor of DNA methylation pathway (original descripti
43 not assigned.ε (original description: pacid=37146499 transcript=Phvul.003G282250.1 locus=Phvul.C
44 RNA processir polynucleotide phosphorylase (PNP) (original description: pacid=37161570 transcript
45 Protein modif protein kinase (LRR-II) (original description: pacid=37161848 transcript=Phvul.004G0

1 Protein modif protein kinase (LRR-II) (original description: pacid=37161848 transcript=Phvul.004G0
2 not assigned.ε (original description: pacid=37154419 transcript=Phvul.005G041300.1 locus=Phvul.C
3 not assigned.ε (original description: pacid=37154419 transcript=Phvul.005G041300.1 locus=Phvul.C
4 not assigned.ε (original description: pacid=37152832 transcript=Phvul.005G069700.1 locus=Phvul.C
5 not assigned.ε (original description: pacid=37152832 transcript=Phvul.005G069700.1 locus=Phvul.C
6 not assigned.ε (original description: pacid=37152508 transcript=Phvul.005G072000.1 locu
7 not assigned.ε (original description: pacid=37172484 transcript=Phvul.006G027500.1 locus=Phvul.C
8 not assigned.ε (original description: pacid=37172484 transcript=Phvul.006G027500.1 locus=Phvul.C
9 Carbohydrate ribose 5-phosphate isomerase (original description: pacid=37173541 transcript=Phvu
10 not assigned.r no hits & (original description: pacid=37171587 transcript=Phvul.006G126400.1 locu
11 not assigned.r no hits & (original description: pacid=37171587 transcript=Phvul.006G126400.1 locu
12 not assigned.r no hits & (original description: pacid=37171863 transcript=Phvul.006G170700.1 locu
13 not assigned.ε (original description: pacid=37161510 transcript=Phvul.008G107400.1 locus=Phvul.C
14 not assigned.ε (original description: pacid=37161510 transcript=Phvul.008G107400.1 locus=Phvul.C
15 RNA processir XRN4-exoribonuclease cofactor (LARP1) (original description: pacid=37159819 transc
16 Protein modif protein kinase (LRR-III) (original description: pacid=37149262 transcript=Phvul.009G1
17 not assigned.ε (original description: pacid=37143651 transcript=Phvul.010G008500.1 locus=Phvul.C
18 RNA biosynthtranscription factor (DOF) (original description: pacid=37142918 transcript=Phvul.010
19 not assigned.r no hits & (original description: pacid=37143088 transcript=Phvul.010G044000.3 locu
20 not assigned.r no hits & (original description: pacid=37143088 transcript=Phvul.010G044000.3 locu
21 not assigned.r no hits & (original description: pacid=37143088 transcript=Phvul.010G044000.3 locu
22 not assigned.r no hits & (original description: pacid=37143088 transcript=Phvul.010G044000.3 locu
23 not assigned.r no hits & (original description: pacid=37143088 transcript=Phvul.010G044000.3 locu
24 not assigned.r no hits & (original description: pacid=37143088 transcript=Phvul.010G044000.3 locu
25 not assigned.r no hits & (original description: pacid=37143088 transcript=Phvul.010G044000.3 locu
26 not assigned.r no hits & (original description: pacid=37143088 transcript=Phvul.010G044000.3 locu
27 not assigned.r no hits & (original description: pacid=37143088 transcript=Phvul.010G044000.3 locu
28 not assigned.ε (original description: pacid=37156104 transcript=Phvul.011G181700.1 locus=Phvul.C
29 not assigned.ε (original description: pacid=37157395 transcript=Phvul.011G200820.1 locus=Phvul.C
30 not assigned.ε (original description: pacid=37156073 transcript=Phvul.011G202100.1 locus=Phvul.C
31 not assigned.ε (original description: pacid=37155566 transcript=Phvul.011G202300.1 locus=Phvul.C
32 not assigned.ε (original description: pacid=37156337 transcript=Phvul.011G203100.1 locus=Phvul.C
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3 J04G048000 ID=Phvul.004G048000.1.v2.1 annot-version=v2.1) & Probable disease resistance prote
4 J01G224800 ID=Phvul.001G224800.2.v2.1 annot-version=v2.1) & no description available(sp|q10az
5 J01G224800 ID=Phvul.001G224800.2.v2.1 annot-version=v2.1) & no description available(sp|q10az
6 J01G224800 ID=Phvul.001G224800.2.v2.1 annot-version=v2.1) & no description available(sp|q10az
7 J01G224800 ID=Phvul.001G224800.2.v2.1 annot-version=v2.1) & no description available(sp|q10az
8 J01G224800 ID=Phvul.001G224800.2.v2.1 annot-version=v2.1) & no description available(sp|q10az
9
10 J07G201700 ID=Phvul.007G201700.1.v2.1 annot-version=v2.1) & Acyl-CoA-binding domain-contain
11 J07G201700 ID=Phvul.007G201700.1.v2.1 annot-version=v2.1) & Acyl-CoA-binding domain-contain
12 J08G061300 ID=Phvul.008G061300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
13 J08G061300 ID=Phvul.008G061300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
14 J08G061300 ID=Phvul.008G061300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
15 J08G061300 ID=Phvul.008G061300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
16 J08G061300 ID=Phvul.008G061300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
17
18 i079200.1 locus=Phvul.002G079200 ID=Phvul.002G079200.1.v2.1 annot-version=v2.1) &
19 Phvul.001G217600.1 locus=Phvul.001G217600 ID=Phvul.001G217600.1.v2.1 annot-version=v2.1) &
20 02G001500.1 locus=Phvul.002G001500 ID=Phvul.002G001500.1.v2.1 annot-version=v2.1) &
21 02G001500.1 locus=Phvul.002G001500 ID=Phvul.002G001500.1.v2.1 annot-version=v2.1) &
22 02G001500.1 locus=Phvul.002G001500 ID=Phvul.002G001500.1.v2.1 annot-version=v2.1) &
23 i072500.1 locus=Phvul.003G072500 ID=Phvul.003G072500.1.v2.1 annot-version=v2.1) &
24 js=Phvul.003G244225 ID=Phvul.003G244225.3.v2.1 annot-version=v2.1)
25 js=Phvul.003G244225 ID=Phvul.003G244225.3.v2.1 annot-version=v2.1)
26 js=Phvul.003G244225 ID=Phvul.003G244225.3.v2.1 annot-version=v2.1)
27 i137300.1 locus=Phvul.004G137300 ID=Phvul.004G137300.1.v2.1 annot-version=v2.1) &
28 i400.3 locus=Phvul.005G029400 ID=Phvul.005G029400.3.v2.1 annot-version=v2.1) &
29 i400.3 locus=Phvul.005G029400 ID=Phvul.005G029400.3.v2.1 annot-version=v2.1) &
30 i400.3 locus=Phvul.005G029400 ID=Phvul.005G029400.3.v2.1 annot-version=v2.1) &
31 i400.3 locus=Phvul.005G029400 ID=Phvul.005G029400.3.v2.1 annot-version=v2.1) &
32 i400.3 locus=Phvul.005G029400 ID=Phvul.005G029400.3.v2.1 annot-version=v2.1) &
33 7G210600.1 locus=Phvul.007G210600 ID=Phvul.007G210600.1.v2.1 annot-version=v2.1) &
34 7G210600.1 locus=Phvul.007G210600 ID=Phvul.007G210600.1.v2.1 annot-version=v2.1) &
35 :37160544 transcript=Phvul.008G055500.1 locus=Phvul.008G055500 ID=Phvul.008G055500.1.v2.1 ;
36 js=Phvul.008G280900 ID=Phvul.008G280900.1.v2.1 annot-version=v2.1)
37 js=Phvul.008G280900 ID=Phvul.008G280900.1.v2.1 annot-version=v2.1)
38
39 J10G064700 ID=Phvul.010G064700.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
40 i136700.1 locus=Phvul.010G136700 ID=Phvul.010G136700.1.v2.1 annot-version=v2.1) &
41 js=Phvul.011G149100 ID=Phvul.011G149100.7.v2.1 annot-version=v2.1)
42 js=Phvul.011G149100 ID=Phvul.011G149100.7.v2.1 annot-version=v2.1)
43 js=Phvul.011G149100 ID=Phvul.011G149100.7.v2.1 annot-version=v2.1)
44 js=Phvul.011G149100 ID=Phvul.011G149100.7.v2.1 annot-version=v2.1)
45 js=Phvul.011G149100 ID=Phvul.011G149100.7.v2.1 annot-version=v2.1)
46 js=Phvul.011G149100 ID=Phvul.011G149100.7.v2.1 annot-version=v2.1)
47 js=Phvul.011G149100 ID=Phvul.011G149100.7.v2.1 annot-version=v2.1)
48 js=Phvul.011G149100 ID=Phvul.011G149100.7.v2.1 annot-version=v2.1)
49 js=Phvul.011G149100 ID=Phvul.011G149100.7.v2.1 annot-version=v2.1)
50 js=Phvul.011G149100 ID=Phvul.011G149100.7.v2.1 annot-version=v2.1)
51
52 J11G166100 ID=Phvul.011G166100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
53 J01G128200 ID=Phvul.001G128200.2.v2.1 annot-version=v2.1) & TMV resistance protein N OS=Nicc
54 J01G134000 ID=Phvul.001G134000.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
55 J01G134000 ID=Phvul.001G134000.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
56 rt=Phvul.001G243900.1 locus=Phvul.001G243900 ID=Phvul.001G243900.1.v2.1 annot-version=v2.1)
57 rt=Phvul.001G243900.1 locus=Phvul.001G243900 ID=Phvul.001G243900.1.v2.1 annot-version=v2.1)
58 js=Phvul.002G057300 ID=Phvul.002G057300.2.v2.1 annot-version=v2.1)
59 js=Phvul.002G057300 ID=Phvul.002G057300.2.v2.1 annot-version=v2.1)
60

1 !G122200.1 locus=Phvul.002G122200 ID=Phvul.002G122200.1.v2.1 annot-version=v2.1) &
2 s=Phvul.002G187600 ID=Phvul.002G187600.1.v2.1 annot-version=v2.1)
3 anscrip=Phvul.002G261500.1 locus=Phvul.002G261500 ID=Phvul.002G261500.1.v2.1 annot-versior
4 anscrip=Phvul.002G261500.1 locus=Phvul.002G261500 ID=Phvul.002G261500.1.v2.1 annot-versior
5 003G101200 ID=Phvul.003G101200.1.v2.1 annot-version=v2.1) & CASP-like protein 1E1 OS=Glycine
6 003G101200 ID=Phvul.003G101200.1.v2.1 annot-version=v2.1) & CASP-like protein 1E1 OS=Glycine
7 : pacid=37146060 transcript=Phvul.003G202900.1 locus=Phvul.003G202900 ID=Phvul.003G202900
8 : pacid=37146060 transcript=Phvul.003G202900.1 locus=Phvul.003G202900 ID=Phvul.003G202900
9 162776 transcript=Phvul.004G026200.1 locus=Phvul.004G026200 ID=Phvul.004G026200.1.v2.1 anr
10 i140400.1 locus=Phvul.004G140400 ID=Phvul.004G140400.1.v2.1 annot-version=v2.1) &
11 i140400.1 locus=Phvul.004G140400 ID=Phvul.004G140400.1.v2.1 annot-version=v2.1) &
12 ript=Phvul.005G038200.1 locus=Phvul.005G038200 ID=Phvul.005G038200.1.v2.1 annot-version=v2
13 ript=Phvul.005G038200.1 locus=Phvul.005G038200 ID=Phvul.005G038200.1.v2.1 annot-version=v2
14 005G087100 ID=Phvul.005G087100.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
15 005G087100 ID=Phvul.005G087100.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
16 3102700.1 locus=Phvul.006G102700 ID=Phvul.006G102700.1.v2.1 annot-version=v2.1) &
17 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
18 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
19 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
20 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
21 acid=37157997 transcript=Phvul.008G202300.1 locus=Phvul.008G202300 ID=Phvul.008G202300.1.
22 ranscrip=Phvul.008G259600.2 locus=Phvul.008G259600 ID=Phvul.008G259600.2.v2.1 annot-versio
23 ranscrip=Phvul.008G259600.2 locus=Phvul.008G259600 ID=Phvul.008G259600.2.v2.1 annot-versio
24 ranscrip=Phvul.008G259600.2 locus=Phvul.008G259600 ID=Phvul.008G259600.2.v2.1 annot-versio
25 ranscrip=Phvul.008G259600.2 locus=Phvul.008G259600 ID=Phvul.008G259600.2.v2.1 annot-versio
26 i131650.1 locus=Phvul.010G131650 ID=Phvul.010G131650.1.v2.1 annot-version=v2.1) &
27 010G132333 ID=Phvul.010G132333.3.v2.1 annot-version=v2.1) & Disease resistance protein RML1A
28 i136800.1 locus=Phvul.010G136800 ID=Phvul.010G136800.1.v2.1 annot-version=v2.1) &
29 s=Phvul.010G151400 ID=Phvul.010G151400.6.v2.1 annot-version=v2.1)
30 s=Phvul.010G151400 ID=Phvul.010G151400.6.v2.1 annot-version=v2.1)
31 s=Phvul.010G151400 ID=Phvul.010G151400.6.v2.1 annot-version=v2.1)
32 s=Phvul.010G151400 ID=Phvul.010G151400.6.v2.1 annot-version=v2.1)
33 i140300.1 locus=Phvul.011G140300 ID=Phvul.011G140300.1.v2.1 annot-version=v2.1) &
34 i140400.1 locus=Phvul.011G140400 ID=Phvul.011G140400.1.v2.1 annot-version=v2.1) &
35 011G151300 ID=Phvul.011G151300.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
36 011G181700 ID=Phvul.011G181700.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
37 011G181700 ID=Phvul.011G181700.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
38 011G192400 ID=Phvul.011G192400.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
39 011G192600 ID=Phvul.011G192600.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
40 011G193100 ID=Phvul.011G193100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
41 011G193500 ID=Phvul.011G193500.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
42 011G193600 ID=Phvul.011G193600.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
43 011G194800 ID=Phvul.011G194800.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
44 011G194900 ID=Phvul.011G194900.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
45 011G195000 ID=Phvul.011G195000.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
46 011G195200 ID=Phvul.011G195200.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13

1 J11G195400 ID=Phvul.011G195400.2.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
2 J11G195500 ID=Phvul.011G195500.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
3 J11G196000 ID=Phvul.011G196000.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
4 J11G196066 ID=Phvul.011G196066.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
5 J11G200820 ID=Phvul.011G200820.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
6 J11G200820 ID=Phvul.011G200820.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
7 J11G202100 ID=Phvul.011G202100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
8 J11G202100 ID=Phvul.011G202100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
9 J11G202300 ID=Phvul.011G202300.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
10 J11G202300 ID=Phvul.011G202300.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
11 J11G202300 ID=Phvul.011G202300.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
12 J11G202300 ID=Phvul.011G202300.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
13 J11G202300 ID=Phvul.011G202300.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
14 J11G203100 ID=Phvul.011G203100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
15 J11G203100 ID=Phvul.011G203100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
16 J11G203100 ID=Phvul.011G203100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
17 337 ID=Phvul.L002337.2.v2.1 annot-version=v2.1) & Alcohol dehydrogenase-like 7 OS=Arabidopsis
18 337 ID=Phvul.L002337.2.v2.1 annot-version=v2.1) & Alcohol dehydrogenase-like 7 OS=Arabidopsis
19 337 ID=Phvul.L002337.2.v2.1 annot-version=v2.1) & Alcohol dehydrogenase-like 7 OS=Arabidopsis
20 337 ID=Phvul.L002337.2.v2.1 annot-version=v2.1) & Alcohol dehydrogenase-like 7 OS=Arabidopsis
21 337 ID=Phvul.L002337.2.v2.1 annot-version=v2.1) & Alcohol dehydrogenase-like 7 OS=Arabidopsis
22 J01G015600 ID=Phvul.001G015600.3.v2.1 annot-version=v2.1) & Lysophospholipid acyltransferase
23 J01G015600 ID=Phvul.001G015600.3.v2.1 annot-version=v2.1) & Lysophospholipid acyltransferase
24 J01G015600 ID=Phvul.001G015600.3.v2.1 annot-version=v2.1) & Lysophospholipid acyltransferase
25 J01G015600 ID=Phvul.001G015600.3.v2.1 annot-version=v2.1) & Lysophospholipid acyltransferase
26 001G085500.2 locus=Phvul.001G085500 ID=Phvul.001G085500.2.v2.1 annot-version=v2.1) &
27 001G085500.2 locus=Phvul.001G085500 ID=Phvul.001G085500.2.v2.1 annot-version=v2.1) &
28 2600.1 locus=Phvul.001G232600 ID=Phvul.001G232600.1.v2.1 annot-version=v2.1) &
29 2600.1 locus=Phvul.001G232600 ID=Phvul.001G232600.1.v2.1 annot-version=v2.1) &
30 J02G041400.4 locus=Phvul.002G041400 ID=Phvul.002G041400.4.v2.1 annot-version=v2.1) &
31 J02G041400.4 locus=Phvul.002G041400 ID=Phvul.002G041400.4.v2.1 annot-version=v2.1) &
32 J02G041400.4 locus=Phvul.002G041400 ID=Phvul.002G041400.4.v2.1 annot-version=v2.1) &
33 J02G041400.4 locus=Phvul.002G041400 ID=Phvul.002G041400.4.v2.1 annot-version=v2.1) &
34 J02G298800 ID=Phvul.002G298800.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At4g10955 (C
35 l description: pacid=37145098 transcript=Phvul.003G010900.1 locus=Phvul.003G010900 ID=Phvul.(C
36 l description: pacid=37145098 transcript=Phvul.003G010900.1 locus=Phvul.003G010900 ID=Phvul.(C
37 =37145330 transcript=Phvul.003G195800.2 locus=Phvul.003G195800 ID=Phvul.003G195800.2.v2.1
38 =37145330 transcript=Phvul.003G195800.2 locus=Phvul.003G195800 ID=Phvul.003G195800.2.v2.1
39 t=Phvul.003G252400.1 locus=Phvul.003G252400 ID=Phvul.003G252400.1.v2.1 annot-version=v2.1)
40 t=Phvul.003G252400.1 locus=Phvul.003G252400 ID=Phvul.003G252400.1.v2.1 annot-version=v2.1)
41 **nal description: pacid=37146502 transcript=Phvul.003G295800.4 locus=Phvul.003G295800 ID=Phvu**
42 **nal description: pacid=37146502 transcript=Phvul.003G295800.4 locus=Phvul.003G295800 ID=Phvu**
43 **nal description: pacid=37146502 transcript=Phvul.003G295800.4 locus=Phvul.003G295800 ID=Phvu**
44 J04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
45 J04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
46 J04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
47 J04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
48 J04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
49 J04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
50 J04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
51 J04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
52 J04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
53 J04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
54 J04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
55 J04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
56 J04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
57 J04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
58 J04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
59 J04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
60 J04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A

1 J04G048000 ID=Phvul.004G048000.1.v2.1 annot-version=v2.1) & Probable disease resistance prote
2 J04G048000 ID=Phvul.004G048000.1.v2.1 annot-version=v2.1) & Probable disease resistance prote
3 rscript=Phvul.004G106800.2 locus=Phvul.004G106800 ID=Phvul.004G106800.2.v2.1 annot-version=
4 rscript=Phvul.004G106800.2 locus=Phvul.004G106800 ID=Phvul.004G106800.2.v2.1 annot-version=
5 J04G133100 ID=Phvul.004G133100.1.v2.1 annot-version=v2.1) & Probable carboxylesterase 18 OS=
6 J05G165800 ID=Phvul.005G165800.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
7 J05G165800 ID=Phvul.005G165800.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
8 J06G066800 ID=Phvul.006G066800.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
9 6800.1 locus=Phvul.006G086800 ID=Phvul.006G086800.1.v2.1 annot-version=v2.1) &
10 rs=Phvul.006G148800 ID=Phvul.006G148800.1.v2.1 annot-version=v2.1)
11 46.0) & Enzyme classification.EC_2 transferases.EC_2.1 transferase transferring one-carbon group(5
12 46.0) & Enzyme classification.EC_2 transferases.EC_2.1 transferase transferring one-carbon group(5
13 rs=Phvul.007G027400 ID=Phvul.007G027400.1.v2.1 annot-version=v2.1)
14 rzyme classification.EC_3 hydrolases.EC_3.6 hydrolase acting on acid anhydride(50.3.6 : 133.9) (orig
15 158100.1 locus=Phvul.008G158100 ID=Phvul.008G158100.1.v2.1 annot-version=v2.1) &
16 il.009G020000.1 locus=Phvul.009G020000 ID=Phvul.009G020000.1.v2.1 annot-version=v2.1) &
17 il.009G020000.1 locus=Phvul.009G020000 ID=Phvul.009G020000.1.v2.1 annot-version=v2.1) &
18 9G065500.2 locus=Phvul.009G065500 ID=Phvul.009G065500.2.v2.1 annot-version=v2.1) &
19 9G065500.2 locus=Phvul.009G065500 ID=Phvul.009G065500.2.v2.1 annot-version=v2.1) &
20 9G065500.2 locus=Phvul.009G065500 ID=Phvul.009G065500.2.v2.1 annot-version=v2.1) &
21 9G065500.2 locus=Phvul.009G065500 ID=Phvul.009G065500.2.v2.1 annot-version=v2.1) &
22 J09G213300 ID=Phvul.009G213300.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat
23 J09G226300 ID=Phvul.009G226300.2.v2.1 annot-version=v2.1) & Protein trichome birefringence-lik
24 J09G226300 ID=Phvul.009G226300.2.v2.1 annot-version=v2.1) & Protein trichome birefringence-lik
25 J09G226300 ID=Phvul.009G226300.2.v2.1 annot-version=v2.1) & Protein trichome birefringence-lik
26 J09G226300 ID=Phvul.009G226300.2.v2.1 annot-version=v2.1) & Protein trichome birefringence-lik
27 J09G233700 ID=Phvul.009G233700.1.v2.1 annot-version=v2.1) & Probable disease resistance RPP8-
28 J09G233700 ID=Phvul.009G233700.1.v2.1 annot-version=v2.1) & Probable disease resistance RPP8-
29 J09G233700 ID=Phvul.009G233700.1.v2.1 annot-version=v2.1) & Probable disease resistance RPP8-
30 J10G008700 ID=Phvul.010G008700.2.v2.1 annot-version=v2.1) & TMV resistance protein N OS=Nicc
31 J10G008700 ID=Phvul.010G008700.2.v2.1 annot-version=v2.1) & TMV resistance protein N OS=Nicc
32 J10G056500 ID=Phvul.010G056500.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
33 J10G056500 ID=Phvul.010G056500.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
34 J10G063100 ID=Phvul.010G063100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
35 J10G070584 ID=Phvul.010G070584.1.v2.1 annot-version=v2.1) & Long-chain-alcohol oxidase FAO1
36 rs=Phvul.010G146900 ID=Phvul.010G146900.7.v2.1 annot-version=v2.1)
37 rs=Phvul.010G146900 ID=Phvul.010G146900.7.v2.1 annot-version=v2.1)
38 rs=Phvul.010G146900 ID=Phvul.010G146900.7.v2.1 annot-version=v2.1)
39 rs=Phvul.010G146900 ID=Phvul.010G146900.7.v2.1 annot-version=v2.1)
40 rs=Phvul.010G146900 ID=Phvul.010G146900.7.v2.1 annot-version=v2.1)
41 rs=Phvul.010G146900 ID=Phvul.010G146900.7.v2.1 annot-version=v2.1)
42 J11G014500 ID=Phvul.011G014500.2.v2.1 annot-version=v2.1) & Disease resistance protein RPP13
43 J11G014500 ID=Phvul.011G014500.2.v2.1 annot-version=v2.1) & Disease resistance protein RPP13
44 J11G014500 ID=Phvul.011G014500.2.v2.1 annot-version=v2.1) & Disease resistance protein RPP13
45 J11G082700 ID=Phvul.011G082700.3.v2.1 annot-version=v2.1) & P-loop NTPase domain-containing
46 J11G082700 ID=Phvul.011G082700.3.v2.1 annot-version=v2.1) & P-loop NTPase domain-containing

1
2 **011G082700 ID=Phvul.011G082700.3.v2.1 annot-version=v2.1) & P-loop NTPase domain-containing**
3
4 011G149400 ID=Phvul.011G149400.1.v2.1 annot-version=v2.1) & Disease resistance protein At4g27
5 011G149400 ID=Phvul.011G149400.1.v2.1 annot-version=v2.1) & Disease resistance protein At4g27
6 011G181500 ID=Phvul.011G181500.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
7
8
9
10 011G191600 ID=Phvul.011G191600.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
11 011G191800 ID=Phvul.011G191800.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
12 011G192200 ID=Phvul.011G192200.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
13 011G192900 ID=Phvul.011G192900.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
14 011G192900 ID=Phvul.011G192900.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
15 011G192900 ID=Phvul.011G192900.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
16 011G195751 ID=Phvul.011G195751.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
17 011G198400 ID=Phvul.011G198400.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
18 011G201000 ID=Phvul.011G201000.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
19 011G201101 ID=Phvul.011G201101.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
20 011G201101 ID=Phvul.011G201101.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
21 001G027100 ID=Phvul.001G027100.1.v2.1 annot-version=v2.1) & F-box/kelch-repeat protein At5g4
22 001G123000 ID=Phvul.001G123000.2.v2.1 annot-version=v2.1) & Alpha-glucosidase OS=Spinacia oler
23 001G132516 ID=Phvul.001G132516.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
24 001G132516 ID=Phvul.001G132516.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
25 001G132701 ID=Phvul.001G132701.1.v2.1 annot-version=v2.1) & Disease resistance protein RGA2 (C
26 001G132701 ID=Phvul.001G132701.1.v2.1 annot-version=v2.1) & Disease resistance protein RGA2 (C
27 001G132800 ID=Phvul.001G132800.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
28 001G132800 ID=Phvul.001G132800.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
29 001G132864 ID=Phvul.001G132864.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
30 001G132864 ID=Phvul.001G132864.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
31 001G133100 ID=Phvul.001G133100.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
32 001G133100 ID=Phvul.001G133100.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
33 001G133101 ID=Phvul.001G133101.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
34 001G133101 ID=Phvul.001G133101.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
35 185400.1 locus=Phvul.001G185400 ID=Phvul.001G185400.1.v2.1 annot-version=v2.1) &
36 185400.1 locus=Phvul.001G185400 ID=Phvul.001G185400.1.v2.1 annot-version=v2.1) &
37 0086 transcript=Phvul.001G217800.1 locus=Phvul.001G217800 ID=Phvul.001G217800.1.v2.1 annot
38 2G063500.1 locus=Phvul.002G063500 ID=Phvul.002G063500.1.v2.1 annot-version=v2.1) &
39 2G063500.1 locus=Phvul.002G063500 ID=Phvul.002G063500.1.v2.1 annot-version=v2.1) &
40 002G104200.1 locus=Phvul.002G104200 ID=Phvul.002G104200.1.v2.1 annot-version=v2.1) &
41 002G104200.1 locus=Phvul.002G104200 ID=Phvul.002G104200.1.v2.1 annot-version=v2.1) &
42 178074 transcript=Phvul.002G279500.1 locus=Phvul.002G279500 ID=Phvul.002G279500.1.v2.1 an
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1 03G162300.1 locus=Phvul.003G162300 ID=Phvul.003G162300.1.v2.1 annot-version=v2.1) &
2 hvul.003G209600.2 locus=Phvul.003G209600 ID=Phvul.003G209600.2.v2.1 annot-version=v2.1) &
3 hvul.003G209600.2 locus=Phvul.003G209600 ID=Phvul.003G209600.2.v2.1 annot-version=v2.1) &
4 ranscript=Phvul.003G288300.1 locus=Phvul.003G288300 ID=Phvul.003G288300.1.v2.1 annot-versic
5 ranscript=Phvul.003G288300.1 locus=Phvul.003G288300 ID=Phvul.003G288300.1.v2.1 annot-versic
6 ranscript=Phvul.003G288300.1 locus=Phvul.003G288300 ID=Phvul.003G288300.1.v2.1 annot-versic
7 ranscript=Phvul.003G288300.1 locus=Phvul.003G288300 ID=Phvul.003G288300.1.v2.1 annot-versic
8 04G011400.1 locus=Phvul.004G011400 ID=Phvul.004G011400.1.v2.1 annot-version=v2.1) &
9 04G064300 ID=Phvul.004G064300.1.v2.1 annot-version=v2.1) & Ultraviolet-B receptor UVR8 OS=A
10 04G064300 ID=Phvul.004G064300.1.v2.1 annot-version=v2.1) & Ultraviolet-B receptor UVR8 OS=A
11 04G131300 ID=Phvul.004G131300.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
12 04G131300 ID=Phvul.004G131300.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
13 05G031200 ID=Phvul.005G031200.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
14 05G071300 ID=Phvul.005G071300.1.v2.1 annot-version=v2.1) &
15 05G071300 ID=Phvul.005G071300.1.v2.1 annot-version=v2.1) &
16 : pacid=37172307 transcript=Phvul.006G057000.1 locus=Phvul.006G057000 ID=Phvul.006G057000
17 : pacid=37172194 transcript=Phvul.006G057100.5 locus=Phvul.006G057100 ID=Phvul.006G057100
18 : pacid=37172194 transcript=Phvul.006G057100.5 locus=Phvul.006G057100 ID=Phvul.006G057100
19 06G057700.2 locus=Phvul.006G057700 ID=Phvul.006G057700.2.v2.1 annot-version=v2.1) &
20 06G066800 ID=Phvul.006G066800.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
21 06G066800 ID=Phvul.006G066800.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
22 07G086300 ID=Phvul.007G086300.2.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
23 07G086300 ID=Phvul.007G086300.2.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
24 08G014700 ID=Phvul.008G014700.1.v2.1 annot-version=v2.1) & Disease resistance protein RPP13
25 08G014700 ID=Phvul.008G014700.1.v2.1 annot-version=v2.1) & Disease resistance protein RPP13
26 08G072032 ID=Phvul.008G072032.1.v2.1 annot-version=v2.1) & Probable disease resistance prote
27 08G072032 ID=Phvul.008G072032.1.v2.1 annot-version=v2.1) & Probable disease resistance prote
28 rs=Phvul.008G168300 ID=Phvul.008G168300.2.v2.1 annot-version=v2.1)
29 rs=Phvul.008G168300 ID=Phvul.008G168300.2.v2.1 annot-version=v2.1)
30 .009G039200.1 locus=Phvul.009G039200 ID=Phvul.009G039200.1.v2.1 annot-version=v2.1) &
31 l.009G079700.1 locus=Phvul.009G079700 ID=Phvul.009G079700.1.v2.1 annot-version=v2.1) &
32 l.009G079700.1 locus=Phvul.009G079700 ID=Phvul.009G079700.1.v2.1 annot-version=v2.1) &
33 09G180800.2 locus=Phvul.009G180800 ID=Phvul.009G180800.2.v2.1 annot-version=v2.1) &
34 09G180800.2 locus=Phvul.009G180800 ID=Phvul.009G180800.2.v2.1 annot-version=v2.1) &
35 09G180800.2 locus=Phvul.009G180800 ID=Phvul.009G180800.2.v2.1 annot-version=v2.1) &
36 09G180800.2 locus=Phvul.009G180800 ID=Phvul.009G180800.2.v2.1 annot-version=v2.1) &
37 rs=Phvul.009G249500 ID=Phvul.009G249500.1.v2.1 annot-version=v2.1)
38 i025000.1 locus=Phvul.010G025000 ID=Phvul.010G025000.1.v2.1 annot-version=v2.1) &
39 i025700.1 locus=Phvul.010G025700 ID=Phvul.010G025700.1.v2.1 annot-version=v2.1) &
40 10G063700 ID=Phvul.010G063700.2.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
41 rs=Phvul.010G101700 ID=Phvul.010G101700.1.v2.1 annot-version=v2.1)
42 **010G141400.1 locus=Phvul.010G141400 ID=Phvul.010G141400.1.v2.1 annot-version=v2.1) &**
43 10G149500 ID=Phvul.010G149500.1.v2.1 annot-version=v2.1) & Regulator of telomere elongation
44 10G149500 ID=Phvul.010G149500.1.v2.1 annot-version=v2.1) & Regulator of telomere elongation
45 11G015000.1 locus=Phvul.011G015000 ID=Phvul.011G015000.1.v2.1 annot-version=v2.1) &
46 11G181500 ID=Phvul.011G181500.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
47 11G181500 ID=Phvul.011G181500.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
48 11G198000 ID=Phvul.011G198000.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13

1 J11G198000 ID=Phvul.011G198000.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
2 J11G200880 ID=Phvul.011G200880.2.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
3 J11G200880 ID=Phvul.011G200880.2.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
4 J11G201000 ID=Phvul.011G201000.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
5 J11G201000 ID=Phvul.011G201000.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
6 J11G201101 ID=Phvul.011G201101.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
7 J11G201101 ID=Phvul.011G201101.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
8 J11G202366 ID=Phvul.011G202366.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
9 J11G202366 ID=Phvul.011G202366.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
10 ath : 469.0) & Enzyme classification.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2 : 354.6) (original des
11 ath : 469.0) & Enzyme classification.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2 : 354.6) (original des
12 J01G183400.4 locus=Phvul.001G183400 ID=Phvul.001G183400.4.v2.1 annot-version=v2.1) &
13 J01G183400.4 locus=Phvul.001G183400 ID=Phvul.001G183400.4.v2.1 annot-version=v2.1) &
14 J01G183400.4 locus=Phvul.001G183400 ID=Phvul.001G183400.4.v2.1 annot-version=v2.1) &
15 J01G183400.4 locus=Phvul.001G183400 ID=Phvul.001G183400.4.v2.1 annot-version=v2.1) &
16 script=Phvul.002G089800.1 locus=Phvul.002G089800 ID=Phvul.002G089800.1.v2.1 annot-version=v
17 script=Phvul.002G089800.1 locus=Phvul.002G089800 ID=Phvul.002G089800.1.v2.1 annot-version=v
18 i171400.1 locus=Phvul.002G171400 ID=Phvul.002G171400.1.v2.1 annot-version=v2.1) &
19 G244900.1 locus=Phvul.002G244900 ID=Phvul.002G244900.1.v2.1 annot-version=v2.1) &
20 G244900.1 locus=Phvul.002G244900 ID=Phvul.002G244900.1.v2.1 annot-version=v2.1) &
21 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
22 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
23 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
24 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
25 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
26 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
27 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
28 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
29 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
30 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
31 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
32 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
33 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
34 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
35 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
36 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
37 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
38 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
39 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
40 G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
41 .44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 anno
42 .44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 anno
43 .44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 anno
44 .44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 anno
45 .44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 anno
46 .44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 anno
47 .44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 anno
48 .44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 anno
49 us=Phvul.003G050200 ID=Phvul.003G050200.2.v2.1 annot-version=v2.1)
50 us=Phvul.003G050200 ID=Phvul.003G050200.2.v2.1 annot-version=v2.1)
51 us=Phvul.003G244225 ID=Phvul.003G244225.3.v2.1 annot-version=v2.1)
52 us=Phvul.003G244225 ID=Phvul.003G244225.3.v2.1 annot-version=v2.1)
53 us=Phvul.003G244225 ID=Phvul.003G244225.3.v2.1 annot-version=v2.1)
54 us=Phvul.003G244225 ID=Phvul.003G244225.3.v2.1 annot-version=v2.1)
55 on: pacid=37145910 transcript=Phvul.003G282200.3 locus=Phvul.003G282200 ID=Phvul.003G28220
56 on: pacid=37145910 transcript=Phvul.003G282200.3 locus=Phvul.003G282200 ID=Phvul.003G28220
57 J03G282250 ID=Phvul.003G282250.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
58 t=Phvul.004G011100.1 locus=Phvul.004G011100 ID=Phvul.004G011100.1.v2.1 annot-version=v2.1)
59 J086300.2 locus=Phvul.004G086300 ID=Phvul.004G086300.2.v2.1 annot-version=v2.1) &

1 086300.2 locus=Phvul.004G086300 ID=Phvul.004G086300.2.v2.1 annot-version=v2.1) &
2 005G041300 ID=Phvul.005G041300.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat
3 005G041300 ID=Phvul.005G041300.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat
4 005G069700 ID=Phvul.005G069700.1.v2.1 annot-version=v2.1) & Nuclear pore complex protein NU
5 005G069700 ID=Phvul.005G069700.1.v2.1 annot-version=v2.1) & Nuclear pore complex protein NU
6 js=Phvul.005G072000 ID=Phvul.005G072000.1.v2.1 annot-version=v2.1)
7 006G027500 ID=Phvul.006G027500.1.v2.1 annot-version=v2.1) & WD repeat-containing protein 26
8 006G027500 ID=Phvul.006G027500.1.v2.1 annot-version=v2.1) & WD repeat-containing protein 26
9 jl.006G100600.1 locus=Phvul.006G100600 ID=Phvul.006G100600.1.v2.1 annot-version=v2.1) &
10 js=Phvul.006G126400 ID=Phvul.006G126400.1.v2.1 annot-version=v2.1)
11 js=Phvul.006G126400 ID=Phvul.006G126400.1.v2.1 annot-version=v2.1)
12 js=Phvul.006G170700 ID=Phvul.006G170700.1.v2.1 annot-version=v2.1)
13 008G107400 ID=Phvul.008G107400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
14 008G107400 ID=Phvul.008G107400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
15 cript=Phvul.008G206300.1 locus=Phvul.008G206300 ID=Phvul.008G206300.1.v2.1 annot-version=v2.1) &
16 103100.1 locus=Phvul.009G103100 ID=Phvul.009G103100.1.v2.1 annot-version=v2.1) &
17 010G008500 ID=Phvul.010G008500.1.v2.1 annot-version=v2.1) & no description available(sp|q9ss8
18 010G013500.1 locus=Phvul.010G013500 ID=Phvul.010G013500.1.v2.1 annot-version=v2.1) &
19 js=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)
20 js=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)
21 js=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)
22 js=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)
23 js=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)
24 js=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)
25 js=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)
26 js=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)
27 010G145600.1 locus=Phvul.010G145600 ID=Phvul.010G145600.1.v2.1 annot-version=v2.1) &
28 011G181700 ID=Phvul.011G181700.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
29 011G200820 ID=Phvul.011G200820.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
30 011G202100 ID=Phvul.011G202100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
31 011G202300 ID=Phvul.011G202300.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
32 011G203100 ID=Phvul.011G203100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 137.0)
4 z7|gpa3_orysj : 136.0)
5 z7|gpa3_orysj : 136.0)
6 z7|gpa3_orysj : 136.0)
7 z7|gpa3_orysj : 136.0)
8 z7|gpa3_orysj : 136.0)
9
10 ing protein 5 OS=Arabidopsis thaliana (sp|q8rwd9|acbp5_arath : 133.0)
11 ing protein 5 OS=Arabidopsis thaliana (sp|q8rwd9|acbp5_arath : 133.0)
12 in At5g63020 OS=Arabidopsis thaliana (sp|q8rxs5|drl40_arath : 433.0)
13 in At5g63020 OS=Arabidopsis thaliana (sp|q8rxs5|drl40_arath : 433.0)
14 in At5g63020 OS=Arabidopsis thaliana (sp|q8rxs5|drl40_arath : 433.0)
15 in At5g63020 OS=Arabidopsis thaliana (sp|q8rxs5|drl40_arath : 433.0)
16 in At5g63020 OS=Arabidopsis thaliana (sp|q8rxs5|drl40_arath : 433.0)
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35

36 annot-version=v2.1) &
37
38
39

40 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 265.0)
41
42
43
44
45
46
47
48
49
50

51
52 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 458.0)
53 otiana glutinosa (sp|q40392|tmvrn_nicgu : 238.0)
54 in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1_solbu : 413.0)
55 in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1_solbu : 413.0)
56) &
57) &
58) &
59) &
60

1
2
3
4 $r=v2.1) \&$

5
6 $r=v2.1) \&$

7 max (sp|c6tbd0|cspl6_soybn : 249.0)

8 max (sp|c6tbd0|cspl6_soybn : 249.0)

9 l.1.v2.1 annot-version=v2.1) &

10 l.1.v2.1 annot-version=v2.1) &

11 not-version=v2.1) &

12
13
14
15
16 2.1) &

17 2.1) &

18 in At4g10780 OS=Arabidopsis thaliana (sp|o82484|drl23_arath : 303.0)

19 in At4g10780 OS=Arabidopsis thaliana (sp|o82484|drl23_arath : 303.0)

20
21
22
23 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)

24 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)

25 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)

26 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)

27 v2.1 annot-version=v2.1) &

28 in=v2.1) &

29 in=v2.1) &

30 in=v2.1) &

31 in=v2.1) &

32
33
34
35
36 \ OS=Arabidopsis thaliana (sp|f4i594|rlm1a_arath : 191.0)

37
38
39
40
41
42
43
44
45
46 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 503.0)

47 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 541.0)

48 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 541.0)

49 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 474.0)

50 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 513.0)

51 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 538.0)

52 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 543.0)

53 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 541.0)

54 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 501.0)

55 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 555.0)

56 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 536.0)

57 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 549.0)

1 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 360.0)
2 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 483.0)
3 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 543.0)
4 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 357.0)
5 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 565.0)
6 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 565.0)
7 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 479.0)
8 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 479.0)
9 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 483.0)
10 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 483.0)
11 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 519.0)
12 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 519.0)
13 thaliana (sp|q9fh04|adh17_arath : 523.0)
14 thaliana (sp|q9fh04|adh17_arath : 523.0)
15 thaliana (sp|q9fh04|adh17_arath : 523.0)
16 thaliana (sp|q9fh04|adh17_arath : 523.0)
17 LPEAT1 OS=Arabidopsis thaliana (sp|q8l7r3|lpct1_arath : 452.0)
18 LPEAT1 OS=Arabidopsis thaliana (sp|q8l7r3|lpct1_arath : 452.0)
19 LPEAT1 OS=Arabidopsis thaliana (sp|q8l7r3|lpct1_arath : 452.0)
20 LPEAT1 OS=Arabidopsis thaliana (sp|q8l7r3|lpct1_arath : 452.0)
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39 OS=Arabidopsis thaliana (sp|q680c0|gdl62_arath : 442.0)
40 J03G010900.1.v2.1 annot-version=v2.1) &
41 J03G010900.1.v2.1 annot-version=v2.1) &
42 annot-version=v2.1) &
43 annot-version=v2.1) &
44 &
45 &
46 &
47 &
48 **!l.003G295800.4.v2.1 annot-version=v2.1) &**
49 **!l.003G295800.4.v2.1 annot-version=v2.1) &**
50 **!l.003G295800.4.v2.1 annot-version=v2.1) &**
51 .rabidopsis thaliana (sp|q6tph1|ppa23_arath : 715.0)
52 .rabidopsis thaliana (sp|q6tph1|ppa23_arath : 715.0)
53 .rabidopsis thaliana (sp|q6tph1|ppa23_arath : 715.0)
54 .rabidopsis thaliana (sp|q6tph1|ppa23_arath : 715.0)
55 .rabidopsis thaliana (sp|q6tph1|ppa23_arath : 715.0)
56 .rabidopsis thaliana (sp|q6tph1|ppa23_arath : 715.0)
57 .rabidopsis thaliana (sp|q6tph1|ppa23_arath : 715.0)
58 .rabidopsis thaliana (sp|q6tph1|ppa23_arath : 715.0)
59 .rabidopsis thaliana (sp|q6tph1|ppa23_arath : 715.0)
60 .rabidopsis thaliana (sp|q6tph1|ppa23_arath : 715.0)

1
 2 :in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 137.0)
 3 :in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 137.0)
 4 =v2.1) &
 5 =v2.1) &
 6 =Arabidopsis thaliana (sp|q9lt10|cxe18_arath : 385.0)
 7 ing protein At3g49730 OS=Arabidopsis thaliana (sp|p0c8a0|pp275_arath : 692.0)
 8 ing protein At3g49730 OS=Arabidopsis thaliana (sp|p0c8a0|pp275_arath : 692.0)
 9 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 446.0)
 10
 11
 12
 13
 14
 15 ;0.2.1 : 182.1) (original description: pacid=37173441 transcript=Phvul.006G180900.1 locus=Phvul.006G180900.1 ID=Phvul.006G180900.1)
 16 ;0.2.1 : 182.1) (original description: pacid=37173441 transcript=Phvul.006G180900.1 locus=Phvul.006G180900.1 ID=Phvul.006G180900.1)
 17
 18
 19 ;original description: pacid=37166954 transcript=Phvul.007G096800.1 locus=Phvul.007G096800 ID=Phvul.007G096800.1
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30 t-containing protein At1g19290 OS=Arabidopsis thaliana (sp|q9ln69|ppr50_arath : 769.0)
 31 ce 16 OS=Arabidopsis thaliana (sp|f4k5l5|tbl16_arath : 573.0)
 32 ce 16 OS=Arabidopsis thaliana (sp|f4k5l5|tbl16_arath : 573.0)
 33 ce 16 OS=Arabidopsis thaliana (sp|f4k5l5|tbl16_arath : 573.0)
 34 ce 16 OS=Arabidopsis thaliana (sp|f4k5l5|tbl16_arath : 573.0)
 35 ce 16 OS=Arabidopsis thaliana (sp|f4k5l5|tbl16_arath : 573.0)
 36 -like protein 2 OS=Arabidopsis thaliana (sp|p0c8s1|rp8l2_arath : 498.0)
 37 -like protein 2 OS=Arabidopsis thaliana (sp|p0c8s1|rp8l2_arath : 498.0)
 38 -like protein 2 OS=Arabidopsis thaliana (sp|p0c8s1|rp8l2_arath : 498.0)
 39 otiana glutinosa (sp|q40392|tmvrn_nicgu : 371.0)
 40 otiana glutinosa (sp|q40392|tmvrn_nicgu : 371.0)
 41 ing protein At2g17670 OS=Arabidopsis thaliana (sp|q84j71|pp161_arath : 496.0)
 42 ing protein At2g17670 OS=Arabidopsis thaliana (sp|q84j71|pp161_arath : 496.0)
 43 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 612.0)
 44 OS=Lotus japonicus (sp|b5wwz8|fao1_lotja : 932.0)
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56 OS=Arabidopsis thaliana (sp|q9m667|rpp13_arath : 310.0)
 57 OS=Arabidopsis thaliana (sp|q9m667|rpp13_arath : 310.0)
 58 OS=Arabidopsis thaliana (sp|q9m667|rpp13_arath : 310.0)
 59 ; protein LPA1 homolog 1 OS=Arabidopsis thaliana (sp|q9fjh9|lpah1_arath : 804.0)
 60 ; protein LPA1 homolog 1 OS=Arabidopsis thaliana (sp|q9fjh9|lpah1_arath : 804.0)

1 ; protein LPA1 homolog 1 OS=Arabidopsis thaliana (sp|q9fjh9|lpah1_arath : 804.0)

2 7190 OS=Arabidopsis thaliana (sp|q9t048|drl27_arath : 177.0)

3 7190 OS=Arabidopsis thaliana (sp|q9t048|drl27_arath : 177.0)

4 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 540.0)

5 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 542.0)

6 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 545.0)

7 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 525.0)

8 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 424.0)

9 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 424.0)

10 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 443.0)

11 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 558.0)

12 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 333.0)

13 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 159.0)

14 3190 OS=Arabidopsis thaliana (sp|q9fhs6|fk119_arath : 285.0)

15 eracea (sp|o04893|aglu_spiol : 80.9)

16 in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1_solbu : 306.0)

17 in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1_solbu : 306.0)

18 OS=Solanum bulbocastanum (sp|q7xbq9|rga2_solbu : 325.0)

19 OS=Solanum bulbocastanum (sp|q7xbq9|rga2_solbu : 325.0)

20 in RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 332.0)

21 in RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 332.0)

22 in RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 367.0)

23 in RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 367.0)

24 in RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 389.0)

25 in RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 389.0)

26 in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1_solbu : 379.0)

27 in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1_solbu : 379.0)

28 t-version=v2.1) &

29 not-version=v2.1) &

30 donor with incorporation or reduction of molecular oxygen(50.1.13 : 208.0) (original description: p

31 donor with incorporation or reduction of molecular oxygen(50.1.13 : 208.0) (original description: p

32 ated plant protein 36 OS=Arabidopsis thaliana (sp|q84j88|hip36_arath : 102.0)

33 ated plant protein 36 OS=Arabidopsis thaliana (sp|q84j88|hip36_arath : 102.0)

34 :Phvul.003G157600.1.v2.1 annot-version=v2.1) &

35

1
2
3
4
5
6 on=v2.1) &

7 on=v2.1) &

8
9
10 Arabidopsis thaliana (sp|q9fn03|uvr8_arath : 171.0)

11 Arabidopsis thaliana (sp|q9fn03|uvr8_arath : 171.0)

12 ing protein At1g12300, mitochondrial OS=Arabidopsis thaliana (sp|q0wkv3|ppr36_arath : 382.0)

13 ing protein At1g12300, mitochondrial OS=Arabidopsis thaliana (sp|q0wkv3|ppr36_arath : 382.0)

14 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 617.0)

15
16
17
18
19 .1.v2.1 annot-version=v2.1) &

20 .5.v2.1 annot-version=v2.1) &

21 .5.v2.1 annot-version=v2.1) &

22
23
24 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 446.0)

25 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 446.0)

26 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 597.0)

27 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 597.0)

28 OS=Arabidopsis thaliana (sp|q9m667|rpp13_arath : 306.0)

29 OS=Arabidopsis thaliana (sp|q9m667|rpp13_arath : 306.0)

30 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 171.0)

31 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 171.0)

32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 528.0)

52
53
54
55 helicase 1 homolog OS=Oryza sativa subsp. japonica (sp|a0a0p0v4r0|rtel1_orysj : 203.0)

56 helicase 1 homolog OS=Oryza sativa subsp. japonica (sp|a0a0p0v4r0|rtel1_orysj : 203.0)

57
58
59 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 540.0)

60 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 540.0)

61 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 559.0)

1 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 559.0)
2 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 489.0)
3 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 489.0)
4 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 489.0)
5 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 333.0)
6 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 333.0)
7 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 333.0)
8 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 159.0)
9 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 159.0)
10 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 159.0)
11 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 203.0)
12 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 203.0)
13 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 203.0)
14 scription: pacid=37163915 transcript=Phvul.L004500.1 locus=Phvul.L004500 ID=Phvul.L004500.1.v2
15 scription: pacid=37163915 transcript=Phvul.L004500.1 locus=Phvul.L004500 ID=Phvul.L004500.1.v2
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40

v2.1) &
v2.1) &

ot-version=v2.1) &
ot-version=v2.1) &
ot-version=v2.1) &
ot-version=v2.1) &
ot-version=v2.1) &
ot-version=v2.1) &

00.3.v2.1 annot-version=v2.1) &
00.3.v2.1 annot-version=v2.1) &
ing protein At2g03380, mitochondrial OS=Arabidopsis thaliana (sp|q9zq74|pp146_arath : 626.0)
&

Do not distribute

1
2
3 t-containing protein At1g03510 OS=Arabidopsis thaliana (sp|q9lr72|ppr7_arath : 388.0)

4 t-containing protein At1g03510 OS=Arabidopsis thaliana (sp|q9lr72|ppr7_arath : 388.0)

5 IP98A OS=Arabidopsis thaliana (sp|q8ry25|nu98a_arath : 109.0)

6 IP98A OS=Arabidopsis thaliana (sp|q8ry25|nu98a_arath : 109.0)

7
8
9 homolog OS=Arabidopsis thaliana (sp|q9fnn2|wdr26_arath : 697.0)

10 homolog OS=Arabidopsis thaliana (sp|q9fnn2|wdr26_arath : 697.0)

11
12
13
14
15
16
17 ing protein At3g09060 OS=Arabidopsis thaliana (sp|q9ss81|pp221_arath : 736.0)

18 ing protein At3g09060 OS=Arabidopsis thaliana (sp|q9ss81|pp221_arath : 736.0)

19
20 2.1) &

21
22
23 :0|ops_arath : 167.0)

24
25
26
27
28
29
30
31
32
33
34
35
36
37 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 541.0)

38 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 565.0)

39 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 479.0)

40 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 483.0)

41 }-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 519.0)

42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

06G180900 ID=Phvul.006G180900.1.v2.1 annot-version=v2.1) &
06G180900 ID=Phvul.006G180900.1.v2.1 annot-version=v2.1) &
vul.007G096800.1.v2.1 annot-version=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

acid=37147806 transcript=Phvul.003G076900.1 locus=Phvul.003G076900 ID=Phvul.003G076900.1:
acid=37147806 transcript=Phvul.003G076900.1 locus=Phvul.003G076900 ID=Phvul.003G076900.1:

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

!.1 annot-version=v2.1) &
!.1 annot-version=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

v2.1 annot-version=v2.1) &
v2.1 annot-version=v2.1) &

| | miRNA_Acc. | Target_Acc. | Expectation | UPE\$ | miRNA_start | miRNA_end |
|----|--------------|--------------------|-------------|-------|-------------|-----------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ccgaccuuagcu | Phvul.005G179400.1 | 2.5 | -1 | 1 | 21 |
| 4 | ccgaccuuagcu | Phvul.001G025900.1 | 3 | -1 | 1 | 21 |
| 5 | ccgaccuuagcu | Phvul.002G321900.1 | 3 | -1 | 1 | 21 |
| 6 | ccgaccuuagcu | Phvul.005G110300.3 | 3 | -1 | 1 | 21 |
| 7 | ccgaccuuagcu | Phvul.005G110300.2 | 3 | -1 | 1 | 21 |
| 8 | ccgaccuuagcu | Phvul.005G110300.1 | 3 | -1 | 1 | 21 |
| 9 | ccgaccuuagcu | Phvul.009G128800.1 | 3 | -1 | 1 | 21 |
| 10 | ccgaccuuagcu | Phvul.002G220500.1 | 3.5 | -1 | 1 | 21 |
| 11 | ccgaccuuagcu | Phvul.006G047700.1 | 3.5 | -1 | 1 | 21 |
| 12 | ccgaccuuagcu | Phvul.006G059900.1 | 3.5 | -1 | 1 | 21 |
| 13 | ccgaccuuagcu | Phvul.002G133400.1 | 4 | -1 | 1 | 21 |
| 14 | ccgaccuuagcu | Phvul.002G302600.1 | 4 | -1 | 1 | 21 |
| 15 | ccgaccuuagcu | Phvul.003G263400.1 | 4 | -1 | 1 | 21 |
| 16 | ccgaccuuagcu | Phvul.005G100500.1 | 4 | -1 | 1 | 21 |
| 17 | ccgaccuuagcu | Phvul.006G017100.1 | 4 | -1 | 1 | 21 |
| 18 | ccgaccuuagcu | Phvul.006G199400.1 | 4 | -1 | 1 | 21 |
| 19 | ccgaccuuagcu | Phvul.008G070100.1 | 4 | -1 | 1 | 21 |
| 20 | ccgaccuuagcu | Phvul.001G119000.1 | 4.5 | -1 | 1 | 21 |
| 21 | ccgaccuuagcu | Phvul.001G259300.1 | 4.5 | -1 | 1 | 21 |
| 22 | ccgaccuuagcu | Phvul.002G003000.1 | 4.5 | -1 | 1 | 21 |
| 23 | ccgaccuuagcu | Phvul.002G278800.1 | 4.5 | -1 | 1 | 21 |
| 24 | ccgaccuuagcu | Phvul.003G138382.1 | 4.5 | -1 | 1 | 21 |
| 25 | ccgaccuuagcu | Phvul.003G155500.1 | 4.5 | -1 | 1 | 21 |
| 26 | ccgaccuuagcu | Phvul.003G185100.1 | 4.5 | -1 | 1 | 21 |
| 27 | ccgaccuuagcu | Phvul.006G015900.1 | 4.5 | -1 | 1 | 21 |
| 28 | ccgaccuuagcu | Phvul.006G015900.2 | 4.5 | -1 | 1 | 21 |
| 29 | ccgaccuuagcu | Phvul.006G086100.1 | 4.5 | -1 | 1 | 21 |
| 30 | ccgaccuuagcu | Phvul.006G117700.1 | 4.5 | -1 | 1 | 21 |
| 31 | ccgaccuuagcu | Phvul.006G125600.1 | 4.5 | -1 | 1 | 21 |
| 32 | ccgaccuuagcu | Phvul.006G142200.1 | 4.5 | -1 | 1 | 21 |
| 33 | ccgaccuuagcu | Phvul.007G042700.1 | 4.5 | -1 | 1 | 21 |
| 34 | ccgaccuuagcu | Phvul.011G012400.1 | 4.5 | -1 | 1 | 21 |
| 35 | ccgaccuuagcu | Phvul.011G024700.1 | 4.5 | -1 | 1 | 21 |
| 36 | ccgaccuuagcu | Phvul.001G016500.2 | 5 | -1 | 1 | 21 |
| 37 | ccgaccuuagcu | Phvul.001G016500.1 | 5 | -1 | 1 | 21 |
| 38 | ccgaccuuagcu | Phvul.001G023100.1 | 5 | -1 | 1 | 21 |
| 39 | ccgaccuuagcu | Phvul.002G208300.1 | 5 | -1 | 1 | 21 |
| 40 | ccgaccuuagcu | Phvul.002G267600.2 | 5 | -1 | 1 | 21 |
| 41 | ccgaccuuagcu | Phvul.002G267600.1 | 5 | -1 | 1 | 21 |
| 42 | ccgaccuuagcu | Phvul.003G011400.1 | 5 | -1 | 1 | 21 |
| 43 | ccgaccuuagcu | Phvul.003G031500.1 | 5 | -1 | 1 | 21 |
| 44 | ccgaccuuagcu | Phvul.003G216800.1 | 5 | -1 | 1 | 21 |
| 45 | ccgaccuuagcu | Phvul.004G041500.2 | 5 | -1 | 1 | 21 |
| 46 | ccgaccuuagcu | Phvul.004G041500.1 | 5 | -1 | 1 | 21 |
| 47 | ccgaccuuagcu | Phvul.004G106700.1 | 5 | -1 | 1 | 21 |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | ccgaccuuagcu Phvul.004G170800.1 | 5 | -1 | 1 | 21 |
| 3 | ccgaccuuagcu Phvul.005G003300.2 | 5 | -1 | 1 | 21 |
| 4 | ccgaccuuagcu Phvul.005G003300.1 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | ccgaccuuagcu Phvul.005G084000.1 | 5 | -1 | 1 | 21 |
| 7 | ccgaccuuagcu Phvul.005G160700.1 | 5 | -1 | 1 | 21 |
| 8 | ccgaccuuagcu Phvul.006G004580.1 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | ccgaccuuagcu Phvul.006G135500.1 | 5 | -1 | 1 | 21 |
| 11 | ccgaccuuagcu Phvul.007G080800.2 | 5 | -1 | 1 | 21 |
| 12 | ccgaccuuagcu Phvul.008G080100.2 | 5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | ccgaccuuagcu Phvul.008G080100.1 | 5 | -1 | 1 | 21 |
| 15 | ccgaccuuagcu Phvul.008G131301.1 | 5 | -1 | 1 | 21 |
| 16 | ccgaccuuagcu Phvul.008G191200.2 | 5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | ccgaccuuagcu Phvul.008G191200.1 | 5 | -1 | 1 | 21 |
| 19 | ccgaccuuagcu Phvul.008G240000.1 | 5 | -1 | 1 | 21 |
| 20 | ccgaccuuagcu Phvul.008G240300.1 | 5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | ccgaccuuagcu Phvul.008G240500.1 | 5 | -1 | 1 | 21 |
| 23 | ccgaccuuagcu Phvul.009G183600.4 | 5 | -1 | 1 | 21 |
| 24 | ccgaccuuagcu Phvul.009G183600.1 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | ccgaccuuagcu Phvul.009G183600.3 | 5 | -1 | 1 | 21 |
| 27 | ccgaccuuagcu Phvul.009G183600.2 | 5 | -1 | 1 | 21 |
| 28 | ccgaccuuagcu Phvul.009G194700.1 | 5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | ccgaccuuagcu Phvul.009G194700.2 | 5 | -1 | 1 | 21 |
| 31 | ccgaccuuagcu Phvul.010G069638.1 | 5 | -1 | 1 | 21 |
| 32 | ccgaccuuagcu Phvul.010G112500.1 | 5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | ccgaccuuagcu Phvul.011G077600.1 | 5 | -1 | 1 | 21 |
| 35 | ccgaccuuagcu Phvul.011G158600.1 | 5 | -1 | 1 | 21 |
| 36 | | | | | |
| 37 | | | | | |
| 38 | | | | | |
| 39 | | | | | |
| 40 | | | | | |
| 41 | | | | | |
| 42 | | | | | |
| 43 | | | | | |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| 1 | Target_start | Target_end | miRNA_alignment | Target_alignment | Inhibition | Target_Desc. |
|----|--------------|------------|-----------------|------------------------|--------------|--------------|
| 2 | 468 | 488 | CCGACCUUAC |: GUUCAUCG | /Cleavage | pacid=371539 |
| 3 | 1494 | 1514 | CCGACCUUAC | : :: ::::: : CUCCAUCUG | /Cleavage | pacid=371692 |
| 4 | 493 | 513 | CCGACCUUAC |: AUUUAACUG | /Cleavage | pacid=371769 |
| 5 | 865 | 885 | CCGACCUUAC | : :: ::: : CUCCAACAGG | Translation | pacid=371530 |
| 6 | 966 | 986 | CCGACCUUAC | : :: ::: : CUCCAACAGG | Translation | pacid=371530 |
| 7 | 1033 | 1053 | CCGACCUUAC | : :: ::: : CUCCAACAGG | Translation | pacid=371529 |
| 8 | 491 | 511 | CCGACCUUAC |: AUUUAACUG | /Cleavage | pacid=371499 |
| 9 | 1612 | 1632 | CCGACCUUAC |: : GAUCAACUG | /Cleavage | pacid=371751 |
| 10 | 1828 | 1848 | CCGACCUUAC |: CUACAGCUG | /Cleavage | pacid=371722 |
| 11 | 2179 | 2199 | CCGACCUUAC |: CUACAGCUG | /Cleavage | pacid=371732 |
| 12 | 632 | 652 | CCGACCUUAC |: AGUUACCUG | /Cleavage | pacid=371771 |
| 13 | 503 | 523 | CCGACCUUAC | : . : : GACUCAUAG | /Cleavage | pacid=371771 |
| 14 | 550 | 570 | CCGACCUUAC | : :: ::: : GCCCAGCGG | /Cleavage | pacid=371470 |
| 15 | 1367 | 1386 | CCGACCUUAC |: AGUCAA-UGA | Cleavage | pacid=371535 |
| 16 | 1847 | 1867 | CCGACCUUAC |: ACUCAAUGG | /Cleavage | pacid=371741 |
| 17 | 2302 | 2322 | CCGACCUUAC |: AAUCAAUUG | /Translation | pacid=371712 |
| 18 | 604 | 624 | CCGACCUUAC | : :: ::: : CUCCAUUUU | /Cleavage | pacid=371602 |
| 19 | 750 | 770 | CCGACCUUAC | : :: ::: : GACCACAUG | /Cleavage | pacid=371700 |
| 20 | 1493 | 1513 | CCGACCUUAC |: GGCCAAUGA | /Cleavage | pacid=371679 |
| 21 | 11011 | 11031 | CCGACCUUAC |: UCUUAAUUG | /Cleavage | pacid=371751 |
| 22 | 155 | 174 | CCGACCUUAC | : :: ::: : UCCAACUG | /Cleavage | pacid=371783 |
| 23 | 328 | 348 | CCGACCUUAC | : :: ::: : AGGCAACUG | /Cleavage | pacid=371474 |
| 24 | 1579 | 1599 | CCGACCUUAC | : :: ::: : UACUAAUUU | /Cleavage | pacid=371481 |
| 25 | 868 | 888 | CCGACCUUAC |: ACCUGAUUG | /Cleavage | pacid=371455 |
| 26 | 1196 | 1216 | CCGACCUUAC | : :: ::: : GGGCAACUG | /Translation | pacid=371726 |
| 27 | 1210 | 1230 | CCGACCUUAC | : :: ::: : GGGCAACUG | /Translation | pacid=371726 |
| 28 | 1859 | 1879 | CCGACCUUAC | : :: ::: : UUUGAAUUA | /Cleavage | pacid=371717 |
| 29 | 1058 | 1078 | CCGACCUUAC |: UUAUAACUG | /Cleavage | pacid=371736 |
| 30 | 927 | 947 | CCGACCUUAC | : . : : AACUAUCAG | /Cleavage | pacid=371722 |
| 31 | 419 | 439 | CCGACCUUAC | : :: ::: : CCUCAUUUC | /Cleavage | pacid=371720 |
| 32 | 822 | 842 | CCGACCUUAC | : :: ::: : AACCGACGG | /Cleavage | pacid=371652 |
| 33 | 1225 | 1245 | CCGACCUUAC | : :: ::: : CAAAACUG | /Translation | pacid=371546 |
| 34 | 313 | 333 | CCGACCUUAC |: ACCUGGUUU | /Cleavage | pacid=371566 |
| 35 | 1535 | 1555 | CCGACCUUAC | : :: ::: : GACCAACUUC | Translation | pacid=371687 |
| 36 | 1672 | 1692 | CCGACCUUAC | : :: ::: : GACCAACUUC | Translation | pacid=371687 |
| 37 | 440 | 460 | CCGACCUUAC |: : UGUCAACUG | /Cleavage | pacid=371701 |
| 38 | 1441 | 1461 | CCGACCUUAC | : :: ::: : AAAUGACUG | /Translation | pacid=371780 |
| 39 | 1929 | 1949 | CCGACCUUAC | : . : : UAUGAACUG | /Cleavage | pacid=371771 |
| 40 | 1933 | 1953 | CCGACCUUAC | : . : : UAUGAACUG | /Cleavage | pacid=371771 |
| 41 | 2267 | 2288 | CCGACCUUAC |: : UACCAAUGG | /Translation | pacid=371482 |
| 42 | 993 | 1013 | CCGACCUUAC | : :: ::: : AACCAAUUG | /Cleavage | pacid=371476 |
| 43 | 1219 | 1239 | CCGACCUUAC | : . : : UAUAUUUG | /Cleavage | pacid=371459 |
| 44 | 698 | 718 | CCGACCUUAC | : : : : CUGCAUCUG | /Cleavage | pacid=371627 |
| 45 | 698 | 718 | CCGACCUUAC | : : : : CUGCAUCUG | /Cleavage | pacid=371627 |
| 46 | 378 | 398 | CCGACCUUAC |: : UGCCAAUGG | /Cleavage | pacid=371634 |

| | | | | |
|----|------|-----------------|---------------------|-------------------------------------|
| 1 | | | | |
| 2 | 1561 | 1581 CCGACCUUAC | :. : | UACCAAUGG/Cleavage pacid=371635 |
| 3 | 1676 | 1696 CCGACCUUAC | :. : | AGUUAACUC/Cleavage pacid=371543 |
| 4 | 1787 | 1807 CCGACCUUAC | :. : | AGUUAACUC/Cleavage pacid=371543 |
| 5 | 2606 | 2626 CCGACCUUAC | :: :. : | CAGCAGCUG/Translation pacid=371531 |
| 6 | 2602 | 2622 CCGACCUUAC | :: :. : | AACUGAUUG/Translation pacid=371527 |
| 7 | | | | |
| 8 | 530 | 550 CCGACCUUAC | :. : | CACUAAUUG/Cleavage pacid=371742 |
| 9 | | | | |
| 10 | 1265 | 1285 CCGACCUUAC | :. : | CAUUGAUGG/Cleavage pacid=371716 |
| 11 | 1827 | 1847 CCGACCUUAC | :. : | AGGGAAUUG/Cleavage pacid=371676 |
| 12 | 2286 | 2306 CCGACCUUAC | :: :. : | CAGCUGCUG/Translation pacid=371612 |
| 13 | | | | |
| 14 | 2271 | 2291 CCGACCUUAC | :: :. : | CAGCUGCUG/Translation pacid=371612 |
| 15 | 517 | 537 CCGACCUUAC | :. : | UACCAAUUG/Cleavage pacid=371609 |
| 16 | 1062 | 1082 CCGACCUUAC | :. : | GGGAGAUUG/Cleavage pacid=371596 |
| 17 | | | | |
| 18 | 1156 | 1176 CCGACCUUAC | :. : | GGGAGAUUG/Cleavage pacid=371596 |
| 19 | 238 | 258 CCGACCUUAC | :. : | AAUCAAGUG/Cleavage pacid=371605 |
| 20 | 517 | 537 CCGACCUUAC | :. : | GAUCAAGUG/Cleavage pacid=371608 |
| 21 | | | | |
| 22 | 685 | 705 CCGACCUUAC | :. : | GAUCAAGUG/Cleavage pacid=371577 |
| 23 | 75 | 95 CCGACCUUAC | :. : | UAUUUACUG/Cleavage pacid=371493 |
| 24 | 75 | 95 CCGACCUUAC | :. : | UAUUUACUG/Cleavage pacid=371493 |
| 25 | 75 | 95 CCGACCUUAC | :. : | UAUUUACUG/Cleavage pacid=371493 |
| 26 | 75 | 95 CCGACCUUAC | :. : | UAUUUACUG/Cleavage pacid=371493 |
| 27 | 75 | 95 CCGACCUUAC | :. : | UAUUUACUG/Cleavage pacid=371493 |
| 28 | 1382 | 1402 CCGACCUUAC | :. : | UACUAAUCU/Cleavage pacid=371491 |
| 29 | 1526 | 1546 CCGACCUUAC | :. : | UACUAAUCU/Cleavage pacid=371491 |
| 30 | | | | |
| 31 | 600 | 620 CCGACCUUAC | :. : | GAUCAAUGG/Cleavage pacid=371437 |
| 32 | 64 | 85 CCGACCUUAC | :. : | UGCCAAGCU/Cleavage pacid=371438 |
| 33 | | | | |
| 34 | 2178 | 2198 CCGACCUUAC | :: :. : | CAGUAACAAA/Cleavage pacid=371546 |
| 35 | 702 | 722 CCGACCUUAC | :. : | CACCACUAGA/Translation pacid=371558 |
| 36 | | | | |
| 37 | | | | |
| 38 | | | | |
| 39 | | | | |
| 40 | | | | |
| 41 | | | | |
| 42 | | | | |
| 43 | | | | |
| 44 | | | | |
| 45 | | | | |
| 46 | | | | |
| 47 | | | | |
| 48 | | | | |
| 49 | | | | |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

| | Multiplicity | Target_Acc. | ID | locusName | Pfam |
|----|--------------|-------------|----|-----------|------|
| 1 | | | | | |
| 2 | | | | | |
| 3 | | | | | |
| 4 | | | | | |
| 5 | | | | | |
| 6 | | | | | |
| 7 | | | | | |
| 8 | | | | | |
| 9 | | | | | |
| 10 | | | | | |
| 11 | | | | | |
| 12 | | | | | |
| 13 | | | | | |
| 14 | | | | | |
| 15 | | | | | |
| 16 | | | | | |
| 17 | | | | | |
| 18 | | | | | |
| 19 | | | | | |
| 20 | | | | | |
| 21 | | | | | |
| 22 | | | | | |
| 23 | | | | | |
| 24 | | | | | |
| 25 | | | | | |
| 26 | | | | | |
| 27 | | | | | |
| 28 | | | | | |
| 29 | | | | | |
| 30 | | | | | |
| 31 | | | | | |
| 32 | | | | | |
| 33 | | | | | |
| 34 | | | | | |
| 35 | | | | | |
| 36 | | | | | |
| 37 | | | | | |
| 38 | | | | | |
| 39 | | | | | |
| 40 | | | | | |
| 41 | | | | | |
| 42 | | | | | |
| 43 | | | | | |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|---|--------------------|------------------|------------------|--------------|
| 1 | | | | | |
| 2 | 1 | Phvul.004G170800.1 | Phvul.004G170800 | Phvul.004G170800 | PF00390,PF03 |
| 3 | 1 | Phvul.005G003300.2 | Phvul.005G003300 | Phvul.005G003300 | PF07714,PF00 |
| 4 | 1 | Phvul.005G003300.1 | Phvul.005G003300 | Phvul.005G003300 | PF07714,PF00 |
| 5 | | | | | |
| 6 | 1 | Phvul.005G084000.1 | Phvul.005G084000 | Phvul.005G084000 | 0 |
| 7 | 1 | Phvul.005G160700.1 | Phvul.005G160700 | Phvul.005G160700 | PF00069 |
| 8 | 1 | Phvul.006G004580.1 | Phvul.006G004580 | Phvul.006G004580 | PF08263 |
| 9 | | | | | |
| 10 | 1 | Phvul.006G135500.1 | Phvul.006G135500 | Phvul.006G135500 | PF05691 |
| 11 | 1 | Phvul.007G080800.2 | Phvul.007G080800 | Phvul.007G080800 | PF03033 |
| 12 | 1 | Phvul.008G080100.2 | Phvul.008G080100 | Phvul.008G080100 | PF00651,PF03 |
| 13 | 1 | Phvul.008G080100.1 | Phvul.008G080100 | Phvul.008G080100 | PF00651,PF03 |
| 14 | 1 | Phvul.008G131301.1 | Phvul.008G131301 | Phvul.008G131301 | PF00498 |
| 15 | 1 | Phvul.008G191200.2 | Phvul.008G191200 | Phvul.008G191200 | 0 |
| 16 | 1 | Phvul.008G191200.1 | Phvul.008G191200 | Phvul.008G191200 | 0 |
| 17 | | | | | |
| 18 | 1 | Phvul.008G240000.1 | Phvul.008G240000 | Phvul.008G240000 | PF03080 |
| 19 | 1 | Phvul.008G240300.1 | Phvul.008G240300 | Phvul.008G240300 | PF14365,PF03 |
| 20 | 1 | Phvul.008G240500.1 | Phvul.008G240500 | Phvul.008G240500 | PF14365,PF03 |
| 21 | 1 | Phvul.009G183600.4 | Phvul.009G183600 | Phvul.009G183600 | PF00010 |
| 22 | 1 | Phvul.009G183600.1 | Phvul.009G183600 | Phvul.009G183600 | PF00010 |
| 23 | 1 | Phvul.009G183600.3 | Phvul.009G183600 | Phvul.009G183600 | PF00010 |
| 24 | 1 | Phvul.009G183600.2 | Phvul.009G183600 | Phvul.009G183600 | PF00010 |
| 25 | 1 | Phvul.009G194700.1 | Phvul.009G194700 | Phvul.009G194700 | PF02881,PF00 |
| 26 | 1 | Phvul.009G194700.2 | Phvul.009G194700 | Phvul.009G194700 | PF02881,PF00 |
| 27 | 1 | Phvul.010G069638.1 | Phvul.010G069638 | Phvul.010G069638 | PF00225 |
| 28 | 1 | Phvul.010G112500.1 | Phvul.010G112500 | Phvul.010G112500 | PF10604 |
| 29 | 1 | Phvul.011G077600.1 | Phvul.011G077600 | Phvul.011G077600 | PF02837,PF02 |
| 30 | 1 | Phvul.011G158600.1 | Phvul.011G158600 | Phvul.011G158600 | PF02485 |
| 31 | | | | | |
| 32 | | | | | |
| 33 | | | | | |
| 34 | | | | | |
| 35 | | | | | |
| 36 | | | | | |
| 37 | | | | | |
| 38 | | | | | |
| 39 | | | | | |
| 40 | | | | | |
| 41 | | | | | |
| 42 | | | | | |
| 43 | | | | | |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | Panther | KOG | KEGG | KOG | GO | Best-hit-arabi-arabi-symbol |
|----|--------------------------------|---------|----------------|-----------------|---------------------|-----------------------------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | PTHR10371,P ⁻ | KOG3196 | 1.6.99.3,1.6.5 | K03943 | | 0 AT4G02580.1 0 |
| 4 | PTHR31300,P ⁻ | | 0 | 0 | 0 | 0 AT3G19540.1 0 |
| 5 | | | | | | |
| 6 | PTHR21431,P ⁻ | KOG3478 | | 0 K04798 | GO:0051082,C | AT1G29990.1 PFD6 |
| 7 | PTHR27002,P ⁻ | KOG1187 | 2.7.11.1 | | 0 GO:0006468,C | AT2G19130.1 0 |
| 8 | PTHR27002,P ⁻ | KOG1187 | 2.7.11.1 | | 0 GO:0006468,C | AT2G19130.1 0 |
| 9 | | | | | | |
| 10 | PTHR27002,P ⁻ | KOG1187 | 2.7.11.1 | | 0 GO:0006468,C | AT2G19130.1 0 |
| 11 | PTHR21431,P ⁻ | | 0 | 0 K04798 | GO:0051082,C | AT1G29990.1 PFD6 |
| 12 | PTHR27002,P ⁻ | KOG1187 | 2.7.11.1 | | 0 GO:0048544,C | AT4G21390.1 B120 |
| 13 | | | | | | |
| 14 | PTHR24015,P ⁻ | | 0 | 0 | 0 | 0 AT4G02750.1 0 |
| 15 | PTHR24015,P ⁻ | | 0 | 0 | 0 | 0 AT4G02750.1 0 |
| 16 | PTHR23155,P ⁻ | KOG4658 | | 0 K13457 | GO:0005515,C | AT3G07040.1 RPM1,RPS3 |
| 17 | PTHR27008,P ⁻ | KOG1187 | 2.7.11.1 | | 0 GO:0005515,C | AT5G35390.1 0 |
| 18 | PTHR31048,P ⁻ | | 0 | 0 | 0 | 0 AT4G38660.1 0 |
| 19 | | | | | | |
| 20 | PTHR24078,P ⁻ | KOG0714 | | 0 K09510 | | 0 AT2G20560.1 0 |
| 21 | | | | | | |
| 22 | PTHR11771,P ⁻ | | 0 1.13.11.12 | K00454 | GO:0005515,C | AT3G45140.1 ATLOX2,LOX2 |
| 23 | PTHR22880,P ⁻ | KOG1474 | | 0 | 0 GO:0005515 | AT5G65630.1 GTE7 |
| 24 | PTHR10778,P ⁻ | KOG1582 | | 0 K15277 | GO:0055085 | AT4G23010.3 ATUTR2,UTR2 |
| 25 | | | | | | |
| 26 | PTHR11654,P ⁻ | | 0 | 0 K14638 | GO:0055085,C | AT1G68570.1 0 |
| 27 | PTHR23061,P ⁻ | KOG1625 | 2.7.7.7 | K02321 | GO:0006260,C | AT1G67630.1 POLA2 |
| 28 | PTHR16166,P ⁻ | KOG1809 | | 0 | 0 | 0 AT4G17140.3 0 |
| 29 | | | | | | |
| 30 | | 0 | 0 | 0 | 0 | 0 0 0 |
| 31 | PTHR31734,P ⁻ | | 0 | 0 K14484 | GO:0006355,C | AT1G04240.1 IAA3,SHY2 |
| 32 | PTHR11564,P⁻ | | 0 | 0 K13431 | GO:0006614,C | AT4G30600.1 0 |
| 33 | PTHR24078,P ⁻ | | 0 | 0 K09506 | | 0 AT1G74250.1 0 |
| 34 | | | | | | |
| 35 | PTHR31482,P ⁻ | | 0 | 0 | 0 GO:0005515 | AT2G32560.1 0 |
| 36 | PTHR31482,P ⁻ | | 0 | 0 | 0 GO:0005515 | AT2G32560.1 0 |
| 37 | | | | | | |
| 38 | PTHR24095,P ⁻ | | 0 | 0 | 0 GO:0008152,C | AT1G65890.1 AAE12 |
| 39 | PTHR23091,P ⁻ | | 0 2.3.1.88 | | 0 GO:0008080 | AT2G23060.1 0 |
| 40 | PTHR32448,P ⁻ | KOG1231 | 1.3.3.8 | | 0 GO:0055114,C | AT4G20840.1 0 |
| 41 | | | | | | |
| 42 | PTHR23130,P ⁻ | | 0 | 0 | 0 | 0 AT5G47530.1 0 |
| 43 | PTHR24015,P ⁻ | | 0 | 0 | 0 | 0 AT5G02860.1 0 |
| 44 | PTHR10209,P ⁻ | | 0 | 0 | 0 | 0 AT4G13400.1 0 |
| 45 | PTHR31989,P ⁻ | | 0 | 0 | 0 GO:0006355,C | AT2G17040.1 anac036,NAC |
| 46 | | | | | | |
| 47 | PTHR10942,P ⁻ | KOG2556 | 3.4.24.36 | | 0 GO:0016020,C | AT5G42620.2 0 |
| 48 | PTHR10942,P ⁻ | KOG2556 | 3.4.24.36 | | 0 GO:0016020,C | AT5G42620.2 0 |
| 49 | PTHR10044,P ⁻ | KOG1100 | | 0 K19042 | | 0 AT1G45976.1 SBP1 |
| 50 | | | | | | |
| 51 | PTHR24015,P ⁻ | | 0 | 0 | 0 | 0 AT5G18390.1 0 |
| 52 | PTHR24006,P ⁻ | | 0 3.4.19.12 | | 0 GO:0036459,C | AT4G39370.1 UBP27 |
| 53 | PTHR24006,P ⁻ | | 0 3.4.19.12 | | 0 GO:0036459,C | AT4G39370.1 UBP27 |
| 54 | | | | | | |
| 55 | PTHR22999,P ⁻ | | 0 | 0 K17925 | GO:0035091 | AT2G15900.1 0 |
| 56 | PTHR12549,P ⁻ | | 0 | 0 K15601 | | 0 AT1G62310.1 0 |
| 57 | PTHR11132,P ⁻ | KOG1441 | | 0 | 0 GO:0055085 | AT1G12500.1 0 |
| 58 | | | | | | |
| 59 | PTHR10631 | | 0 2.1.1.216 | K00555 | GO:0008033,C | AT5G15810.1 0 |
| 60 | PTHR10631 | | 0 2.1.1.216 | K00555 | GO:0008033,C | AT5G15810.1 0 |
| | PTHR34575,P ⁻ | | 0 | 0 | 0 | 0 AT5G52780.1 0 |

| 1 | arabi-defline | ID | Annot_defline |
|----|--|-----------------------|---------------|
| 2 | NADH-ubiquinone oxidoreductase 24 kDa subunit, putative | Phvul.005G17K03943 | - NAD |
| 3 | Protein of unknown function (DUF620) | Phvul.001G02PTHR31300 | :SF |
| 4 | prefoldin 6 | Phvul.002G32K04798 | - pref |
| 5 | S-locus lectin protein kinase family protein | Phvul.005G11PF00069 | //PFC |
| 6 | S-locus lectin protein kinase family protein | Phvul.005G11PF00069 | //PFC |
| 7 | S-locus lectin protein kinase family protein | Phvul.005G11PF00069 | //PFC |
| 8 | prefoldin 6 | Phvul.009G12K04798 | - pref |
| 9 | S-locus lectin protein kinase family protein | Phvul.002G22PF00954 | //PFC |
| 10 | Tetratricopeptide repeat (TPR)-like superfamily protein | Phvul.006G04PF01535 | //PF1 |
| 11 | Tetratricopeptide repeat (TPR)-like superfamily protein | Phvul.006G05PF01535 | //PF1 |
| 12 | NB-ARC domain-containing disease resistance protein | Phvul.002G13PTHR23155 | //I |
| 13 | Leucine-rich repeat protein kinase family protein | Phvul.002G30PTHR27008 | :SF |
| 14 | Pathogenesis-related thaumatin superfamily protein | Phvul.003G26PTHR31048 | :SF |
| 15 | DNAJ heat shock family protein | Phvul.005G10PTHR24078 | :SF |
| 16 | lipoxygenase 2 | Phvul.006G01PTHR11771 | :SF |
| 17 | global transcription factor group E7 | Phvul.006G19PTHR22880 | //I |
| 18 | UDP-galactose transporter 2 | Phvul.008G07K15277 | - solut |
| 19 | Major facilitator superfamily protein | Phvul.001G11PTHR11654 | //I |
| 20 | DNA polymerase alpha 2 | Phvul.001G25K02321 | - DNA |
| 21 | pleckstrin homology (PH) domain-containing protein | Phvul.002G00PTHR16166 | :SF |
| 22 | | 0 | 0 |
| 23 | AUX/IAA transcriptional regulator family protein | Phvul.003G13PTHR31734 | :SF |
| 24 | signal recognition particle receptor alpha subunit family prot | Phvul.003G15K13431 | - signa |
| 25 | DNAJ heat shock N-terminal domain-containing protein | Phvul.003G18K09506 | - DnaJ |
| 26 | F-box family protein | Phvul.006G01PF00646 | - F-b |
| 27 | F-box family protein | Phvul.006G01PF00646 | - F-b |
| 28 | acyl activating enzyme 12 | Phvul.006G08PF00501 | //PF1 |
| 29 | Acyl-CoA N-acyltransferases (NAT) superfamily protein | Phvul.006G11PTHR23091 | :SF |
| 30 | FAD-binding Berberine family protein | Phvul.006G12PTHR32448 | :SF |
| 31 | Auxin-responsive family protein | Phvul.006G14PTHR23130 | :SF |
| 32 | Pentatricopeptide repeat (PPR) superfamily protein | Phvul.007G04PF12854 | //PF1 |
| 33 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super | Phvul.011G01PTHR10209 | :SF |
| 34 | NAC domain containing protein 36 | Phvul.011G02PTHR31989 | :SF |
| 35 | metalloendopeptidases;zinc ion binding | Phvul.001G013.4.24.36 | - Lei |
| 36 | metalloendopeptidases;zinc ion binding | Phvul.001G013.4.24.36 | - Lei |
| 37 | S-ribonuclease binding protein 1 | Phvul.001G02PTHR10044 | :SF |
| 38 | Pentatricopeptide repeat (PPR) superfamily protein | Phvul.002G20PF01535 | //PF1 |
| 39 | ubiquitin-specific protease 27 | Phvul.002G26K11851 | - ubiq |
| 40 | ubiquitin-specific protease 27 | Phvul.002G26K11851 | - ubiq |
| 41 | Phox-associated domain;Phox-like;Sorting nexin, C-terminal | Phvul.003G01K17925 | - sorti |
| 42 | transcription factor jumonji (jmjC) domain-containing proteir | Phvul.003G03K15601 | - lysin |
| 43 | Nucleotide-sugar transporter family protein | Phvul.003G21PTHR11132 | //I |
| 44 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G042.1.1.216 | - tRI |
| 45 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G042.1.1.216 | - tRI |
| 46 | Protein of unknown function (DUF3464) | Phvul.004G10PF11947 | - Pro |

| | | | |
|----|--|----------------------------|---|
| 1 | | | |
| 2 | NADP-malic enzyme 4 | Phvul.004G17PTHR23406:SI | |
| 3 | KCBP-interacting protein kinase | Phvul.005G00PTHR24351//I | |
| 4 | KCBP-interacting protein kinase | Phvul.005G00PTHR24351//I | |
| 5 | COP1-interacting protein 7 | Phvul.005G08PTHR31008:SI | |
| 6 | Protein kinase protein with adenine nucleotide alpha hydrolyz | Phvul.005G16PTHR27001:SI | |
| 7 | receptor like protein 48 | Phvul.006G00PF08263 - Leu | |
| 8 | seed imbibition 2 | Phvul.006G13PF05691 - Raf | |
| 9 | UDP-Glycosyltransferase superfamily protein | Phvul.007G08PTHR11926:SI | |
| 10 | Phototropic-responsive NPH3 family protein | Phvul.008G08PF00651//PFC | |
| 11 | Phototropic-responsive NPH3 family protein | Phvul.008G08PF00651//PFC | |
| 12 | SMAD/FHA domain-containing protein | Phvul.008G13PF00498 - FHA | |
| 13 | | 0 | 0 |
| 14 | | 0 | 0 |
| 15 | | 0 | 0 |
| 16 | Protein of Unknown Function (DUF239) | Phvul.008G24PF03080 - Dor | |
| 17 | Protein of Unknown Function (DUF239) | Phvul.008G24PF14365 - Dor | |
| 18 | Protein of Unknown Function (DUF239) | Phvul.008G24PF14365 - Dor | |
| 19 | BIG PETAL P | Phvul.009G18PTHR12565//I | |
| 20 | BIG PETAL P | Phvul.009G18PTHR12565//I | |
| 21 | BIG PETAL P | Phvul.009G18PTHR12565//I | |
| 22 | BIG PETAL P | Phvul.009G18PTHR12565//I | |
| 23 | signal recognition particle receptor alpha subunit family prot | Phvul.009G19K13431 - signa | |
| 24 | signal recognition particle receptor alpha subunit family prot | Phvul.009G19K13431 - signa | |
| 25 | P-loop containing nucleoside triphosphate hydrolases superf | Phvul.010G06PTHR24115:SI | |
| 26 | regulatory component of ABA receptor 1 | Phvul.010G11PTHR31213:SI | |
| 27 | beta-galactosidase 8 | Phvul.011G07PF01301//PFC | |
| 28 | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferas | Phvul.011G15PTHR19297:SI | |
| 29 | | | |
| 30 | | | |
| 31 | | | |
| 32 | | | |
| 33 | | | |
| 34 | | | |
| 35 | | | |
| 36 | | | |
| 37 | | | |
| 38 | | | |
| 39 | | | |
| 40 | | | |
| 41 | | | |
| 42 | | | |
| 43 | | | |
| 44 | | | |
| 45 | | | |
| 46 | | | |
| 47 | | | |
| 48 | | | |
| 49 | | | |
| 50 | | | |
| 51 | | | |
| 52 | | | |
| 53 | | | |
| 54 | | | |
| 55 | | | |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

| IDENTIFIER | NAME | DESCRIPTION |
|--------------|---------------------------|--|
| Phvul.005G17 | Cellular respir component | NQO2 of NADH dehydrogenase electron input (module N) |
| Phvul.001G02 | Multi-process | GTPase effector (BDR) (original description: pacid=37169232 transcript= |
| Phvul.002G32 | Cytoskeleton | component PFD6 of Prefoldin co-chaperone complex (original descript |
| Phvul.005G11 | Enzyme classif | G-type lectin S-receptor-like serine/threonine-protein kinase At2g1913 |
| Phvul.005G11 | Enzyme classif | G-type lectin S-receptor-like serine/threonine-protein kinase At2g1913 |
| Phvul.005G11 | Enzyme classif | G-type lectin S-receptor-like serine/threonine-protein kinase At2g1913 |
| Phvul.009G12 | Cytoskeleton | component PFD6 of Prefoldin co-chaperone complex (original descript |
| Phvul.002G22 | Protein modif | protein kinase (SD-1) (original description: pacid=37175156 transcript= |
| Phvul.006G04 | not assigned. | (original description: pacid=37172255 transcript=Phvul.006G047700.1 |
| Phvul.006G05 | not assigned. | (original description: pacid=37173205 transcript=Phvul.006G059900.1 |
| Phvul.002G13 | not assigned. | (original description: pacid=37177101 transcript=Phvul.002G133400.1 |
| Phvul.002G30 | Protein modif | protein kinase (LRR-III) (original description: pacid=37177113 transcrip |
| Phvul.003G26 | not assigned. | (original description: pacid=37147040 transcript=Phvul.003G263400.1 |
| Phvul.005G10 | not assigned. | (original description: pacid=37153534 transcript=Phvul.005G100500.1 |
| Phvul.006G01 | Phytohormon | 13-lipoxygenase (original description: pacid=37174172 transcript=Phvu |
| Phvul.006G19 | RNA biosynth | transcriptional co-activator (BET/GTE) (original description: pacid=371: |
| Phvul.008G07 | Solute transp | nucleotide sugar transporter (UTR1 5) (original description: pacid=371 |
| Phvul.001G11 | Solute transp | anion transporter (NRT1/PTR) (original description: pacid=37170064 tr |
| Phvul.001G25 | Cell cycle orga | replication fork tethering component POLA2 of DNA polymerase alpha |
| Phvul.002G00 | not assigned. | r no hits & (original description: pacid=37175146 transcript=Phvul.002G |
| Phvul.002G27 | not assigned. | r no hits & (original description: pacid=37178371 transcript=Phvul.002G |
| Phvul.003G13 | not assigned. | (original description: pacid=37147466 transcript=Phvul.003G138382.1 |
| Phvul.003G15 | Protein transla | component SR-alpha of SRP (signal recognition particle) receptor comp |
| Phvul.003G18 | Protein home | co-chaperone (Jjj1) (original description: pacid=37145570 transcript=Pl |
| Phvul.006G01 | Protein home | component FBX of SCF E3 ubiquitin ligase complex (original descriptio |
| Phvul.006G01 | Protein home | component FBX of SCF E3 ubiquitin ligase complex (original descriptio |
| Phvul.006G08 | not assigned. | (original description: pacid=37171712 transcript=Phvul.006G086100.1 |
| Phvul.006G11 | not assigned. | (original description: pacid=37173640 transcript=Phvul.006G117700.1 |
| Phvul.006G12 | Enzyme classif | Berberine bridge enzyme-like 21 OS=Arabidopsis thaliana (sp q9svg3 |
| Phvul.006G14 | not assigned. | (original description: pacid=37172040 transcript=Phvul.006G142200.1 |
| Phvul.007G04 | RNA processir | plastidial mRNA processing factor (PPR10) (original description: pacid= |
| Phvul.011G01 | not assigned. | r no hits & (original description: pacid=37154680 transcript=Phvul.011G |
| Phvul.011G02 | RNA biosynth | transcription factor (NAC) (original description: pacid=37156658 transc |
| Phvul.001G01 | Protein home | Leishmanolysin-type protease (original description: pacid=37168734 tr |
| Phvul.001G01 | Protein home | Leishmanolysin-type protease (original description: pacid=37168734 tr |
| Phvul.001G02 | not assigned. | (original description: pacid=37170145 transcript=Phvul.001G023100.1 |
| Phvul.002G20 | not assigned. | (original description: pacid=37178018 transcript=Phvul.002G208300.1 |
| Phvul.002G26 | Protein home | deubiquitinase (UBP27) (original description: pacid=37177124 transcrip |
| Phvul.002G26 | Protein home | deubiquitinase (UBP27) (original description: pacid=37177124 transcrip |
| Phvul.003G01 | not assigned. | r no hits & (original description: pacid=37148267 transcript=Phvul.003G |
| Phvul.003G03 | RNA biosynth | transcription factor (JUMONJI) (original description: pacid=37147655 t |
| Phvul.003G21 | not assigned. | (original description: pacid=37145919 transcript=Phvul.003G216800.1 |
| Phvul.004G04 | RNA processir | tRNA guanosine-methyltransferase (TRM1) (original description: pacid: |
| Phvul.004G04 | RNA processir | tRNA guanosine-methyltransferase (TRM1) (original description: pacid: |
| Phvul.004G10 | Photosynthesi | PAM68 protein involved in PS-II assembly (original description: pacid=: |

1 Phvul.004G17Lipid metabolic cytosolic NADP-dependent malic enzyme (original description: pacid=3
2 Phvul.005G00Protein modif protein kinase (AGC-VIII) (original description: pacid=37154375 transcr
3 Phvul.005G00Protein modif protein kinase (AGC-VIII) (original description: pacid=37154375 transcr
4 Phvul.005G08not assigned.ε (original description: pacid=37153134 transcript=Phvul.005G084000.1
5 Phvul.005G16Protein modif protein kinase (PERK-related) (original description: pacid=37152765 tra
6 Phvul.006G00not assigned.ε (original description: pacid=37174231 transcript=Phvul.006G004580.1
7 Phvul.006G13not assigned.ε (original description: pacid=37171646 transcript=Phvul.006G135500.1
8 Phvul.007G08Lipid metaboli UDP-glucose:sterol glucosyltransferase (original description: pacid=371
9 Phvul.008G08not assigned.ε (original description: pacid=37161262 transcript=Phvul.008G080100.2
10 Phvul.008G08not assigned.ε (original description: pacid=37161262 transcript=Phvul.008G080100.2
11 Phvul.008G13not assigned.ε (original description: pacid=37160906 transcript=Phvul.008G131301.1
12 Phvul.008G19not assigned.r no hits & (original description: pacid=37159620 transcript=Phvul.008G
13 Phvul.008G19not assigned.r no hits & (original description: pacid=37159620 transcript=Phvul.008G
14 Phvul.008G24not assigned.r no hits & (original description: pacid=37160578 transcript=Phvul.008G
15 Phvul.008G24not assigned.r no hits & (original description: pacid=37160890 transcript=Phvul.008G
16 Phvul.008G24not assigned.r no hits & (original description: pacid=37157759 transcript=Phvul.008G
17 Phvul.009G18External stimu transcriptional regulator (CIB) (original description: pacid=37149341 tr
18 Phvul.009G18External stimu transcriptional regulator (CIB) (original description: pacid=37149341 tr
19 Phvul.009G18External stimu transcriptional regulator (CIB) (original description: pacid=37149341 tr
20 Phvul.009G18External stimu transcriptional regulator (CIB) (original description: pacid=37149341 tr
21 Phvul.009G19Protein transk component SR-alpha of SRP (signal recognition particle) receptor comp
22 Phvul.009G19Protein transk component SR-alpha of SRP (signal recognition particle) receptor comp
23 Phvul.010G06Cytoskeleton motor protein (Kinesin-10) (original description: pacid=37143788 trans
24 Phvul.010G11Phytohormon receptor component PYL/RCAR of cytoplasm-localized abscisic acid rec
25 Phvul.011G07Cell wall orgar beta-galactosidase (BGAL) (original description: pacid=37154665 trans
26 Phvul.011G15not assigned.ε (original description: pacid=37155876 transcript=Phvul.011G158600.1
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

(original description: pacid=37153994 transcript=Phvul.005G179400.1 locus=Phvul.005G179400 ID=Phvul.005G179400.1.v2.1 annot-version=v2.1)
 t=Phvul.001G025900.1 locus=Phvul.001G025900 ID=Phvul.001G025900.1.v2.1 annot-version=v2.1)
 ion: pacid=37176929 transcript=Phvul.002G321900.1 locus=Phvul.002G321900 ID=Phvul.002G321900.1.v2.1 annot-version=v2.1) & Enzyme classification.EC_2 transfer
 30 OS=Arabidopsis thaliana (sp|o64477|y2913_arath : 511.0) & Enzyme classification.EC_2 transfer
 30 OS=Arabidopsis thaliana (sp|o64477|y2913_arath : 511.0) & Enzyme classification.EC_2 transfer
 30 OS=Arabidopsis thaliana (sp|o64477|y2913_arath : 511.0) & Enzyme classification.EC_2 transfer
 ion: pacid=37149943 transcript=Phvul.009G128800.1 locus=Phvul.009G128800 ID=Phvul.009G128800.1.v2.1 annot-version=v2.1) &
 =Phvul.002G220500.1 locus=Phvul.002G220500 ID=Phvul.002G220500.1.v2.1 annot-version=v2.1) &
 L locus=Phvul.006G047700 ID=Phvul.006G047700.1.v2.1 annot-version=v2.1) & Pentatricopeptide r
 L locus=Phvul.006G059900 ID=Phvul.006G059900.1.v2.1 annot-version=v2.1) & Pentatricopeptide r
 L locus=Phvul.002G133400 ID=Phvul.002G133400.1.v2.1 annot-version=v2.1) & Disease resistance p
 pt=Phvul.002G302600.1 locus=Phvul.002G302600 ID=Phvul.002G302600.1.v2.1 annot-version=v2.1)
 L locus=Phvul.003G263400 ID=Phvul.003G263400.1.v2.1 annot-version=v2.1) & Thaumatin-like prot
 L locus=Phvul.005G100500 ID=Phvul.005G100500.1.v2.1 annot-version=v2.1) & DnaJ protein ERDJ3
 ul.006G017100.1 locus=Phvul.006G017100 ID=Phvul.006G017100.1.v2.1 annot-version=v2.1) &
 71293 transcript=Phvul.006G199400.1 locus=Phvul.006G199400 ID=Phvul.006G199400.1.v2.1 anno
 L60296 transcript=Phvul.008G070100.1 locus=Phvul.008G070100 ID=Phvul.008G070100.1.v2.1 anno
 ranscript=Phvul.001G119000.1 locus=Phvul.001G119000 ID=Phvul.001G119000.1.v2.1 annot-versio
 i complex (original description: pacid=37167920 transcript=Phvul.001G259300.1 locus=Phvul.001G259300.1.v2.1 annot-version=v2.1)
 5003000.1 locus=Phvul.002G003000 ID=Phvul.002G003000.1.v2.1 annot-version=v2.1)
 5278800.1 locus=Phvul.002G278800 ID=Phvul.002G278800.1.v2.1 annot-version=v2.1)
 L locus=Phvul.003G138382 ID=Phvul.003G138382.1.v2.1 annot-version=v2.1) & Auxin-induced prot
olex (original description: pacid=37148117 transcript=Phvul.003G155500.1 locus=Phvul.003G155500.1.v2.1 annot-version=v2.1) &
 hvul.003G185100.1 locus=Phvul.003G185100 ID=Phvul.003G185100.1.v2.1 annot-version=v2.1) &
 r: pacid=37172683 transcript=Phvul.006G015900.2 locus=Phvul.006G015900 ID=Phvul.006G015900.1.v2.1 annot-version=v2.1)
 r: pacid=37172683 transcript=Phvul.006G015900.2 locus=Phvul.006G015900 ID=Phvul.006G015900.1.v2.1 annot-version=v2.1)
 L locus=Phvul.006G086100 ID=Phvul.006G086100.1.v2.1 annot-version=v2.1) & Probable acyl-activa
 L locus=Phvul.006G117700 ID=Phvul.006G117700.1.v2.1 annot-version=v2.1) & Probable N-acetyltr
 bbe21_arath : 580.0) & Enzyme classification.EC_1 oxidoreductases.EC_1.1 oxidoreductase acting c
 L locus=Phvul.006G142200 ID=Phvul.006G142200.1.v2.1 annot-version=v2.1) & Cytochrome b561 a
 :37165270 transcript=Phvul.007G042700.1 locus=Phvul.007G042700 ID=Phvul.007G042700.1.v2.1 a
 5012400.1 locus=Phvul.011G012400 ID=Phvul.011G012400.1.v2.1 annot-version=v2.1)
 ript=Phvul.011G024700.1 locus=Phvul.011G024700 ID=Phvul.011G024700.1.v2.1 annot-version=v2.1)
 ranscript=Phvul.001G016500.2 locus=Phvul.001G016500 ID=Phvul.001G016500.2.v2.1 annot-versio
 ranscript=Phvul.001G016500.2 locus=Phvul.001G016500 ID=Phvul.001G016500.2.v2.1 annot-versio
 L locus=Phvul.001G023100 ID=Phvul.001G023100.1.v2.1 annot-version=v2.1) & Probable BOI-relate
 L locus=Phvul.002G208300 ID=Phvul.002G208300.1.v2.1 annot-version=v2.1) & Pentatricopeptide r
 pt=Phvul.002G267600.2 locus=Phvul.002G267600 ID=Phvul.002G267600.2.v2.1 annot-version=v2.1
 pt=Phvul.002G267600.2 locus=Phvul.002G267600 ID=Phvul.002G267600.2.v2.1 annot-version=v2.1
 5011400.1 locus=Phvul.003G011400 ID=Phvul.003G011400.1.v2.1 annot-version=v2.1)
 ranscript=Phvul.003G031500.1 locus=Phvul.003G031500 ID=Phvul.003G031500.1.v2.1 annot-versio
 L locus=Phvul.003G216800 ID=Phvul.003G216800.1.v2.1 annot-version=v2.1) & Probable sugar pho
 =37162701 transcript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1
 =37162701 transcript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1
 37163415 transcript=Phvul.004G106700.1 locus=Phvul.004G106700 ID=Phvul.004G106700.1.v2.1 a

1
2 37163561 transcript=Phvul.004G170800.1 locus=Phvul.004G170800 ID=Phvul.004G170800.1.v2.1 ai
3 ript=Phvul.005G003300.2 locus=Phvul.005G003300 ID=Phvul.005G003300.2.v2.1 annot-version=v2.
4 ript=Phvul.005G003300.2 locus=Phvul.005G003300 ID=Phvul.005G003300.2.v2.1 annot-version=v2.
5 L locus=Phvul.005G084000 ID=Phvul.005G084000.1.v2.1 annot-version=v2.1) & COP1-interacting pr
6 anscrip=Phvul.005G160700.1 locus=Phvul.005G160700 ID=Phvul.005G160700.1.v2.1 annot-versior
7 L locus=Phvul.006G004580 ID=Phvul.006G004580.1.v2.1 annot-version=v2.1) & Receptor-like protei
8 L locus=Phvul.006G135500 ID=Phvul.006G135500.1.v2.1 annot-version=v2.1) & Probable galactinol-
9 167623 transcript=Phvul.007G080800.2 locus=Phvul.007G080800 ID=Phvul.007G080800.2.v2.1 ann
10 ? locus=Phvul.008G080100 ID=Phvul.008G080100.2.v2.1 annot-version=v2.1) & BTB/POZ domain-cc
11 ? locus=Phvul.008G080100 ID=Phvul.008G080100.2.v2.1 annot-version=v2.1) & BTB/POZ domain-cc
12 L locus=Phvul.008G131301 ID=Phvul.008G131301.1.v2.1 annot-version=v2.1) & FHA domain-contain
13 191200.2 locus=Phvul.008G191200 ID=Phvul.008G191200.2.v2.1 annot-version=v2.1)
14 191200.2 locus=Phvul.008G191200 ID=Phvul.008G191200.2.v2.1 annot-version=v2.1)
15 240000.1 locus=Phvul.008G240000 ID=Phvul.008G240000.1.v2.1 annot-version=v2.1)
16 240300.1 locus=Phvul.008G240300 ID=Phvul.008G240300.1.v2.1 annot-version=v2.1)
17 240500.1 locus=Phvul.008G240500 ID=Phvul.008G240500.1.v2.1 annot-version=v2.1)
18 ranscript=Phvul.009G183600.4 locus=Phvul.009G183600 ID=Phvul.009G183600.4.v2.1 annot-versio
19 ranscript=Phvul.009G183600.4 locus=Phvul.009G183600 ID=Phvul.009G183600.4.v2.1 annot-versio
20 ranscript=Phvul.009G183600.4 locus=Phvul.009G183600 ID=Phvul.009G183600.4.v2.1 annot-versio
21 ranscript=Phvul.009G183600.4 locus=Phvul.009G183600 ID=Phvul.009G183600.4.v2.1 annot-versio
22 olex (original description: pacid=37149160 transcript=Phvul.009G194700.2 locus=Phvul.009G19470
23 olex (original description: pacid=37149160 transcript=Phvul.009G194700.2 locus=Phvul.009G19470
24 ript=Phvul.010G069638.1 locus=Phvul.010G069638 ID=Phvul.010G069638.1.v2.1 annot-version=v
25 eceptor complex (original description: pacid=37143807 transcript=Phvul.010G112500.1 locus=Phvul.(
26 ript=Phvul.011G077600.1 locus=Phvul.011G077600 ID=Phvul.011G077600.1.v2.1 annot-version=v
27 L locus=Phvul.011G158600 ID=Phvul.011G158600.1.v2.1 annot-version=v2.1) & Beta-glucuronosyltr
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
 2
 3 ID=Phvul.005G179400.1.v2.1 annot-version=v2.1) &
 4 &
 5
 6 900.1.v2.1 annot-version=v2.1) &
 7 ases.EC_2.7 transferase transferring phosphorus-containing group(50.2.7 : 114.9) (original descript
 8 ases.EC_2.7 transferase transferring phosphorus-containing group(50.2.7 : 114.9) (original descript
 9 ases.EC_2.7 transferase transferring phosphorus-containing group(50.2.7 : 114.9) (original descript
 10 800.1.v2.1 annot-version=v2.1) &
 11 &
 12
 13
 14 repeat-containing protein At4g02750 OS=Arabidopsis thaliana (sp|q9sy02|pp301_arath : 429.0)
 15 repeat-containing protein At4g02750 OS=Arabidopsis thaliana (sp|q9sy02|pp301_arath : 469.0)
 16 protein RPM1 OS=Arabidopsis thaliana (sp|q39214|rpm1_arath : 432.0)
 17) &
 18 tein 1 OS=Arabidopsis thaliana (sp|a0a1p8b554|thlp1_arath : 285.0)
 19 B OS=Arabidopsis thaliana (sp|q9lzk5|dnj19_arath : 137.0)
 20
 21
 22
 23 ot-version=v2.1) &
 24 ot-version=v2.1) &
 25 in=v2.1) &
 26 259300 ID=Phvul.001G259300.1.v2.1 annot-version=v2.1) &
 27
 28
 29
 30
 31 ein 22B OS=Vigna radiata var. radiata (sp|p32294|ax22b_vigrr : 291.0)
 32 ID=Phvul.003G155500.1.v2.1 annot-version=v2.1) &
 33
 34
 35 J.2.v2.1 annot-version=v2.1) &
 36 J.2.v2.1 annot-version=v2.1) &
 37 ating enzyme 12, peroxisomal OS=Arabidopsis thaliana (sp|q9ss00|aae12_arath : 670.0)
 38 ansferase HLS1-like OS=Arabidopsis thaliana (sp|o64815|hls1_arath : 254.0)
 39 on CH-OH group of donor(50.1.1 : 461.0) (original description: pacid=37172282 transcript=Phvul.006
 40 ind DOMON domain-containing protein At5g47530 OS=Arabidopsis thaliana (sp|q9fgk4|b561j_arat
 41 annot-version=v2.1) &
 42
 43
 44
 45 2.1) &
 46 in=v2.1) &
 47 in=v2.1) &
 48 ed E3 ubiquitin-protein ligase 3 OS=Arabidopsis thaliana (sp|q9ldd1|brg3_arath : 117.0)
 49 repeat-containing protein At5g18390, mitochondrial OS=Arabidopsis thaliana (sp|q94jx6|pp391_ar
 50 1) &
 51 1) &
 52
 53
 54
 55
 56 on=v2.1) &
 57 sphate/phosphate translocator At1g12500 OS=Arabidopsis thaliana (sp|q9ldh3|pt112_arath : 462.0
 58 . annot-version=v2.1) &
 59 . annot-version=v2.1) &
 60 innot-version=v2.1) &

1
2 nnot-version=v2.1) &
3 .1) &
4 .1) &
5
6 rotein 7 OS=Arabidopsis thaliana (sp|o80386|cip7_arath : 505.0)
7 n=v2.1) &
8 in EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2_sollc : 120.0)
9 --sucrose galactosyltransferase 2 OS=Arabidopsis thaliana (sp|q94a08|rfs2_arath : 732.0)
10
11 not-version=v2.1) &
12 ontaining protein At3g08570 OS=Arabidopsis thaliana (sp|q9c9z7|y3857_arath : 661.0)
13 ontaining protein At3g08570 OS=Arabidopsis thaliana (sp|q9c9z7|y3857_arath : 661.0)
14 ning protein FHA2 OS=Arabidopsis thaliana (sp|q9sfv2|fha2_arath : 431.0)
15
16
17
18
19
20
21
22
23 n=v2.1) &
24 n=v2.1) &
25 n=v2.1) &
26 n=v2.1) &
27 n=v2.1) &
28 0 ID=Phvul.009G194700.2.v2.1 annot-version=v2.1) &
29 0 ID=Phvul.009G194700.2.v2.1 annot-version=v2.1) &
30 v2.1) &
31 010G112500 ID=Phvul.010G112500.1.v2.1 annot-version=v2.1) &
32 v2.1) &
33
34
35 ransferase GlcAT14A OS=Arabidopsis thaliana (sp|q9fld7|gt14a_arath : 462.0)
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

ion: pacid=37153001 transcript=Phvul.005G110300.3 locus=Phvul.005G110300 ID=Phvul.005G110300
ion: pacid=37153001 transcript=Phvul.005G110300.3 locus=Phvul.005G110300 ID=Phvul.005G110300
ion: pacid=37153001 transcript=Phvul.005G110300.3 locus=Phvul.005G110300 ID=Phvul.005G110300

Do not distribute

6G125600.1 locus=Phvul.006G125600 ID=Phvul.006G125600.1.v2.1 annot-version=v2.1) &
ath : 147.0)

ath : 590.0)

0)

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7 300.3.v2.1 annot-version=v2.1) &
8 300.3.v2.1 annot-version=v2.1) &
9 300.3.v2.1 annot-version=v2.1) &
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

| | miRNA_Acc. | Target_Acc. | Expectation | UPE\$ | miRNA_start | miRNA_end |
|----|---------------|--------------------|-------------|-------|-------------|-----------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | gauccccggcaar | Phvul.004G110400.1 | 3 | -1 | 1 | 20 |
| 4 | gauccccggcaar | Phvul.005G120700.1 | 3 | -1 | 1 | 20 |
| 5 | gauccccggcaar | Phvul.005G120700.2 | 3 | -1 | 1 | 20 |
| 6 | gauccccggcaar | Phvul.006G001600.1 | 3 | -1 | 1 | 20 |
| 7 | gauccccggcaar | Phvul.007G023000.1 | 3.5 | -1 | 1 | 20 |
| 8 | gauccccggcaar | Phvul.008G271000.1 | 3.5 | -1 | 1 | 20 |
| 9 | gauccccggcaar | Phvul.008G271000.1 | 3.5 | -1 | 1 | 20 |
| 10 | gauccccggcaar | Phvul.008G271000.1 | 3.5 | -1 | 1 | 20 |
| 11 | gauccccggcaar | Phvul.001G240600.1 | 4 | -1 | 1 | 20 |
| 12 | gauccccggcaar | Phvul.003G220500.1 | 4 | -1 | 1 | 20 |
| 13 | gauccccggcaar | Phvul.003G237300.1 | 4 | -1 | 1 | 20 |
| 14 | gauccccggcaar | Phvul.003G237300.1 | 4 | -1 | 1 | 20 |
| 15 | gauccccggcaar | Phvul.003G285700.1 | 4 | -1 | 1 | 20 |
| 16 | gauccccggcaar | Phvul.004G086300.2 | 4 | -1 | 1 | 20 |
| 17 | gauccccggcaar | Phvul.004G086300.2 | 4 | -1 | 1 | 20 |
| 18 | gauccccggcaar | Phvul.004G086300.1 | 4 | -1 | 1 | 20 |
| 19 | gauccccggcaar | Phvul.006G068400.1 | 4 | -1 | 1 | 20 |
| 20 | gauccccggcaar | Phvul.006G130200.1 | 4 | -1 | 1 | 20 |
| 21 | gauccccggcaar | Phvul.006G130200.1 | 4 | -1 | 1 | 20 |
| 22 | gauccccggcaar | Phvul.007G268300.1 | 4 | -1 | 1 | 20 |
| 23 | gauccccggcaar | Phvul.008G036200.1 | 4 | -1 | 1 | 20 |
| 24 | gauccccggcaar | Phvul.008G290700.1 | 4 | -1 | 1 | 20 |
| 25 | gauccccggcaar | Phvul.008G290700.1 | 4 | -1 | 1 | 20 |
| 26 | gauccccggcaar | Phvul.009G144300.1 | 4 | -1 | 1 | 20 |
| 27 | gauccccggcaar | Phvul.001G028400.1 | 4.5 | -1 | 1 | 20 |
| 28 | gauccccggcaar | Phvul.001G071200.1 | 4.5 | -1 | 1 | 20 |
| 29 | gauccccggcaar | Phvul.001G071200.1 | 4.5 | -1 | 1 | 20 |
| 30 | gauccccggcaar | Phvul.001G146900.1 | 4.5 | -1 | 1 | 20 |
| 31 | gauccccggcaar | Phvul.001G147001.1 | 4.5 | -1 | 1 | 20 |
| 32 | gauccccggcaar | Phvul.001G147001.2 | 4.5 | -1 | 1 | 20 |
| 33 | gauccccggcaar | Phvul.001G147001.2 | 4.5 | -1 | 1 | 20 |
| 34 | gauccccggcaar | Phvul.002G006700.1 | 4.5 | -1 | 1 | 20 |
| 35 | gauccccggcaar | Phvul.002G059000.1 | 4.5 | -1 | 1 | 20 |
| 36 | gauccccggcaar | Phvul.002G092900.2 | 4.5 | -1 | 1 | 20 |
| 37 | gauccccggcaar | Phvul.002G092900.2 | 4.5 | -1 | 1 | 20 |
| 38 | gauccccggcaar | Phvul.002G092900.1 | 4.5 | -1 | 1 | 20 |
| 39 | gauccccggcaar | Phvul.002G274500.1 | 4.5 | -1 | 1 | 20 |
| 40 | gauccccggcaar | Phvul.002G274500.1 | 4.5 | -1 | 1 | 20 |
| 41 | gauccccggcaar | Phvul.002G315300.1 | 4.5 | -1 | 1 | 20 |
| 42 | gauccccggcaar | Phvul.003G076700.2 | 4.5 | -1 | 1 | 20 |
| 43 | gauccccggcaar | Phvul.003G076700.1 | 4.5 | -1 | 1 | 20 |
| 44 | gauccccggcaar | Phvul.003G076700.1 | 4.5 | -1 | 1 | 20 |
| 45 | gauccccggcaar | Phvul.003G099100.1 | 4.5 | -1 | 1 | 20 |
| 46 | gauccccggcaar | Phvul.003G099100.3 | 4.5 | -1 | 1 | 20 |
| 47 | gauccccggcaar | Phvul.003G099100.2 | 4.5 | -1 | 1 | 20 |
| 48 | gauccccggcaar | Phvul.003G099100.2 | 4.5 | -1 | 1 | 20 |
| 49 | gauccccggcaar | Phvul.004G037600.3 | 4.5 | -1 | 1 | 20 |
| 50 | gauccccggcaar | Phvul.004G037600.2 | 4.5 | -1 | 1 | 20 |
| 51 | gauccccggcaar | Phvul.004G037600.2 | 4.5 | -1 | 1 | 20 |
| 52 | gauccccggcaar | Phvul.004G049200.1 | 4.5 | -1 | 1 | 20 |
| 53 | gauccccggcaar | Phvul.004G110200.2 | 4.5 | -1 | 1 | 20 |
| 54 | gauccccggcaar | Phvul.004G171500.6 | 4.5 | -1 | 1 | 20 |
| 55 | gauccccggcaar | Phvul.004G171500.2 | 4.5 | -1 | 1 | 20 |
| 56 | gauccccggcaar | Phvul.004G171500.3 | 4.5 | -1 | 1 | 20 |
| 57 | gauccccggcaar | Phvul.004G171500.3 | 4.5 | -1 | 1 | 20 |
| 58 | gauccccggcaar | Phvul.004G171500.1 | 4.5 | -1 | 1 | 20 |
| 59 | gauccccggcaar | Phvul.004G171500.5 | 4.5 | -1 | 1 | 20 |
| 60 | gauccccggcaar | Phvul.004G171500.4 | 4.5 | -1 | 1 | 20 |
| | gauccccggcaar | Phvul.005G022300.1 | 4.5 | -1 | 1 | 20 |

| | | | | | |
|----|----------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | gauccccggcaar Phvul.005G159600.1 | 4.5 | -1 | 1 | 20 |
| 3 | gauccccggcaar Phvul.006G049100.1 | 4.5 | -1 | 1 | 20 |
| 4 | gauccccggcaar Phvul.006G068100.1 | 4.5 | -1 | 1 | 20 |
| 5 | gauccccggcaar Phvul.006G087700.1 | 4.5 | -1 | 1 | 20 |
| 6 | gauccccggcaar Phvul.007G208400.1 | 4.5 | -1 | 1 | 20 |
| 7 | gauccccggcaar Phvul.008G042900.1 | 4.5 | -1 | 1 | 20 |
| 8 | gauccccggcaar Phvul.008G124000.2 | 4.5 | -1 | 1 | 20 |
| 9 | gauccccggcaar Phvul.008G124000.1 | 4.5 | -1 | 1 | 20 |
| 10 | gauccccggcaar Phvul.008G233100.1 | 4.5 | -1 | 1 | 20 |
| 11 | gauccccggcaar Phvul.009G157200.2 | 4.5 | -1 | 1 | 20 |
| 12 | gauccccggcaar Phvul.009G157200.1 | 4.5 | -1 | 1 | 20 |
| 13 | gauccccggcaar Phvul.010G024866.1 | 4.5 | -1 | 1 | 20 |
| 14 | gauccccggcaar Phvul.010G082300.1 | 4.5 | -1 | 1 | 20 |
| 15 | gauccccggcaar Phvul.010G119800.1 | 4.5 | -1 | 1 | 20 |
| 16 | gauccccggcaar Phvul.011G029450.1 | 4.5 | -1 | 1 | 20 |
| 17 | gauccccggcaar Phvul.001G025101.1 | 5 | -1 | 1 | 20 |
| 18 | gauccccggcaar Phvul.001G183700.1 | 5 | -1 | 1 | 20 |
| 19 | gauccccggcaar Phvul.001G209500.2 | 5 | -1 | 1 | 20 |
| 20 | gauccccggcaar Phvul.001G209900.2 | 5 | -1 | 1 | 20 |
| 21 | gauccccggcaar Phvul.001G250100.2 | 5 | -1 | 1 | 20 |
| 22 | gauccccggcaar Phvul.001G250100.1 | 5 | -1 | 1 | 20 |
| 23 | gauccccggcaar Phvul.002G063100.1 | 5 | -1 | 1 | 20 |
| 24 | gauccccggcaar Phvul.002G111100.1 | 5 | -1 | 1 | 20 |
| 25 | gauccccggcaar Phvul.002G132600.2 | 5 | -1 | 1 | 20 |
| 26 | gauccccggcaar Phvul.002G132600.1 | 5 | -1 | 1 | 20 |
| 27 | gauccccggcaar Phvul.002G188300.1 | 5 | -1 | 1 | 20 |
| 28 | gauccccggcaar Phvul.002G252700.1 | 5 | -1 | 1 | 20 |
| 29 | gauccccggcaar Phvul.002G324600.1 | 5 | -1 | 1 | 20 |
| 30 | gauccccggcaar Phvul.003G043600.2 | 5 | -1 | 1 | 20 |
| 31 | gauccccggcaar Phvul.003G064900.1 | 5 | -1 | 1 | 20 |
| 32 | gauccccggcaar Phvul.003G076900.1 | 5 | -1 | 1 | 20 |
| 33 | gauccccggcaar Phvul.003G192900.1 | 5 | -1 | 1 | 20 |
| 34 | gauccccggcaar Phvul.003G192900.2 | 5 | -1 | 1 | 20 |
| 35 | gauccccggcaar Phvul.004G017600.1 | 5 | -1 | 1 | 20 |
| 36 | gauccccggcaar Phvul.005G035400.1 | 5 | -1 | 1 | 20 |
| 37 | gauccccggcaar Phvul.005G080800.2 | 5 | -1 | 1 | 20 |
| 38 | gauccccggcaar Phvul.005G080800.1 | 5 | -1 | 1 | 20 |
| 39 | gauccccggcaar Phvul.005G095300.1 | 5 | -1 | 1 | 20 |
| 40 | gauccccggcaar Phvul.005G176600.1 | 5 | -1 | 1 | 20 |
| 41 | gauccccggcaar Phvul.006G034100.1 | 5 | -1 | 1 | 20 |
| 42 | gauccccggcaar Phvul.007G196100.2 | 5 | -1 | 1 | 20 |
| 43 | gauccccggcaar Phvul.007G196100.1 | 5 | -1 | 1 | 20 |
| 44 | gauccccggcaar Phvul.007G268300.1 | 5 | -1 | 1 | 20 |
| 45 | gauccccggcaar Phvul.008G015300.3 | 5 | -1 | 1 | 20 |
| 46 | gauccccggcaar Phvul.008G015300.4 | 5 | -1 | 1 | 20 |
| 47 | gauccccggcaar Phvul.008G015300.2 | 5 | -1 | 1 | 20 |

| | | | | | |
|----|----------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | gaucgccggcaar Phvul.008G015300.5 | 5 | -1 | 1 | 20 |
| 3 | gaucgccggcaar Phvul.008G015300.1 | 5 | -1 | 1 | 20 |
| 4 | gaucgccggcaar Phvul.008G050200.1 | 5 | -1 | 1 | 20 |
| 5 | | | | | |
| 6 | gaucgccggcaar Phvul.008G092200.2 | 5 | -1 | 1 | 20 |
| 7 | gaucgccggcaar Phvul.008G092200.3 | 5 | -1 | 1 | 20 |
| 8 | gaucgccggcaar Phvul.008G106950.2 | 5 | -1 | 1 | 20 |
| 9 | | | | | |
| 10 | gaucgccggcaar Phvul.008G106950.1 | 5 | -1 | 1 | 20 |
| 11 | gaucgccggcaar Phvul.008G114300.1 | 5 | -1 | 1 | 20 |
| 12 | gaucgccggcaar Phvul.008G130400.1 | 5 | -1 | 1 | 20 |
| 13 | | | | | |
| 14 | gaucgccggcaar Phvul.008G203314.1 | 5 | -1 | 1 | 20 |
| 15 | gaucgccggcaar Phvul.009G108800.1 | 5 | -1 | 1 | 20 |
| 16 | gaucgccggcaar Phvul.009G128500.2 | 5 | -1 | 1 | 20 |
| 17 | | | | | |
| 18 | gaucgccggcaar Phvul.009G128500.3 | 5 | -1 | 1 | 20 |
| 19 | gaucgccggcaar Phvul.009G128500.1 | 5 | -1 | 1 | 20 |
| 20 | gaucgccggcaar Phvul.009G128500.4 | 5 | -1 | 1 | 20 |
| 21 | | | | | |
| 22 | gaucgccggcaar Phvul.009G255500.1 | 5 | -1 | 1 | 20 |
| 23 | gaucgccggcaar Phvul.009G255500.2 | 5 | -1 | 1 | 20 |
| 24 | gaucgccggcaar Phvul.010G032000.1 | 5 | -1 | 1 | 20 |
| 25 | | | | | |
| 26 | gaucgccggcaar Phvul.011G062200.1 | 5 | -1 | 1 | 20 |
| 27 | gaucgccggcaar Phvul.011G175000.2 | 5 | -1 | 1 | 20 |
| 28 | gaucgccggcaar Phvul.011G175000.1 | 5 | -1 | 1 | 20 |
| 29 | | | | | |
| 30 | | | | | |
| 31 | | | | | |
| 32 | | | | | |
| 33 | | | | | |
| 34 | | | | | |
| 35 | | | | | |
| 36 | | | | | |
| 37 | | | | | |
| 38 | | | | | |
| 39 | | | | | |
| 40 | | | | | |
| 41 | | | | | |
| 42 | | | | | |
| 43 | | | | | |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | Target_start | Target_end | miRNA_align | alignment | Target_align | Inhibition | Target_Desc. |
|----|--------------|------------|-------------|---------------------------|--------------|----------------|--------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | | 1053 | 1072 | GAUCCCCGGC :::: ::::: :: | GGGCGCGG | UI Cleavage | pacid=371628 |
| 4 | | 222 | 241 | GAUCCCCGGC ::::: ::::: :: | CGGCGCCG | UL Cleavage | pacid=371525 |
| 5 | | 367 | 386 | GAUCCCCGGC ::::: ::::: :: | CGGCGCCG | UL Cleavage | pacid=371525 |
| 6 | | 716 | 735 | GAUCCCCGGC ::::: ::::: :: | CGGCGCAG | UL Cleavage | pacid=371718 |
| 7 | | 559 | 578 | GAUCCCCGGC ::::: ::::: :: | CGGCGCCG | UL Cleavage | pacid=371640 |
| 8 | | 1667 | 1686 | GAUCCCCGGC ::::: ::::: :: | AGGCGCCG | U Translation | pacid=371600 |
| 9 | | 945 | 964 | GAUCCCCGGC ::::: ::::: :: | UGGCGCUG | UI Cleavage | pacid=371707 |
| 10 | | 623 | 642 | GAUCCCCGGC ::::: ::::: :: | CGGCGCCG | AL Cleavage | pacid=371463 |
| 11 | | 619 | 638 | GAUCCCCGGC ::::: ::::: :: | UGGCGGUG | U Cleavage | pacid=371472 |
| 12 | | 1454 | 1473 | GAUCCCCGGC ::::: ::::: :: | UGGUGCCG | UI Cleavage | pacid=371474 |
| 13 | | 1131 | 1150 | GAUCCCCGGC ::::: ::::: :: | UGAGGCUG | UI Cleavage | pacid=371618 |
| 14 | | 1663 | 1682 | GAUCCCCGGC ::::: ::::: :: | UGAGGCUG | UI Cleavage | pacid=371618 |
| 15 | | 238 | 257 | GAUCCCCGGC ::::: ::::: :: | CGGUGUCG | U Translation | pacid=371737 |
| 16 | | 1177 | 1196 | GAUCCCCGGC ::::: ::::: :: | CGGUUCUG | UI Cleavage | pacid=371732 |
| 17 | | 560 | 579 | GAUCCCCGGC ::::: ::::: :: | CCGCGCCG | CC Translation | pacid=371658 |
| 18 | | 316 | 335 | GAUCCCCGGC ::::: ::::: :: | CGGUGCCG | UI Cleavage | pacid=371600 |
| 19 | | 221 | 240 | GAUCCCCGGC ::::: ::::: :: | AGGCGCGG | UI Cleavage | pacid=371609 |
| 20 | | 681 | 700 | GAUCCCCGGC ::::: ::::: :: | GGGCGCCU | U Cleavage | pacid=371502 |
| 21 | | 596 | 615 | GAUCCCCGGC ::::: ::::: :: | AGGAGCUG | UI Cleavage | pacid=371709 |
| 22 | | 702 | 721 | GAUCCCCGGC ::::: ::::: :: | GGGUGCUG | U Cleavage | pacid=371698 |
| 23 | | 1160 | 1179 | GAUCCCCGGC ::::: ::::: :: | UUGUUCUG | U Cleavage | pacid=371680 |
| 24 | | 816 | 835 | GAUCCCCGGC ::::: ::::: :: | UUGUUCUG | U Cleavage | pacid=371704 |
| 25 | | 928 | 947 | GAUCCCCGGC ::::: ::::: :: | UUGUUCUG | U Cleavage | pacid=371704 |
| 26 | | 1011 | 1030 | GAUCCCCGGC ::::: ::::: :: | UGGUGAAG | U Cleavage | pacid=371753 |
| 27 | | 680 | 699 | GAUCCCCGGC ::::: ::::: :: | CUCCGCUG | UI Cleavage | pacid=371755 |
| 28 | | 5389 | 5408 | GAUCCCCGGC ::::: ::::: :: | AUGAGCCG | UI Cleavage | pacid=371766 |
| 29 | | 5401 | 5420 | GAUCCCCGGC ::::: ::::: :: | AUGAGCCG | UI Cleavage | pacid=371766 |
| 30 | | 710 | 729 | GAUCCCCGGC ::::: ::::: :: | GGGCACCG | UI Cleavage | pacid=371760 |
| 31 | | 1178 | 1197 | GAUCCCCGGC ::::: ::::: :: | UGGGGUUG | U Cleavage | pacid=371744 |
| 32 | | 247 | 266 | GAUCCCCGGC ::::: ::::: :: | UGGCGAUG | UI Cleavage | pacid=371472 |
| 33 | | 247 | 266 | GAUCCCCGGC ::::: ::::: :: | UGGCGAUG | UI Cleavage | pacid=371472 |
| 34 | | 2013 | 2032 | GAUCCCCGGC ::::: ::::: :: | AGGCGCAG | UI Cleavage | pacid=371449 |
| 35 | | 2411 | 2430 | GAUCCCCGGC ::::: ::::: :: | AGGCGCAG | UI Cleavage | pacid=371449 |
| 36 | | 2449 | 2468 | GAUCCCCGGC ::::: ::::: :: | AGGCGCAG | UI Cleavage | pacid=371449 |
| 37 | | 1246 | 1265 | GAUCCCCGGC ::::: ::::: :: | UGGGGAUG | U Cleavage | pacid=371632 |
| 38 | | 1246 | 1265 | GAUCCCCGGC ::::: ::::: :: | UGGGGAUG | U Cleavage | pacid=371632 |
| 39 | | 1075 | 1094 | GAUCCCCGGC ::::: ::::: :: | UGUUGGUG | U Cleavage | pacid=371636 |
| 40 | | 705 | 724 | GAUCCCCGGC ::::: ::::: :: | GGGCGCGG | U Translation | pacid=371636 |
| 41 | | 463 | 482 | GAUCCCCGGC ::::: ::::: :: | UGGUGCUG | U Cleavage | pacid=371623 |
| 42 | | 472 | 491 | GAUCCCCGGC ::::: ::::: :: | UGGUGCUG | U Cleavage | pacid=371623 |
| 43 | | 463 | 482 | GAUCCCCGGC ::::: ::::: :: | UGGUGCUG | U Cleavage | pacid=371623 |
| 44 | | 472 | 491 | GAUCCCCGGC ::::: ::::: :: | UGGUGCUG | U Cleavage | pacid=371623 |
| 45 | | 463 | 482 | GAUCCCCGGC ::::: ::::: :: | UGGUGCUG | U Cleavage | pacid=371623 |
| 46 | | 472 | 491 | GAUCCCCGGC ::::: ::::: :: | UGGUGCUG | U Cleavage | pacid=371623 |
| 47 | | 463 | 482 | GAUCCCCGGC ::::: ::::: :: | UGGUGCUG | U Cleavage | pacid=371623 |
| 48 | | 472 | 491 | GAUCCCCGGC ::::: ::::: :: | UGGUGCUG | U Cleavage | pacid=371623 |
| 49 | | 998 | 1017 | GAUCCCCGGC ::::: ::::: :: | GGGUGUUG | U Cleavage | pacid=371537 |

| | | | | | |
|----|------|-----------------|----------------------------|-------------|--------------|
| 1 | | | | | |
| 2 | 513 | 532 GAUCCCCGGC | ::: : ::: ::::: AGGUGGCCUI | Cleavage | pacid=371545 |
| 3 | 1225 | 1244 GAUCCCCGGC | ::: ::::: : ::: UGGUGCCGUI | Cleavage | pacid=371719 |
| 4 | 511 | 530 GAUCCCCGGC | ::: ::::: : ::: GGGUGUUGU | Cleavage | pacid=371741 |
| 5 | 861 | 880 GAUCCCCGGC | :: : ::::: : GGGGGCUGU | Cleavage | pacid=371738 |
| 6 | 576 | 595 GAUCCCCGGC | ::: : ::::: : CGGCACAGU | Cleavage | pacid=371665 |
| 7 | 432 | 451 GAUCCCCGGC | : : ::::: : UCCCACUGU | Cleavage | pacid=371596 |
| 8 | 773 | 792 GAUCCCCGGC | ::: ::::: : AAGUGCUGU | Cleavage | pacid=371580 |
| 9 | 1132 | 1151 GAUCCCCGGC | ::: ::::: : AAGUGCUGU | Cleavage | pacid=371580 |
| 10 | 516 | 535 GAUCCCCGGC | ::: : ::::: : UGGUGUAGU | Cleavage | pacid=371605 |
| 11 | 1341 | 1360 GAUCCCCGGC | ::: : ::::: : UGGUUCUGU | Cleavage | pacid=371499 |
| 12 | 1368 | 1387 GAUCCCCGGC | ::: : ::::: : UGGUUCUGU | Cleavage | pacid=371499 |
| 13 | 154 | 173 GAUCCCCGGC | ::: : ::::: : UGGUGUAGU | Cleavage | pacid=371422 |
| 14 | 1652 | 1671 GAUCCCCGGC | ::: : ::::: : UGGCACCGU | Cleavage | pacid=371438 |
| 15 | 597 | 616 GAUCCCCGGC | ::: : ::::: : UGUCGCUGU | Translation | pacid=371439 |
| 16 | 2765 | 2784 GAUCCCCGGC | : : ::::: : GGCUGCUGU | Cleavage | pacid=371573 |
| 17 | 276 | 295 GAUCCCCGGC | ::: : ::::: : AGGUGGCGU | Cleavage | pacid=371681 |
| 18 | 871 | 890 GAUCCCCGGC | ::: : ::::: : UGGCGGCGU | Cleavage | pacid=371692 |
| 19 | 1254 | 1273 GAUCCCCGGC | ::: ::::: : GGGUGCCGU | Cleavage | pacid=371677 |
| 20 | 1156 | 1175 GAUCCCCGGC | ::: : ::::: : UGGCGAAGU | Cleavage | pacid=371689 |
| 21 | 48 | 67 GAUCCCCGGC | ::: : ::::: : UGGAGCUGU | Cleavage | pacid=371707 |
| 22 | 57 | 76 GAUCCCCGGC | ::: : ::::: : UGGAGCUGU | Cleavage | pacid=371707 |
| 23 | 707 | 726 GAUCCCCGGC | ::: : ::::: : CUGCCCAAL | Cleavage | pacid=371743 |
| 24 | 1118 | 1137 GAUCCCCGGC | ::: : ::::: : ACGCGCCGUC | Translation | pacid=371761 |
| 25 | 1742 | 1761 GAUCCCCGGC | ::: ::::: : AGGUGCUGU | Cleavage | pacid=371787 |
| 26 | 1708 | 1727 GAUCCCCGGC | ::: ::::: : AGGUGCUGU | Cleavage | pacid=371787 |
| 27 | 624 | 643 GAUCCCCGGC | ::: : ::::: : UGUCACUGU | Translation | pacid=371749 |
| 28 | 896 | 915 GAUCCCCGGC | ::: : ::::: : CGGUGCUGU | Translation | pacid=371746 |
| 29 | 1576 | 1595 GAUCCCCGGC | ::: : ::::: : UGUUGUUGU | Cleavage | pacid=371755 |
| 30 | 89 | 108 GAUCCCCGGC | ::: : ::::: : UGGUGAUGU | Cleavage | pacid=371474 |
| 31 | 900 | 919 GAUCCCCGGC | ::: ::::: : GGGCGCUGU | Cleavage | pacid=371461 |
| 32 | 1207 | 1227 GAUCC-CCGG | ::: : ::::: : CGGCGUGGU | Cleavage | pacid=371478 |
| 33 | 81 | 100 GAUCCCCGGC | ::: : ::::: : UCUCGUCGU | Cleavage | pacid=371457 |
| 34 | 81 | 100 GAUCCCCGGC | ::: : ::::: : UCUCGUCGU | Cleavage | pacid=371457 |
| 35 | 3869 | 3888 GAUCCCCGGC | ::: : ::::: : UCGUGUUGU | Translation | pacid=371629 |
| 36 | 842 | 861 GAUCCCCGGC | ::: : ::::: : AGGCGCUGU | Cleavage | pacid=371525 |
| 37 | 860 | 879 GAUCCCCGGC | ::: : ::::: : UGGUUCUGU | Cleavage | pacid=371543 |
| 38 | 863 | 882 GAUCCCCGGC | ::: : ::::: : UGGUUCUGU | Cleavage | pacid=371543 |
| 39 | 542 | 561 GAUCCCCGGC | ::: : ::::: : UGGUCUUGA | Cleavage | pacid=371545 |
| 40 | 1260 | 1279 GAUCCCCGGC | : : ::::: : AGUUGUCGU | Cleavage | pacid=371526 |
| 41 | 472 | 491 GAUCCCCGGC | ::: : ::::: : UGGUGUUGG | Cleavage | pacid=371721 |
| 42 | 1295 | 1314 GAUCCCCGGC | ::: : ::::: : UGGUGCCGG | Cleavage | pacid=371642 |
| 43 | 1580 | 1599 GAUCCCCGGC | ::: : ::::: : UGGUGCCGG | Cleavage | pacid=371642 |
| 44 | 293 | 312 GAUCCCCGGC | ::: : ::::: : CGGCACUGU | Cleavage | pacid=371658 |
| 45 | 876 | 895 GAUCCCCGGC | ::: : ::::: : UGAUGCUGU | Cleavage | pacid=371611 |
| 46 | 876 | 895 GAUCCCCGGC | ::: : ::::: : UGAUGCUGU | Cleavage | pacid=371611 |
| 47 | 875 | 894 GAUCCCCGGC | ::: : ::::: : UGAUGCUGU | Cleavage | pacid=371611 |

| | | | | |
|----|------|-------------------------------|------------------------|--------------|
| 1 | | | | |
| 2 | 876 | 895 GAUCCCCGGC :: :.:.:. .:.: | UGAUGCUGU Cleavage | pacid=371611 |
| 3 | 875 | 894 GAUCCCCGGC :: :.:.:. .:.: | UGAUGCUGU Cleavage | pacid=371611 |
| 4 | 242 | 261 GAUCCCCGGC : : :.:. .:.: | UUGCUCUGU Translation | pacid=371607 |
| 5 | 558 | 577 GAUCCCCGGC :.:. :.:. :.: | UGGCGGUGC Cleavage | pacid=371595 |
| 6 | 558 | 577 GAUCCCCGGC :.:. :.:. :.: | UGGCGGUGC Cleavage | pacid=371595 |
| 7 | | | | |
| 8 | 3937 | 3956 GAUCCCCGGC :.:.:. :.: | GAGCGCUGU Cleavage | pacid=371594 |
| 9 | 3937 | 3956 GAUCCCCGGC :.:.:. :.: | GAGCGCUGU Cleavage | pacid=371594 |
| 10 | | | | |
| 11 | 1330 | 1349 GAUCCCCGGC : :.:. .:.: | UGGAGUUGU Cleavage | pacid=371598 |
| 12 | 1154 | 1173 GAUCCCCGGC :.:.:. :.: | AGGUGUUGU Cleavage | pacid=371589 |
| 13 | | | | |
| 14 | 709 | 728 GAUCCCCGGC :.:. :.: | UGGUGGUGU Cleavage | pacid=371614 |
| 15 | 388 | 407 GAUCCCCGGC :.:. :.: | UGGCCUCCUL Cleavage | pacid=371499 |
| 16 | 1505 | 1524 GAUCCCCGGC :.:.:. :.: | UGGCUCUGU Cleavage | pacid=371492 |
| 17 | | | | |
| 18 | 1517 | 1536 GAUCCCCGGC :.:.:. :.: | UGGCUCUGU Cleavage | pacid=371492 |
| 19 | 1544 | 1563 GAUCCCCGGC :.:.:. :.: | UGGCUCUGU Cleavage | pacid=371492 |
| 20 | 1767 | 1786 GAUCCCCGGC :.:.:. :.: | UGGCUCUGU Cleavage | pacid=371493 |
| 21 | | | | |
| 22 | 741 | 760 GAUCCCCGGC :.:. :.: | UGGAGCUGU Translation | pacid=371491 |
| 23 | 843 | 862 GAUCCCCGGC :.:. :.: | UGGAGCUGU Translation | pacid=371491 |
| 24 | 2180 | 2199 GAUCCCCGGC :.:.:. :.: | GGGUGUUGU Cleavage | pacid=371428 |
| 25 | | | | |
| 26 | 752 | 771 GAUCCCCGGC :.:.:. :.: | CGGUGCUGU Cleavage | pacid=371564 |
| 27 | 382 | 401 GAUCCCCGGC :.:.:. :.: | CCAACCUGUL Cleavage | pacid=371553 |
| 28 | 382 | 401 GAUCCCCGGC :.:.:. :.: | CCAACCUGUL Cleavage | pacid=371553 |
| 29 | | | | |
| 30 | | | | |
| 31 | | | | |
| 32 | | | | |
| 33 | | | | |
| 34 | | | | |
| 35 | | | | |
| 36 | | | | |
| 37 | | | | |
| 38 | | | | |
| 39 | | | | |
| 40 | | | | |
| 41 | | | | |
| 42 | | | | |
| 43 | | | | |
| 44 | | | | |
| 45 | | | | |
| 46 | | | | |
| 47 | | | | |
| 48 | | | | |
| 49 | | | | |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

bioRxiv preprint doi: <https://doi.org/10.1101/2019.01.15.864314>; this version posted January 15, 2019. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

| Multiplicity | Target_Acc. | ID | locusName | Pfam |
|--------------|--------------------|------------------|------------------|--------------|
| 1 | Phvul.004G110400.1 | Phvul.004G110400 | Phvul.004G110400 | PF00168 |
| 1 | Phvul.005G120700.1 | Phvul.005G120700 | Phvul.005G120700 | PF00069 |
| 1 | Phvul.005G120700.2 | Phvul.005G120700 | Phvul.005G120700 | PF00069 |
| 1 | Phvul.006G001600.1 | Phvul.006G001600 | Phvul.006G001600 | PF00012 |
| 1 | Phvul.007G023000.1 | Phvul.007G023000 | Phvul.007G023000 | PF01814 |
| 1 | Phvul.008G271000.1 | Phvul.008G271000 | Phvul.008G271000 | PF07983,PF00 |
| 1 | Phvul.001G240600.1 | Phvul.001G240600 | Phvul.001G240600 | PF00168 |
| 1 | Phvul.003G220500.1 | Phvul.003G220500 | Phvul.003G220500 | PF01095 |
| 1 | Phvul.003G237300.1 | Phvul.003G237300 | Phvul.003G237300 | PF05922,PF02 |
| 1 | Phvul.003G285700.1 | Phvul.003G285700 | Phvul.003G285700 | PF00010,PF14 |
| 1 | Phvul.004G086300.2 | Phvul.004G086300 | Phvul.004G086300 | PF00069 |
| 1 | Phvul.004G086300.1 | Phvul.004G086300 | Phvul.004G086300 | PF00069 |
| 1 | Phvul.006G068400.1 | Phvul.006G068400 | Phvul.006G068400 | PF13540,PF00 |
| 1 | Phvul.006G130200.1 | Phvul.006G130200 | Phvul.006G130200 | PF04146 |
| 2 | Phvul.007G268300.1 | Phvul.007G268300 | Phvul.007G268300 | 0 |
| 1 | Phvul.008G036200.1 | Phvul.008G036200 | Phvul.008G036200 | PF00520 |
| 1 | Phvul.008G290700.1 | Phvul.008G290700 | Phvul.008G290700 | PF05678 |
| 1 | Phvul.009G144300.1 | Phvul.009G144300 | Phvul.009G144300 | PF03479 |
| 1 | Phvul.001G028400.1 | Phvul.001G028400 | Phvul.001G028400 | PF03081 |
| 1 | Phvul.001G071200.1 | Phvul.001G071200 | Phvul.001G071200 | PF00069 |
| 1 | Phvul.001G146900.1 | Phvul.001G146900 | Phvul.001G146900 | PF00069 |
| 1 | Phvul.001G147001.1 | Phvul.001G147001 | Phvul.001G147001 | PF07714 |
| 1 | Phvul.001G147001.2 | Phvul.001G147001 | Phvul.001G147001 | PF07714 |
| 1 | Phvul.002G006700.1 | Phvul.002G006700 | Phvul.002G006700 | PF03479 |
| 1 | Phvul.002G059000.1 | Phvul.002G059000 | Phvul.002G059000 | 0 |
| 1 | Phvul.002G092900.2 | Phvul.002G092900 | Phvul.002G092900 | PF00118,PF01 |
| 1 | Phvul.002G092900.1 | Phvul.002G092900 | Phvul.002G092900 | PF00118,PF01 |
| 1 | Phvul.002G274500.1 | Phvul.002G274500 | Phvul.002G274500 | PF01764 |
| 1 | Phvul.002G315300.1 | Phvul.002G315300 | Phvul.002G315300 | PF03456,PF00 |
| 1 | Phvul.003G076700.2 | Phvul.003G076700 | Phvul.003G076700 | PF00232 |
| 1 | Phvul.003G076700.1 | Phvul.003G076700 | Phvul.003G076700 | PF00232 |
| 1 | Phvul.003G099100.1 | Phvul.003G099100 | Phvul.003G099100 | PF01156 |
| 1 | Phvul.003G099100.3 | Phvul.003G099100 | Phvul.003G099100 | PF01156 |
| 1 | Phvul.003G099100.2 | Phvul.003G099100 | Phvul.003G099100 | PF01156 |
| 1 | Phvul.004G037600.3 | Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00 |
| 1 | Phvul.004G037600.2 | Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00 |
| 1 | Phvul.004G049200.1 | Phvul.004G049200 | Phvul.004G049200 | PF03639 |
| 1 | Phvul.004G110200.2 | Phvul.004G110200 | Phvul.004G110200 | PF00168 |
| 1 | Phvul.004G171500.6 | Phvul.004G171500 | Phvul.004G171500 | PF00132 |
| 1 | Phvul.004G171500.2 | Phvul.004G171500 | Phvul.004G171500 | PF00132 |
| 1 | Phvul.004G171500.3 | Phvul.004G171500 | Phvul.004G171500 | PF00132 |
| 1 | Phvul.004G171500.1 | Phvul.004G171500 | Phvul.004G171500 | PF00132 |
| 1 | Phvul.004G171500.5 | Phvul.004G171500 | Phvul.004G171500 | PF00132 |
| 1 | Phvul.004G171500.4 | Phvul.004G171500 | Phvul.004G171500 | PF00132 |
| 1 | Phvul.005G022300.1 | Phvul.005G022300 | Phvul.005G022300 | PF03151 |

| | | | | |
|----|----------------------|------------------|------------------|--------------|
| 1 | | | | |
| 2 | 1 Phvul.005G159600.1 | Phvul.005G159600 | Phvul.005G159600 | PF05879 |
| 3 | 1 Phvul.006G049100.1 | Phvul.006G049100 | Phvul.006G049100 | PF12327,PF00 |
| 4 | 1 Phvul.006G068100.1 | Phvul.006G068100 | Phvul.006G068100 | PF01713,PF08 |
| 5 | | | | |
| 6 | 1 Phvul.006G087700.1 | Phvul.006G087700 | Phvul.006G087700 | PF00069,PF00 |
| 7 | 1 Phvul.007G208400.1 | Phvul.007G208400 | Phvul.007G208400 | PF00249 |
| 8 | 1 Phvul.008G042900.1 | Phvul.008G042900 | Phvul.008G042900 | PF13360 |
| 9 | | | | |
| 10 | 1 Phvul.008G124000.2 | Phvul.008G124000 | Phvul.008G124000 | PF12452 |
| 11 | 1 Phvul.008G124000.1 | Phvul.008G124000 | Phvul.008G124000 | PF12452 |
| 12 | 1 Phvul.008G233100.1 | Phvul.008G233100 | Phvul.008G233100 | PF01841,PF10 |
| 13 | | | | |
| 14 | 1 Phvul.009G157200.2 | Phvul.009G157200 | Phvul.009G157200 | PF02493,PF01 |
| 15 | 1 Phvul.009G157200.1 | Phvul.009G157200 | Phvul.009G157200 | PF02493,PF01 |
| 16 | 1 Phvul.010G024866.1 | Phvul.010G024866 | Phvul.010G024866 | PF10404,PF10 |
| 17 | | | | |
| 18 | 1 Phvul.010G082300.1 | Phvul.010G082300 | Phvul.010G082300 | PF01073 |
| 19 | 1 Phvul.010G119800.1 | Phvul.010G119800 | Phvul.010G119800 | PF03168 |
| 20 | 1 Phvul.011G029450.1 | Phvul.011G029450 | Phvul.011G029450 | PF04818,PF00 |
| 21 | | | | |
| 22 | 1 Phvul.001G025101.1 | Phvul.001G025101 | Phvul.001G025101 | PF03629 |
| 23 | 1 Phvul.001G183700.1 | Phvul.001G183700 | Phvul.001G183700 | PF03465,PF03 |
| 24 | 1 Phvul.001G209500.2 | Phvul.001G209500 | Phvul.001G209500 | PF00759 |
| 25 | | | | |
| 26 | 1 Phvul.001G209900.2 | Phvul.001G209900 | Phvul.001G209900 | PF01966,PF04 |
| 27 | 1 Phvul.001G250100.2 | Phvul.001G250100 | Phvul.001G250100 | PF00168,PF00 |
| 28 | 1 Phvul.001G250100.1 | Phvul.001G250100 | Phvul.001G250100 | PF00168,PF00 |
| 29 | | | | |
| 30 | 1 Phvul.002G063100.1 | Phvul.002G063100 | Phvul.002G063100 | PF01095 |
| 31 | 1 Phvul.002G111100.1 | Phvul.002G111100 | Phvul.002G111100 | PF08263,PF07 |
| 32 | 1 Phvul.002G132600.2 | Phvul.002G132600 | Phvul.002G132600 | 0 |
| 33 | 1 Phvul.002G132600.1 | Phvul.002G132600 | Phvul.002G132600 | 0 |
| 34 | | | | |
| 35 | 1 Phvul.002G188300.1 | Phvul.002G188300 | Phvul.002G188300 | PF00646 |
| 36 | 1 Phvul.002G252700.1 | Phvul.002G252700 | Phvul.002G252700 | PF00400 |
| 37 | | | | |
| 38 | 1 Phvul.002G324600.1 | Phvul.002G324600 | Phvul.002G324600 | PF08263,PF13 |
| 39 | 1 Phvul.003G043600.2 | Phvul.003G043600 | Phvul.003G043600 | PF00232 |
| 40 | 1 Phvul.003G064900.1 | Phvul.003G064900 | Phvul.003G064900 | PF01384 |
| 41 | 1 Phvul.003G076900.1 | Phvul.003G076900 | Phvul.003G076900 | PF00067 |
| 42 | | | | |
| 43 | 1 Phvul.003G192900.1 | Phvul.003G192900 | Phvul.003G192900 | PF02183,PF00 |
| 44 | 1 Phvul.003G192900.2 | Phvul.003G192900 | Phvul.003G192900 | PF02183,PF00 |
| 45 | | | | |
| 46 | 1 Phvul.004G017600.1 | Phvul.004G017600 | Phvul.004G017600 | PF15612,PF01 |
| 47 | 1 Phvul.005G035400.1 | Phvul.005G035400 | Phvul.005G035400 | PF08799,PF02 |
| 48 | 1 Phvul.005G080800.2 | Phvul.005G080800 | Phvul.005G080800 | PF09507 |
| 49 | 1 Phvul.005G080800.1 | Phvul.005G080800 | Phvul.005G080800 | PF09507 |
| 50 | | | | |
| 51 | 1 Phvul.005G095300.1 | Phvul.005G095300 | Phvul.005G095300 | PF00311 |
| 52 | 1 Phvul.005G176600.1 | Phvul.005G176600 | Phvul.005G176600 | PF13041 |
| 53 | 1 Phvul.006G034100.1 | Phvul.006G034100 | Phvul.006G034100 | PF01501 |
| 54 | | | | |
| 55 | 1 Phvul.007G196100.2 | Phvul.007G196100 | Phvul.007G196100 | 0 |
| 56 | 1 Phvul.007G196100.1 | Phvul.007G196100 | Phvul.007G196100 | 0 |
| 57 | | | | |
| 58 | 2 Phvul.007G268300.1 | Phvul.007G268300 | Phvul.007G268300 | 0 |
| 59 | 1 Phvul.008G015300.3 | Phvul.008G015300 | Phvul.008G015300 | 0 |
| 60 | 1 Phvul.008G015300.4 | Phvul.008G015300 | Phvul.008G015300 | 0 |
| | 1 Phvul.008G015300.2 | Phvul.008G015300 | Phvul.008G015300 | 0 |

| | | | | | |
|----|---|--------------------|------------------|------------------|--------------|
| 1 | | | | | |
| 2 | 1 | Phvul.008G015300.5 | Phvul.008G015300 | Phvul.008G015300 | 0 |
| 3 | 1 | Phvul.008G015300.1 | Phvul.008G015300 | Phvul.008G015300 | 0 |
| 4 | 1 | Phvul.008G050200.1 | Phvul.008G050200 | Phvul.008G050200 | 0 |
| 5 | | | | | |
| 6 | 1 | Phvul.008G092200.2 | Phvul.008G092200 | Phvul.008G092200 | 0 |
| 7 | 1 | Phvul.008G092200.3 | Phvul.008G092200 | Phvul.008G092200 | 0 |
| 8 | 1 | Phvul.008G106950.2 | Phvul.008G106950 | Phvul.008G106950 | PF02207 |
| 9 | | | | | |
| 10 | 1 | Phvul.008G106950.1 | Phvul.008G106950 | Phvul.008G106950 | PF02207 |
| 11 | 1 | Phvul.008G114300.1 | Phvul.008G114300 | Phvul.008G114300 | PF05920,PF07 |
| 12 | 1 | Phvul.008G130400.1 | Phvul.008G130400 | Phvul.008G130400 | PF10510 |
| 13 | | | | | |
| 14 | 1 | Phvul.008G203314.1 | Phvul.008G203314 | Phvul.008G203314 | PF02298 |
| 15 | 1 | Phvul.009G108800.1 | Phvul.009G108800 | Phvul.009G108800 | PF00230 |
| 16 | 1 | Phvul.009G128500.2 | Phvul.009G128500 | Phvul.009G128500 | PF01490 |
| 17 | | | | | |
| 18 | 1 | Phvul.009G128500.3 | Phvul.009G128500 | Phvul.009G128500 | PF01490 |
| 19 | 1 | Phvul.009G128500.1 | Phvul.009G128500 | Phvul.009G128500 | PF01490 |
| 20 | 1 | Phvul.009G128500.4 | Phvul.009G128500 | Phvul.009G128500 | PF01490 |
| 21 | | | | | |
| 22 | 1 | Phvul.009G255500.1 | Phvul.009G255500 | Phvul.009G255500 | 0 |
| 23 | 1 | Phvul.009G255500.2 | Phvul.009G255500 | Phvul.009G255500 | 0 |
| 24 | 1 | Phvul.010G032000.1 | Phvul.010G032000 | Phvul.010G032000 | PF01453,PF00 |
| 25 | | | | | |
| 26 | 1 | Phvul.011G062200.1 | Phvul.011G062200 | Phvul.011G062200 | PF00806,PF07 |
| 27 | 1 | Phvul.011G175000.2 | Phvul.011G175000 | Phvul.011G175000 | PF08276,PF07 |
| 28 | 1 | Phvul.011G175000.1 | Phvul.011G175000 | Phvul.011G175000 | PF08276,PF07 |
| 29 | | | | | |
| 30 | | | | | |
| 31 | | | | | |
| 32 | | | | | |
| 33 | | | | | |
| 34 | | | | | |
| 35 | | | | | |
| 36 | | | | | |
| 37 | | | | | |
| 38 | | | | | |
| 39 | | | | | |
| 40 | | | | | |
| 41 | | | | | |
| 42 | | | | | |
| 43 | | | | | |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | Panther | KOG | KEGG | KOG | GO | Best-hit-arabi |
|----|----------------------------------|-----|---------------------------|----------|---------------------|----------------------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | PTHR32246,P ⁻ | | 0 | 0 | 0 GO:0005515 | AT5G23950.1 |
| 4 | PTHR24362,P ⁻ | | 0 2.7.11.1 | | 0 GO:0006468,C | AT3G44200.1 |
| 5 | PTHR24362,P ⁻ | | 0 2.7.11.1 | | 0 GO:0006468,C | AT3G44200.1 |
| 6 | PTHR19375,P ⁻ | | 0 | 0 K09486 | | 0 AT4G16660.1 |
| 7 | PTHR19375,P ⁻ | | 0 | 0 K09486 | | 0 AT4G16660.1 |
| 8 | PTHR35739,P ⁻ | | 0 | 0 | 0 | 0 AT3G54290.1 |
| 9 | PTHR32227,P ⁻ | | 0 3.2.1.39 | | 0 GO:0005975,C | AT5G55180.1 |
| 10 | PTHR32227,P ⁻ | | 0 3.2.1.39 | | 0 GO:0005975,C | AT5G55180.1 |
| 11 | PTHR32246,P⁻ | | 0 | 0 | 0 GO:0005515 | AT1G07310.1 |
| 12 | PTHR31321,P ⁻ | | 0 3.1.1.11 | | 0 GO:0042545,C | AT5G47500.1 |
| 13 | PTHR10795,P ⁻ | | 0 3.4.14.10 | | 0 GO:0006508,C | AT5G67360.1 |
| 14 | PTHR10795,P ⁻ | | 0 3.4.14.10 | | 0 GO:0006508,C | AT5G67360.1 |
| 15 | PTHR11514,P ⁻ | | 0 | 0 K13422 | GO:0046983 | AT1G32640.1 |
| 16 | PTHR27001,P ⁻ KOG1187 | | 2.7.11.1,2.7.11.1 | | 0 GO:0006468,C | AT1G71830.1 |
| 17 | PTHR27001,P ⁻ KOG1187 | | 2.7.11.1,2.7.11.1 | | 0 GO:0006468,C | AT1G71830.1 |
| 18 | PTHR27001,P ⁻ KOG1187 | | 2.7.11.1,2.7.11.1 | | 0 GO:0006468,C | AT1G71830.1 |
| 19 | PTHR27003,P ⁻ KOG1187 | | 2.7.11.1 | | 0 GO:0006468,C | AT3G55950.1 |
| 20 | PTHR27003,P ⁻ KOG1187 | | 2.7.11.1 | | 0 GO:0006468,C | AT3G55950.1 |
| 21 | PTHR12357,P ⁻ KOG1902 | | | 0 K14404 | | 0 AT1G30460.1 |
| 22 | PTHR12357,P ⁻ KOG1902 | | | 0 K14404 | | 0 AT1G30460.1 |
| 23 | PTHR36351,P ⁻ | | 0 | 0 | 0 | 0 |
| 24 | PTHR10217,P ⁻ | | 0 | 0 K05391 | GO:0055085,C | AT5G15410.2 |
| 25 | PTHR10217,P ⁻ | | 0 | 0 K05391 | GO:0055085,C | AT5G15410.2 |
| 26 | PTHR33179,P ⁻ | | 0 | 0 | 0 | 0 AT3G22160.1 |
| 27 | PTHR33179,P ⁻ | | 0 | 0 | 0 | 0 AT3G22160.1 |
| 28 | PTHR31100,P ⁻ | | 0 | 0 | 0 | 0 AT5G49700.1 |
| 29 | PTHR31100,P ⁻ | | 0 | 0 | 0 | 0 AT5G49700.1 |
| 30 | PTHR12542,P ⁻ | | 0 | 0 K07195 | GO:0006887,C | AT4G31540.1 |
| 31 | PTHR12542,P ⁻ | | 0 | 0 K07195 | GO:0006887,C | AT4G31540.1 |
| 32 | PTHR27006,P ⁻ KOG1187 | | 2.7.11.1 | | 0 GO:0006468,C | AT1G11050.1 |
| 33 | PTHR27006,P ⁻ KOG1187 | | 2.7.11.1 | | 0 GO:0006468,C | AT1G11050.1 |
| 34 | PTHR27006,P ⁻ KOG1187 | | 2.7.11.1 | | 0 GO:0006468,C | AT2G48010.1 |
| 35 | PTHR27006,P ⁻ KOG1187 | | 2.7.11.1 | | 0 GO:0006468,C | AT2G48010.1 |
| 36 | PTHR27006,P ⁻ KOG1187 | | 2.7.11.1 | | 0 GO:0006468,C | AT2G48010.1 |
| 37 | PTHR27006,P ⁻ KOG1187 | | 2.7.11.1 | | 0 GO:0006468,C | AT2G48010.1 |
| 38 | PTHR31500,P ⁻ | | 0 | 0 | 0 | 0 AT4G17950.1 |
| 39 | PTHR34043,P⁻ | | 0 3.1.1.32,3.1.1.1 | | 0 | 0 AT1G10740.3 |
| 40 | PTHR11353,P ⁻ | | 0 2.7.1.150 | K00921 | GO:0005524,C | AT1G71010.1 |
| 41 | PTHR11353,P ⁻ | | 0 2.7.1.150 | K00921 | GO:0005524,C | AT1G71010.1 |
| 42 | PTHR11353,P ⁻ | | 0 2.7.1.150 | K00921 | GO:0005524,C | AT1G71010.1 |
| 43 | PTHR21493,P⁻ | | 0 3.1.1.1 | | 0 GO:0006629 | AT3G52430.1 |
| 44 | PTHR22844,P ⁻ KOG3569 | | | 0 | 0 GO:0005515 | AT1G49040.1 |
| 45 | PTHR10353,P ⁻ | | 0 3.2.1.21 | | 0 GO:0005975,C | AT1G61820.1 |
| 46 | PTHR10353,P ⁻ | | 0 3.2.1.21 | | 0 GO:0005975,C | AT1G61820.1 |
| 47 | PTHR10353,P ⁻ | | 0 3.2.1.21 | | 0 GO:0005975,C | AT1G61820.1 |
| 48 | PTHR12304,P ⁻ KOG2938 | | | 0 | 0 | 0 AT5G18860.1 |
| 49 | PTHR12304,P ⁻ KOG2938 | | | 0 | 0 | 0 AT5G18860.1 |
| 50 | PTHR12304,P ⁻ KOG2938 | | | 0 | 0 | 0 AT5G18860.1 |
| 51 | PTHR12304,P ⁻ KOG2938 | | | 0 | 0 | 0 AT5G18860.1 |
| 52 | PTHR27000,P ⁻ KOG1187 | | 2.7.11.1 | | 0 GO:0005515,C | AT3G02130.1 |
| 53 | PTHR27000,P ⁻ KOG1187 | | 2.7.11.1 | | 0 GO:0005515,C | AT3G02130.1 |
| 54 | PTHR27000,P ⁻ KOG1187 | | 2.7.11.1 | | 0 GO:0005515,C | AT3G02130.1 |
| 55 | PTHR31983 | | 0 3.2.1.39 | K01180 | GO:0052862,C | AT5G15870.1 |
| 56 | PTHR32246,P ⁻ | | 0 | 0 | 0 GO:0005515 | AT5G23950.1 |
| 57 | PTHR23416,P ⁻ | | 0 2.3.1.129 | | 0 | 0 AT4G29540.2 |
| 58 | PTHR23416,P ⁻ | | 0 2.3.1.129 | | 0 | 0 AT4G29540.2 |
| 59 | PTHR23416,P ⁻ | | 0 2.3.1.129 | | 0 | 0 AT4G29540.2 |
| 60 | PTHR23416,P ⁻ | | 0 2.3.1.129 | | 0 | 0 AT4G29540.2 |
| 61 | PTHR23416,P ⁻ | | 0 2.3.1.129 | | 0 | 0 AT4G29540.2 |
| 62 | PTHR23416,P ⁻ | | 0 2.3.1.129 | | 0 | 0 AT4G29540.2 |
| 63 | PTHR23416,P ⁻ | | 0 2.3.1.129 | | 0 | 0 AT4G29540.2 |
| 64 | PTHR23416,P ⁻ | | 0 2.3.1.129 | | 0 | 0 AT4G29540.2 |
| 65 | PTHR23416,P ⁻ | | 0 2.3.1.129 | | 0 | 0 AT4G29540.2 |
| 66 | PTHR23416,P ⁻ | | 0 2.3.1.129 | | 0 | 0 AT4G29540.2 |
| 67 | PTHR23416,P ⁻ | | 0 2.3.1.129 | | 0 | 0 AT4G29540.2 |
| 68 | PTHR23416,P ⁻ | | 0 2.3.1.129 | | 0 | 0 AT4G29540.2 |
| 69 | PTHR23416,P ⁻ | | 0 2.3.1.129 | | 0 | 0 AT4G29540.2 |
| 70 | PTHR23416,P ⁻ | | 0 2.3.1.129 | | 0 | 0 AT4G29540.2 |
| 71 | PTHR11132,P ⁻ KOG1441 | | | 0 K15283 | | 0 AT5G17630.1 |

| | | | | | |
|----|--|----------------|-----------------|---------------------|--------------------|
| 1 | | | | | |
| 2 | PTHR11649,P ⁻ | 0 | 0 | 0 | 0 AT1G72960.1 |
| 3 | PTHR30314,P ⁻ | 0 3.6.5.6 | K03531 | GO:0003924 | AT5G55280.1 |
| 4 | PTHR13308,P ⁻ KOG2401 | | 0 | 0 | 0 AT5G58720.1 |
| 5 | | | | | |
| 6 | PTHR27007,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0006468,(| AT3G53380.1 |
| 7 | PTHR10641,P ⁻ KOG0048 | | 0 K09422 | | 0 AT4G01680.1 |
| 8 | PTHR32303,P ⁻ | 0 1.1.2.6 | | 0 | 0 0 |
| 9 | | | | | |
| 10 | PTHR36807,P ⁻ | 0 | 0 | 0 | 0 AT5G48830.1 |
| 11 | PTHR36807,P ⁻ | 0 | 0 | 0 | 0 AT5G48830.1 |
| 12 | PTHR12135,P ⁻ KOG2179 | | 0 K10838 | GO:0003677,(| AT5G16630.1 |
| 13 | | | | | |
| 14 | PTHR23086,P ⁻ | 0 2.7.1.68 | K00889 | GO:0046488,(| AT1G21980.1 |
| 15 | PTHR23086,P ⁻ | 0 2.7.1.68 | K00889 | GO:0046488,(| AT1G21980.1 |
| 16 | PTHR12135,P ⁻ KOG2179 | | 0 K10838 | GO:0003677,(| AT5G16630.1 |
| 17 | | | | | |
| 18 | PTHR10366,P⁻ KOG1371 | 5.1.3.6 | K08679 | GO:0055114,(| AT4G00110.1 |
| 19 | PTHR31415,P ⁻ | 0 | 0 | 0 | 0 AT4G01410.1 |
| 20 | PTHR12550,P ⁻ | 0 | 0 | 0 | 0 AT5G08230.1 |
| 21 | | | | | |
| 22 | PTHR31988 | 0 3.1.1.73 | | 0 | 0 AT4G34215.1 |
| 23 | PTHR10853 KOG2869 | | 0 K06965 | GO:0071025,(| AT4G27650.1 |
| 24 | PTHR22298,P ⁻ | 0 3.2.1.4 | | 0 GO:0005975,(| AT4G02290.1 |
| 25 | | | | | |
| 26 | PTHR21262,P ⁻ | 0 2.7.6.5 | | 0 GO:0015969 | AT4G02260.2 |
| 27 | PTHR23315,P ⁻ KOG2160,KOG | | 0 | 0 GO:0005515 | AT2G22125.1 |
| 28 | PTHR23315,P ⁻ KOG2160,KOG | | 0 | 0 GO:0005515 | AT2G22125.1 |
| 29 | | | | | |
| 30 | PTHR31321,P ⁻ | 0 3.1.1.11 | | 0 GO:0042545,(| AT5G47500.1 |
| 31 | PTHR27000,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0006468,(| AT4G36180.1 |
| 32 | PTHR37891,P ⁻ | 0 | 0 | 0 | 0 0 |
| 33 | PTHR37891,P ⁻ | 0 | 0 | 0 | 0 0 |
| 34 | | | | | |
| 35 | PTHR32133,P ⁻ | 0 | 0 | 0 GO:0005515 | AT1G30950.1 |
| 36 | PTHR22844,P ⁻ KOG0645 | 2.7.11.7 | | 0 GO:0005515 | AT1G24530.1 |
| 37 | PTHR27001,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0005515,(| AT1G66150.1 |
| 38 | | | | | |
| 39 | PTHR10353,P ⁻ | 0 3.2.1.21 | K01188 | GO:0005975,(| AT1G26560.1 |
| 40 | PTHR11101 KOG2493 | | 0 K14640 | GO:0016020,(| AT3G26570.2 |
| 41 | PTHR24298,P ⁻ KOG0156 | | 0 | 0 GO:0055114,(| AT1G11600.1 |
| 42 | | | | | |
| 43 | PTHR24326,P ⁻ | 0 | 0 | 0 GO:0043565,(| AT3G01470.1 |
| 44 | PTHR24326,P ⁻ | 0 | 0 | 0 GO:0043565,(| AT3G01470.1 |
| 45 | PTHR14140,P ⁻ | 0 2.3.1.48 | | 0 GO:0005634,(| AT3G01460.1 |
| 46 | | | | | |
| 47 | PTHR13007,P⁻ KOG2808 | | 0 K12817 | GO:0008380,(| AT1G03140.1 |
| 48 | PTHR17598 | 0 | 0 K03504 | GO:0006260,(| AT1G78650.1 |
| 49 | PTHR17598 | 0 | 0 K03504 | GO:0006260,(| AT1G78650.1 |
| 50 | | | | | |
| 51 | PTHR30523,P ⁻ | 0 4.1.1.31 | K01595 | GO:0015977,(| AT2G42600.2 |
| 52 | PTHR24015,P ⁻ | 0 | 0 | 0 | 0 AT1G52620.1 |
| 53 | PTHR32116,P ⁻ | 0 2.4.1.43 | K13648 | GO:0016757,(| AT3G58790.1 |
| 54 | | | | | |
| 55 | PTHR10593,P ⁻ | 0 | 0 | 0 | 0 AT3G50700.1 |
| 56 | PTHR10593,P ⁻ | 0 | 0 | 0 | 0 AT3G50700.1 |
| 57 | PTHR36351,P ⁻ | 0 | 0 | 0 | 0 0 |
| 58 | | | | | |
| 59 | PTHR10159,P ⁻ | 0 3.1.3.48 | | 0 | 0 AT3G55270.1 |
| 60 | PTHR10159,P ⁻ | 0 3.1.3.48 | | 0 | 0 AT3G55270.1 |
| | PTHR10159,P ⁻ | 0 3.1.3.48 | | 0 | 0 AT3G55270.1 |

| | | | | | |
|----|----------------------------------|---|-----------------------|---|--------------------------|
| 1 | | | | | |
| 2 | PTHR10159,P ⁻ | 0 | 3.1.3.48 | 0 | 0 AT3G55270.1 |
| 3 | PTHR10159,P ⁻ | 0 | 3.1.3.48 | 0 | 0 AT3G55270.1 |
| 4 | PTHR12655,P ⁻ KOG2763 | | 3.1.2.2,3.1.2.2K17361 | | 0 AT5G48370.1 |
| 5 | | | | | |
| 6 | PTHR20938,P ⁻ | 0 | 0 K13141 | | 0 AT3G08800.1 |
| 7 | PTHR20938,P ⁻ | 0 | 0 K13141 | | 0 AT3G08800.1 |
| 8 | PTHR21497,P ⁻ KOG1139 | | 3.4.17.20 | 0 | GO:0008270 AT5G02310.1 |
| 9 | | | | | |
| 10 | PTHR21497,P ⁻ KOG1139 | | 3.4.17.20 | 0 | GO:0008270 AT5G02310.1 |
| 11 | PTHR11850,P ⁻ KOG0773 | | 0 | 0 | GO:0006355,C AT5G02030.1 |
| 12 | PTHR21072 KOG2459 | | 0 K05291 | | GO:0042765,C AT3G07180.1 |
| 13 | | | | | |
| 14 | PTHR33021,P ⁻ | 0 | 0 | 0 | GO:0009055 AT1G08500.1 |
| 15 | PTHR19139 KOG0223 | | 0 K09873 | | GO:0016020,C AT2G25810.1 |
| 16 | PTHR22950,P ⁻ KOG1303 | | 0 | 0 | 0 AT1G77380.1 |
| 17 | | | | | |
| 18 | PTHR22950,P ⁻ KOG1303 | | 0 | 0 | 0 AT1G77380.1 |
| 19 | PTHR22950,P ⁻ KOG1303 | | 0 | 0 | 0 AT1G77380.1 |
| 20 | PTHR22950,P ⁻ KOG1303 | | 0 | 0 | 0 AT1G77380.1 |
| 21 | | | | | |
| 22 | 0 | 0 | 0 | 0 | 0 0 |
| 23 | 0 | 0 | 0 | 0 | 0 0 |
| 24 | PTHR27002,P ⁻ KOG1187 | | 2.7.11.1 | 0 | GO:0006468,C AT5G60900.1 |
| 25 | | | | | |
| 26 | PTHR12537,P ⁻ | 0 | 0 K17943 | | GO:0003723 AT2G29190.2 |
| 27 | PTHR27002,P ⁻ | 0 | 2.7.11.1 | 0 | GO:0006468,C AT1G67520.1 |
| 28 | PTHR27002,P ⁻ | 0 | 2.7.11.1 | 0 | GO:0006468,C AT1G67520.1 |
| 29 | | | | | |
| 30 | | | | | |
| 31 | | | | | |
| 32 | | | | | |
| 33 | | | | | |
| 34 | | | | | |
| 35 | | | | | |
| 36 | | | | | |
| 37 | | | | | |
| 38 | | | | | |
| 39 | | | | | |
| 40 | | | | | |
| 41 | | | | | |
| 42 | | | | | |
| 43 | | | | | |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| arabi-symbol | arabi-defline | ID |
|--------------------|--|----------------|
| | 0 Calcium-dependent lipid-binding (CaLB domain) family | Phvul.004G11 |
| ATNEK6,IBO1,NEK6 | NIMA (never in mitosis, gene A)-related 6 | Phvul.005G12 |
| ATNEK6,IBO1,NEK6 | NIMA (never in mitosis, gene A)-related 6 | Phvul.005G12 |
| | 0 heat shock protein 70 (Hsp 70) family protein | Phvul.006G00 |
| | 0 | 0 Phvul.007G02 |
| | 0 O-Glycosyl hydrolases family 17 protein | Phvul.008G27 |
| | 0 Calcium-dependent lipid-binding (CaLB domain) family | Phvul.001G24 |
| | 0 Pectin lyase-like superfamily protein | Phvul.003G22 |
| ARA12 | Subtilase family protein | Phvul.003G23 |
| ATMYC2,JAI1,JIN1,M | Basic helix-loop-helix (bHLH) DNA-binding family protei | Phvul.003G28 |
| ATSERK1,SERK1 | somatic embryogenesis receptor-like kinase 1 | Phvul.004G08 |
| ATSERK1,SERK1 | somatic embryogenesis receptor-like kinase 1 | Phvul.004G08 |
| ATCRR3,CCR3 | CRINKLY4 related 3 | Phvul.006G06 |
| ATCPSF30,CPSF30 | cleavage and polyadenylation specificity factor 30 | Phvul.006G13 |
| | 0 | 0 Phvul.007G26 |
| ATCNGC2,CNGC2,DN | Cyclic nucleotide-regulated ion channel family protein | Phvul.008G03 |
| | 0 VQ motif-containing protein | Phvul.008G29 |
| | 0 Predicted AT-hook DNA-binding family protein | Phvul.009G14 |
| ATEXO70G1,EXO70G | exocyst subunit exo70 family protein G1 | Phvul.001G02 |
| | 0 Protein kinase superfamily protein | Phvul.001G07 |
| RKF3 | receptor-like kinase in in flowers 3 | Phvul.001G14 |
| RKF3 | receptor-like kinase in in flowers 3 | Phvul.001G14 |
| RKF3 | receptor-like kinase in in flowers 3 | Phvul.001G14 |
| | 0 AT hook motif DNA-binding family protein | Phvul.002G00 |
| | 0 alpha/beta-Hydrolases superfamily protein | Phvul.002G05 |
| FAB1C | FORMS APLOID AND BINUCLEATE CELLS 1C | Phvul.002G09 |
| FAB1C | FORMS APLOID AND BINUCLEATE CELLS 1C | Phvul.002G09 |
| ATPAD4,PAD4 | alpha/beta-Hydrolases superfamily protein | Phvul.002G27 |
| SCD1 | stomatal cytokinesis defective / SCD1 protein (SCD1) | Phvul.002G31 |
| BGLU46 | beta glucosidase 46 | Phvul.003G07 |
| BGLU46 | beta glucosidase 46 | Phvul.003G07 |
| | 0 inosine-uridine preferring nucleoside hydrolase family | Phvul.003G09 |
| | 0 inosine-uridine preferring nucleoside hydrolase family | Phvul.003G09 |
| | 0 inosine-uridine preferring nucleoside hydrolase family | Phvul.003G09 |
| RPK2,TOAD2 | receptor-like protein kinase 2 | Phvul.004G03 |
| RPK2,TOAD2 | receptor-like protein kinase 2 | Phvul.004G03 |
| | 0 glycosyl hydrolase family 81 protein | Phvul.004G04 |
| | 0 Calcium-dependent lipid-binding (CaLB domain) family | Phvul.004G11 |
| | 0 bacterial transferase hexapeptide repeat-containing pr | Phvul.004G17 |
| | 0 bacterial transferase hexapeptide repeat-containing pr | Phvul.004G17 |
| | 0 bacterial transferase hexapeptide repeat-containing pr | Phvul.004G17 |
| | 0 bacterial transferase hexapeptide repeat-containing pr | Phvul.004G17 |
| | 0 bacterial transferase hexapeptide repeat-containing pr | Phvul.004G17 |
| | 0 bacterial transferase hexapeptide repeat-containing pr | Phvul.004G17 |
| | 0 Nucleotide/sugar transporter family protein | Phvul.005G02 |

| | | | |
|----|---------------------|--|---------------------|
| 1 | | | |
| 2 | | 0 Root hair defective 3 GTP-binding protein (RHD3) | Phvul.005G15 |
| 3 | ATFTSZ1-1,CPFTSZ,FT | homolog of bacterial cytokinesis Z-ring protein FTSZ 1- | Phvul.006G04 |
| 4 | | 0 smr (Small MutS Related) domain-containing protein | Phvul.006G06 |
| 5 | | 0 Concanavalin A-like lectin protein kinase family protein | Phvul.006G08 |
| 6 | | | |
| 7 | AtMYB55,MYB55 | myb domain protein 55 | Phvul.007G20 |
| 8 | | 0 | 0 Phvul.008G04 |
| 9 | | 0 | 0 Phvul.008G12 |
| 10 | | 0 | 0 Phvul.008G12 |
| 11 | | | |
| 12 | ATRAD4,RAD4 | DNA repair protein Rad4 family | Phvul.008G23 |
| 13 | | | |
| 14 | ATPIP5K1,ATPIP1K,PI | phosphatidylinositol-4-phosphate 5-kinase 1 | Phvul.009G15 |
| 15 | ATPIP5K1,ATPIP1K,PI | phosphatidylinositol-4-phosphate 5-kinase 1 | Phvul.009G15 |
| 16 | ATRAD4,RAD4 | DNA repair protein Rad4 family | Phvul.010G02 |
| 17 | | | |
| 18 | GAE3 | UDP-D-glucuronate 4-epimerase 3 | Phvul.010G08 |
| 19 | | 0 Late embryogenesis abundant (LEA) hydroxyproline-ric | Phvul.010G11 |
| 20 | | 0 Tudor/PWWP/MBT domain-containing protein | Phvul.011G02 |
| 21 | | 0 Domain of unknown function (DUF303) | Phvul.001G02 |
| 22 | | | |
| 23 | PEL1 | Eukaryotic release factor 1 (eRF1) family protein | Phvul.001G18 |
| 24 | AtGH9B13,GH9B13 | glycosyl hydrolase 9B13 | Phvul.001G20 |
| 25 | | | |
| 26 | AT-RSH1,ATRSH1,RSR | RELA/SPOT homolog 1 | Phvul.001G20 |
| 27 | CSI1 | binding | Phvul.001G25 |
| 28 | CSI1 | binding | Phvul.001G25 |
| 29 | | 0 Pectin lyase-like superfamily protein | Phvul.002G06 |
| 30 | | 0 Leucine-rich receptor-like protein kinase family protein | Phvul.002G11 |
| 31 | | 0 | 0 0 |
| 32 | | 0 | 0 0 |
| 33 | | 0 | 0 0 |
| 34 | | | |
| 35 | UFO | F-box family protein | Phvul.002G18 |
| 36 | | 0 Transducin/WD40 repeat-like superfamily protein | Phvul.002G25 |
| 37 | | | |
| 38 | TMK1 | transmembrane kinase 1 | Phvul.002G32 |
| 39 | BGLU40 | beta glucosidase 40 | Phvul.003G04 |
| 40 | ORF02,PHT2;1 | phosphate transporter 2;1 | Phvul.003G06 |
| 41 | CYP77B1 | cytochrome P450, family 77, subfamily B, polypeptide | Phvul.003G07 |
| 42 | | | |
| 43 | ATHB-1,ATHB1,HAT5 | homeobox 1 | Phvul.003G19 |
| 44 | ATHB-1,ATHB1,HAT5 | homeobox 1 | Phvul.003G19 |
| 45 | ATMBD9,MBD9 | methyl-CPG-binding domain 9 | Phvul.004G01 |
| 46 | | | |
| 47 | | 0 splicing factor Prp18 family protein | Phvul.005G03 |
| 48 | POLD3 | DNA-directed DNA polymerases | Phvul.005G08 |
| 49 | POLD3 | DNA-directed DNA polymerases | Phvul.005G08 |
| 50 | | | |
| 51 | ATPPC2,PPC2 | phosphoenolpyruvate carboxylase 2 | Phvul.005G09 |
| 52 | | 0 Pentatricopeptide repeat (PPR) superfamily protein | Phvul.005G17 |
| 53 | | | |
| 54 | GAUT15 | galacturonosyltransferase 15 | Phvul.006G03 |
| 55 | AtIDD2,IDD2 | indeterminate(ID)-domain 2 | Phvul.007G19 |
| 56 | AtIDD2,IDD2 | indeterminate(ID)-domain 2 | Phvul.007G19 |
| 57 | | 0 | 0 Phvul.007G26 |
| 58 | | | |
| 59 | ATMKP1,MKP1 | mitogen-activated protein kinase phosphatase 1 | Phvul.008G01 |
| 60 | ATMKP1,MKP1 | mitogen-activated protein kinase phosphatase 1 | Phvul.008G01 |
| | ATMKP1,MKP1 | mitogen-activated protein kinase phosphatase 1 | Phvul.008G01 |

| | | | |
|----|---------------------|---|--------------|
| 1 | | | |
| 2 | ATMKP1,MKP1 | mitogen-activated protein kinase phosphatase 1 | Phvul.008G01 |
| 3 | ATMKP1,MKP1 | mitogen-activated protein kinase phosphatase 1 | Phvul.008G01 |
| 4 | | 0 Thioesterase/thiol ester dehydrase-isomerase superfar | Phvul.008G05 |
| 5 | | 0 ARM repeat superfamily protein | Phvul.008G09 |
| 6 | | 0 ARM repeat superfamily protein | Phvul.008G09 |
| 7 | | 0 ARM repeat superfamily protein | Phvul.008G09 |
| 8 | PRT6 | proteolysis 6 | Phvul.008G10 |
| 9 | PRT6 | proteolysis 6 | Phvul.008G10 |
| 10 | PRT6 | proteolysis 6 | Phvul.008G10 |
| 11 | BLH9,BLR,HB-6,LSN,P | POX (plant homeobox) family protein | Phvul.008G11 |
| 12 | | 0 GPI transamidase component PIG-S-related | Phvul.008G13 |
| 13 | AtENODL18,ENODL18 | early nodulin-like protein 18 | Phvul.008G20 |
| 14 | TIP4;1 | tonoplast intrinsic protein 4;1 | Phvul.009G10 |
| 15 | AAP3,ATAAP3 | amino acid permease 3 | Phvul.009G12 |
| 16 | AAP3,ATAAP3 | amino acid permease 3 | Phvul.009G12 |
| 17 | AAP3,ATAAP3 | amino acid permease 3 | Phvul.009G12 |
| 18 | AAP3,ATAAP3 | amino acid permease 3 | Phvul.009G12 |
| 19 | AAP3,ATAAP3 | amino acid permease 3 | Phvul.009G12 |
| 20 | AAP3,ATAAP3 | amino acid permease 3 | Phvul.009G12 |
| 21 | | | |
| 22 | | 0 | 0 0 |
| 23 | | 0 | 0 0 |
| 24 | RLK1 | receptor-like protein kinase 1 | Phvul.010G03 |
| 25 | APUM2,PUM2 | pumilio 2 | Phvul.011G06 |
| 26 | | 0 lectin protein kinase family protein | Phvul.011G17 |
| 27 | | 0 lectin protein kinase family protein | Phvul.011G17 |
| 28 | | | |
| 29 | | | |
| 30 | | | |
| 31 | | | |
| 32 | | | |
| 33 | | | |
| 34 | | | |
| 35 | | | |
| 36 | | | |
| 37 | | | |
| 38 | | | |
| 39 | | | |
| 40 | | | |
| 41 | | | |
| 42 | | | |
| 43 | | | |
| 44 | | | |
| 45 | | | |
| 46 | | | |
| 47 | | | |
| 48 | | | |
| 49 | | | |
| 50 | | | |
| 51 | | | |
| 52 | | | |
| 53 | | | |
| 54 | | | |
| 55 | | | |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

| Annot_defline | IDENTIFIER | NAME | DESCRIPTION |
|---------------|----------------|--------------|---|
| | PF00168 - C2 | Phvul.004G11 | not assigned.r no hits & (original description: pacid=37162836 transcri |
| | PTHR24362:SI | Phvul.005G12 | Protein modif protein kinase (NEK) (original description: pacid=371525 |
| | PTHR24362:SI | Phvul.005G12 | Protein modif protein kinase (NEK) (original description: pacid=371525 |
| | K09486 - hyc | Phvul.006G00 | Protein home nucleotide exchange factor (Grp170) (original descriptio |
| | PF01814 - Her | Phvul.007G02 | not assigned.r no hits & (original description: pacid=37164059 transcri |
| | PTHR32227:SI | Phvul.008G27 | Enzyme classii Glucan endo-1,3-beta-glucosidase 12 OS=Arabidopsis th |
| | PTHR32246:SI | Phvul.001G24 | not assigned.r no hits & (original description: pacid=37170768 transcri |
| | PTHR31321:SI | Phvul.003G22 | Cell wall orgar pectin methylesterase (original description: pacid=37146 |
| | PTHR10795://I | Phvul.003G23 | Protein home protease (SBT1) (original description: pacid=37147285 tr |
| | K13422 - tran | Phvul.003G28 | RNA biosynthi transcription factor (bHLH) (original description: pacid=3 |
| | K13418 - som | Phvul.004G08 | Protein modif protein kinase (LRR-II) (original description: pacid=37161 |
| | K13418 - som | Phvul.004G08 | Protein modif protein kinase (LRR-II) (original description: pacid=37161 |
| | PF00069://PF1 | Phvul.006G06 | Protein modif protein kinase (Crinkly-like) (original description: pacid= |
| | PTHR12357:SI | Phvul.006G13 | RNA processir component CPSF30/Yth1 of Cleavage and Polyadenylatic |
| | PTHR36351:SI | Phvul.007G26 | not assigned.r no hits & (original description: pacid=37165888 transcri |
| | PTHR10217:SI | Phvul.008G03 | External stimu temperature sensor protein (CNGC2) (original descriptio |
| | PTHR33179:SI | Phvul.008G29 | not assigned.r no hits & (original description: pacid=37160918 transcri |
| | PTHR31100:SI | Phvul.009G14 | not assigned.r (original description: pacid=37150218 transcript=Phvul.(|
| | PTHR12542://I | Phvul.001G02 | Vesicle trafficl component EXO70 of Exocyst complex (original descripti |
| | 2.7.11.1 - Non | Phvul.001G07 | Protein modif protein kinase (RKF3) (original description: pacid=37169 |
| | PTHR27006:SI | Phvul.001G14 | Protein modif protein kinase (RKF3) (original description: pacid=37168 |
| | PTHR27006:SI | Phvul.001G14 | Enzyme classii Probable LRR receptor-like serine/threonine-protein kin |
| | PTHR27006:SI | Phvul.001G14 | Enzyme classii Probable LRR receptor-like serine/threonine-protein kin |
| | PTHR31500:SI | Phvul.002G00 | not assigned.r (original description: pacid=37175392 transcript=Phvul.(|
| | 3.1.1.3//3.1.1 | Phvul.002G05 | not assigned.r no hits & (original description: pacid=37175506 transcri |
| | PTHR11353:SI | Phvul.002G09 | Multi-process phosphatidylinositol 3-phosphate 5-kinase (FAB1) (origir |
| | PTHR11353:SI | Phvul.002G09 | Multi-process phosphatidylinositol 3-phosphate 5-kinase (FAB1) (origir |
| | PTHR21493://I | Phvul.002G27 | External stimu PAD4 effector-triggered immunity co-regulator (original |
| | PTHR22844:SI | Phvul.002G31 | Vesicle trafficl SCD1 component of post-Golgi trafficking SCD complex (|
| | PTHR10353:SI | Phvul.003G07 | Enzyme classii Beta-glucosidase 46 OS=Arabidopsis thaliana (sp o8069 |
| | PTHR10353:SI | Phvul.003G07 | Enzyme classii Beta-glucosidase 46 OS=Arabidopsis thaliana (sp o8069 |
| | PTHR12304:SI | Phvul.003G09 | Nucleotide mε nucleoside hydrolase (original description: pacid=37144 |
| | PTHR12304:SI | Phvul.003G09 | Nucleotide mε nucleoside hydrolase (original description: pacid=37144 |
| | PTHR12304:SI | Phvul.003G09 | Nucleotide mε nucleoside hydrolase (original description: pacid=37144 |
| | PTHR27000:SI | Phvul.004G03 | Protein modif protein kinase (LRR-XV) (original description: pacid=371 |
| | PTHR27000:SI | Phvul.004G03 | Protein modif protein kinase (LRR-XV) (original description: pacid=371 |
| | K01180 - end | Phvul.004G04 | not assigned.r no hits & (original description: pacid=37163654 transcri |
| | PF00168 - C2 | Phvul.004G11 | not assigned.r no hits & (original description: pacid=37163692 transcri |
| | 2.3.1.129 - Ac | Phvul.004G17 | Lipid metaboli UDP-N-acetylglucosamine O-acyltransferase (LpxA) (orig |
| | 2.3.1.129 - Ac | Phvul.004G17 | Lipid metaboli UDP-N-acetylglucosamine O-acyltransferase (LpxA) (orig |
| | 2.3.1.129 - Ac | Phvul.004G17 | Lipid metaboli UDP-N-acetylglucosamine O-acyltransferase (LpxA) (orig |
| | 2.3.1.129 - Ac | Phvul.004G17 | Lipid metaboli UDP-N-acetylglucosamine O-acyltransferase (LpxA) (orig |
| | 2.3.1.129 - Ac | Phvul.004G17 | Lipid metaboli UDP-N-acetylglucosamine O-acyltransferase (LpxA) (orig |
| | 2.3.1.129 - Ac | Phvul.004G17 | Lipid metaboli UDP-N-acetylglucosamine O-acyltransferase (LpxA) (orig |
| | PTHR11132:SI | Phvul.005G02 | Solute transpc phosphometabolite transporter (TPT PPT GPT XPT) (ori |

1 PTHR11649:SlPhvul.005G15Cell cycle orgaER tubulae formation factor (RHD3/RL) (original descript
 2 PTHR30314:SlPhvul.006G04Cell cycle orgacomponent FtsZ1 of plastid division FtsZ prokaryotic-tub
 3 KOG2401 - PrPhvul.006G06not assigned.ε (original description: pacid=37174192 transcript=Phvul.
 4 PTHR27007:SlPhvul.006G08Protein modif protein kinase (L-lectin) (original description: pacid=3717
 5 PTHR10641:SlPhvul.007G20RNA biosynthtranscription factor (MYB) (original description: pacid=37
 6 1.1.2.6 - PolyvPhvul.008G04not assigned.r no hits & (original description: pacid=37159669 transcri
 7 PF12452 - ProPhvul.008G12not assigned.r no hits & (original description: pacid=37158036 transcri
 8 PF12452 - ProPhvul.008G12not assigned.r no hits & (original description: pacid=37158036 transcri
 9 K10838 - xeroPhvul.008G23DNA damage DNA repair protein (XPC) (original description: pacid=37:
 10 PTHR23086:SlPhvul.009G15Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (origi
 11 PTHR23086:SlPhvul.009G15Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (origi
 12 K10838 - xeroPhvul.010G02DNA damage DNA repair protein (XPC) (original description: pacid=37:
 13 **PTHR10366:SlPhvul.010G08Carbohydrate UDP-D-glucuronic acid 4-epimerase (original description:**
 14 PF03168 - LatPhvul.010G11not assigned.ε (original description: pacid=37143932 transcript=Phvul.
 15 PTHR12550:SlPhvul.011G02RNA biosynthtranscription factor (HUA2) (original description: pacid=ε
 16 3.1.1.73 - FeruPhvul.001G02not assigned.ε (original description: pacid=37168114 transcript=Phvul.
 17 K06965 - protPhvul.001G18Protein biosyr component DOM34 of DOM34-HBS1 aberrant mRNA del
 18 PTHR22298:SlPhvul.001G20not assigned.ε (original description: pacid=37167724 transcript=Phvul.
 19 PTHR21262:SlPhvul.001G20not assigned.ε (original description: pacid=37168990 transcript=Phvul.
 20 KOG2160//KCPPhvul.001G25Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (origi
 21 KOG2160//KCPPhvul.001G25Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (origi
 22 PTHR31321:SlPhvul.002G06Cell wall orgar pectin methylesterase (original description: pacid=37174
 23 PTHR27000:SlPhvul.002G11Protein modif protein kinase (LRR-VII) (original description: pacid=3717
 24 O Phvul.002G13not assigned.r no hits & (original description: pacid=37178726 transcri
 25 O Phvul.002G13not assigned.r no hits & (original description: pacid=37178726 transcri
 26 PTHR32133:SlPhvul.002G18Protein home component UFO of SCF E3 ubiquitin ligase complex (orig
 27 PTHR22844:SlPhvul.002G25not assigned.ε (original description: pacid=37174658 transcript=Phvul.
 28 PTHR27001:SlPhvul.002G32Protein modif protein kinase (LRR-IX) (original description: pacid=3717:
 29 PTHR10353:SlPhvul.003G04Enzyme classiiBeta-glucosidase 40 OS=Arabidopsis thaliana (sp|q9fze0
 30 K14640 - soluiPhvul.003G06Solute transpc phosphate transporter (PHT2) (original description: pacid
 31 PTHR24298:SlPhvul.003G07Enzyme classiiCytochrome P450 77A1 (Fragment) OS=Solanum melong
 32 KOG0483 - TrPhvul.003G19RNA biosynthtranscription factor (HD-ZIP I/II) (original description: pac
 33 KOG0483 - TrPhvul.003G19RNA biosynthtranscription factor (HD-ZIP I/II) (original description: pac
 34 PTHR14140:SlPhvul.004G01not assigned.ε (original description: pacid=37162939 transcript=Phvul.
 35 **K12817 - pre-iPhvul.005G03not assigned.r no hits & (original description: pacid=37152518 transcri**
 36 K03504 - DNAPhvul.005G08Cell cycle orgacomponent POLD3 of DNA polymerase delta complex (oi
 37 K03504 - DNAPhvul.005G08Cell cycle orgacomponent POLD3 of DNA polymerase delta complex (oi
 38 K01595 - phosPhvul.005G09PhotosynthesiPEP carboxylase (original description: pacid=37154500 tr
 39 PF13041 - PPFPhvul.005G17not assigned.ε (original description: pacid=37152686 transcript=Phvul.
 40 PTHR32116:SlPhvul.006G03not assigned.ε (original description: pacid=37172111 transcript=Phvul.
 41 PTHR10593:SlPhvul.007G19RNA biosynthC2H2 zinc finger transcription factor (original description
 42 PTHR10593:SlPhvul.007G19RNA biosynthC2H2 zinc finger transcription factor (original description
 43 PTHR36351:SlPhvul.007G26not assigned.r no hits & (original description: pacid=37165888 transcri
 44 PTHR10159:SlPhvul.008G01not assigned.ε (original description: pacid=37161122 transcript=Phvul.
 45 PTHR10159:SlPhvul.008G01not assigned.ε (original description: pacid=37161122 transcript=Phvul.
 46 PTHR10159:SlPhvul.008G01not assigned.ε (original description: pacid=37161122 transcript=Phvul.

1 PTHR10159:SlPhvul.008G01 not assigned.ε (original description: pacid=37161122 transcript=Phvul.0
2 PTHR10159:SlPhvul.008G01 not assigned.ε (original description: pacid=37161122 transcript=Phvul.0
3 3.1.2.2//3.1.2 Phvul.008G05 not assigned.r no hits & (original description: pacid=37160794 transcri
4 K13141 - inteḡPhvul.008G09 Protein transi SIEL plasmodesmata intercellular trafficking regulator pr
5 K13141 - inteḡPhvul.008G09 Protein transi SIEL plasmodesmata intercellular trafficking regulator pr
6 3.4.17.20 - CaPhvul.008G10 Protein home type-I-residues E3 ubiquitin ligase (PRT6) (original descri
7 3.4.17.20 - CaPhvul.008G10 Protein home type-I-residues E3 ubiquitin ligase (PRT6) (original descri
8 PTHR11850:SlPhvul.008G11 RNA biosynth transcription factor (BEL) (original description: pacid=371
9 K05291 - phosPhvul.008G13 Protein modif component PIG-S of GPI transamidase complex (original
10 PTHR33021:SlPhvul.008G20 not assigned.r no hits & (original description: pacid=37161432 transcri
11 K09873 - aquaPhvul.009G10 Solute transp tonoplast intrinsic protein (TIP) (original description: pac
12 PTHR22950:SlPhvul.009G12 Solute transp amino acid transporter (AAP) (original description: pacid
13 PTHR22950:SlPhvul.009G12 Solute transp amino acid transporter (AAP) (original description: pacid
14 PTHR22950:SlPhvul.009G12 Solute transp amino acid transporter (AAP) (original description: pacid
15 PTHR22950:SlPhvul.009G12 Solute transp amino acid transporter (AAP) (original description: pacid
16 0 Phvul.009G25 not assigned.r no hits & (original description: pacid=37149126 transcri
17 0 Phvul.009G25 not assigned.r no hits & (original description: pacid=37149126 transcri
18 PF00069//PF0Phvul.010G03 Enzyme classii G-type lectin S-receptor-like serine/threonine-protein kin
19 PTHR12537:SlPhvul.011G06 not assigned.ε (original description: pacid=37156482 transcript=Phvul.0
20 PF01453//PF0Phvul.011G17 Enzyme classii G-type lectin S-receptor-like serine/threonine-protein kin
21 PF01453//PF0Phvul.011G17 Enzyme classii G-type lectin S-receptor-like serine/threonine-protein kin
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

pt=Phvul.004G110400.1 locus=Phvul.004G110400 ID=Phvul.004G110400.1.v2.1 annot-version=v2.1
 59 transcript=Phvul.005G120700.3 locus=Phvul.005G120700 ID=Phvul.005G120700.3.v2.1 annot-v
 59 transcript=Phvul.005G120700.3 locus=Phvul.005G120700 ID=Phvul.005G120700.3.v2.1 annot-v
 n: pacid=37171820 transcript=Phvul.006G001600.1 locus=Phvul.006G001600 ID=Phvul.006G001600
 pt=Phvul.007G023000.1 locus=Phvul.007G023000 ID=Phvul.007G023000.1.v2.1 annot-version=v2.1
 aliana (sp|q8vye5|e1312_arath : 362.0) & Enzyme classification.EC_3 hydrolases.EC_3.2 glycosylase
 pt=Phvul.001G240600.1 locus=Phvul.001G240600 ID=Phvul.001G240600.1.v2.1 annot-version=v2.1
 5318 transcript=Phvul.003G220500.1 locus=Phvul.003G220500 ID=Phvul.003G220500.1.v2.1 annot-
 ranscript=Phvul.003G237300.1 locus=Phvul.003G237300 ID=Phvul.003G237300.1.v2.1 annot-versio
 37147468 transcript=Phvul.003G285700.1 locus=Phvul.003G285700 ID=Phvul.003G285700.1.v2.1 ar
 L848 transcript=Phvul.004G086300.2 locus=Phvul.004G086300 ID=Phvul.004G086300.2.v2.1 annot-
 L848 transcript=Phvul.004G086300.2 locus=Phvul.004G086300 ID=Phvul.004G086300.2.v2.1 annot-
 37173758 transcript=Phvul.006G068400.1 locus=Phvul.006G068400 ID=Phvul.006G068400.1.v2.1 a
 on Specificity Factor (CPSF) complex (original description: pacid=37173223 transcript=Phvul.006G13
 pt=Phvul.007G268300.1 locus=Phvul.007G268300 ID=Phvul.007G268300.1.v2.1 annot-version=v2.1
 n: pacid=37160007 transcript=Phvul.008G036200.1 locus=Phvul.008G036200 ID=Phvul.008G03620
 pt=Phvul.008G290700.1 locus=Phvul.008G290700 ID=Phvul.008G290700.1.v2.1 annot-version=v2.1
 009G144300.1 locus=Phvul.009G144300 ID=Phvul.009G144300.1.v2.1 annot-version=v2.1) & AT-hc
 ion: pacid=37170939 transcript=Phvul.001G028400.1 locus=Phvul.001G028400 ID=Phvul.001G0284
 865 transcript=Phvul.001G071200.1 locus=Phvul.001G071200 ID=Phvul.001G071200.1.v2.1 annot-
 019 transcript=Phvul.001G146900.1 locus=Phvul.001G146900 ID=Phvul.001G146900.1.v2.1 annot-
 ase RKF3 OS=Arabidopsis thaliana (sp|p93050|rkf3_arath : 454.0) & Enzyme classification.EC_2 trar
 ase RKF3 OS=Arabidopsis thaliana (sp|p93050|rkf3_arath : 454.0) & Enzyme classification.EC_2 trar
 002G006700.1 locus=Phvul.002G006700 ID=Phvul.002G006700.1.v2.1 annot-version=v2.1) & AT-hc
 pt=Phvul.002G059000.1 locus=Phvul.002G059000 ID=Phvul.002G059000.1.v2.1 annot-version=v2.1
 al description: pacid=37176675 transcript=Phvul.002G092900.2 locus=Phvul.002G092900 ID=Phvu
 al description: pacid=37176675 transcript=Phvul.002G092900.2 locus=Phvul.002G092900 ID=Phvu
 description: pacid=37176037 transcript=Phvul.002G274500.1 locus=Phvul.002G274500 ID=Phvul.00
 original description: pacid=37174440 transcript=Phvul.002G315300.1 locus=Phvul.002G315300 ID=
 0|bgl46_arath : 462.0) & Enzyme classification.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2 : 272.9) (c
 0|bgl46_arath : 462.0) & Enzyme classification.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2 : 272.9) (c
 950 transcript=Phvul.003G099100.3 locus=Phvul.003G099100 ID=Phvul.003G099100.3.v2.1 annot-
 950 transcript=Phvul.003G099100.3 locus=Phvul.003G099100 ID=Phvul.003G099100.3.v2.1 annot-
 950 transcript=Phvul.003G099100.3 locus=Phvul.003G099100 ID=Phvul.003G099100.3.v2.1 annot-
 53248 transcript=Phvul.004G037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 anno
 53248 transcript=Phvul.004G037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 anno
 pt=Phvul.004G049200.1 locus=Phvul.004G049200 ID=Phvul.004G049200.1.v2.1 annot-version=v2.1
 pt=Phvul.004G110200.2 locus=Phvul.004G110200 ID=Phvul.004G110200.2.v2.1 annot-version=v2.1
 inal description: pacid=37162324 transcript=Phvul.004G171500.6 locus=Phvul.004G171500 ID=Phv
 inal description: pacid=37162324 transcript=Phvul.004G171500.6 locus=Phvul.004G171500 ID=Phv
 inal description: pacid=37162324 transcript=Phvul.004G171500.6 locus=Phvul.004G171500 ID=Phv
 inal description: pacid=37162324 transcript=Phvul.004G171500.6 locus=Phvul.004G171500 ID=Phv
 inal description: pacid=37162324 transcript=Phvul.004G171500.6 locus=Phvul.004G171500 ID=Phv
 inal description: pacid=37162324 transcript=Phvul.004G171500.6 locus=Phvul.004G171500 ID=Phv
 inal description: pacid=37153709 transcript=Phvul.005G022300.1 locus=Phvul.005G022300 ID=Ph

1
 2 :ion: pacid=37154537 transcript=Phvul.005G159600.1 locus=Phvul.005G159600 ID=Phvul.005G1596
 3 ulin filaments (original description: pacid=37171983 transcript=Phvul.006G049100.1 locus=Phvul.006
 4 006G068100.1 locus=Phvul.006G068100 ID=Phvul.006G068100.1.v2.1 annot-version=v2.1) & SMR (G
 5 73870 transcript=Phvul.006G087700.1 locus=Phvul.006G087700 ID=Phvul.006G087700.1.v2.1 anno
 6 7166531 transcript=Phvul.007G208400.1 locus=Phvul.007G208400 ID=Phvul.007G208400.1.v2.1 an
 7 pt=Phvul.008G042900.1 locus=Phvul.008G042900 ID=Phvul.008G042900.1.v2.1 annot-version=v2.1
 8
 9 pt=Phvul.008G124000.2 locus=Phvul.008G124000 ID=Phvul.008G124000.2.v2.1 annot-version=v2.1
 10
 11 pt=Phvul.008G124000.2 locus=Phvul.008G124000 ID=Phvul.008G124000.2.v2.1 annot-version=v2.1
 12
 13 160521 transcript=Phvul.008G233100.1 locus=Phvul.008G233100 ID=Phvul.008G233100.1.v2.1 ann
 14 inal description: pacid=37149983 transcript=Phvul.009G157200.2 locus=Phvul.009G157200 ID=Phv
 15 inal description: pacid=37149983 transcript=Phvul.009G157200.2 locus=Phvul.009G157200 ID=Phv
 16 142287 transcript=Phvul.010G024866.1 locus=Phvul.010G024866 ID=Phvul.010G024866.1.v2.1 ann
 17
 18 : pacid=37143837 transcript=Phvul.010G082300.1 locus=Phvul.010G082300 ID=Phvul.010G082300
 19 010G119800.1 locus=Phvul.010G119800 ID=Phvul.010G119800.1.v2.1 annot-version=v2.1) & NDR1
 20 37157305 transcript=Phvul.011G029450.1 locus=Phvul.011G029450 ID=Phvul.011G029450.1.v2.1 a
 21
 22 001G025101.1 locus=Phvul.001G025101 ID=Phvul.001G025101.1.v2.1 annot-version=v2.1) & Proba
 23
 24 tection complex (original description: pacid=37169227 transcript=Phvul.001G183700.1 locus=Phvul
 25 001G209500.2 locus=Phvul.001G209500 ID=Phvul.001G209500.2.v2.1 annot-version=v2.1) & Endo
 26 001G209900.2 locus=Phvul.001G209900 ID=Phvul.001G209900.2.v2.1 annot-version=v2.1) & Puta
 27
 28 inal description: pacid=37170740 transcript=Phvul.001G250100.2 locus=Phvul.001G250100 ID=Phv
 29 inal description: pacid=37170740 transcript=Phvul.001G250100.2 locus=Phvul.001G250100 ID=Phv
 30 4340 transcript=Phvul.002G063100.1 locus=Phvul.002G063100 ID=Phvul.002G063100.1.v2.1 annot-
 31 76115 transcript=Phvul.002G111100.1 locus=Phvul.002G111100 ID=Phvul.002G111100.1.v2.1 anno
 32
 33 pt=Phvul.002G132600.2 locus=Phvul.002G132600 ID=Phvul.002G132600.2.v2.1 annot-version=v2.1
 34
 35 pt=Phvul.002G132600.2 locus=Phvul.002G132600 ID=Phvul.002G132600.2.v2.1 annot-version=v2.1
 36
 37 inal description: pacid=37174959 transcript=Phvul.002G188300.1 locus=Phvul.002G188300 ID=Phv
 38 002G252700.1 locus=Phvul.002G252700 ID=Phvul.002G252700.1.v2.1 annot-version=v2.1) & Prote
 39 5507 transcript=Phvul.002G324600.1 locus=Phvul.002G324600 ID=Phvul.002G324600.1.v2.1 annot
 40
 41 |bgl40_arath : 657.0) & Enzyme classification.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2 : 409.7) (c
 42 d=37146149 transcript=Phvul.003G064900.1 locus=Phvul.003G064900 ID=Phvul.003G064900.1.v2.
 43
 44 gena (sp|p37123|c77a1_solme : 391.0) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxid
 45 cid=37145774 transcript=Phvul.003G192900.2 locus=Phvul.003G192900 ID=Phvul.003G192900.2.v.
 46
 47 cid=37145774 transcript=Phvul.003G192900.2 locus=Phvul.003G192900 ID=Phvul.003G192900.2.v.
 48 004G017600.1 locus=Phvul.004G017600 ID=Phvul.004G017600.1.v2.1 annot-version=v2.1) & Meth
 49
 50 pt=Phvul.005G035400.1 locus=Phvul.005G035400 ID=Phvul.005G035400.1.v2.1 annot-version=v2.1
 51
 52 iginal description: pacid=37154337 transcript=Phvul.005G080800.2 locus=Phvul.005G080800 ID=P
 53 iginal description: pacid=37154337 transcript=Phvul.005G080800.2 locus=Phvul.005G080800 ID=P
 54
 55 ranscript=Phvul.005G095300.1 locus=Phvul.005G095300 ID=Phvul.005G095300.1.v2.1 annot-versic
 56 005G176600.1 locus=Phvul.005G176600 ID=Phvul.005G176600.1.v2.1 annot-version=v2.1) & Penta
 57
 58 006G034100.1 locus=Phvul.006G034100 ID=Phvul.006G034100.1.v2.1 annot-version=v2.1) & Proba
 59
 60 ra: pacid=37164279 transcript=Phvul.007G196100.2 locus=Phvul.007G196100 ID=Phvul.007G196100
 ra: pacid=37164279 transcript=Phvul.007G196100.2 locus=Phvul.007G196100 ID=Phvul.007G196100
 pt=Phvul.007G268300.1 locus=Phvul.007G268300 ID=Phvul.007G268300.1.v2.1 annot-version=v2.1
 008G015300.5 locus=Phvul.008G015300 ID=Phvul.008G015300.5.v2.1 annot-version=v2.1) & Prote
 008G015300.5 locus=Phvul.008G015300 ID=Phvul.008G015300.5.v2.1 annot-version=v2.1) & Prote
 008G015300.5 locus=Phvul.008G015300 ID=Phvul.008G015300.5.v2.1 annot-version=v2.1) & Prote

1
2 008G015300.5 locus=Phvul.008G015300 ID=Phvul.008G015300.5.v2.1 annot-version=v2.1) & Prote
3 008G015300.5 locus=Phvul.008G015300 ID=Phvul.008G015300.5.v2.1 annot-version=v2.1) & Prote
4 pt=Phvul.008G050200.1 locus=Phvul.008G050200 ID=Phvul.008G050200.1.v2.1 annot-version=v2.1
5
6 protein (original description: pacid=37159576 transcript=Phvul.008G092200.3 locus=Phvul.008G0922
7
8 protein (original description: pacid=37159576 transcript=Phvul.008G092200.3 locus=Phvul.008G0922
9
10 ption: pacid=37159444 transcript=Phvul.008G106950.2 locus=Phvul.008G106950 ID=Phvul.008G10
11
12 ption: pacid=37159444 transcript=Phvul.008G106950.2 locus=Phvul.008G106950 ID=Phvul.008G10
13
14 159820 transcript=Phvul.008G114300.1 locus=Phvul.008G114300 ID=Phvul.008G114300.1.v2.1 ann
15
16 description: pacid=37158932 transcript=Phvul.008G130400.1 locus=Phvul.008G130400 ID=Phvul.0
17
18 pt=Phvul.008G203314.1 locus=Phvul.008G203314 ID=Phvul.008G203314.1.v2.1 annot-version=v2.1
19
20 id=37149974 transcript=Phvul.009G108800.1 locus=Phvul.009G108800 ID=Phvul.009G108800.1.v2
21
22 l=37149300 transcript=Phvul.009G128500.4 locus=Phvul.009G128500 ID=Phvul.009G128500.4.v2.1
23
24 l=37149300 transcript=Phvul.009G128500.4 locus=Phvul.009G128500 ID=Phvul.009G128500.4.v2.1
25
26 l=37149300 transcript=Phvul.009G128500.4 locus=Phvul.009G128500 ID=Phvul.009G128500.4.v2.1
27
28 l=37149300 transcript=Phvul.009G128500.4 locus=Phvul.009G128500 ID=Phvul.009G128500.4.v2.1
29
30 pt=Phvul.009G255500.2 locus=Phvul.009G255500 ID=Phvul.009G255500.2.v2.1 annot-version=v2.1
31
32 pt=Phvul.009G255500.2 locus=Phvul.009G255500 ID=Phvul.009G255500.2.v2.1 annot-version=v2.1
33
34 nase RLK1 OS=Arabidopsis thaliana (sp|q39202|rlk1_arath : 652.0) & Enzyme classification.EC_2 tra
35
36 011G062200.1 locus=Phvul.011G062200 ID=Phvul.011G062200.1.v2.1 annot-version=v2.1) & Pumil
37
38 nase At1g67520 OS=Arabidopsis thaliana (sp|o64793|y1675_arath : 249.0) & Enzyme classification
39
40 nase At1g67520 OS=Arabidopsis thaliana (sp|o64793|y1675_arath : 249.0) & Enzyme classification
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
 2
 3 1)
 4 ersion=v2.1) &
 5 ersion=v2.1) &
 6 0.1.v2.1 annot-version=v2.1) &
 7 1)
 8
 9 e(50.3.2 : 323.5) (original description: pacid=37160089 transcript=Phvul.008G271000.1 locus=Phvul
 10 1)
 11
 12 -version=v2.1) &
 13 ersion=v2.1) &
 14 nnot-version=v2.1) &
 15 -version=v2.1) &
 16 -version=v2.1) &
 17 ersion=v2.1) &
 18 ersion=v2.1) &
 19 ersion=v2.1) &
 20 30200.1 locus=Phvul.006G130200 ID=Phvul.006G130200.1.v2.1 annot-version=v2.1) &
 21 1)
 22 0.1.v2.1 annot-version=v2.1) &
 23 1)
 24
 25 ok motif nuclear-localized protein 17 OS=Arabidopsis thaliana (sp|q9lta2|ahl17_arath : 179.0)
 26 0.1.v2.1 annot-version=v2.1) &
 27 version=v2.1) &
 28 version=v2.1) &
 29
 30 nsferases.EC_2.7 transferase transferring phosphorus-containing group(50.2.7 : 109.2) (original des
 31 nsferases.EC_2.7 transferase transferring phosphorus-containing group(50.2.7 : 109.2) (original des
 32 ok motif nuclear-localized protein 13 OS=Arabidopsis thaliana (sp|q940i0|ahl13_arath : 144.0)
 33 1)
 34
 35 il.002G092900.2.v2.1 annot-version=v2.1) &
 36 il.002G092900.2.v2.1 annot-version=v2.1) &
 37 02G274500.1.v2.1 annot-version=v2.1) &
 38 =Phvul.002G315300.1.v2.1 annot-version=v2.1) &
 39 original description: pacid=37147256 transcript=Phvul.003G076700.2 locus=Phvul.003G076700 ID=
 40 original description: pacid=37147256 transcript=Phvul.003G076700.2 locus=Phvul.003G076700 ID=
 41 version=v2.1) &
 42 version=v2.1) &
 43 version=v2.1) &
 44 ersion=v2.1) &
 45 ersion=v2.1) &
 46 1)
 47 1)
 48
 49 ul.004G171500.6.v2.1 annot-version=v2.1) &
 50 ul.004G171500.6.v2.1 annot-version=v2.1) &
 51 ul.004G171500.6.v2.1 annot-version=v2.1) &
 52 ul.004G171500.6.v2.1 annot-version=v2.1) &
 53 ul.004G171500.6.v2.1 annot-version=v2.1) &
 54 ul.004G171500.6.v2.1 annot-version=v2.1) &
 55 ul.004G171500.6.v2.1 annot-version=v2.1) &
 56 ul.004G171500.6.v2.1 annot-version=v2.1) &
 57 ul.004G171500.6.v2.1 annot-version=v2.1) &
 58 ul.004G171500.6.v2.1 annot-version=v2.1) &
 59 ul.004G171500.6.v2.1 annot-version=v2.1) &
 60 ul.005G022300.1.v2.1 annot-version=v2.1) &

1 600.1.v2.1 annot-version=v2.1) &
2 06G049100 ID=Phvul.006G049100.1.v2.1 annot-version=v2.1) &
3 domain-containing protein At5g58720 OS=Arabidopsis thaliana (sp|o65573|y5872_arath : 334.0)
4 nt-version=v2.1) &
5 not-version=v2.1) &
6 1)
7 1)
8 1)
9 not-version=v2.1) &
10 ul.009G157200.2.v2.1 annot-version=v2.1) &
11 ul.009G157200.2.v2.1 annot-version=v2.1) &
12 not-version=v2.1) &
13 **1.v2.1 annot-version=v2.1) &**
14 l/HIN1-like protein 12 OS=Arabidopsis thaliana (sp|q9sj54|nhl12_arath : 94.7)
15 not-version=v2.1) &
16 able carbohydrate esterase At4g34215 OS=Arabidopsis thaliana (sp|q8l9j9|caes_arath : 216.0)
17 l.001G183700 ID=Phvul.001G183700.1.v2.1 annot-version=v2.1) &
18 glucanase 17 OS=Arabidopsis thaliana (sp|o81416|gun17_arath : 701.0)
19 utive GTP diphosphokinase RSH1, chloroplastic OS=Arabidopsis thaliana (sp|p0dkg8|rsh1l_arath : 111)
20 ul.001G250100.2.v2.1 annot-version=v2.1) &
21 ul.001G250100.2.v2.1 annot-version=v2.1) &
22 -version=v2.1) &
23 nt-version=v2.1) &
24 1)
25 1)
26 ul.002G188300.1.v2.1 annot-version=v2.1) &
27 in JINGUBANG OS=Arabidopsis thaliana (sp|o48716|jgb_arath : 234.0)
28 t-version=v2.1) &
29 original description: pacid=37147449 transcript=Phvul.003G043600.2 locus=Phvul.003G043600 ID=F
30 1 annot-version=v2.1) &
31 oreductase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 2
32 2.1 annot-version=v2.1) &
33 2.1 annot-version=v2.1) &
34 yl-CpG-binding domain-containing protein 9 OS=Arabidopsis thaliana (sp|q9sgh2|mbd9_arath : 151
35 **1)**
36 Phvul.005G080800.2.v2.1 annot-version=v2.1) &
37 Phvul.005G080800.2.v2.1 annot-version=v2.1) &
38 on=v2.1) &
39 atricopeptide repeat-containing protein At1g52620 OS=Arabidopsis thaliana (sp|q9ssr4|ppr77_arat
40 able galacturonosyltransferase 15 OS=Arabidopsis thaliana (sp|q8l4b0|gautf_arath : 590.0)
41).2.v2.1 annot-version=v2.1) &
42).2.v2.1 annot-version=v2.1) &
43 1)
44 in-tyrosine-phosphatase MKP1 OS=Arabidopsis thaliana (sp|q9c5s1|mkp1_arath : 348.0)
45 in-tyrosine-phosphatase MKP1 OS=Arabidopsis thaliana (sp|q9c5s1|mkp1_arath : 348.0)
46 in-tyrosine-phosphatase MKP1 OS=Arabidopsis thaliana (sp|q9c5s1|mkp1_arath : 348.0)

1
2 in-tyrosine-phosphatase MKP1 OS=Arabidopsis thaliana (sp|q9c5s1|mkp1_arath : 348.0)
3 in-tyrosine-phosphatase MKP1 OS=Arabidopsis thaliana (sp|q9c5s1|mkp1_arath : 348.0)
4 1)
5
6 200 ID=Phvul.008G092200.3.v2.1 annot-version=v2.1) &
7 200 ID=Phvul.008G092200.3.v2.1 annot-version=v2.1) &
8)6950.2.v2.1 annot-version=v2.1) &
9)6950.2.v2.1 annot-version=v2.1) &
10)6950.2.v2.1 annot-version=v2.1) &
11 rot-version=v2.1) &
12 08G130400.1.v2.1 annot-version=v2.1) &
13 1)
14 2.1 annot-version=v2.1) &
15 L annot-version=v2.1) &
16 L annot-version=v2.1) &
17 L annot-version=v2.1) &
18 L annot-version=v2.1) &
19 L annot-version=v2.1) &
20 L annot-version=v2.1) &
21 1)
22 1)
23
24 ansferases.EC_2.7 transferase transferring phosphorus-containing group(50.2.7 : 103.4) (original de
25 lio homolog 2 OS=Arabidopsis thaliana (sp|q9zw06|pum2_arath : 992.0)
26
27 i.EC_2 transferases.EC_2.7 transferase transferring phosphorus-containing group(50.2.7 : 57.7) (orig
28 i.EC_2 transferases.EC_2.7 transferase transferring phosphorus-containing group(50.2.7 : 57.7) (orig
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10 l.008G271000 ID=Phvul.008G271000.1.v2.1 annot-version=v2.1) &
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31 ;cription: pacid=37170420 transcript=Phvul.001G147001.2 locus=Phvul.001G147001 ID=Phvul.001G
32 ;cription: pacid=37170420 transcript=Phvul.001G147001.2 locus=Phvul.001G147001 ID=Phvul.001G
33
34
35
36
37
38
39
40
41 =Phvul.003G076700.2.v2.1 annot-version=v2.1) &
42 =Phvul.003G076700.2.v2.1 annot-version=v2.1) &
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

83.0)

Phvul.003G043600.2.v2.1 annot-version=v2.1) &

.08.0) (original description: pacid=37147806 transcript=Phvul.003G076900.1 locus=Phvul.003G0769

65.0)

th : 801.0)

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

description: pacid=37142844 transcript=Phvul.010G032000.1 locus=Phvul.010G032000 ID=Phvul.010

ginal description: pacid=37155309 transcript=Phvul.011G175000.2 locus=Phvul.011G175000 ID=Phv

ginal description: pacid=37155309 transcript=Phvul.011G175000.2 locus=Phvul.011G175000 ID=Phv

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

¡147001.2.v2.1 annot-version=v2.1) &
¡147001.2.v2.1 annot-version=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

00 ID=Phvul.003G076900.1.v2.1 annot-version=v2.1) &

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

!G032000.1.v2.1 annot-version=v2.1) &

vul.011G175000.2.v2.1 annot-version=v2.1) &

vul.011G175000.2.v2.1 annot-version=v2.1) &

Don't distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| ld | H42_1 | H42_2 | H42_3 | X42_1 | X42_2 | |
|----------------|-------|-------|-------|-------|-------|----|
| cfa-miR-31 | 13 | | 0 | 2 | 17 | 3 |
| cpo-miR-31-5p | 13 | | 0 | 2 | 17 | 3 |
| dno-miR-31-5p | 13 | | 0 | 2 | 17 | 3 |
| ocu-miR-31-5p | 13 | | 0 | 2 | 17 | 3 |
| aly-miR164a-5p | 477 | 598 | | 177 | 50 | 83 |
| aly-miR164b-5p | 477 | 598 | | 177 | 50 | 83 |
| aof-miR164 | 477 | 598 | | 177 | 50 | 83 |
| ata-miR164b-5p | 477 | 598 | | 177 | 50 | 83 |
| ata-miR164c-5p | 477 | 598 | | 177 | 50 | 83 |
| ath-miR164a | 477 | 598 | | 177 | 50 | 83 |
| ath-miR164b-5p | 477 | 598 | | 177 | 50 | 83 |
| atr-miR164a | 477 | 598 | | 177 | 50 | 83 |
| atr-miR164b | 477 | 598 | | 177 | 50 | 83 |
| bdi-miR164a-5p | 477 | 598 | | 177 | 50 | 83 |
| bdi-miR164b | 477 | 598 | | 177 | 50 | 83 |
| bdi-miR164e | 477 | 598 | | 177 | 50 | 83 |
| bna-miR164a | 477 | 598 | | 177 | 50 | 83 |
| bra-miR164a | 477 | 598 | | 177 | 50 | 83 |
| cas-miR164 | 477 | 598 | | 177 | 50 | 83 |
| cme-miR164c | 477 | 598 | | 177 | 50 | 83 |
| cme-miR164d | 477 | 598 | | 177 | 50 | 83 |
| cpa-miR164a | 477 | 598 | | 177 | 50 | 83 |
| cpa-miR164b | 477 | 598 | | 177 | 50 | 83 |
| cpa-miR164c | 477 | 598 | | 177 | 50 | 83 |
| csi-miR164a-5p | 477 | 598 | | 177 | 50 | 83 |
| csi-miR164b-5p | 477 | 598 | | 177 | 50 | 83 |
| csi-miR164c-5p | 477 | 598 | | 177 | 50 | 83 |
| csi-miR164d-5p | 477 | 598 | | 177 | 50 | 83 |
| ctr-miR164 | 477 | 598 | | 177 | 50 | 83 |
| fve-miR164a-5p | 477 | 598 | | 177 | 50 | 83 |
| fve-miR164b | 477 | 598 | | 177 | 50 | 83 |
| ghr-miR164 | 477 | 598 | | 177 | 50 | 83 |
| gma-miR164a | 477 | 598 | | 177 | 50 | 83 |
| gma-miR164e | 477 | 598 | | 177 | 50 | 83 |
| gma-miR164f | 477 | 598 | | 177 | 50 | 83 |
| gma-miR164g | 477 | 598 | | 177 | 50 | 83 |
| gma-miR164h | 477 | 598 | | 177 | 50 | 83 |
| gma-miR164i | 477 | 598 | | 177 | 50 | 83 |
| gma-miR164j | 477 | 598 | | 177 | 50 | 83 |
| gma-miR164k | 477 | 598 | | 177 | 50 | 83 |
| lus-miR164a | 477 | 598 | | 177 | 50 | 83 |
| lus-miR164b | 477 | 598 | | 177 | 50 | 83 |

| | | | | | | |
|----|----------------|-----|-----|-----|----|----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | lus-miR164c | 477 | 598 | 177 | 50 | 83 |
| 4 | lus-miR164d | 477 | 598 | 177 | 50 | 83 |
| 5 | lus-miR164e | 477 | 598 | 177 | 50 | 83 |
| 6 | mdm-miR164b | 477 | 598 | 177 | 50 | 83 |
| 7 | mdm-miR164c | 477 | 598 | 177 | 50 | 83 |
| 8 | mdm-miR164d | 477 | 598 | 177 | 50 | 83 |
| 9 | mdm-miR164e | 477 | 598 | 177 | 50 | 83 |
| 10 | mdm-miR164f | 477 | 598 | 177 | 50 | 83 |
| 11 | mes-miR164a | 477 | 598 | 177 | 50 | 83 |
| 12 | mes-miR164b | 477 | 598 | 177 | 50 | 83 |
| 13 | mes-miR164c | 477 | 598 | 177 | 50 | 83 |
| 14 | mtr-miR164a | 477 | 598 | 177 | 50 | 83 |
| 15 | mtr-miR164b | 477 | 598 | 177 | 50 | 83 |
| 16 | mtr-miR164c | 477 | 598 | 177 | 50 | 83 |
| 17 | nta-miR164a | 477 | 598 | 177 | 50 | 83 |
| 18 | nta-miR164b | 477 | 598 | 177 | 50 | 83 |
| 19 | osa-miR164a | 477 | 598 | 177 | 50 | 83 |
| 20 | osa-miR164b | 477 | 598 | 177 | 50 | 83 |
| 21 | osa-miR164f | 477 | 598 | 177 | 50 | 83 |
| 22 | ppe-miR164a | 477 | 598 | 177 | 50 | 83 |
| 23 | ppe-miR164b | 477 | 598 | 177 | 50 | 83 |
| 24 | ppe-miR164c | 477 | 598 | 177 | 50 | 83 |
| 25 | ptc-miR164a | 477 | 598 | 177 | 50 | 83 |
| 26 | ptc-miR164b | 477 | 598 | 177 | 50 | 83 |
| 27 | ptc-miR164c | 477 | 598 | 177 | 50 | 83 |
| 28 | ptc-miR164d | 477 | 598 | 177 | 50 | 83 |
| 29 | ptc-miR164e | 477 | 598 | 177 | 50 | 83 |
| 30 | rco-miR164a | 477 | 598 | 177 | 50 | 83 |
| 31 | rco-miR164b | 477 | 598 | 177 | 50 | 83 |
| 32 | rco-miR164c | 477 | 598 | 177 | 50 | 83 |
| 33 | sbi-miR164a | 477 | 598 | 177 | 50 | 83 |
| 34 | sbi-miR164d | 477 | 598 | 177 | 50 | 83 |
| 35 | sbi-miR164e | 477 | 598 | 177 | 50 | 83 |
| 36 | sly-miR164a-5p | 477 | 598 | 177 | 50 | 83 |
| 37 | sly-miR164b-5p | 477 | 598 | 177 | 50 | 83 |
| 38 | ssl-miR164a | 477 | 598 | 177 | 50 | 83 |
| 39 | ssl-miR164b | 477 | 598 | 177 | 50 | 83 |
| 40 | tae-miR164 | 477 | 598 | 177 | 50 | 83 |
| 41 | tcc-miR164a | 477 | 598 | 177 | 50 | 83 |
| 42 | tcc-miR164b | 477 | 598 | 177 | 50 | 83 |
| 43 | vvi-miR164a | 477 | 598 | 177 | 50 | 83 |
| 44 | vvi-miR164c | 477 | 598 | 177 | 50 | 83 |
| 45 | vvi-miR164d | 477 | 598 | 177 | 50 | 83 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-------------------|-----|-----|------|----|----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | zma-miR164a-5p | 477 | 598 | 177 | 50 | 83 |
| 4 | zma-miR164b-5p | 477 | 598 | 177 | 50 | 83 |
| 5 | zma-miR164c-5p | 477 | 598 | 177 | 50 | 83 |
| 6 | zma-miR164d-5p | 477 | 598 | 177 | 50 | 83 |
| 7 | zma-miR164e-5p | 477 | 598 | 177 | 50 | 83 |
| 8 | zma-miR164g-5p | 477 | 598 | 177 | 50 | 83 |
| 9 | bra-miR164e-5p | 482 | 598 | 180 | 50 | 83 |
| 10 | bta-miR-451 | 86 | 276 | 3131 | 81 | 55 |
| 11 | cja-miR-451 | 86 | 276 | 3131 | 81 | 55 |
| 12 | cpo-miR-451-5p | 86 | 276 | 3131 | 81 | 55 |
| 13 | dno-miR-451-5p | 86 | 276 | 3131 | 81 | 55 |
| 14 | gga-miR-451 | 86 | 276 | 3131 | 81 | 55 |
| 15 | oan-miR-451 | 86 | 276 | 3131 | 81 | 55 |
| 16 | ocu-miR-451-5p | 86 | 276 | 3131 | 81 | 55 |
| 17 | oha-miR-451-?? | 86 | 276 | 3131 | 81 | 55 |
| 18 | tgu-miR-451 | 86 | 276 | 3131 | 81 | 55 |
| 19 | aca-miR-451-5p | 33 | 261 | 1822 | 29 | 15 |
| 20 | cfa-miR-451 | 33 | 261 | 1822 | 29 | 15 |
| 21 | cgr-miR-451a | 33 | 261 | 1822 | 29 | 15 |
| 22 | dre-miR-451 | 33 | 261 | 1822 | 29 | 15 |
| 23 | hsa-miR-451a | 33 | 261 | 1822 | 29 | 15 |
| 24 | mml-miR-451 | 33 | 261 | 1822 | 29 | 15 |
| 25 | mmu-miR-451a | 33 | 261 | 1822 | 29 | 15 |
| 26 | ppy-miR-451 | 33 | 261 | 1822 | 29 | 15 |
| 27 | ptr-miR-451 | 33 | 261 | 1822 | 29 | 15 |
| 28 | rno-miR-451-5p | 33 | 261 | 1822 | 29 | 15 |
| 29 | ssc-miR-451 | 33 | 261 | 1822 | 29 | 15 |
| 30 | xtr-miR-451 | 33 | 261 | 1822 | 29 | 15 |
| 31 | ebv-miR-BART8-3p | 0 | 0 | 1 | 0 | 0 |
| 32 | ebv-miR-BART1-3p | 0 | 0 | 1 | 0 | 0 |
| 33 | ebv-miR-BART1-5p | 0 | 0 | 1 | 0 | 0 |
| 34 | ebv-miR-BART17-5p | 0 | 0 | 0 | 0 | 0 |
| 35 | ebv-miR-BART6-3p | 0 | 0 | 0 | 0 | 0 |
| 36 | ebv-miR-BART17-3p | 0 | 0 | 0 | 0 | 0 |
| 37 | ebv-miR-BART6-5p | 0 | 0 | 1 | 0 | 0 |
| 38 | ebv-miR-BART7-5p | 0 | 0 | 0 | 0 | 0 |
| 39 | ebv-miR-BART19-3p | 0 | 0 | 0 | 0 | 0 |
| 40 | ebv-miR-BART14-5p | 0 | 0 | 0 | 0 | 0 |
| 41 | ebv-miR-BART2-5p | 0 | 0 | 1 | 0 | 0 |
| 42 | ebv-miR-BART5-5p | 0 | 0 | 1 | 0 | 0 |
| 43 | ebv-miR-BART9-3p | 0 | 0 | 2 | 0 | 0 |
| 44 | ebv-miR-BART22 | 0 | 0 | 5 | 0 | 0 |
| 45 | rlcv-miR-rL1-6-3p | 0 | 0 | 11 | 0 | 0 |
| 46 | ebv-miR-BART10-3p | 0 | 0 | 2 | 0 | 0 |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-------------------|---|---|----|---|---|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ebv-miR-BART7-3p | 0 | 0 | 2 | 0 | 0 |
| 4 | ebv-miR-BART11-5p | 0 | 0 | 2 | 0 | 0 |
| 5 | ebv-miR-BART8-5p | 0 | 0 | 3 | 0 | 0 |
| 6 | efu-miR-192 | 3 | 5 | 9 | 5 | 2 |
| 7 | cfa-miR-192 | 0 | 2 | 3 | 2 | 1 |
| 8 | chi-miR-192-5p | 0 | 2 | 3 | 2 | 1 |
| 9 | cpo-miR-192-5p | 0 | 2 | 3 | 2 | 1 |
| 10 | eca-miR-192 | 0 | 2 | 3 | 2 | 1 |
| 11 | ggo-miR-192 | 0 | 2 | 3 | 2 | 1 |
| 12 | hsa-miR-192-5p | 0 | 2 | 3 | 2 | 1 |
| 13 | mml-miR-192-5p | 0 | 2 | 3 | 2 | 1 |
| 14 | mmu-miR-192-5p | 0 | 2 | 3 | 2 | 1 |
| 15 | nle-miR-192 | 0 | 2 | 3 | 2 | 1 |
| 16 | oan-miR-192-5p | 0 | 2 | 3 | 2 | 1 |
| 17 | oga-miR-192 | 0 | 2 | 3 | 2 | 1 |
| 18 | ppa-miR-192 | 0 | 2 | 3 | 2 | 1 |
| 19 | ppy-miR-192 | 0 | 2 | 3 | 2 | 1 |
| 20 | ptr-miR-192 | 0 | 2 | 3 | 2 | 1 |
| 21 | rno-miR-192-5p | 0 | 2 | 3 | 2 | 1 |
| 22 | ssc-miR-192 | 0 | 2 | 3 | 2 | 1 |
| 23 | tch-miR-192-5p | 0 | 2 | 3 | 2 | 1 |
| 24 | bta-miR-192 | 3 | 5 | 5 | 4 | 2 |
| 25 | cgr-miR-192 | 2 | 4 | 4 | 3 | 2 |
| 26 | oar-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 27 | age-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 28 | bta-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 29 | cfa-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 30 | cgr-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 31 | cpo-miR-127-3p | 5 | 2 | 39 | 5 | 6 |
| 32 | dma-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 33 | dno-miR-127-3p | 5 | 2 | 39 | 5 | 6 |
| 34 | eca-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 35 | hsa-miR-127-3p | 5 | 2 | 39 | 5 | 6 |
| 36 | lla-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 37 | mml-miR-127-3p | 5 | 2 | 39 | 5 | 6 |
| 38 | mmu-miR-127-3p | 5 | 2 | 39 | 5 | 6 |
| 39 | mne-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 40 | nle-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 41 | ocu-miR-127-3p | 5 | 2 | 39 | 5 | 6 |
| 42 | oga-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 43 | pal-miR-127-3p | 5 | 2 | 39 | 5 | 6 |
| 44 | pha-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 45 | ppa-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|----|----|----|---|---|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ppy-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 4 | ptr-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 5 | rno-miR-127-3p | 5 | 2 | 39 | 5 | 6 |
| 6 | sbo-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 7 | sla-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 8 | sla-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 9 | ssc-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 10 | ssc-miR-127 | 5 | 2 | 39 | 5 | 6 |
| 11 | tch-miR-127-3p | 5 | 2 | 39 | 5 | 6 |
| 12 | efu-miR-127 | 5 | 2 | 40 | 5 | 6 |
| 13 | efu-miR-127 | 5 | 2 | 40 | 5 | 6 |
| 14 | ola-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 15 | aae-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 16 | abu-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 17 | abu-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 18 | aca-miR-7-5p | 14 | 28 | 15 | 9 | 6 |
| 19 | aga-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 20 | aga-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 21 | ame-miR-7-5p | 14 | 28 | 15 | 9 | 6 |
| 22 | ami-miR-7a-5p | 14 | 28 | 15 | 9 | 6 |
| 23 | bbe-miR-7-5p | 14 | 28 | 15 | 9 | 6 |
| 24 | bfl-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 25 | bfl-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 26 | bmo-miR-7-5p | 14 | 28 | 15 | 9 | 6 |
| 27 | cfa-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 28 | cgr-miR-7a | 14 | 28 | 15 | 9 | 6 |
| 29 | cgr-miR-7a | 14 | 28 | 15 | 9 | 6 |
| 30 | cqu-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 31 | csa-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 32 | csa-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 33 | dan-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 34 | der-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 35 | dgr-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 36 | dme-miR-7-5p | 14 | 28 | 15 | 9 | 6 |
| 37 | dme-miR-7-5p | 14 | 28 | 15 | 9 | 6 |
| 38 | dmo-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 39 | dpe-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 40 | dps-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 41 | dps-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 42 | dpu-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 43 | dre-miR-7a | 14 | 28 | 15 | 9 | 6 |
| 44 | dse-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 45 | dse-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 46 | dsi-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 47 | dwi-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 48 | dya-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 49 | dya-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 50 | eca-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 51 | gmo-miR-7c-5p | 14 | 28 | 15 | 9 | 6 |
| 52 | ipu-miR-7a | 14 | 28 | 15 | 9 | 6 |
| 53 | ipu-miR-7a | 14 | 28 | 15 | 9 | 6 |
| 54 | isc-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 55 | lva-miR-7-5p | 14 | 28 | 15 | 9 | 6 |
| 56 | mml-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 57 | mml-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 58 | mmu-miR-7a-5p | 14 | 28 | 15 | 9 | 6 |
| 59 | mze-miR-7b | 14 | 28 | 15 | 9 | 6 |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|----|----|----|---|---|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | nbr-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 4 | nlo-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 5 | nvi-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 6 | oan-miR-7-5p | 14 | 28 | 15 | 9 | 6 |
| 7 | oni-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 8 | pma-miR-7a-5p | 14 | 28 | 15 | 9 | 6 |
| 9 | pmi-miR-7-5p | 14 | 28 | 15 | 9 | 6 |
| 10 | pony-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 11 | ptr-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 12 | rno-miR-7a-5p | 14 | 28 | 15 | 9 | 6 |
| 13 | sko-miR-7-5p | 14 | 28 | 15 | 9 | 6 |
| 14 | spu-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 15 | ssa-miR-7a-5p | 14 | 28 | 15 | 9 | 6 |
| 16 | tgu-miR-7-5p | 14 | 28 | 15 | 9 | 6 |
| 17 | tni-miR-7 | 14 | 28 | 15 | 9 | 6 |
| 18 | bta-miR-411a | 6 | 1 | 21 | 8 | 2 |
| 19 | cfa-miR-411 | 6 | 1 | 21 | 8 | 2 |
| 20 | ggo-miR-411 | 6 | 1 | 21 | 8 | 2 |
| 21 | oar-miR-411a-5p | 6 | 1 | 21 | 8 | 2 |
| 22 | cja-miR-411 | 6 | 1 | 14 | 6 | 1 |
| 23 | cpo-miR-411-5p | 6 | 1 | 14 | 6 | 1 |
| 24 | dno-miR-411-5p | 6 | 1 | 14 | 6 | 1 |
| 25 | eca-miR-411 | 6 | 1 | 14 | 6 | 1 |
| 26 | hsa-miR-411-5p | 6 | 1 | 14 | 6 | 1 |
| 27 | mml-miR-411-5p | 6 | 1 | 14 | 6 | 1 |
| 28 | mmr-miR-411a | 6 | 1 | 14 | 6 | 1 |
| 29 | mmu-miR-411-5p | 6 | 1 | 14 | 6 | 1 |
| 30 | ocu-miR-411-5p | 6 | 1 | 14 | 6 | 1 |
| 31 | oga-miR-411a | 6 | 1 | 14 | 6 | 1 |
| 32 | pha-miR-411a | 6 | 1 | 14 | 6 | 1 |
| 33 | ppa-miR-411a | 6 | 1 | 14 | 6 | 1 |
| 34 | ppy-miR-411 | 6 | 1 | 14 | 6 | 1 |
| 35 | ptr-miR-411 | 6 | 1 | 14 | 6 | 1 |
| 36 | rno-miR-411-5p | 6 | 1 | 14 | 6 | 1 |
| 37 | tch-miR-411-5p | 6 | 1 | 14 | 6 | 1 |
| 38 | aca-miR-10a-5p | 8 | 5 | 15 | 4 | 5 |
| 39 | age-miR-10a | 8 | 5 | 15 | 4 | 5 |
| 40 | ami-miR-10a-5p | 8 | 5 | 15 | 4 | 5 |
| 41 | bfl-miR-10a-5p | 8 | 5 | 15 | 4 | 5 |
| 42 | bta-miR-10a | 8 | 5 | 15 | 4 | 5 |
| 43 | cli-miR-10a-5p | 8 | 5 | 15 | 4 | 5 |
| 44 | dno-miR-10a-5p | 8 | 5 | 15 | 4 | 5 |
| 45 | eca-miR-10a | 8 | 5 | 15 | 4 | 5 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|----|-----|----|-----|----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ggo-miR-10a | 8 | 5 | 15 | 4 | 5 |
| 4 | hsa-miR-10a-5p | 8 | 5 | 15 | 4 | 5 |
| 5 | mdo-miR-10a-5p | 8 | 5 | 15 | 4 | 5 |
| 6 | mml-miR-10a-5p | 8 | 5 | 15 | 4 | 5 |
| 7 | mmu-miR-10a-5p | 8 | 5 | 15 | 4 | 5 |
| 8 | oha-miR-10a-5p | 8 | 5 | 15 | 4 | 5 |
| 9 | oha-miR-10a-5p | 8 | 5 | 15 | 4 | 5 |
| 10 | oha-miR-10a-5p | 8 | 5 | 15 | 4 | 5 |
| 11 | pbv-miR-10a-5p | 8 | 5 | 15 | 4 | 5 |
| 12 | ppa-miR-10a | 8 | 5 | 15 | 4 | 5 |
| 13 | ppy-miR-10a | 8 | 5 | 15 | 4 | 5 |
| 14 | ptr-miR-10a | 8 | 5 | 15 | 4 | 5 |
| 15 | rno-miR-10a-5p | 8 | 5 | 15 | 4 | 5 |
| 16 | rno-miR-10a-5p | 8 | 5 | 15 | 4 | 5 |
| 17 | rno-miR-10a-5p | 8 | 5 | 15 | 4 | 5 |
| 18 | ska-miR-10a | 8 | 5 | 15 | 4 | 5 |
| 19 | sla-miR-10a | 8 | 5 | 15 | 4 | 5 |
| 20 | xtr-miR-10a | 8 | 5 | 15 | 4 | 5 |
| 21 | xtr-miR-10a | 8 | 5 | 15 | 4 | 5 |
| 22 | xla-miR-10a-5p | 8 | 5 | 16 | 4 | 5 |
| 23 | api-miR-7 | 97 | 187 | 35 | 103 | 49 |
| 24 | bdo-miR-7 | 97 | 187 | 35 | 103 | 49 |
| 25 | bdo-miR-7 | 97 | 187 | 35 | 103 | 49 |
| 26 | bta-miR-7 | 97 | 187 | 35 | 103 | 49 |
| 27 | ccr-miR-7a | 97 | 187 | 35 | 103 | 49 |
| 28 | chi-miR-7-5p | 97 | 187 | 35 | 103 | 49 |
| 29 | chi-miR-7-5p | 97 | 187 | 35 | 103 | 49 |
| 30 | cja-miR-7 | 97 | 187 | 35 | 103 | 49 |
| 31 | cli-miR-7a-5p | 97 | 187 | 35 | 103 | 49 |
| 32 | cli-miR-7a-5p | 97 | 187 | 35 | 103 | 49 |
| 33 | cpo-miR-7-5p | 97 | 187 | 35 | 103 | 49 |
| 34 | dno-miR-7-5p | 97 | 187 | 35 | 103 | 49 |
| 35 | dqu-miR-7-5p | 97 | 187 | 35 | 103 | 49 |
| 36 | dvi-miR-7-5p | 97 | 187 | 35 | 103 | 49 |
| 37 | dvi-miR-7-5p | 97 | 187 | 35 | 103 | 49 |
| 38 | efu-miR-7a | 97 | 187 | 35 | 103 | 49 |
| 39 | efu-miR-7b | 97 | 187 | 35 | 103 | 49 |
| 40 | efu-miR-7c | 97 | 187 | 35 | 103 | 49 |
| 41 | efu-miR-7c | 97 | 187 | 35 | 103 | 49 |
| 42 | gmo-miR-7a-5p | 97 | 187 | 35 | 103 | 49 |
| 43 | hsa-miR-7-5p | 97 | 187 | 35 | 103 | 49 |
| 44 | lgi-miR-7 | 97 | 187 | 35 | 103 | 49 |
| 45 | lgi-miR-7 | 97 | 187 | 35 | 103 | 49 |
| 46 | mse-miR-7 | 97 | 187 | 35 | 103 | 49 |
| 47 | mze-miR-7a | 97 | 187 | 35 | 103 | 49 |
| 48 | ocu-miR-7a-5p | 97 | 187 | 35 | 103 | 49 |
| 49 | ocu-miR-7a-5p | 97 | 187 | 35 | 103 | 49 |
| 50 | oha-miR-7-5p | 97 | 187 | 35 | 103 | 49 |
| 51 | pal-miR-7b-5p | 97 | 187 | 35 | 103 | 49 |
| 52 | pbv-miR-7-5p | 97 | 187 | 35 | 103 | 49 |
| 53 | pbv-miR-7-5p | 97 | 187 | 35 | 103 | 49 |
| 54 | pca-miR-7-5p | 97 | 187 | 35 | 103 | 49 |
| 55 | ssc-miR-7-5p | 97 | 187 | 35 | 103 | 49 |
| 56 | tca-miR-7-5p | 97 | 187 | 35 | 103 | 49 |
| 57 | tca-miR-7-5p | 97 | 187 | 35 | 103 | 49 |
| 58 | tcf-miR-7 | 97 | 187 | 35 | 103 | 49 |
| 59 | tch-miR-7-5p | 97 | 187 | 35 | 103 | 49 |
| 60 | | | | | | |

| | | | | | | |
|----|---------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | tur-miR-7-5p | 97 | 187 | 35 | 103 | 49 |
| 4 | abu-let-7a | 261 | 217 | 212 | 242 | 138 |
| 5 | aca-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 6 | ami-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 7 | asu-let-7-5p | 261 | 217 | 212 | 242 | 138 |
| 8 | bbe-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 9 | bfl-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 10 | bma-let-7 | 261 | 217 | 212 | 242 | 138 |
| 11 | bta-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 12 | cbn-let-7 | 261 | 217 | 212 | 242 | 138 |
| 13 | cbr-let-7 | 261 | 217 | 212 | 242 | 138 |
| 14 | ccr-let-7a | 261 | 217 | 212 | 242 | 138 |
| 15 | cel-let-7-5p | 261 | 217 | 212 | 242 | 138 |
| 16 | cfa-let-7a | 261 | 217 | 212 | 242 | 138 |
| 17 | cgr-let-7a | 261 | 217 | 212 | 242 | 138 |
| 18 | chi-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 19 | cja-let-7a | 261 | 217 | 212 | 242 | 138 |
| 20 | cli-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 21 | cpi-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 22 | cpo-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 23 | crm-let-7 | 261 | 217 | 212 | 242 | 138 |
| 24 | dma-let-7a | 261 | 217 | 212 | 242 | 138 |
| 25 | dno-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 26 | dre-let-7a | 261 | 217 | 212 | 242 | 138 |
| 27 | eca-let-7a | 261 | 217 | 212 | 242 | 138 |
| 28 | fru-let-7a | 261 | 217 | 212 | 242 | 138 |
| 29 | gga-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 30 | gga-let-7j-5p | 261 | 217 | 212 | 242 | 138 |
| 31 | gmo-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 32 | hpo-let-7-5p | 261 | 217 | 212 | 242 | 138 |
| 33 | hsa-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 34 | ipu-let-7a | 261 | 217 | 212 | 242 | 138 |
| 35 | lgi-let-7 | 261 | 217 | 212 | 242 | 138 |
| 36 | mdo-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 37 | mml-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 38 | mmr-let-7a | 261 | 217 | 212 | 242 | 138 |
| 39 | mmu-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 40 | mze-let-7a | 261 | 217 | 212 | 242 | 138 |
| 41 | nbr-let-7a | 261 | 217 | 212 | 242 | 138 |
| 42 | nle-let-7a | 261 | 217 | 212 | 242 | 138 |
| 43 | oar-let-7a | 261 | 217 | 212 | 242 | 138 |
| 44 | ocu-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 45 | oga-let-7a | 261 | 217 | 212 | 242 | 138 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | oha-let-7a | 261 | 217 | 212 | 242 | 138 |
| 4 | oha-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 5 | ola-let-7a | 261 | 217 | 212 | 242 | 138 |
| 6 | oni-let-7a | 261 | 217 | 212 | 242 | 138 |
| 7 | oni-let-7a | 261 | 217 | 212 | 242 | 138 |
| 8 | pal-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 9 | pal-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 10 | pbv-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 11 | pha-let-7a | 261 | 217 | 212 | 242 | 138 |
| 12 | pha-let-7a | 261 | 217 | 212 | 242 | 138 |
| 13 | pma-let-7a | 261 | 217 | 212 | 242 | 138 |
| 14 | ppy-let-7a | 261 | 217 | 212 | 242 | 138 |
| 15 | ppa-let-7a | 261 | 217 | 212 | 242 | 138 |
| 16 | ppc-let-7 | 261 | 217 | 212 | 242 | 138 |
| 17 | ppc-let-7 | 261 | 217 | 212 | 242 | 138 |
| 18 | ppy-let-7a | 261 | 217 | 212 | 242 | 138 |
| 19 | pte-let-7-5p | 261 | 217 | 212 | 242 | 138 |
| 20 | ptr-let-7a | 261 | 217 | 212 | 242 | 138 |
| 21 | ptr-let-7a | 261 | 217 | 212 | 242 | 138 |
| 22 | rno-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 23 | sbo-let-7a | 261 | 217 | 212 | 242 | 138 |
| 24 | sbo-let-7a | 261 | 217 | 212 | 242 | 138 |
| 25 | sbo-let-7a | 261 | 217 | 212 | 242 | 138 |
| 26 | ssa-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 27 | ssc-let-7a | 261 | 217 | 212 | 242 | 138 |
| 28 | tgu-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 29 | tgu-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 30 | tni-let-7a | 261 | 217 | 212 | 242 | 138 |
| 31 | xla-let-7a-5p | 261 | 217 | 212 | 242 | 138 |
| 32 | xtr-let-7a | 261 | 217 | 212 | 242 | 138 |
| 33 | xtr-let-7a | 261 | 217 | 212 | 242 | 138 |
| 34 | prd-let-7-5p | 264 | 220 | 219 | 248 | 141 |
| 35 | cgr-miR-196b | 39 | 3 | 4 | 18 | 27 |
| 36 | cja-miR-196b | 39 | 3 | 4 | 18 | 27 |
| 37 | cja-miR-196b | 39 | 3 | 4 | 18 | 27 |
| 38 | eca-miR-196b | 39 | 3 | 4 | 18 | 27 |
| 39 | ggo-miR-196b | 39 | 3 | 4 | 18 | 27 |
| 40 | ggo-miR-196b | 39 | 3 | 4 | 18 | 27 |
| 41 | hsa-miR-196b-5p | 39 | 3 | 4 | 18 | 27 |
| 42 | mdo-miR-196a-5p | 39 | 3 | 4 | 18 | 27 |
| 43 | mml-miR-196b-5p | 39 | 3 | 4 | 18 | 27 |
| 44 | mml-miR-196b-5p | 39 | 3 | 4 | 18 | 27 |
| 45 | mmr-miR-196b | 39 | 3 | 4 | 18 | 27 |
| 46 | mmu-miR-196b-5p | 39 | 3 | 4 | 18 | 27 |
| 47 | nle-miR-196b | 39 | 3 | 4 | 18 | 27 |
| 48 | oga-miR-196b | 39 | 3 | 4 | 18 | 27 |
| 49 | oga-miR-196b | 39 | 3 | 4 | 18 | 27 |
| 50 | pal-miR-196b-5p | 39 | 3 | 4 | 18 | 27 |
| 51 | ppy-miR-196b | 39 | 3 | 4 | 18 | 27 |
| 52 | ppy-miR-196b | 39 | 3 | 4 | 18 | 27 |
| 53 | ptr-miR-196b | 39 | 3 | 4 | 18 | 27 |
| 54 | rno-miR-196b-5p | 39 | 3 | 4 | 18 | 27 |
| 55 | ssc-miR-196b-5p | 39 | 3 | 4 | 18 | 27 |
| 56 | efu-miR-34a | 69 | 10 | 99 | 57 | 33 |
| 57 | ami-miR-34a-5p | 69 | 10 | 99 | 57 | 33 |
| 58 | ami-miR-34a-5p | 69 | 10 | 99 | 57 | 33 |
| 59 | cja-miR-34a | 69 | 10 | 99 | 57 | 33 |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | gga-miR-34a-5p | 69 | 10 | 99 | 57 | 33 |
| 4 | mdo-miR-34a-5p | 69 | 10 | 99 | 57 | 33 |
| 5 | oha-miR-34a-5p | 69 | 10 | 99 | 57 | 33 |
| 6 | tch-miR-34a-5p | 69 | 10 | 99 | 57 | 33 |
| 7 | tch-miR-34a-5p | 69 | 10 | 99 | 57 | 33 |
| 8 | xtr-miR-34a | 69 | 10 | 99 | 57 | 33 |
| 9 | xtr-miR-34a | 69 | 10 | 99 | 57 | 33 |
| 10 | bta-miR-196b | 45 | 4 | 4 | 26 | 31 |
| 11 | cfa-miR-196b | 45 | 4 | 4 | 26 | 31 |
| 12 | cpo-miR-196b-5p | 45 | 4 | 4 | 26 | 31 |
| 13 | cpo-miR-196b-5p | 45 | 4 | 4 | 26 | 31 |
| 14 | dno-miR-196b-5p | 45 | 4 | 4 | 26 | 31 |
| 15 | ocu-miR-196b-5p | 45 | 4 | 4 | 26 | 31 |
| 16 | abu-let-7b | 262 | 161 | 189 | 198 | 135 |
| 17 | abu-let-7b | 262 | 161 | 189 | 198 | 135 |
| 18 | ami-let-7b-5p | 262 | 161 | 189 | 198 | 135 |
| 19 | bta-let-7b | 262 | 161 | 189 | 198 | 135 |
| 20 | ccb-let-7b | 262 | 161 | 189 | 198 | 135 |
| 21 | ccb-let-7b | 262 | 161 | 189 | 198 | 135 |
| 22 | cfa-let-7b | 262 | 161 | 189 | 198 | 135 |
| 23 | cgr-let-7b | 262 | 161 | 189 | 198 | 135 |
| 24 | chi-let-7b-5p | 262 | 161 | 189 | 198 | 135 |
| 25 | chi-let-7b-5p | 262 | 161 | 189 | 198 | 135 |
| 26 | cja-let-7b | 262 | 161 | 189 | 198 | 135 |
| 27 | cpi-let-7b-5p | 262 | 161 | 189 | 198 | 135 |
| 28 | cpo-let-7b-5p | 262 | 161 | 189 | 198 | 135 |
| 29 | cpo-let-7b-5p | 262 | 161 | 189 | 198 | 135 |
| 30 | dma-let-7b | 262 | 161 | 189 | 198 | 135 |
| 31 | dno-let-7b-5p | 262 | 161 | 189 | 198 | 135 |
| 32 | dre-let-7b | 262 | 161 | 189 | 198 | 135 |
| 33 | dre-let-7b | 262 | 161 | 189 | 198 | 135 |
| 34 | fru-let-7b | 262 | 161 | 189 | 198 | 135 |
| 35 | gga-let-7b | 262 | 161 | 189 | 198 | 135 |
| 36 | hsa-let-7b-5p | 262 | 161 | 189 | 198 | 135 |
| 37 | hsa-let-7b-5p | 262 | 161 | 189 | 198 | 135 |
| 38 | mdo-let-7b | 262 | 161 | 189 | 198 | 135 |
| 39 | mml-let-7b-5p | 262 | 161 | 189 | 198 | 135 |
| 40 | mmr-let-7b | 262 | 161 | 189 | 198 | 135 |
| 41 | mmr-let-7b | 262 | 161 | 189 | 198 | 135 |
| 42 | mmu-let-7b-5p | 262 | 161 | 189 | 198 | 135 |
| 43 | mze-let-7b | 262 | 161 | 189 | 198 | 135 |
| 44 | nbr-let-7b | 262 | 161 | 189 | 198 | 135 |
| 45 | nbr-let-7b | 262 | 161 | 189 | 198 | 135 |
| 46 | oan-let-7b-5p | 262 | 161 | 189 | 198 | 135 |
| 47 | ocu-let-7b-5p | 262 | 161 | 189 | 198 | 135 |
| 48 | oga-let-7b | 262 | 161 | 189 | 198 | 135 |
| 49 | oga-let-7b | 262 | 161 | 189 | 198 | 135 |
| 50 | oha-let-7b-5p | 262 | 161 | 189 | 198 | 135 |
| 51 | oni-let-7b | 262 | 161 | 189 | 198 | 135 |
| 52 | pbv-let-7b-5p | 262 | 161 | 189 | 198 | 135 |
| 53 | pha-let-7b | 262 | 161 | 189 | 198 | 135 |
| 54 | pha-let-7b | 262 | 161 | 189 | 198 | 135 |
| 55 | ppy-let-7b | 262 | 161 | 189 | 198 | 135 |
| 56 | pol-let-7b-5p | 262 | 161 | 189 | 198 | 135 |
| 57 | ppa-let-7b | 262 | 161 | 189 | 198 | 135 |
| 58 | ppa-let-7b | 262 | 161 | 189 | 198 | 135 |
| 59 | ppy-let-7b | 262 | 161 | 189 | 198 | 135 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ptr-let-7b | 262 | 161 | 189 | 198 | 135 |
| 4 | rno-let-7b-5p | 262 | 161 | 189 | 198 | 135 |
| 5 | sbo-let-7b | 262 | 161 | 189 | 198 | 135 |
| 6 | ssa-let-7b-5p | 262 | 161 | 189 | 198 | 135 |
| 7 | tgu-let-7b-5p | 262 | 161 | 189 | 198 | 135 |
| 8 | tni-let-7b | 262 | 161 | 189 | 198 | 135 |
| 9 | | | | | | |
| 10 | abu-miR-34 | 58 | 9 | 85 | 42 | 29 |
| 11 | age-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 12 | bta-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 13 | ccb-miR-34 | 58 | 9 | 85 | 42 | 29 |
| 14 | cfa-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 15 | cgr-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 16 | chi-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 17 | cli-miR-34a-5p | 58 | 9 | 85 | 42 | 29 |
| 18 | cpi-miR-34a-5p | 58 | 9 | 85 | 42 | 29 |
| 19 | cpo-miR-34a-5p | 58 | 9 | 85 | 42 | 29 |
| 20 | dno-miR-34a-5p | 58 | 9 | 85 | 42 | 29 |
| 21 | dre-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 22 | eca-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 23 | ggo-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 24 | gmo-miR-34-5p | 58 | 9 | 85 | 42 | 29 |
| 25 | hsa-miR-34a-5p | 58 | 9 | 85 | 42 | 29 |
| 26 | ipu-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 27 | lla-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 28 | mml-miR-34a-5p | 58 | 9 | 85 | 42 | 29 |
| 29 | mmr-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 30 | mmu-miR-34a-5p | 58 | 9 | 85 | 42 | 29 |
| 31 | mne-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 32 | mze-miR-34 | 58 | 9 | 85 | 42 | 29 |
| 33 | nbr-miR-34 | 58 | 9 | 85 | 42 | 29 |
| 34 | nle-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 35 | ocu-miR-34a-5p | 58 | 9 | 85 | 42 | 29 |
| 36 | oga-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 37 | oni-miR-34 | 58 | 9 | 85 | 42 | 29 |
| 38 | pal-miR-34a-5p | 58 | 9 | 85 | 42 | 29 |
| 39 | pbv-miR-34a-5p | 58 | 9 | 85 | 42 | 29 |
| 40 | pony-miR-34 | 58 | 9 | 85 | 42 | 29 |
| 41 | ppa-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 42 | ppy-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 43 | ptr-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 44 | rno-miR-34a-5p | 58 | 9 | 85 | 42 | 29 |
| 45 | sla-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 46 | ssc-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-----|-----|-----|-----|----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | tgu-miR-34a | 58 | 9 | 85 | 42 | 29 |
| 4 | cja-miR-222 | 28 | 20 | 33 | 32 | 14 |
| 5 | cpi-miR-222a-3p | 28 | 20 | 33 | 32 | 14 |
| 6 | gmo-miR-222-3p | 28 | 20 | 33 | 32 | 14 |
| 7 | gmo-miR-222-3p | 28 | 20 | 33 | 32 | 14 |
| 8 | mmu-miR-222-3p | 28 | 20 | 33 | 32 | 14 |
| 9 | mmu-miR-222-3p | 28 | 20 | 33 | 32 | 14 |
| 10 | pal-miR-222-3p | 28 | 20 | 33 | 32 | 14 |
| 11 | xla-miR-222-3p | 28 | 20 | 33 | 32 | 14 |
| 12 | xla-miR-222-3p | 28 | 20 | 33 | 32 | 14 |
| 13 | ccr-miR-100 | 31 | 0 | 40 | 10 | 8 |
| 14 | cgr-miR-100-5p | 31 | 0 | 40 | 10 | 8 |
| 15 | chi-miR-100-5p | 31 | 0 | 40 | 10 | 8 |
| 16 | cpi-miR-100-5p | 31 | 0 | 40 | 10 | 8 |
| 17 | cpi-miR-100-5p | 31 | 0 | 40 | 10 | 8 |
| 18 | dma-miR-100 | 31 | 0 | 40 | 10 | 8 |
| 19 | mdo-miR-100-5p | 31 | 0 | 40 | 10 | 8 |
| 20 | mdo-miR-100-5p | 31 | 0 | 40 | 10 | 8 |
| 21 | pmi-miR-100-5p | 31 | 0 | 40 | 10 | 8 |
| 22 | sbo-miR-100 | 31 | 0 | 40 | 10 | 8 |
| 23 | sha-miR-100 | 31 | 0 | 40 | 10 | 8 |
| 24 | sha-miR-100 | 31 | 0 | 40 | 10 | 8 |
| 25 | tgu-miR-100-5p | 31 | 0 | 40 | 10 | 8 |
| 26 | hme-let-7 | 86 | 41 | 76 | 62 | 44 |
| 27 | pca-let-7-5p | 86 | 41 | 76 | 62 | 44 |
| 28 | ame-let-7-5p | 86 | 41 | 76 | 62 | 43 |
| 29 | ame-let-7-5p | 86 | 41 | 76 | 62 | 43 |
| 30 | bdo-let-7 | 86 | 41 | 76 | 62 | 43 |
| 31 | bmo-let-7-5p | 86 | 41 | 76 | 62 | 43 |
| 32 | bmo-let-7-5p | 86 | 41 | 76 | 62 | 43 |
| 33 | cte-let-7 | 86 | 41 | 76 | 62 | 43 |
| 34 | dan-let-7 | 86 | 41 | 76 | 62 | 43 |
| 35 | der-let-7 | 86 | 41 | 76 | 62 | 43 |
| 36 | dgr-let-7 | 86 | 41 | 76 | 62 | 43 |
| 37 | dgr-let-7 | 86 | 41 | 76 | 62 | 43 |
| 38 | dme-let-7-5p | 86 | 41 | 76 | 62 | 43 |
| 39 | dmo-let-7 | 86 | 41 | 76 | 62 | 43 |
| 40 | dpe-let-7 | 86 | 41 | 76 | 62 | 43 |
| 41 | dpe-let-7 | 86 | 41 | 76 | 62 | 43 |
| 42 | dps-let-7 | 86 | 41 | 76 | 62 | 43 |
| 43 | dqu-let-7-5p | 86 | 41 | 76 | 62 | 43 |
| 44 | dse-let-7 | 86 | 41 | 76 | 62 | 43 |
| 45 | dse-let-7 | 86 | 41 | 76 | 62 | 43 |
| 46 | dsi-let-7 | 86 | 41 | 76 | 62 | 43 |
| 47 | dvi-let-7 | 86 | 41 | 76 | 62 | 43 |
| 48 | dwi-let-7 | 86 | 41 | 76 | 62 | 43 |
| 49 | dwi-let-7 | 86 | 41 | 76 | 62 | 43 |
| 50 | dya-let-7 | 86 | 41 | 76 | 62 | 43 |
| 51 | ggo-let-7a | 86 | 41 | 76 | 62 | 43 |
| 52 | isc-let-7 | 86 | 41 | 76 | 62 | 43 |
| 53 | isc-let-7 | 86 | 41 | 76 | 62 | 43 |
| 54 | ngi-let-7 | 86 | 41 | 76 | 62 | 43 |
| 55 | nvi-let-7 | 86 | 41 | 76 | 62 | 43 |
| 56 | ola-let-7a-5p | 86 | 41 | 76 | 62 | 43 |
| 57 | ola-let-7a-5p | 86 | 41 | 76 | 62 | 43 |
| 58 | sha-let-7a | 86 | 41 | 76 | 62 | 43 |
| 59 | abu-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | age-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 4 | ami-miR-222a-3p | 123 | 106 | 185 | 150 | 53 |
| 5 | cgr-miR-222-3p | 123 | 106 | 185 | 150 | 53 |
| 6 | chi-miR-222-3p | 123 | 106 | 185 | 150 | 53 |
| 7 | cli-miR-222a-3p | 123 | 106 | 185 | 150 | 53 |
| 8 | cli-miR-222a-3p | 123 | 106 | 185 | 150 | 53 |
| 9 | cli-miR-222a-3p | 123 | 106 | 185 | 150 | 53 |
| 10 | cpo-miR-222-3p | 123 | 106 | 185 | 150 | 53 |
| 11 | dma-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 12 | dno-miR-222-3p | 123 | 106 | 185 | 150 | 53 |
| 13 | dno-miR-222-3p | 123 | 106 | 185 | 150 | 53 |
| 14 | dre-miR-222a-3p | 123 | 106 | 185 | 150 | 53 |
| 15 | fru-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 16 | gga-miR-222a | 123 | 106 | 185 | 150 | 53 |
| 17 | gga-miR-222a | 123 | 106 | 185 | 150 | 53 |
| 18 | mdo-miR-222a | 123 | 106 | 185 | 150 | 53 |
| 19 | mmr-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 20 | mze-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 21 | mze-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 22 | nbr-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 23 | nle-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 24 | ocu-miR-222-3p | 123 | 106 | 185 | 150 | 53 |
| 25 | ocu-miR-222-3p | 123 | 106 | 185 | 150 | 53 |
| 26 | oga-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 27 | oha-miR-222a-3p | 123 | 106 | 185 | 150 | 53 |
| 28 | oni-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 29 | oni-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 30 | pbv-miR-222a-3p | 123 | 106 | 185 | 150 | 53 |
| 31 | pha-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 32 | pha-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 33 | ppy-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 34 | ppa-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 35 | ssa-miR-222a-3p | 123 | 106 | 185 | 150 | 53 |
| 36 | ssc-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 37 | ssc-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 38 | tgu-miR-222-3p | 123 | 106 | 185 | 150 | 53 |
| 39 | tni-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 40 | xtr-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 41 | xtr-miR-222 | 123 | 106 | 185 | 150 | 53 |
| 42 | efu-let-7f | 201 | 112 | 115 | 183 | 125 |
| 43 | aca-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 44 | bta-let-7f | 199 | 112 | 115 | 182 | 125 |
| 45 | bta-let-7f | 199 | 112 | 115 | 182 | 125 |
| 46 | cfa-let-7f | 199 | 112 | 115 | 182 | 125 |
| 47 | cgr-let-7f | 199 | 112 | 115 | 182 | 125 |
| 48 | chi-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 49 | chi-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 50 | cja-let-7f | 199 | 112 | 115 | 182 | 125 |
| 51 | cli-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 52 | cpi-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 53 | cpi-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 54 | cpo-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 55 | dma-let-7f | 199 | 112 | 115 | 182 | 125 |
| 56 | dno-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 57 | dno-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 58 | dre-let-7f | 199 | 112 | 115 | 182 | 125 |
| 59 | eca-let-7f | 199 | 112 | 115 | 182 | 125 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | gga-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 4 | gmo-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 5 | hsa-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 6 | ipu-let-7f | 199 | 112 | 115 | 182 | 125 |
| 7 | mdo-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 8 | mml-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 9 | mmr-let-7f | 199 | 112 | 115 | 182 | 125 |
| 10 | mmu-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 11 | nle-let-7f | 199 | 112 | 115 | 182 | 125 |
| 12 | oan-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 13 | ocu-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 14 | oga-let-7f | 199 | 112 | 115 | 182 | 125 |
| 15 | oha-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 16 | oni-let-7f | 199 | 112 | 115 | 182 | 125 |
| 17 | pal-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 18 | pav-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 19 | pha-let-7f | 199 | 112 | 115 | 182 | 125 |
| 20 | ppa-let-7f | 199 | 112 | 115 | 182 | 125 |
| 21 | ppy-let-7f | 199 | 112 | 115 | 182 | 125 |
| 22 | ptr-let-7f | 199 | 112 | 115 | 182 | 125 |
| 23 | rno-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 24 | sbo-let-7f | 199 | 112 | 115 | 182 | 125 |
| 25 | ssc-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 26 | tch-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 27 | tgu-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 28 | xla-let-7f-5p | 199 | 112 | 115 | 182 | 125 |
| 29 | xtr-let-7f | 199 | 112 | 115 | 182 | 125 |
| 30 | bfl-miR-100-5p | 57 | 2 | 301 | 35 | 20 |
| 31 | dpu-miR-100 | 57 | 2 | 301 | 35 | 20 |
| 32 | hpo-miR-100-5p | 57 | 2 | 301 | 35 | 20 |
| 33 | isc-miR-100 | 57 | 2 | 301 | 35 | 20 |
| 34 | abu-let-7i | 305 | 162 | 122 | 253 | 165 |
| 35 | aca-let-7i-5p | 305 | 162 | 122 | 253 | 165 |
| 36 | bta-let-7i | 305 | 162 | 122 | 253 | 165 |
| 37 | chi-let-7i-5p | 305 | 162 | 122 | 253 | 165 |
| 38 | cja-let-7i | 305 | 162 | 122 | 253 | 165 |
| 39 | cpi-let-7i-5p | 305 | 162 | 122 | 253 | 165 |
| 40 | cpo-let-7i-5p | 305 | 162 | 122 | 253 | 165 |
| 41 | dno-let-7i-5p | 305 | 162 | 122 | 253 | 165 |
| 42 | dre-let-7i | 305 | 162 | 122 | 253 | 165 |
| 43 | fru-let-7i | 305 | 162 | 122 | 253 | 165 |
| 44 | gmo-let-7i-5p | 305 | 162 | 122 | 253 | 165 |
| 45 | hsa-let-7i-5p | 305 | 162 | 122 | 253 | 165 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ipu-let-7i | 305 | 162 | 122 | 253 | 165 |
| 4 | mml-let-7i-5p | 305 | 162 | 122 | 253 | 165 |
| 5 | mmu-let-7i-5p | 305 | 162 | 122 | 253 | 165 |
| 6 | mze-let-7i | 305 | 162 | 122 | 253 | 165 |
| 7 | nbr-let-7i | 305 | 162 | 122 | 253 | 165 |
| 8 | nle-let-7i | 305 | 162 | 122 | 253 | 165 |
| 9 | oar-let-7i | 305 | 162 | 122 | 253 | 165 |
| 10 | ocu-let-7i-5p | 305 | 162 | 122 | 253 | 165 |
| 11 | oga-let-7i | 305 | 162 | 122 | 253 | 165 |
| 12 | oha-let-7i-5p | 305 | 162 | 122 | 253 | 165 |
| 13 | oni-let-7i | 305 | 162 | 122 | 253 | 165 |
| 14 | pal-let-7i-5p | 305 | 162 | 122 | 253 | 165 |
| 15 | pbv-let-7i-5p | 305 | 162 | 122 | 253 | 165 |
| 16 | pha-let-7i | 305 | 162 | 122 | 253 | 165 |
| 17 | ppy-let-7i | 305 | 162 | 122 | 253 | 165 |
| 18 | ppa-let-7i | 305 | 162 | 122 | 253 | 165 |
| 19 | ppy-let-7i | 305 | 162 | 122 | 253 | 165 |
| 20 | ptr-let-7i | 305 | 162 | 122 | 253 | 165 |
| 21 | rno-let-7i-5p | 305 | 162 | 122 | 253 | 165 |
| 22 | ssa-let-7i-5p | 305 | 162 | 122 | 253 | 165 |
| 23 | tch-let-7i-5p | 305 | 162 | 122 | 253 | 165 |
| 24 | tgu-let-7i-5p | 305 | 162 | 122 | 253 | 165 |
| 25 | tni-let-7i | 305 | 162 | 122 | 253 | 165 |
| 26 | cli-let-7i-5p | 309 | 162 | 123 | 256 | 165 |
| 27 | asu-miR-100a-5p | 57 | 3 | 311 | 35 | 20 |
| 28 | prd-miR-100-5p | 57 | 3 | 311 | 35 | 20 |
| 29 | oha-miR-100-5p | 47 | 2 | 288 | 32 | 16 |
| 30 | aae-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 31 | abu-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 32 | aca-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 33 | aga-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 34 | age-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 35 | ame-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 36 | ami-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 37 | bbe-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 38 | bma-miR-100b | 47 | 2 | 288 | 31 | 16 |
| 39 | bmo-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 40 | bta-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 41 | cja-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 42 | cli-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 43 | cpo-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 44 | cqu-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 45 | dno-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|----|----|-----|----|----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | dre-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 4 | eca-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 5 | fru-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 6 | gga-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 7 | ggo-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 8 | gmo-miR-100a-5p | 47 | 2 | 288 | 31 | 16 |
| 9 | gmo-miR-100a-5p | 47 | 2 | 288 | 31 | 16 |
| 10 | gmo-miR-100a-5p | 47 | 2 | 288 | 31 | 16 |
| 11 | hsa-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 12 | ipu-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 13 | ipu-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 14 | lgi-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 15 | lla-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 16 | mml-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 17 | mml-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 18 | mmr-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 19 | mmu-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 20 | mse-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 21 | mse-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 22 | mze-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 23 | nbr-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 24 | nle-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 25 | nle-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 26 | nvi-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 27 | oan-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 28 | ocu-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 29 | ocu-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 30 | oga-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 31 | oni-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 32 | oni-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 33 | pal-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 34 | pbv-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 35 | pha-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 36 | pma-miR-100a-5p | 47 | 2 | 288 | 31 | 16 |
| 37 | pma-miR-100a-5p | 47 | 2 | 288 | 31 | 16 |
| 38 | pny-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 39 | ppa-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 40 | ppy-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 41 | ppy-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 42 | pte-miR-100b-5p | 47 | 2 | 288 | 31 | 16 |
| 43 | ptr-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 44 | rno-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 45 | rno-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 46 | sko-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 47 | sla-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 48 | ssa-miR-100a-5p | 47 | 2 | 288 | 31 | 16 |
| 49 | ssc-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 50 | ssc-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 51 | tcf-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 52 | tch-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 53 | tni-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 54 | tni-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 55 | xla-miR-100-5p | 47 | 2 | 288 | 31 | 16 |
| 56 | xtr-miR-100 | 47 | 2 | 288 | 31 | 16 |
| 57 | tca-miR-100-5p | 47 | 2 | 290 | 31 | 16 |
| 58 | tca-miR-100-5p | 47 | 2 | 290 | 31 | 16 |
| 59 | ami-let-7f-5p | 54 | 16 | 39 | 51 | 36 |
| 60 | | | | | | |

| | | | | | | |
|----|------------------|-----|----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ggo-let-7f | 54 | 16 | 39 | 51 | 36 |
| 4 | oar-let-7f | 54 | 16 | 39 | 51 | 36 |
| 5 | cli-miR-199-3p | 450 | 16 | 114 | 402 | 242 |
| 6 | efu-miR-199 | 450 | 16 | 114 | 402 | 242 |
| 7 | dre-miR-199-3p | 426 | 15 | 111 | 375 | 227 |
| 8 | oha-miR-199c-3p | 426 | 15 | 111 | 375 | 227 |
| 9 | ssc-miR-199b-3p | 426 | 15 | 111 | 375 | 227 |
| 10 | xtr-miR-199a-3p | 426 | 15 | 111 | 375 | 227 |
| 11 | xla-miR-199-3p | 379 | 12 | 105 | 334 | 200 |
| 12 | ami-miR-199-3p | 379 | 12 | 105 | 334 | 200 |
| 13 | bta-miR-199a-3p | 379 | 12 | 105 | 334 | 200 |
| 14 | cpi-miR-199-3p | 379 | 12 | 105 | 334 | 200 |
| 15 | cpo-miR-199-3p | 379 | 12 | 105 | 334 | 200 |
| 16 | dno-miR-199-3p | 379 | 12 | 105 | 334 | 200 |
| 17 | eca-miR-199a-3p | 379 | 12 | 105 | 334 | 200 |
| 18 | eca-miR-199b-3p | 379 | 12 | 105 | 334 | 200 |
| 19 | gmo-miR-199-3p | 379 | 12 | 105 | 334 | 200 |
| 20 | hsa-miR-199a-3p | 379 | 12 | 105 | 334 | 200 |
| 21 | hsa-miR-199b-3p | 379 | 12 | 105 | 334 | 200 |
| 22 | mml-miR-199a-3p | 379 | 12 | 105 | 334 | 200 |
| 23 | mmu-miR-199a-3p | 379 | 12 | 105 | 334 | 200 |
| 24 | mmu-miR-199b-3p | 379 | 12 | 105 | 334 | 200 |
| 25 | ocu-miR-199a-3p | 379 | 12 | 105 | 334 | 200 |
| 26 | oha-miR-199a-3p | 379 | 12 | 105 | 334 | 200 |
| 27 | ola-miR-199a-3p | 379 | 12 | 105 | 334 | 200 |
| 28 | pol-miR-199a-3p | 379 | 12 | 105 | 334 | 200 |
| 29 | ptr-miR-199a-3p | 379 | 12 | 105 | 334 | 200 |
| 30 | ptr-miR-199b | 379 | 12 | 105 | 334 | 200 |
| 31 | rno-miR-199a-3p | 379 | 12 | 105 | 334 | 200 |
| 32 | ssc-miR-199a-3p | 379 | 12 | 105 | 334 | 200 |
| 33 | abu-miR-199-3p | 358 | 11 | 102 | 309 | 185 |
| 34 | ccr-miR-199-3p | 358 | 11 | 102 | 309 | 185 |
| 35 | cfa-miR-199 | 358 | 11 | 102 | 309 | 185 |
| 36 | cgr-miR-199a-3p | 358 | 11 | 102 | 309 | 185 |
| 37 | chi-miR-199a-3p | 358 | 11 | 102 | 309 | 185 |
| 38 | chi-miR-199b-3p | 358 | 11 | 102 | 309 | 185 |
| 39 | chi-miR-199c-3p | 358 | 11 | 102 | 309 | 185 |
| 40 | cja-miR-199 | 358 | 11 | 102 | 309 | 185 |
| 41 | dma-miR-199 | 358 | 11 | 102 | 309 | 185 |
| 42 | gmo-miR-199-4-3p | 358 | 11 | 102 | 309 | 185 |
| 43 | ipu-miR-199a-3p | 358 | 11 | 102 | 309 | 185 |
| 44 | mdo-miR-199b-3p | 358 | 11 | 102 | 309 | 185 |
| 45 | mmr-miR-199 | 358 | 11 | 102 | 309 | 185 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-----|----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | mze-miR-199 | 358 | 11 | 102 | 309 | 185 |
| 4 | nbr-miR-199 | 358 | 11 | 102 | 309 | 185 |
| 5 | nle-miR-199a | 358 | 11 | 102 | 309 | 185 |
| 6 | nle-miR-199b | 358 | 11 | 102 | 309 | 185 |
| 7 | oan-miR-199-3p | 358 | 11 | 102 | 309 | 185 |
| 8 | oar-miR-199a-3p | 358 | 11 | 102 | 309 | 185 |
| 9 | oga-miR-199 | 358 | 11 | 102 | 309 | 185 |
| 10 | oni-miR-199a | 358 | 11 | 102 | 309 | 185 |
| 11 | pal-miR-199-3p | 358 | 11 | 102 | 309 | 185 |
| 12 | pbv-miR-199-3p | 358 | 11 | 102 | 309 | 185 |
| 13 | pha-miR-199 | 358 | 11 | 102 | 309 | 185 |
| 14 | ppy-miR-199 | 358 | 11 | 102 | 309 | 185 |
| 15 | ppa-miR-199b | 358 | 11 | 102 | 309 | 185 |
| 16 | sbo-miR-199 | 358 | 11 | 102 | 309 | 185 |
| 17 | sha-miR-199a | 358 | 11 | 102 | 309 | 185 |
| 18 | ssa-miR-199a-3p | 358 | 11 | 102 | 309 | 185 |
| 19 | tch-miR-199a-3p | 358 | 11 | 102 | 309 | 185 |
| 20 | tch-miR-199b-3p | 358 | 11 | 102 | 309 | 185 |
| 21 | tgu-miR-199-3p | 358 | 11 | 102 | 309 | 185 |
| 22 | aae-miR-125-5p | 75 | 5 | 62 | 39 | 22 |
| 23 | abu-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 24 | aca-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 25 | aga-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 26 | age-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 27 | ami-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 28 | bbe-miR-125a-5p | 75 | 5 | 62 | 39 | 22 |
| 29 | bdo-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 30 | bfl-miR-125a-5p | 75 | 5 | 62 | 39 | 22 |
| 31 | bta-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 32 | ccb-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 33 | cfa-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 34 | cgr-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 35 | cja-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 36 | cja-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 37 | cli-miR-125-5p | 75 | 5 | 62 | 39 | 22 |
| 38 | cpi-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 39 | cpo-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 40 | cqu-miR-125-5p | 75 | 5 | 62 | 39 | 22 |
| 41 | cte-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 42 | dan-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 43 | der-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 44 | dgr-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 45 | dma-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|----|---|----|----|----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | dme-miR-125-5p | 75 | 5 | 62 | 39 | 22 |
| 4 | dmo-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 5 | dno-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 6 | dpe-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 7 | dps-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 8 | dps-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 9 | dps-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 10 | dqu-miR-125-5p | 75 | 5 | 62 | 39 | 22 |
| 11 | dre-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 12 | dse-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 13 | dse-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 14 | dsi-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 15 | dwi-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 16 | dya-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 17 | dya-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 18 | eca-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 19 | efu-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 20 | fru-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 21 | fru-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 22 | gga-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 23 | ggo-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 24 | ggo-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 25 | gmo-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 26 | hsa-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 27 | ipu-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 28 | lca-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 29 | lca-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 30 | lla-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 31 | lva-miR-125-5p | 75 | 5 | 62 | 39 | 22 |
| 32 | mdo-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 33 | mdo-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 34 | mml-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 35 | mmr-miR-125a | 75 | 5 | 62 | 39 | 22 |
| 36 | mmu-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 37 | mmu-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 38 | mne-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 39 | mze-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 40 | nbr-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 41 | nbr-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 42 | nle-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 43 | nlo-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 44 | nvi-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 45 | nvi-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 46 | oan-miR-125-5p | 75 | 5 | 62 | 39 | 22 |
| 47 | ocu-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 48 | oga-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 49 | oga-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 50 | oha-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 51 | ola-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 52 | ola-miR-125c | 75 | 5 | 62 | 39 | 22 |
| 53 | oni-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 54 | oni-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 55 | pal-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 56 | pbv-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 57 | pbv-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 58 | pha-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 59 | pma-miR-125-5p | 75 | 5 | 62 | 39 | 22 |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|----|----|----|----|----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | pmi-miR-125-5p | 75 | 5 | 62 | 39 | 22 |
| 4 | pony-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 5 | ppa-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 6 | ppy-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 7 | ptr-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 8 | rno-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 9 | sha-miR-125a | 75 | 5 | 62 | 39 | 22 |
| 10 | sko-miR-125a | 75 | 5 | 62 | 39 | 22 |
| 11 | sla-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 12 | spu-miR-125-5p | 75 | 5 | 62 | 39 | 22 |
| 13 | ssa-miR-125a-5p | 75 | 5 | 62 | 39 | 22 |
| 14 | ssc-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 15 | tca-miR-125-5p | 75 | 5 | 62 | 39 | 22 |
| 16 | tcf-miR-125 | 75 | 5 | 62 | 39 | 22 |
| 17 | tch-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 18 | tgu-miR-125-5p | 75 | 5 | 62 | 39 | 22 |
| 19 | tni-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 20 | xla-miR-125b-5p | 75 | 5 | 62 | 39 | 22 |
| 21 | xtr-miR-125b | 75 | 5 | 62 | 39 | 22 |
| 22 | aca-let-7b-5p | 66 | 35 | 74 | 42 | 30 |
| 23 | ggo-let-7b | 66 | 35 | 74 | 42 | 30 |
| 24 | ipu-let-7b | 66 | 35 | 74 | 42 | 30 |
| 25 | oar-let-7b | 66 | 35 | 74 | 42 | 30 |
| 26 | ola-let-7b | 66 | 35 | 74 | 42 | 30 |
| 27 | cgr-miR-125a-5p | 43 | 2 | 23 | 26 | 18 |
| 28 | cpo-miR-125a-5p | 43 | 2 | 23 | 26 | 18 |
| 29 | eca-miR-125a-5p | 43 | 2 | 23 | 26 | 18 |
| 30 | hsa-miR-125a-5p | 43 | 2 | 23 | 26 | 18 |
| 31 | mml-miR-125a-5p | 43 | 2 | 23 | 26 | 18 |
| 32 | mmu-miR-125a-5p | 43 | 2 | 23 | 26 | 18 |
| 33 | oga-miR-125a | 43 | 2 | 23 | 26 | 18 |
| 34 | ppy-miR-125a-5p | 43 | 2 | 23 | 26 | 18 |
| 35 | rno-miR-125a-5p | 43 | 2 | 23 | 26 | 18 |
| 36 | sbo-miR-125a | 43 | 2 | 23 | 26 | 18 |
| 37 | efu-miR-99b | 42 | 1 | 76 | 17 | 18 |
| 38 | bta-miR-99b | 42 | 1 | 76 | 17 | 18 |
| 39 | cfa-miR-99b | 42 | 1 | 76 | 17 | 18 |
| 40 | chi-miR-99b-5p | 42 | 1 | 76 | 17 | 18 |
| 41 | cpo-miR-99b-5p | 42 | 1 | 76 | 17 | 18 |
| 42 | eca-miR-99b | 42 | 1 | 76 | 17 | 18 |
| 43 | hsa-miR-99b-5p | 42 | 1 | 76 | 17 | 18 |
| 44 | mml-miR-99b-5p | 42 | 1 | 76 | 17 | 18 |
| 45 | mmu-miR-99b-5p | 42 | 1 | 76 | 17 | 18 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|------------------|-----|----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | oga-miR-99b | 42 | 1 | 76 | 17 | 18 |
| 4 | pal-miR-99b-5p | 42 | 1 | 76 | 17 | 18 |
| 5 | ptr-miR-99b | 42 | 1 | 76 | 17 | 18 |
| 6 | rno-miR-99b-5p | 42 | 1 | 76 | 17 | 18 |
| 7 | ssc-miR-99b | 42 | 1 | 76 | 17 | 18 |
| 8 | tch-miR-99b-5p | 42 | 1 | 76 | 17 | 18 |
| 9 | abu-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 10 | aca-miR-26-3-5p | 615 | 49 | 348 | 440 | 277 |
| 11 | ami-miR-26-5p | 615 | 49 | 348 | 440 | 277 |
| 12 | bta-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 13 | cca-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 14 | cfa-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 15 | chi-miR-26a-5p | 615 | 49 | 348 | 440 | 277 |
| 16 | cja-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 17 | cli-miR-26-5p | 615 | 49 | 348 | 440 | 277 |
| 18 | cpi-miR-26-5p | 615 | 49 | 348 | 440 | 277 |
| 19 | cpo-miR-26a-5p | 615 | 49 | 348 | 440 | 277 |
| 20 | dma-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 21 | dno-miR-26a-5p | 615 | 49 | 348 | 440 | 277 |
| 22 | dre-miR-26a-5p | 615 | 49 | 348 | 440 | 277 |
| 23 | eca-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 24 | fru-miR-26 | 615 | 49 | 348 | 440 | 277 |
| 25 | gga-miR-26a-2-5p | 615 | 49 | 348 | 440 | 277 |
| 26 | ggo-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 27 | gmo-miR-26a-5p | 615 | 49 | 348 | 440 | 277 |
| 28 | hsa-miR-26a-5p | 615 | 49 | 348 | 440 | 277 |
| 29 | ipu-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 30 | lla-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 31 | mml-miR-26a-5p | 615 | 49 | 348 | 440 | 277 |
| 32 | mmr-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 33 | mmu-miR-26a-5p | 615 | 49 | 348 | 440 | 277 |
| 34 | mne-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 35 | mze-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 36 | nbr-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 37 | nle-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 38 | oan-miR-26-5p | 615 | 49 | 348 | 440 | 277 |
| 39 | oar-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 40 | ocu-miR-26a-5p | 615 | 49 | 348 | 440 | 277 |
| 41 | oga-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 42 | oha-miR-26-5p | 615 | 49 | 348 | 440 | 277 |
| 43 | oni-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 44 | pal-miR-26a-5p | 615 | 49 | 348 | 440 | 277 |
| 45 | pav-miR-26-5p | 615 | 49 | 348 | 440 | 277 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | pha-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 4 | pma-miR-26a-5p | 615 | 49 | 348 | 440 | 277 |
| 5 | ppy-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 6 | ppa-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 7 | ppa-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 8 | ppa-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 9 | ppa-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 10 | ptr-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 11 | rno-miR-26a-5p | 615 | 49 | 348 | 440 | 277 |
| 12 | sbo-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 13 | ssa-miR-26a-5p | 615 | 49 | 348 | 440 | 277 |
| 14 | ssa-miR-26a-5p | 615 | 49 | 348 | 440 | 277 |
| 15 | ssc-miR-26a | 615 | 49 | 348 | 440 | 277 |
| 16 | tch-miR-26a-5p | 615 | 49 | 348 | 440 | 277 |
| 17 | tch-miR-26a-5p | 615 | 49 | 348 | 440 | 277 |
| 18 | tgu-miR-26-5p | 615 | 49 | 348 | 440 | 277 |
| 19 | tni-miR-26 | 615 | 49 | 348 | 440 | 277 |
| 20 | xla-miR-26-5p | 615 | 49 | 348 | 440 | 277 |
| 21 | xla-miR-26-5p | 615 | 49 | 348 | 440 | 277 |
| 22 | efu-miR-26a | 618 | 49 | 351 | 447 | 278 |
| 23 | efu-miR-26c | 618 | 49 | 351 | 447 | 278 |
| 24 | bta-miR-21-5p | 2370 | 1990 | 2099 | 2260 | 1180 |
| 25 | cpo-miR-21-5p | 2370 | 1990 | 2099 | 2260 | 1180 |
| 26 | cpo-miR-21-5p | 2370 | 1990 | 2099 | 2260 | 1180 |
| 27 | dno-miR-21-5p | 2370 | 1990 | 2099 | 2260 | 1180 |
| 28 | ocu-miR-21-5p | 2370 | 1990 | 2099 | 2260 | 1180 |
| 29 | ocu-miR-21-5p | 2370 | 1990 | 2099 | 2260 | 1180 |
| 30 | sha-miR-21 | 2370 | 1990 | 2099 | 2260 | 1180 |
| 31 | ami-miR-21-5p | 2354 | 1975 | 2085 | 2242 | 1167 |
| 32 | chi-miR-21-5p | 2354 | 1975 | 2085 | 2242 | 1167 |
| 33 | chi-miR-21-5p | 2354 | 1975 | 2085 | 2242 | 1167 |
| 34 | dma-miR-21 | 2354 | 1975 | 2085 | 2242 | 1167 |
| 35 | mmr-miR-21 | 2354 | 1975 | 2085 | 2242 | 1167 |
| 36 | nle-miR-21 | 2354 | 1975 | 2085 | 2242 | 1167 |
| 37 | nle-miR-21 | 2354 | 1975 | 2085 | 2242 | 1167 |
| 38 | oar-miR-21 | 2354 | 1975 | 2085 | 2242 | 1167 |
| 39 | oga-miR-21 | 2354 | 1975 | 2085 | 2242 | 1167 |
| 40 | pbv-miR-21-5p | 2354 | 1975 | 2085 | 2242 | 1167 |
| 41 | pbv-miR-21-5p | 2354 | 1975 | 2085 | 2242 | 1167 |
| 42 | pha-miR-21 | 2354 | 1975 | 2085 | 2242 | 1167 |
| 43 | sbo-miR-21 | 2354 | 1975 | 2085 | 2242 | 1167 |
| 44 | aca-miR-181a | 530 | 24 | 204 | 364 | 281 |
| 45 | ami-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 46 | ami-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 47 | cgr-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 48 | cja-miR-181a | 530 | 24 | 204 | 364 | 281 |
| 49 | cja-miR-181a | 530 | 24 | 204 | 364 | 281 |
| 50 | cpi-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 51 | dma-miR-181a | 530 | 24 | 204 | 364 | 281 |
| 52 | dre-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 53 | dre-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 54 | eca-miR-181a | 530 | 24 | 204 | 364 | 281 |
| 55 | fru-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 56 | gga-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 57 | gga-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 58 | ggo-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 59 | gmo-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|------|------|------|------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | hsa-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 4 | lla-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 5 | mdo-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 6 | mml-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 7 | mmu-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 8 | mne-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 9 | nle-miR-181a | 530 | 24 | 204 | 364 | 281 |
| 10 | oan-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 11 | oar-miR-181a | 530 | 24 | 204 | 364 | 281 |
| 12 | oga-miR-181a | 530 | 24 | 204 | 364 | 281 |
| 13 | pha-miR-181a | 530 | 24 | 204 | 364 | 281 |
| 14 | pma-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 15 | ppa-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 16 | ppy-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 17 | ptr-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 18 | rno-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 19 | sla-miR-181a | 530 | 24 | 204 | 364 | 281 |
| 20 | ssa-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 21 | tch-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 22 | tgu-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 23 | tni-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 24 | xtr-miR-181a-5p | 530 | 24 | 204 | 364 | 281 |
| 25 | gma-miR169k | 4455 | 4521 | 1104 | 4737 | 10493 |
| 26 | gma-miR169l-5p | 4455 | 4521 | 1104 | 4737 | 10493 |
| 27 | mes-miR169l | 4455 | 4521 | 1104 | 4737 | 10493 |
| 28 | mes-miR169m | 4455 | 4521 | 1104 | 4737 | 10493 |
| 29 | bta-miR-181a | 573 | 27 | 235 | 389 | 301 |
| 30 | cli-miR-181a-5p | 573 | 27 | 235 | 389 | 301 |
| 31 | cpo-miR-181a-5p | 573 | 27 | 235 | 389 | 301 |
| 32 | dno-miR-181a-5p | 573 | 27 | 235 | 389 | 301 |
| 33 | ocu-miR-181a-5p | 573 | 27 | 235 | 389 | 301 |
| 34 | oha-miR-181a-5p | 573 | 27 | 235 | 389 | 301 |
| 35 | pal-miR-181a-5p | 573 | 27 | 235 | 389 | 301 |
| 36 | pbv-miR-181a-5p | 573 | 27 | 235 | 389 | 301 |
| 37 | ssc-miR-181a | 573 | 27 | 235 | 389 | 301 |
| 38 | ami-let-7i-5p | 41 | 17 | 46 | 40 | 27 |
| 39 | ccr-let-7i | 41 | 17 | 46 | 40 | 27 |
| 40 | gga-let-7i | 41 | 17 | 46 | 40 | 27 |
| 41 | ggo-let-7i | 41 | 17 | 46 | 40 | 27 |
| 42 | mdo-let-7i-5p | 41 | 17 | 46 | 40 | 27 |
| 43 | sha-let-7i | 41 | 17 | 46 | 40 | 27 |
| 44 | xla-let-7i-5p | 41 | 17 | 46 | 40 | 27 |
| 45 | xtr-let-7i | 41 | 17 | 46 | 40 | 27 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | bta-miR-26b | 46 | 28 | 38 | 40 | 14 |
| 4 | cfa-miR-26b | 46 | 28 | 38 | 40 | 14 |
| 5 | cgr-miR-26b-5p | 46 | 28 | 38 | 40 | 14 |
| 6 | chi-miR-26b-5p | 46 | 28 | 38 | 40 | 14 |
| 7 | chi-miR-26b-5p | 46 | 28 | 38 | 40 | 14 |
| 8 | cja-miR-26b | 46 | 28 | 38 | 40 | 14 |
| 9 | cja-miR-26b | 46 | 28 | 38 | 40 | 14 |
| 10 | cpo-miR-26b-5p | 46 | 28 | 38 | 40 | 14 |
| 11 | dma-miR-26b | 46 | 28 | 38 | 40 | 14 |
| 12 | dma-miR-26b | 46 | 28 | 38 | 40 | 14 |
| 13 | dno-miR-26b-5p | 46 | 28 | 38 | 40 | 14 |
| 14 | mmr-miR-26b | 46 | 28 | 38 | 40 | 14 |
| 15 | ocu-miR-26b-5p | 46 | 28 | 38 | 40 | 14 |
| 16 | pal-miR-26b-5p | 46 | 28 | 38 | 40 | 14 |
| 17 | pal-miR-26b-5p | 46 | 28 | 38 | 40 | 14 |
| 18 | pha-miR-26b | 46 | 28 | 38 | 40 | 14 |
| 19 | ppa-miR-26b | 46 | 28 | 38 | 40 | 14 |
| 20 | ppa-miR-26b | 46 | 28 | 38 | 40 | 14 |
| 21 | ssc-miR-26b-5p | 46 | 28 | 38 | 40 | 14 |
| 22 | tch-miR-26b-5p | 46 | 28 | 38 | 40 | 14 |
| 23 | efu-miR-26b | 47 | 30 | 39 | 41 | 14 |
| 24 | cfa-miR-24 | 507 | 314 | 364 | 538 | 238 |
| 25 | cfa-miR-24 | 507 | 314 | 364 | 538 | 238 |
| 26 | cgr-miR-24-3p | 507 | 314 | 364 | 538 | 238 |
| 27 | ipu-miR-24 | 507 | 314 | 364 | 538 | 238 |
| 28 | ipu-miR-24 | 507 | 314 | 364 | 538 | 238 |
| 29 | oga-miR-24 | 507 | 314 | 364 | 538 | 238 |
| 30 | oha-miR-24-3p | 507 | 314 | 364 | 538 | 238 |
| 31 | abu-miR-24b-3p | 505 | 314 | 364 | 538 | 237 |
| 32 | aca-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 33 | aca-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 34 | ami-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 35 | bta-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 36 | ccb-miR-24 | 505 | 314 | 364 | 538 | 237 |
| 37 | ccb-miR-24 | 505 | 314 | 364 | 538 | 237 |
| 38 | cja-miR-24 | 505 | 314 | 364 | 538 | 237 |
| 39 | cpo-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 40 | dno-miR-24a-3p | 505 | 314 | 364 | 538 | 237 |
| 41 | dno-miR-24a-3p | 505 | 314 | 364 | 538 | 237 |
| 42 | dre-miR-24 | 505 | 314 | 364 | 538 | 237 |
| 43 | eca-miR-24 | 505 | 314 | 364 | 538 | 237 |
| 44 | fru-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 45 | fru-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 46 | gga-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 47 | ggo-miR-24 | 505 | 314 | 364 | 538 | 237 |
| 48 | ggo-miR-24 | 505 | 314 | 364 | 538 | 237 |
| 49 | hsa-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 50 | mml-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 51 | mmu-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 52 | mne-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 53 | nbr-miR-24a | 505 | 314 | 364 | 538 | 237 |
| 54 | nbr-miR-24a | 505 | 314 | 364 | 538 | 237 |
| 55 | oan-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 56 | ocu-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 57 | ocu-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 58 | ola-miR-24a | 505 | 314 | 364 | 538 | 237 |
| 59 | oni-miR-24a | 505 | 314 | 364 | 538 | 237 |
| 60 | | | | | | |

| | | | | | | |
|----|------------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | pbv-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 4 | pma-miR-24 | 505 | 314 | 364 | 538 | 237 |
| 5 | ppy-miR-24a | 505 | 314 | 364 | 538 | 237 |
| 6 | ppa-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 7 | ppa-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 8 | ppp-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 9 | ptr-miR-24 | 505 | 314 | 364 | 538 | 237 |
| 10 | ptr-miR-24 | 505 | 314 | 364 | 538 | 237 |
| 11 | rno-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 12 | ssc-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 13 | ssc-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 14 | tgu-miR-24-3p | 505 | 314 | 364 | 538 | 237 |
| 15 | tni-miR-24 | 505 | 314 | 364 | 538 | 237 |
| 16 | xla-miR-24a-3p | 505 | 314 | 364 | 538 | 237 |
| 17 | xtr-miR-24a-3p | 505 | 314 | 364 | 538 | 237 |
| 18 | xtr-miR-24a-3p | 505 | 314 | 364 | 538 | 237 |
| 19 | abu-miR-181c | 64 | 15 | 28 | 42 | 45 |
| 20 | chi-miR-181b-5p | 64 | 15 | 28 | 42 | 45 |
| 21 | chi-miR-181b-5p | 64 | 15 | 28 | 42 | 45 |
| 22 | eca-miR-181b | 64 | 15 | 28 | 42 | 45 |
| 23 | hsa-miR-181b-5p | 64 | 15 | 28 | 42 | 45 |
| 24 | hsa-miR-181b-5p | 64 | 15 | 28 | 42 | 45 |
| 25 | mdo-miR-181b-5p | 64 | 15 | 28 | 42 | 45 |
| 26 | oha-miR-181b-5p | 64 | 15 | 28 | 42 | 45 |
| 27 | ppy-miR-181b | 64 | 15 | 28 | 42 | 45 |
| 28 | ptr-miR-181b | 64 | 15 | 28 | 42 | 45 |
| 29 | ptr-miR-181b | 64 | 15 | 28 | 42 | 45 |
| 30 | rno-miR-181b-5p | 64 | 15 | 28 | 42 | 45 |
| 31 | tch-miR-181b-5p | 64 | 15 | 28 | 42 | 45 |
| 32 | tch-miR-181b-5p | 64 | 15 | 28 | 42 | 45 |
| 33 | pde-miR159 | 342 | 153 | 44 | 381 | 330 |
| 34 | ssa-miR-23b-3p | 153 | 17 | 36 | 119 | 64 |
| 35 | bta-miR-10174-3p | 155 | 17 | 35 | 118 | 64 |
| 36 | oga-miR-23b | 155 | 17 | 35 | 118 | 64 |
| 37 | oga-miR-23b | 155 | 17 | 35 | 118 | 64 |
| 38 | tch-miR-23b-3p | 155 | 17 | 35 | 118 | 64 |
| 39 | cpi-miR-93-5p | 11 | 10 | 75 | 9 | 5 |
| 40 | sha-miR-93 | 11 | 10 | 75 | 9 | 5 |
| 41 | sha-miR-93 | 11 | 10 | 75 | 9 | 5 |
| 42 | gga-let-7g-5p | 33 | 17 | 56 | 30 | 20 |
| 43 | ggo-let-7g | 33 | 17 | 56 | 30 | 20 |
| 44 | ggo-let-7g | 33 | 17 | 56 | 30 | 20 |
| 45 | mdo-let-7g-5p | 33 | 17 | 56 | 30 | 20 |
| 46 | oar-let-7g | 33 | 17 | 56 | 30 | 20 |
| 47 | sha-let-7g | 33 | 17 | 56 | 30 | 20 |
| 48 | sha-let-7g | 33 | 17 | 56 | 30 | 20 |
| 49 | cli-miR-23b-3p | 155 | 18 | 35 | 119 | 63 |
| 50 | efu-miR-23b | 156 | 17 | 36 | 118 | 65 |
| 51 | aca-let-7g | 99 | 80 | 152 | 91 | 48 |
| 52 | ami-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 53 | ami-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 54 | bta-let-7g | 99 | 80 | 152 | 91 | 48 |
| 55 | cfa-let-7g | 99 | 80 | 152 | 91 | 48 |
| 56 | cgr-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 57 | cgr-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 58 | chi-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 59 | cja-let-7g | 99 | 80 | 152 | 91 | 48 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | cli-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 4 | cpi-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 5 | cpo-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 6 | dma-let-7g | 99 | 80 | 152 | 91 | 48 |
| 7 | dno-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 8 | eca-let-7g | 99 | 80 | 152 | 91 | 48 |
| 9 | hsa-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 10 | mml-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 11 | mmr-let-7g | 99 | 80 | 152 | 91 | 48 |
| 12 | mmu-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 13 | nle-let-7g | 99 | 80 | 152 | 91 | 48 |
| 14 | oan-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 15 | ocu-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 16 | oga-let-7g | 99 | 80 | 152 | 91 | 48 |
| 17 | oha-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 18 | pal-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 19 | pbv-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 20 | pha-let-7g | 99 | 80 | 152 | 91 | 48 |
| 21 | ppa-let-7g | 99 | 80 | 152 | 91 | 48 |
| 22 | ppy-let-7g | 99 | 80 | 152 | 91 | 48 |
| 23 | ptr-let-7g | 99 | 80 | 152 | 91 | 48 |
| 24 | rno-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 25 | ssc-let-7g | 99 | 80 | 152 | 91 | 48 |
| 26 | tch-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 27 | tgu-let-7g-5p | 99 | 80 | 152 | 91 | 48 |
| 28 | ami-miR-23b-3p | 153 | 17 | 35 | 116 | 63 |
| 29 | bta-miR-23b-3p | 153 | 17 | 35 | 116 | 63 |
| 30 | cpo-miR-23b-3p | 153 | 17 | 35 | 116 | 63 |
| 31 | dno-miR-23b-3p | 153 | 17 | 35 | 116 | 63 |
| 32 | dre-miR-23b-3p | 153 | 17 | 35 | 116 | 63 |
| 33 | hsa-miR-23b-3p | 153 | 17 | 35 | 116 | 63 |
| 34 | ocu-miR-23b-3p | 153 | 17 | 35 | 116 | 63 |
| 35 | oha-miR-23b-3p | 153 | 17 | 35 | 116 | 63 |
| 36 | ola-miR-23b | 153 | 17 | 35 | 116 | 63 |
| 37 | pbv-miR-23b-3p | 153 | 17 | 35 | 116 | 63 |
| 38 | pma-miR-23b | 153 | 17 | 35 | 116 | 63 |
| 39 | ppa-miR-23b | 153 | 17 | 35 | 116 | 63 |
| 40 | ppy-miR-23b | 153 | 17 | 35 | 116 | 63 |
| 41 | ptr-miR-23b | 153 | 17 | 35 | 116 | 63 |
| 42 | aca-miR-23a-3p | 403 | 112 | 128 | 342 | 207 |
| 43 | age-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 44 | ccr-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 45 | cgr-miR-23a-3p | 403 | 112 | 128 | 342 | 207 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | chi-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 4 | cpi-miR-23a-3p | 403 | 112 | 128 | 342 | 207 |
| 5 | eca-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 6 | ggo-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 7 | ggo-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 8 | hsa-miR-23a-3p | 403 | 112 | 128 | 342 | 207 |
| 9 | ipu-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 10 | ipu-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 11 | lca-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 12 | lca-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 13 | mml-miR-23a-3p | 403 | 112 | 128 | 342 | 207 |
| 14 | mmu-miR-23a-3p | 403 | 112 | 128 | 342 | 207 |
| 15 | mne-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 16 | pbv-miR-23a-3p | 403 | 112 | 128 | 342 | 207 |
| 17 | pbv-miR-23a-3p | 403 | 112 | 128 | 342 | 207 |
| 18 | pha-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 19 | phn-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 20 | ppa-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 21 | ppa-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 22 | ppy-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 23 | ppy-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 24 | ptr-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 25 | rno-miR-23a-3p | 403 | 112 | 128 | 342 | 207 |
| 26 | sla-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 27 | ssa-miR-23a-3p | 403 | 112 | 128 | 342 | 207 |
| 28 | ssc-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 29 | ssc-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 30 | xla-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 31 | xtr-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 32 | xtr-miR-23a | 403 | 112 | 128 | 342 | 207 |
| 33 | bta-miR-93 | 14 | 16 | 76 | 13 | 8 |
| 34 | cpo-miR-151-5p | 38 | 45 | 24 | 48 | 27 |
| 35 | dno-miR-151-5p | 38 | 45 | 24 | 48 | 27 |
| 36 | ami-miR-181b-5p | 95 | 27 | 50 | 66 | 59 |
| 37 | ami-miR-181b-5p | 95 | 27 | 50 | 66 | 59 |
| 38 | bta-miR-181b | 95 | 27 | 50 | 66 | 59 |
| 39 | cli-miR-181b-5p | 95 | 27 | 50 | 66 | 59 |
| 40 | cpi-miR-181b-5p | 95 | 27 | 50 | 66 | 59 |
| 41 | cpi-miR-181b-5p | 95 | 27 | 50 | 66 | 59 |
| 42 | cpo-miR-181b-5p | 95 | 27 | 50 | 66 | 59 |
| 43 | dno-miR-181b-5p | 95 | 27 | 50 | 66 | 59 |
| 44 | efu-miR-181e | 95 | 27 | 50 | 66 | 59 |
| 45 | efu-miR-181e | 95 | 27 | 50 | 66 | 59 |
| 46 | ggo-miR-181b | 95 | 27 | 50 | 66 | 59 |
| 47 | gmo-miR-181b-5p | 95 | 27 | 50 | 66 | 59 |
| 48 | hhi-miR-181b | 95 | 27 | 50 | 66 | 59 |
| 49 | hhi-miR-181b | 95 | 27 | 50 | 66 | 59 |
| 50 | lla-miR-181b | 95 | 27 | 50 | 66 | 59 |
| 51 | mml-miR-181b-5p | 95 | 27 | 50 | 66 | 59 |
| 52 | mmu-miR-181b-5p | 95 | 27 | 50 | 66 | 59 |
| 53 | mmu-miR-181b-5p | 95 | 27 | 50 | 66 | 59 |
| 54 | mne-miR-181b | 95 | 27 | 50 | 66 | 59 |
| 55 | ocu-miR-181b-5p | 95 | 27 | 50 | 66 | 59 |
| 56 | ola-miR-181b-5p | 95 | 27 | 50 | 66 | 59 |
| 57 | ola-miR-181b-5p | 95 | 27 | 50 | 66 | 59 |
| 58 | pal-miR-181b-5p | 95 | 27 | 50 | 66 | 59 |
| 59 | ppa-miR-181b | 95 | 27 | 50 | 66 | 59 |
| 60 | ppa-miR-181b | 95 | 27 | 50 | 66 | 59 |

| | | | | | | |
|----|-----------------|-----|----|----|----|----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ssc-miR-181b | 95 | 27 | 50 | 66 | 59 |
| 4 | tgu-miR-181b-5p | 95 | 27 | 50 | 66 | 59 |
| 5 | abu-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 6 | ami-miR-221-3p | 34 | 21 | 39 | 23 | 11 |
| 7 | ami-miR-221-3p | 34 | 21 | 39 | 23 | 11 |
| 8 | cgr-miR-221-3p | 34 | 21 | 39 | 23 | 11 |
| 9 | cgr-miR-221-3p | 34 | 21 | 39 | 23 | 11 |
| 10 | cpo-miR-221-3p | 34 | 21 | 39 | 23 | 11 |
| 11 | dma-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 12 | dma-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 13 | dno-miR-221-3p | 34 | 21 | 39 | 23 | 11 |
| 14 | dre-miR-221-3p | 34 | 21 | 39 | 23 | 11 |
| 15 | eca-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 16 | eca-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 17 | fru-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 18 | gga-miR-221-3p | 34 | 21 | 39 | 23 | 11 |
| 19 | ggo-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 20 | ggo-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 21 | hsa-miR-221-3p | 34 | 21 | 39 | 23 | 11 |
| 22 | mdo-miR-221-3p | 34 | 21 | 39 | 23 | 11 |
| 23 | mml-miR-221-3p | 34 | 21 | 39 | 23 | 11 |
| 24 | mml-miR-221-3p | 34 | 21 | 39 | 23 | 11 |
| 25 | mmr-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 26 | mmu-miR-221-3p | 34 | 21 | 39 | 23 | 11 |
| 27 | mze-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 28 | nbr-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 29 | nbr-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 30 | nle-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 31 | ocu-miR-221-3p | 34 | 21 | 39 | 23 | 11 |
| 32 | oga-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 33 | oga-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 34 | oha-miR-221-3p | 34 | 21 | 39 | 23 | 11 |
| 35 | ola-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 36 | oni-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 37 | oni-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 38 | pha-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 39 | phn-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 40 | ppy-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 41 | ppa-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 42 | ppy-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 43 | ptr-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 44 | rno-miR-221-3p | 34 | 21 | 39 | 23 | 11 |
| 45 | rno-miR-221-3p | 34 | 21 | 39 | 23 | 11 |
| 46 | sbo-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 47 | tgu-miR-221-3p | 34 | 21 | 39 | 23 | 11 |
| 48 | tni-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 49 | tni-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 50 | xtr-miR-221 | 34 | 21 | 39 | 23 | 11 |
| 51 | abu-miR-23b | 106 | 6 | 23 | 67 | 42 |
| 52 | aca-miR-23b-3p | 106 | 6 | 23 | 67 | 42 |
| 53 | aca-miR-23b-3p | 106 | 6 | 23 | 67 | 42 |
| 54 | ccb-miR-23b | 106 | 6 | 23 | 67 | 42 |
| 55 | cgr-miR-23b-3p | 106 | 6 | 23 | 67 | 42 |
| 56 | chi-miR-23b-3p | 106 | 6 | 23 | 67 | 42 |
| 57 | chi-miR-23b-3p | 106 | 6 | 23 | 67 | 42 |
| 58 | cja-miR-23b | 106 | 6 | 23 | 67 | 42 |
| 59 | cpi-miR-23b-3p | 106 | 6 | 23 | 67 | 42 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | dma-miR-23b | 106 | 6 | 23 | 67 | 42 |
| 4 | eca-miR-23b | 106 | 6 | 23 | 67 | 42 |
| 5 | gga-miR-23b-3p | 106 | 6 | 23 | 67 | 42 |
| 6 | ipu-miR-23b | 106 | 6 | 23 | 67 | 42 |
| 7 | mdu-miR-23b-3p | 106 | 6 | 23 | 67 | 42 |
| 8 | mml-miR-23b-3p | 106 | 6 | 23 | 67 | 42 |
| 9 | mmr-miR-23b | 106 | 6 | 23 | 67 | 42 |
| 10 | mmu-miR-23b-3p | 106 | 6 | 23 | 67 | 42 |
| 11 | mze-miR-23b | 106 | 6 | 23 | 67 | 42 |
| 12 | nbr-miR-23b | 106 | 6 | 23 | 67 | 42 |
| 13 | nle-miR-23b | 106 | 6 | 23 | 67 | 42 |
| 14 | oni-miR-23b | 106 | 6 | 23 | 67 | 42 |
| 15 | pha-miR-23b | 106 | 6 | 23 | 67 | 42 |
| 16 | pma-miR-23a-3p | 106 | 6 | 23 | 67 | 42 |
| 17 | ppy-miR-23b | 106 | 6 | 23 | 67 | 42 |
| 18 | rno-miR-23b-3p | 106 | 6 | 23 | 67 | 42 |
| 19 | tgu-miR-23-3p | 106 | 6 | 23 | 67 | 42 |
| 20 | xla-miR-23b-3p | 106 | 6 | 23 | 67 | 42 |
| 21 | xtr-miR-23b | 106 | 6 | 23 | 67 | 42 |
| 22 | efu-miR-23a | 692 | 247 | 187 | 626 | 335 |
| 23 | ami-miR-30d-5p | 57 | 28 | 69 | 62 | 22 |
| 24 | bta-miR-30d | 57 | 28 | 69 | 62 | 22 |
| 25 | cfa-miR-30d | 57 | 28 | 69 | 62 | 22 |
| 26 | cli-miR-30d-5p | 57 | 28 | 69 | 62 | 22 |
| 27 | cpo-miR-30d-5p | 57 | 28 | 69 | 62 | 22 |
| 28 | dno-miR-30d-5p | 57 | 28 | 69 | 62 | 22 |
| 29 | gmo-miR-30a-5p | 57 | 28 | 69 | 62 | 22 |
| 30 | nle-miR-30d | 57 | 28 | 69 | 62 | 22 |
| 31 | ocu-miR-30d-5p | 57 | 28 | 69 | 62 | 22 |
| 32 | oga-miR-30d | 57 | 28 | 69 | 62 | 22 |
| 33 | oha-miR-30d-5p | 57 | 28 | 69 | 62 | 22 |
| 34 | pal-miR-30d-5p | 57 | 28 | 69 | 62 | 22 |
| 35 | pbv-miR-30d-5p | 57 | 28 | 69 | 62 | 22 |
| 36 | pha-miR-30d | 57 | 28 | 69 | 62 | 22 |
| 37 | ssa-miR-30b-5p | 57 | 28 | 69 | 62 | 22 |
| 38 | ssc-miR-30d | 57 | 28 | 69 | 62 | 22 |
| 39 | tgu-miR-30d-5p | 57 | 28 | 69 | 62 | 22 |
| 40 | xla-miR-30d-5p | 57 | 28 | 69 | 62 | 22 |
| 41 | abu-miR-24a | 90 | 32 | 44 | 67 | 41 |
| 42 | chi-miR-24-3p | 90 | 32 | 44 | 67 | 41 |
| 43 | dma-miR-24 | 90 | 32 | 44 | 67 | 41 |
| 44 | dre-miR-24b-3p | 90 | 32 | 44 | 67 | 41 |
| 45 | gmo-miR-24a-3p | 90 | 32 | 44 | 67 | 41 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|------|-----|------|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ipu-miR-24b | 90 | 32 | 44 | 67 | 41 |
| 4 | mnr-miR-24 | 90 | 32 | 44 | 67 | 41 |
| 5 | mze-miR-24a | 90 | 32 | 44 | 67 | 41 |
| 6 | nbr-miR-24c | 90 | 32 | 44 | 67 | 41 |
| 7 | nle-miR-24 | 90 | 32 | 44 | 67 | 41 |
| 8 | oni-miR-24a-3 | 90 | 32 | 44 | 67 | 41 |
| 9 | oni-miR-24a-4 | 90 | 32 | 44 | 67 | 41 |
| 10 | oni-miR-24b-3p | 90 | 32 | 44 | 67 | 41 |
| 11 | pha-miR-24 | 90 | 32 | 44 | 67 | 41 |
| 12 | ppy-miR-24a-3 | 90 | 32 | 44 | 67 | 41 |
| 13 | ppy-miR-24a-4 | 90 | 32 | 44 | 67 | 41 |
| 14 | ssa-miR-24a-3p | 90 | 32 | 44 | 67 | 41 |
| 15 | dre-miR-23b | 138 | 9 | 32 | 97 | 54 |
| 16 | fru-miR-23b | 138 | 9 | 32 | 97 | 54 |
| 17 | ggo-miR-23b | 138 | 9 | 32 | 97 | 54 |
| 18 | gmo-miR-23b-3p | 138 | 9 | 32 | 97 | 54 |
| 19 | pal-miR-23b-3p | 138 | 9 | 32 | 97 | 54 |
| 20 | ssc-miR-23b | 138 | 9 | 32 | 97 | 54 |
| 21 | tni-miR-23b | 138 | 9 | 32 | 97 | 54 |
| 22 | cpo-miR-23a-3p | 672 | 228 | 184 | 607 | 324 |
| 23 | dno-miR-23a-3p | 672 | 228 | 184 | 607 | 324 |
| 24 | bta-miR-423-3p | 130 | 129 | 28 | 140 | 71 |
| 25 | sbo-miR-423 | 130 | 129 | 28 | 140 | 71 |
| 26 | dno-miR-24b-3p | 91 | 32 | 44 | 67 | 42 |
| 27 | efu-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 28 | abu-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 29 | aca-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 30 | age-miR-92 | 967 | 1113 | 97 | 1161 | 475 |
| 31 | ami-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 32 | bta-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 33 | ccr-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 34 | cfa-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 35 | cgr-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 36 | chi-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 37 | chi-miR-92b | 967 | 1113 | 97 | 1161 | 475 |
| 38 | cja-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 39 | cli-miR-92-3p | 967 | 1113 | 97 | 1161 | 475 |
| 40 | cpo-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 41 | dma-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 42 | dno-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 43 | dre-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 44 | eca-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 45 | fru-miR-92 | 967 | 1113 | 97 | 1161 | 475 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|------|-----|------|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ggo-miR-92 | 967 | 1113 | 97 | 1161 | 475 |
| 4 | hsa-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 5 | ipu-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 6 | lca-miR-92 | 967 | 1113 | 97 | 1161 | 475 |
| 7 | lla-miR-92 | 967 | 1113 | 97 | 1161 | 475 |
| 8 | lla-miR-92 | 967 | 1113 | 97 | 1161 | 475 |
| 9 | lla-miR-92 | 967 | 1113 | 97 | 1161 | 475 |
| 10 | mdo-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 11 | mml-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 12 | mmr-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 13 | mmr-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 14 | mmr-miR-92b | 967 | 1113 | 97 | 1161 | 475 |
| 15 | mne-miR-92 | 967 | 1113 | 97 | 1161 | 475 |
| 16 | mze-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 17 | mze-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 18 | nbr-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 19 | nle-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 20 | oan-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 21 | oan-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 22 | ocu-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 23 | oga-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 24 | oha-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 25 | oha-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 26 | oha-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 27 | oni-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 28 | pal-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 29 | pal-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 30 | pbv-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 31 | pha-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 32 | pha-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 33 | ppy-miR-92 | 967 | 1113 | 97 | 1161 | 475 |
| 34 | ppa-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 35 | ppy-miR-92 | 967 | 1113 | 97 | 1161 | 475 |
| 36 | ptr-miR-92 | 967 | 1113 | 97 | 1161 | 475 |
| 37 | ptr-miR-92 | 967 | 1113 | 97 | 1161 | 475 |
| 38 | sbo-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 39 | sla-miR-92 | 967 | 1113 | 97 | 1161 | 475 |
| 40 | ssa-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 41 | ssa-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 42 | ssc-miR-92a | 967 | 1113 | 97 | 1161 | 475 |
| 43 | tch-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 44 | tgu-miR-92-3p | 967 | 1113 | 97 | 1161 | 475 |
| 45 | tgu-miR-92-3p | 967 | 1113 | 97 | 1161 | 475 |
| 46 | tni-miR-92 | 967 | 1113 | 97 | 1161 | 475 |
| 47 | xla-miR-92a-3p | 967 | 1113 | 97 | 1161 | 475 |
| 48 | abu-miR-23a | 651 | 218 | 181 | 584 | 309 |
| 49 | ami-miR-23a-3p | 651 | 218 | 181 | 584 | 309 |
| 50 | ami-miR-23a-3p | 651 | 218 | 181 | 584 | 309 |
| 51 | bta-miR-23a | 651 | 218 | 181 | 584 | 309 |
| 52 | cja-miR-23a | 651 | 218 | 181 | 584 | 309 |
| 53 | cja-miR-23a | 651 | 218 | 181 | 584 | 309 |
| 54 | dre-miR-23a-3p | 651 | 218 | 181 | 584 | 309 |
| 55 | fru-miR-23a | 651 | 218 | 181 | 584 | 309 |
| 56 | gmo-miR-23a-3p | 651 | 218 | 181 | 584 | 309 |
| 57 | gmo-miR-23a-3p | 651 | 218 | 181 | 584 | 309 |
| 58 | hhi-miR-23a | 651 | 218 | 181 | 584 | 309 |
| 59 | mze-miR-23a | 651 | 218 | 181 | 584 | 309 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | nbr-miR-23a | 651 | 218 | 181 | 584 | 309 |
| 4 | oan-miR-23a-3p | 651 | 218 | 181 | 584 | 309 |
| 5 | oar-miR-23a | 651 | 218 | 181 | 584 | 309 |
| 6 | oga-miR-23a | 651 | 218 | 181 | 584 | 309 |
| 7 | oha-miR-23a-3p | 651 | 218 | 181 | 584 | 309 |
| 8 | ola-miR-23a | 651 | 218 | 181 | 584 | 309 |
| 9 | oni-miR-23a | 651 | 218 | 181 | 584 | 309 |
| 10 | pal-miR-23a-3p | 651 | 218 | 181 | 584 | 309 |
| 11 | tni-miR-23a | 651 | 218 | 181 | 584 | 309 |
| 12 | xla-miR-23a-3p | 651 | 218 | 181 | 584 | 309 |
| 13 | gma-miR396e | 610 | 282 | 349 | 380 | 635 |
| 14 | aa-miR396 | 610 | 282 | 348 | 380 | 635 |
| 15 | aly-miR396a-5p | 610 | 282 | 348 | 380 | 635 |
| 16 | amg-miR396 | 610 | 282 | 348 | 380 | 635 |
| 17 | aof-miR396b | 610 | 282 | 348 | 380 | 635 |
| 18 | aqc-miR396a | 610 | 282 | 348 | 380 | 635 |
| 19 | ata-miR396e-5p | 610 | 282 | 348 | 380 | 635 |
| 20 | ath-miR396a-5p | 610 | 282 | 348 | 380 | 635 |
| 21 | bcy-miR396a | 610 | 282 | 348 | 380 | 635 |
| 22 | bdi-miR396c-5p | 610 | 282 | 348 | 380 | 635 |
| 23 | bdi-miR396d-5p | 610 | 282 | 348 | 380 | 635 |
| 24 | bg-miR396a | 610 | 282 | 348 | 380 | 635 |
| 25 | cas-miR396a | 610 | 282 | 348 | 380 | 635 |
| 26 | cme-miR396b | 610 | 282 | 348 | 380 | 635 |
| 27 | cpa-miR396 | 610 | 282 | 348 | 380 | 635 |
| 28 | csi-miR396a-5p | 610 | 282 | 348 | 380 | 635 |
| 29 | csi-miR396b-5p | 610 | 282 | 348 | 380 | 635 |
| 30 | dpr-miR396 | 610 | 282 | 348 | 380 | 635 |
| 31 | eun-miR396b-5p | 610 | 282 | 348 | 380 | 635 |
| 32 | fve-miR396a-5p | 610 | 282 | 348 | 380 | 635 |
| 33 | fve-miR396c-5p | 610 | 282 | 348 | 380 | 635 |
| 34 | fve-miR396d | 610 | 282 | 348 | 380 | 635 |
| 35 | ghr-miR396a | 610 | 282 | 348 | 380 | 635 |
| 36 | ghr-miR396b | 610 | 282 | 348 | 380 | 635 |
| 37 | gma-miR396a-5p | 610 | 282 | 348 | 380 | 635 |
| 38 | gma-miR396i-5p | 610 | 282 | 348 | 380 | 635 |
| 39 | hbr-miR396b | 610 | 282 | 348 | 380 | 635 |
| 40 | lja-miR396 | 610 | 282 | 348 | 380 | 635 |
| 41 | lus-miR396a | 610 | 282 | 348 | 380 | 635 |
| 42 | lus-miR396c | 610 | 282 | 348 | 380 | 635 |
| 43 | mdm-miR396b | 610 | 282 | 348 | 380 | 635 |
| 44 | mes-miR396a | 610 | 282 | 348 | 380 | 635 |
| 45 | mes-miR396b | 610 | 282 | 348 | 380 | 635 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | mtr-miR396b-5p | 610 | 282 | 348 | 380 | 635 |
| 4 | nta-miR396a | 610 | 282 | 348 | 380 | 635 |
| 5 | osa-miR396a-5p | 610 | 282 | 348 | 380 | 635 |
| 6 | osa-miR396b-5p | 610 | 282 | 348 | 380 | 635 |
| 7 | osa-miR396b-5p | 610 | 282 | 348 | 380 | 635 |
| 8 | ptc-miR396a | 610 | 282 | 348 | 380 | 635 |
| 9 | ptc-miR396b | 610 | 282 | 348 | 380 | 635 |
| 10 | ptc-miR396b | 610 | 282 | 348 | 380 | 635 |
| 11 | sbi-miR396a | 610 | 282 | 348 | 380 | 635 |
| 12 | sbi-miR396b | 610 | 282 | 348 | 380 | 635 |
| 13 | sbi-miR396b | 610 | 282 | 348 | 380 | 635 |
| 14 | sly-miR396a-5p | 610 | 282 | 348 | 380 | 635 |
| 15 | sof-miR396 | 610 | 282 | 348 | 380 | 635 |
| 16 | ssl-miR396 | 610 | 282 | 348 | 380 | 635 |
| 17 | ssl-miR396 | 610 | 282 | 348 | 380 | 635 |
| 18 | ssp-miR396 | 610 | 282 | 348 | 380 | 635 |
| 19 | tcc-miR396a | 610 | 282 | 348 | 380 | 635 |
| 20 | tcc-miR396b | 610 | 282 | 348 | 380 | 635 |
| 21 | tcc-miR396b | 610 | 282 | 348 | 380 | 635 |
| 22 | vvi-miR396c | 610 | 282 | 348 | 380 | 635 |
| 23 | vvi-miR396d | 610 | 282 | 348 | 380 | 635 |
| 24 | vvi-miR396d | 610 | 282 | 348 | 380 | 635 |
| 25 | zma-miR396a-5p | 610 | 282 | 348 | 380 | 635 |
| 26 | zma-miR396b-5p | 610 | 282 | 348 | 380 | 635 |
| 27 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 28 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 29 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 30 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 31 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 32 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 33 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 34 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 35 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 36 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 37 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 38 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 39 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 40 | ami-miR-140 | 150 | 17 | 4 | 108 | 74 |
| 41 | ami-miR-140 | 150 | 17 | 4 | 108 | 74 |
| 42 | ami-miR-140 | 150 | 17 | 4 | 108 | 74 |
| 43 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 44 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 45 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 46 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 47 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 48 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 49 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 50 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 51 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 52 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 53 | ami-miR-140 | 150 | 17 | 4 | 108 | 74 |
| 54 | ami-miR-140 | 150 | 17 | 4 | 108 | 74 |
| 55 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 56 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 57 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 58 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 59 | ami-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | tgu-miR-140-5p | 150 | 17 | 4 | 108 | 74 |
| 4 | tni-miR-140 | 150 | 17 | 4 | 108 | 74 |
| 5 | xla-miR-140-5p | 152 | 18 | 4 | 110 | 74 |
| 6 | cgr-miR-423-3p | 123 | 121 | 27 | 134 | 63 |
| 7 | chi-miR-423-3p | 123 | 121 | 27 | 134 | 63 |
| 8 | cja-miR-423-3p | 123 | 121 | 27 | 134 | 63 |
| 9 | cpo-miR-423-3p | 123 | 121 | 27 | 134 | 63 |
| 10 | dma-miR-423 | 123 | 121 | 27 | 134 | 63 |
| 11 | dno-miR-423-3p | 123 | 121 | 27 | 134 | 63 |
| 12 | eca-miR-423-3p | 123 | 121 | 27 | 134 | 63 |
| 13 | hsa-miR-423-3p | 123 | 121 | 27 | 134 | 63 |
| 14 | mml-miR-423-3p | 123 | 121 | 27 | 134 | 63 |
| 15 | mmu-miR-423-3p | 123 | 121 | 27 | 134 | 63 |
| 16 | nle-miR-423 | 123 | 121 | 27 | 134 | 63 |
| 17 | ocu-miR-423-3p | 123 | 121 | 27 | 134 | 63 |
| 18 | oga-miR-423 | 123 | 121 | 27 | 134 | 63 |
| 19 | pal-miR-423-3p | 123 | 121 | 27 | 134 | 63 |
| 20 | ppa-miR-423 | 123 | 121 | 27 | 134 | 63 |
| 21 | ppy-miR-423-3p | 123 | 121 | 27 | 134 | 63 |
| 22 | ptr-miR-423 | 123 | 121 | 27 | 134 | 63 |
| 23 | rno-miR-423-3p | 123 | 121 | 27 | 134 | 63 |
| 24 | ssc-miR-423-3p | 123 | 121 | 27 | 134 | 63 |
| 25 | tch-miR-423-3p | 123 | 121 | 27 | 134 | 63 |
| 26 | ahy-miR408-3p | 38 | 40 | 43 | 72 | 52 |
| 27 | aly-miR408-3p | 38 | 40 | 43 | 72 | 52 |
| 28 | ath-miR408-3p | 38 | 40 | 43 | 72 | 52 |
| 29 | cas-miR408 | 38 | 40 | 43 | 72 | 52 |
| 30 | cme-miR408 | 38 | 40 | 43 | 72 | 52 |
| 31 | csi-miR408-3p | 38 | 40 | 43 | 72 | 52 |
| 32 | gma-miR408a-3p | 38 | 40 | 43 | 72 | 52 |
| 33 | gma-miR408b-3p | 38 | 40 | 43 | 72 | 52 |
| 34 | gma-miR408c-3p | 38 | 40 | 43 | 72 | 52 |
| 35 | lus-miR408a | 38 | 40 | 43 | 72 | 52 |
| 36 | mdm-miR408a | 38 | 40 | 43 | 72 | 52 |
| 37 | mes-miR408 | 38 | 40 | 43 | 72 | 52 |
| 38 | mtr-miR408-3p | 38 | 40 | 43 | 72 | 52 |
| 39 | pta-miR408 | 38 | 40 | 43 | 72 | 52 |
| 40 | ptc-miR408-3p | 38 | 40 | 43 | 72 | 52 |
| 41 | vun-miR408 | 38 | 40 | 43 | 72 | 52 |
| 42 | vvi-miR408 | 38 | 40 | 43 | 72 | 52 |
| 43 | dre-miR-27a-3p | 526 | 304 | 354 | 521 | 256 |
| 44 | ipu-miR-27a | 526 | 304 | 354 | 521 | 256 |
| 45 | ssa-miR-27a-3p | 526 | 304 | 354 | 521 | 256 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | aly-miR396a-3p | 127 | 102 | 90 | 94 | 201 |
| 4 | ath-miR396a-3p | 127 | 102 | 90 | 94 | 201 |
| 5 | csi-miR396b-3p | 127 | 102 | 90 | 94 | 201 |
| 6 | eun-miR396a-3p | 127 | 102 | 90 | 94 | 201 |
| 7 | fve-miR396a-3p | 127 | 102 | 90 | 94 | 201 |
| 8 | fve-miR396c-3p | 127 | 102 | 90 | 94 | 201 |
| 9 | gma-miR396i-3p | 127 | 102 | 90 | 94 | 201 |
| 10 | mtr-miR396b-3p | 127 | 102 | 90 | 94 | 201 |
| 11 | sly-miR396a-3p | 127 | 102 | 90 | 94 | 201 |
| 12 | abu-miR-27a | 466 | 289 | 340 | 482 | 226 |
| 13 | aca-miR-27a-3p | 466 | 289 | 340 | 482 | 226 |
| 14 | ami-miR-27a-3p | 466 | 289 | 340 | 482 | 226 |
| 15 | ccr-miR-27a | 466 | 289 | 340 | 482 | 226 |
| 16 | cgr-miR-27a-3p | 466 | 289 | 340 | 482 | 226 |
| 17 | cja-miR-27a | 466 | 289 | 340 | 482 | 226 |
| 18 | cpi-miR-27a-3p | 466 | 289 | 340 | 482 | 226 |
| 19 | dno-miR-27a-3p | 466 | 289 | 340 | 482 | 226 |
| 20 | eca-miR-27a | 466 | 289 | 340 | 482 | 226 |
| 21 | hsa-miR-27a-3p | 466 | 289 | 340 | 482 | 226 |
| 22 | mdo-miR-27a-3p | 466 | 289 | 340 | 482 | 226 |
| 23 | mmu-miR-27a-3p | 466 | 289 | 340 | 482 | 226 |
| 24 | mze-miR-27a | 466 | 289 | 340 | 482 | 226 |
| 25 | nbr-miR-27a | 466 | 289 | 340 | 482 | 226 |
| 26 | oan-miR-27a-3p | 466 | 289 | 340 | 482 | 226 |
| 27 | oar-miR-27a | 466 | 289 | 340 | 482 | 226 |
| 28 | oni-miR-27a | 466 | 289 | 340 | 482 | 226 |
| 29 | pbv-miR-27a-3p | 466 | 289 | 340 | 482 | 226 |
| 30 | ppy-miR-27a | 466 | 289 | 340 | 482 | 226 |
| 31 | rno-miR-27a-3p | 466 | 289 | 340 | 482 | 226 |
| 32 | sbo-miR-27a | 466 | 289 | 340 | 482 | 226 |
| 33 | ssc-miR-27a | 466 | 289 | 340 | 482 | 226 |
| 34 | xtr-miR-27a | 466 | 289 | 340 | 482 | 226 |
| 35 | age-miR-27a | 466 | 290 | 340 | 483 | 226 |
| 36 | ggo-miR-27a | 466 | 290 | 340 | 483 | 226 |
| 37 | lca-miR-27a | 466 | 290 | 340 | 483 | 226 |
| 38 | mml-miR-27a-3p | 466 | 290 | 340 | 483 | 226 |
| 39 | mne-miR-27a | 466 | 290 | 340 | 483 | 226 |
| 40 | oha-miR-27a-3p | 466 | 290 | 340 | 483 | 226 |
| 41 | ppa-miR-27a | 466 | 290 | 340 | 483 | 226 |
| 42 | ppy-miR-27a | 466 | 290 | 340 | 483 | 226 |
| 43 | ptr-miR-27a | 466 | 290 | 340 | 483 | 226 |
| 44 | sla-miR-27a | 466 | 290 | 340 | 483 | 226 |
| 45 | cpo-miR-27a-3p | 178 | 92 | 314 | 181 | 109 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | tch-miR-27a-3p | 178 | 92 | 314 | 181 | 109 |
| 4 | efu-miR-93 | 52 | 85 | 87 | 71 | 35 |
| 5 | ami-miR-93-5p | 48 | 75 | 85 | 63 | 28 |
| 6 | cfa-miR-93 | 48 | 75 | 85 | 63 | 28 |
| 7 | cgr-miR-93-5p | 48 | 75 | 85 | 63 | 28 |
| 8 | chi-miR-93-5p | 48 | 75 | 85 | 63 | 28 |
| 9 | chi-miR-93-5p | 48 | 75 | 85 | 63 | 28 |
| 10 | chi-miR-93-5p | 48 | 75 | 85 | 63 | 28 |
| 11 | cja-miR-93 | 48 | 75 | 85 | 63 | 28 |
| 12 | cpo-miR-93-5p | 48 | 75 | 85 | 63 | 28 |
| 13 | cpo-miR-93-5p | 48 | 75 | 85 | 63 | 28 |
| 14 | dma-miR-93 | 48 | 75 | 85 | 63 | 28 |
| 15 | dno-miR-93-5p | 48 | 75 | 85 | 63 | 28 |
| 16 | eca-miR-93 | 48 | 75 | 85 | 63 | 28 |
| 17 | eca-miR-93 | 48 | 75 | 85 | 63 | 28 |
| 18 | hsa-miR-93-5p | 48 | 75 | 85 | 63 | 28 |
| 19 | mmu-miR-93-5p | 48 | 75 | 85 | 63 | 28 |
| 20 | nle-miR-93 | 48 | 75 | 85 | 63 | 28 |
| 21 | nle-miR-93 | 48 | 75 | 85 | 63 | 28 |
| 22 | ocu-miR-93-5p | 48 | 75 | 85 | 63 | 28 |
| 23 | oga-miR-93 | 48 | 75 | 85 | 63 | 28 |
| 24 | pal-miR-93-5p | 48 | 75 | 85 | 63 | 28 |
| 25 | pal-miR-93-5p | 48 | 75 | 85 | 63 | 28 |
| 26 | pha-miR-93 | 48 | 75 | 85 | 63 | 28 |
| 27 | rno-miR-93-5p | 48 | 75 | 85 | 63 | 28 |
| 28 | tch-miR-93-5p | 48 | 75 | 85 | 63 | 28 |
| 29 | tch-miR-93-5p | 48 | 75 | 85 | 63 | 28 |
| 30 | xla-miR-93-5p | 48 | 75 | 85 | 63 | 28 |
| 31 | ptc-miR6478 | 2152 | 3721 | 7602 | 2350 | 8982 |
| 32 | pvu-miR482-5p | 4383 | 5090 | 697 | 3076 | 6462 |
| 33 | pvu-miR482-5p | 4383 | 5090 | 697 | 3076 | 6462 |
| 34 | aca-miR-27b-3p | 213 | 40 | 135 | 172 | 87 |
| 35 | dre-miR-27b-3p | 213 | 40 | 135 | 172 | 87 |
| 36 | fru-miR-27b | 213 | 40 | 135 | 172 | 87 |
| 37 | fru-miR-27b | 213 | 40 | 135 | 172 | 87 |
| 38 | oha-miR-27b-3p | 213 | 40 | 135 | 172 | 87 |
| 39 | tni-miR-27b | 213 | 40 | 135 | 172 | 87 |
| 40 | xla-miR-27b-3p | 213 | 40 | 135 | 172 | 87 |
| 41 | xla-miR-27b-3p | 213 | 40 | 135 | 172 | 87 |
| 42 | abu-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 43 | bta-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 44 | bta-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 45 | cfa-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 46 | cgr-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 47 | chi-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 48 | chi-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 49 | cja-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 50 | cli-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 51 | cpi-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 52 | cpo-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 53 | cpo-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 54 | dno-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 55 | eca-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 56 | gga-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 57 | ggo-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 58 | ggo-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 59 | hsa-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ipu-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 4 | mdo-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 5 | mml-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 6 | mmr-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 7 | mmu-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 8 | mze-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 9 | nbr-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 10 | oan-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 11 | ocu-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 12 | oni-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 13 | pal-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 14 | pbv-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 15 | pma-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 16 | ppy-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 17 | ppa-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 18 | ppp-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 19 | ptr-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 20 | rno-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 21 | sbo-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 22 | sha-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 23 | ssa-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 24 | ssc-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 25 | tch-miR-27b-3p | 171 | 33 | 131 | 134 | 76 |
| 26 | tgu-miR-27-3p | 171 | 33 | 131 | 134 | 76 |
| 27 | xtr-miR-27b | 171 | 33 | 131 | 134 | 76 |
| 28 | efu-miR-27b | 217 | 42 | 137 | 172 | 87 |
| 29 | ggo-let-7c | 95 | 32 | 29 | 90 | 55 |
| 30 | ola-let-7c | 95 | 32 | 29 | 90 | 55 |
| 31 | cpi-miR-24-3p | 202 | 107 | 198 | 200 | 94 |
| 32 | sbo-miR-24 | 202 | 107 | 198 | 200 | 94 |
| 33 | bcy-miR156 | 497 | 289 | 178 | 259 | 317 |
| 34 | bgp-miR156 | 497 | 289 | 178 | 259 | 317 |
| 35 | ahy-miR156b-5p | 497 | 289 | 177 | 259 | 317 |
| 36 | aly-miR157a-5p | 497 | 289 | 177 | 259 | 317 |
| 37 | aly-miR157b-5p | 497 | 289 | 177 | 259 | 317 |
| 38 | aly-miR157c-5p | 497 | 289 | 177 | 259 | 317 |
| 39 | aof-miR156b | 497 | 289 | 177 | 259 | 317 |
| 40 | ath-miR157a-5p | 497 | 289 | 177 | 259 | 317 |
| 41 | ath-miR157b-5p | 497 | 289 | 177 | 259 | 317 |
| 42 | ath-miR157c-5p | 497 | 289 | 177 | 259 | 317 |
| 43 | atr-miR156a | 497 | 289 | 177 | 259 | 317 |
| 44 | atr-miR156c | 497 | 289 | 177 | 259 | 317 |
| 45 | bnm-miR156b | 497 | 289 | 177 | 259 | 317 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | bna-miR156c | 497 | 289 | 177 | 259 | 317 |
| 4 | bna-miR156g | 497 | 289 | 177 | 259 | 317 |
| 5 | bol-miR157a | 497 | 289 | 177 | 259 | 317 |
| 6 | bra-miR157a | 497 | 289 | 177 | 259 | 317 |
| 7 | cca-miR156c | 497 | 289 | 177 | 259 | 317 |
| 8 | cme-miR156b | 497 | 289 | 177 | 259 | 317 |
| 9 | cpa-miR156e | 497 | 289 | 177 | 259 | 317 |
| 10 | cpa-miR156f | 497 | 289 | 177 | 259 | 317 |
| 11 | fve-miR156f | 497 | 289 | 177 | 259 | 317 |
| 12 | fve-miR156g-5p | 497 | 289 | 177 | 259 | 317 |
| 13 | gma-miR156c | 497 | 289 | 177 | 259 | 317 |
| 14 | gma-miR156d | 497 | 289 | 177 | 259 | 317 |
| 15 | gma-miR156i | 497 | 289 | 177 | 259 | 317 |
| 16 | gma-miR156j | 497 | 289 | 177 | 259 | 317 |
| 17 | gma-miR156l | 497 | 289 | 177 | 259 | 317 |
| 18 | gma-miR156m | 497 | 289 | 177 | 259 | 317 |
| 19 | gra-miR157a | 497 | 289 | 177 | 259 | 317 |
| 20 | gra-miR157b | 497 | 289 | 177 | 259 | 317 |
| 21 | han-miR156c | 497 | 289 | 177 | 259 | 317 |
| 22 | lus-miR156b | 497 | 289 | 177 | 259 | 317 |
| 23 | lus-miR156c | 497 | 289 | 177 | 259 | 317 |
| 24 | lus-miR156e | 497 | 289 | 177 | 259 | 317 |
| 25 | lus-miR156f | 497 | 289 | 177 | 259 | 317 |
| 26 | lus-miR156h | 497 | 289 | 177 | 259 | 317 |
| 27 | lus-miR156i | 497 | 289 | 177 | 259 | 317 |
| 28 | mdm-miR156ab | 497 | 289 | 177 | 259 | 317 |
| 29 | mdm-miR156ac | 497 | 289 | 177 | 259 | 317 |
| 30 | mes-miR156h | 497 | 289 | 177 | 259 | 317 |
| 31 | mes-miR156i | 497 | 289 | 177 | 259 | 317 |
| 32 | mes-miR156j | 497 | 289 | 177 | 259 | 317 |
| 33 | mtr-miR156e | 497 | 289 | 177 | 259 | 317 |
| 34 | mtr-miR156f | 497 | 289 | 177 | 259 | 317 |
| 35 | mtr-miR156h-5p | 497 | 289 | 177 | 259 | 317 |
| 36 | ppe-miR156g | 497 | 289 | 177 | 259 | 317 |
| 37 | ppe-miR156h | 497 | 289 | 177 | 259 | 317 |
| 38 | ppe-miR156i | 497 | 289 | 177 | 259 | 317 |
| 39 | ptc-miR156g | 497 | 289 | 177 | 259 | 317 |
| 40 | ptc-miR156h | 497 | 289 | 177 | 259 | 317 |
| 41 | ptc-miR156i | 497 | 289 | 177 | 259 | 317 |
| 42 | ptc-miR156j | 497 | 289 | 177 | 259 | 317 |
| 43 | rco-miR156f | 497 | 289 | 177 | 259 | 317 |
| 44 | rco-miR156g | 497 | 289 | 177 | 259 | 317 |
| 45 | rco-miR156h | 497 | 289 | 177 | 259 | 317 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | sly-miR156a | 497 | 289 | 177 | 259 | 317 |
| 4 | sly-miR156b | 497 | 289 | 177 | 259 | 317 |
| 5 | sly-miR156c | 497 | 289 | 177 | 259 | 317 |
| 6 | stu-miR156a | 497 | 289 | 177 | 259 | 317 |
| 7 | stu-miR156b | 497 | 289 | 177 | 259 | 317 |
| 8 | stu-miR156c | 497 | 289 | 177 | 259 | 317 |
| 9 | stu-miR156d-5p | 497 | 289 | 177 | 259 | 317 |
| 10 | tcc-miR156e | 497 | 289 | 177 | 259 | 317 |
| 11 | tcc-miR156f | 497 | 289 | 177 | 259 | 317 |
| 12 | vca-miR156b-5p | 497 | 289 | 177 | 259 | 317 |
| 13 | vun-miR156b | 497 | 289 | 177 | 259 | 317 |
| 14 | vvi-miR156f | 497 | 289 | 177 | 259 | 317 |
| 15 | vvi-miR156g | 497 | 289 | 177 | 259 | 317 |
| 16 | vvi-miR156i | 497 | 289 | 177 | 259 | 317 |
| 17 | pta-miR159a | 214 | 147 | 5 | 235 | 134 |
| 18 | osa-miR159c | 221 | 151 | 6 | 236 | 138 |
| 19 | aof-miR319b | 4361 | 1697 | 3131 | 4130 | 2409 |
| 20 | atr-miR319b | 4361 | 1697 | 3131 | 4130 | 2409 |
| 21 | atr-miR319d | 4361 | 1697 | 3131 | 4130 | 2409 |
| 22 | atr-miR319e | 4361 | 1697 | 3131 | 4130 | 2409 |
| 23 | cas-miR319c | 4361 | 1697 | 3131 | 4130 | 2409 |
| 24 | csi-miR159d | 4361 | 1697 | 3131 | 4130 | 2409 |
| 25 | fve-miR319 | 4361 | 1697 | 3131 | 4130 | 2409 |
| 26 | tcc-miR319 | 4361 | 1697 | 3131 | 4130 | 2409 |
| 27 | vvi-miR319e | 4361 | 1697 | 3131 | 4130 | 2409 |
| 28 | abu-let-7c | 435 | 201 | 101 | 374 | 235 |
| 29 | aca-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 30 | ami-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 31 | bta-let-7c | 435 | 201 | 101 | 374 | 235 |
| 32 | cfa-let-7c | 435 | 201 | 101 | 374 | 235 |
| 33 | chi-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 34 | cja-let-7c | 435 | 201 | 101 | 374 | 235 |
| 35 | cli-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 36 | cpi-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 37 | cpo-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 38 | dma-let-7c | 435 | 201 | 101 | 374 | 235 |
| 39 | dno-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 40 | dre-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 41 | eca-let-7c | 435 | 201 | 101 | 374 | 235 |
| 42 | gga-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 43 | gmo-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 44 | hhi-let-7c | 435 | 201 | 101 | 374 | 235 |
| 45 | hsa-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ipu-let-7c | 435 | 201 | 101 | 374 | 235 |
| 4 | mml-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 5 | mmr-let-7c | 435 | 201 | 101 | 374 | 235 |
| 6 | mmu-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 7 | mze-let-7c | 435 | 201 | 101 | 374 | 235 |
| 8 | nbr-let-7c | 435 | 201 | 101 | 374 | 235 |
| 9 | nle-let-7c | 435 | 201 | 101 | 374 | 235 |
| 10 | oan-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 11 | oar-let-7c | 435 | 201 | 101 | 374 | 235 |
| 12 | ocu-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 13 | oga-let-7c | 435 | 201 | 101 | 374 | 235 |
| 14 | oha-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 15 | oni-let-7c | 435 | 201 | 101 | 374 | 235 |
| 16 | pal-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 17 | pbv-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 18 | pha-let-7c | 435 | 201 | 101 | 374 | 235 |
| 19 | ppy-let-7c | 435 | 201 | 101 | 374 | 235 |
| 20 | pol-let-7a-5p | 435 | 201 | 101 | 374 | 235 |
| 21 | ppa-let-7c | 435 | 201 | 101 | 374 | 235 |
| 22 | ppy-let-7c | 435 | 201 | 101 | 374 | 235 |
| 23 | ptr-let-7c | 435 | 201 | 101 | 374 | 235 |
| 24 | rno-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 25 | ssa-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 26 | ssc-let-7c | 435 | 201 | 101 | 374 | 235 |
| 27 | tcf-let-7-5p | 435 | 201 | 101 | 374 | 235 |
| 28 | tgu-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 29 | xla-let-7c-5p | 435 | 201 | 101 | 374 | 235 |
| 30 | xtr-let-7c | 435 | 201 | 101 | 374 | 235 |
| 31 | efu-let-7c | 448 | 209 | 111 | 385 | 247 |
| 32 | abu-miR-143 | 115 | 4 | 328 | 51 | 30 |
| 33 | aca-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 34 | aja-miR-143 | 115 | 4 | 328 | 51 | 30 |
| 35 | ami-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 36 | bta-miR-143 | 115 | 4 | 328 | 51 | 30 |
| 37 | cfa-miR-143 | 115 | 4 | 328 | 51 | 30 |
| 38 | cgr-miR-143 | 115 | 4 | 328 | 51 | 30 |
| 39 | chi-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 40 | cli-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 41 | cpi-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 42 | cpo-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 43 | dno-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 44 | dre-miR-143 | 115 | 4 | 328 | 51 | 30 |
| 45 | eca-miR-143 | 115 | 4 | 328 | 51 | 30 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | gga-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 4 | hsa-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 5 | ipu-miR-143 | 115 | 4 | 328 | 51 | 30 |
| 6 | mdo-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 7 | mml-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 8 | mmu-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 9 | nle-miR-143 | 115 | 4 | 328 | 51 | 30 |
| 10 | oan-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 11 | oar-miR-143 | 115 | 4 | 328 | 51 | 30 |
| 12 | ocu-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 13 | oga-miR-143 | 115 | 4 | 328 | 51 | 30 |
| 14 | oni-miR-143 | 115 | 4 | 328 | 51 | 30 |
| 15 | pal-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 16 | pbv-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 17 | pha-miR-143 | 115 | 4 | 328 | 51 | 30 |
| 18 | ssa-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 19 | ssc-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 20 | tch-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 21 | xla-miR-143-3p | 115 | 4 | 328 | 51 | 30 |
| 22 | xtr-miR-143 | 115 | 4 | 328 | 51 | 30 |
| 23 | efu-miR-143 | 115 | 4 | 329 | 51 | 30 |
| 24 | mes-miR319h | 237 | 83 | 202 | 210 | 130 |
| 25 | vun-miR319b | 237 | 83 | 202 | 210 | 130 |
| 26 | cme-miR319c | 218 | 77 | 198 | 201 | 122 |
| 27 | cme-miR319d | 218 | 77 | 198 | 201 | 122 |
| 28 | gma-miR319c | 218 | 77 | 198 | 201 | 122 |
| 29 | ptc-miR319e | 218 | 77 | 198 | 201 | 122 |
| 30 | ptc-miR319f | 218 | 77 | 198 | 201 | 122 |
| 31 | ptc-miR319g | 218 | 77 | 198 | 201 | 122 |
| 32 | ptc-miR319h | 218 | 77 | 198 | 201 | 122 |
| 33 | stu-miR319b | 218 | 77 | 198 | 201 | 122 |
| 34 | ipu-miR-99b | 629 | 10 | 298 | 423 | 321 |
| 35 | efu-miR-99a | 615 | 9 | 287 | 415 | 310 |
| 36 | gma-miR169n-5p | 703 | 297 | 415 | 379 | 640 |
| 37 | mtr-miR169c | 703 | 297 | 415 | 379 | 640 |
| 38 | oga-miR-99a | 585 | 9 | 284 | 397 | 295 |
| 39 | pbv-miR-99a-5p | 585 | 9 | 284 | 397 | 295 |
| 40 | pha-miR-99a | 585 | 9 | 284 | 397 | 295 |
| 41 | aca-miR-99a-5p | 585 | 9 | 284 | 396 | 294 |
| 42 | ami-miR-99a-5p | 585 | 9 | 284 | 396 | 294 |
| 43 | cli-miR-99-5p | 585 | 9 | 284 | 396 | 294 |
| 44 | cpi-miR-99a-5p | 585 | 9 | 284 | 396 | 294 |
| 45 | cpo-miR-99a-5p | 585 | 9 | 284 | 396 | 294 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | dno-miR-99a-5p | 585 | 9 | 284 | 396 | 294 |
| 4 | dre-miR-99 | 585 | 9 | 284 | 396 | 294 |
| 5 | eca-miR-99a | 585 | 9 | 284 | 396 | 294 |
| 6 | gga-miR-99a-5p | 585 | 9 | 284 | 396 | 294 |
| 7 | ggo-miR-99a | 585 | 9 | 284 | 396 | 294 |
| 8 | gmo-miR-99-5p | 585 | 9 | 284 | 396 | 294 |
| 9 | gmo-miR-99-5p | 585 | 9 | 284 | 396 | 294 |
| 10 | gmo-miR-99-5p | 585 | 9 | 284 | 396 | 294 |
| 11 | hsa-miR-99a-5p | 585 | 9 | 284 | 396 | 294 |
| 12 | ipu-miR-99a | 585 | 9 | 284 | 396 | 294 |
| 13 | ipu-miR-99a | 585 | 9 | 284 | 396 | 294 |
| 14 | lla-miR-99a | 585 | 9 | 284 | 396 | 294 |
| 15 | mml-miR-99a-5p | 585 | 9 | 284 | 396 | 294 |
| 16 | mmr-miR-99a | 585 | 9 | 284 | 396 | 294 |
| 17 | mmr-miR-99a | 585 | 9 | 284 | 396 | 294 |
| 18 | mmu-miR-99a-5p | 585 | 9 | 284 | 396 | 294 |
| 19 | mne-miR-99a | 585 | 9 | 284 | 396 | 294 |
| 20 | mze-miR-99b | 585 | 9 | 284 | 396 | 294 |
| 21 | mze-miR-99b | 585 | 9 | 284 | 396 | 294 |
| 22 | nbr-miR-99b | 585 | 9 | 284 | 396 | 294 |
| 23 | ocu-miR-99a-5p | 585 | 9 | 284 | 396 | 294 |
| 24 | oha-miR-99a-5p | 585 | 9 | 284 | 396 | 294 |
| 25 | oha-miR-99a-5p | 585 | 9 | 284 | 396 | 294 |
| 26 | oni-miR-99b | 585 | 9 | 284 | 396 | 294 |
| 27 | ony-miR-99b | 585 | 9 | 284 | 396 | 294 |
| 28 | ppa-miR-99a | 585 | 9 | 284 | 396 | 294 |
| 29 | ppa-miR-99a | 585 | 9 | 284 | 396 | 294 |
| 30 | ppy-miR-99a | 585 | 9 | 284 | 396 | 294 |
| 31 | ptr-miR-99a | 585 | 9 | 284 | 396 | 294 |
| 32 | ptr-miR-99a | 585 | 9 | 284 | 396 | 294 |
| 33 | rno-miR-99a-5p | 585 | 9 | 284 | 396 | 294 |
| 34 | ssa-miR-99-5p | 585 | 9 | 284 | 396 | 294 |
| 35 | ssc-miR-99a-5p | 585 | 9 | 284 | 396 | 294 |
| 36 | tch-miR-99a-5p | 585 | 9 | 284 | 396 | 294 |
| 37 | tch-miR-99a-5p | 585 | 9 | 284 | 396 | 294 |
| 38 | xtr-miR-99 | 585 | 9 | 284 | 396 | 294 |
| 39 | gma-miR171n | 100 | 118 | 70 | 64 | 161 |
| 40 | gma-miR171p | 100 | 118 | 70 | 64 | 161 |
| 41 | aly-miR319c-3p | 246 | 84 | 228 | 218 | 126 |
| 42 | aly-miR319c-3p | 246 | 84 | 228 | 218 | 126 |
| 43 | aly-miR319d-3p | 246 | 84 | 228 | 218 | 126 |
| 44 | ath-miR319c | 246 | 84 | 228 | 218 | 126 |
| 45 | ath-miR319c | 246 | 84 | 228 | 218 | 126 |
| 46 | mes-miR319g | 246 | 84 | 228 | 218 | 126 |
| 47 | pvu-miR319c | 246 | 84 | 228 | 218 | 126 |
| 48 | rco-miR319d | 246 | 84 | 228 | 218 | 126 |
| 49 | rco-miR319d | 246 | 84 | 228 | 218 | 126 |
| 50 | sly-miR319c-3p | 246 | 84 | 228 | 218 | 126 |
| 51 | dma-miR-143 | 122 | 6 | 361 | 56 | 36 |
| 52 | ggo-miR-143 | 122 | 6 | 361 | 56 | 36 |
| 53 | ggo-miR-143 | 122 | 6 | 361 | 56 | 36 |
| 54 | lla-miR-143 | 122 | 6 | 361 | 56 | 36 |
| 55 | oha-miR-143-3p | 122 | 6 | 361 | 56 | 36 |
| 56 | ppa-miR-143 | 122 | 6 | 361 | 56 | 36 |
| 57 | ppy-miR-143 | 122 | 6 | 361 | 56 | 36 |
| 58 | ppy-miR-143 | 122 | 6 | 361 | 56 | 36 |
| 59 | ptr-miR-143 | 122 | 6 | 361 | 56 | 36 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|-----|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | rno-miR-143-3p | 122 | 6 | 361 | 56 | 36 |
| 4 | bta-miR-27a-3p | 136 | 65 | 270 | 137 | 76 |
| 5 | cfa-miR-27a | 136 | 65 | 270 | 137 | 76 |
| 6 | chi-miR-27a-3p | 136 | 65 | 270 | 137 | 76 |
| 7 | gmo-miR-27d-3p | 136 | 65 | 270 | 137 | 76 |
| 8 | oga-miR-27a | 136 | 65 | 270 | 137 | 76 |
| 9 | ola-miR-27a | 136 | 65 | 270 | 137 | 76 |
| 10 | pal-miR-27a-3p | 136 | 65 | 270 | 137 | 76 |
| 11 | xla-miR-27a-3p | 136 | 65 | 270 | 137 | 76 |
| 12 | cfa-miR-181a | 163 | 6 | 105 | 105 | 85 |
| 13 | ipu-miR-181a | 163 | 6 | 105 | 105 | 85 |
| 14 | mmr-miR-181a | 163 | 6 | 105 | 105 | 85 |
| 15 | oni-miR-181c | 163 | 6 | 105 | 105 | 85 |
| 16 | sbo-miR-181a | 163 | 6 | 105 | 105 | 85 |
| 17 | bta-miR-29a | 105 | 39 | 119 | 96 | 50 |
| 18 | ssc-miR-29a-3p | 105 | 39 | 119 | 96 | 50 |
| 19 | efu-miR-29a | 109 | 41 | 122 | 97 | 52 |
| 20 | age-miR-29a | 65 | 23 | 96 | 58 | 29 |
| 21 | ggo-miR-29a | 65 | 23 | 96 | 58 | 29 |
| 22 | lla-miR-29a | 65 | 23 | 96 | 58 | 29 |
| 23 | mml-miR-29a-3p | 65 | 23 | 96 | 58 | 29 |
| 24 | mne-miR-29a | 65 | 23 | 96 | 58 | 29 |
| 25 | ppa-miR-29a | 65 | 23 | 96 | 58 | 29 |
| 26 | ppy-miR-29a | 65 | 23 | 96 | 58 | 29 |
| 27 | ptr-miR-29a | 65 | 23 | 96 | 58 | 29 |
| 28 | sbo-miR-29a | 65 | 23 | 96 | 58 | 29 |
| 29 | sla-miR-29a | 65 | 23 | 96 | 58 | 29 |
| 30 | abu-miR-99b | 366 | 1 | 184 | 239 | 176 |
| 31 | bta-miR-99a-5p | 366 | 1 | 184 | 239 | 176 |
| 32 | ccr-miR-99 | 366 | 1 | 184 | 239 | 176 |
| 33 | cfa-miR-99a | 366 | 1 | 184 | 239 | 176 |
| 34 | cgr-miR-99a-5p | 366 | 1 | 184 | 239 | 176 |
| 35 | chi-miR-99a-5p | 366 | 1 | 184 | 239 | 176 |
| 36 | cja-miR-99 | 366 | 1 | 184 | 239 | 176 |
| 37 | nle-miR-99a | 366 | 1 | 184 | 239 | 176 |
| 38 | oan-miR-99-5p | 366 | 1 | 184 | 239 | 176 |
| 39 | pal-miR-99a-5p | 366 | 1 | 184 | 239 | 176 |
| 40 | sbo-miR-99a | 366 | 1 | 184 | 239 | 176 |
| 41 | tgu-miR-99-5p | 366 | 1 | 184 | 239 | 176 |
| 42 | xla-miR-99-5p | 366 | 1 | 184 | 239 | 176 |
| 43 | cpo-miR-652-3p | 101 | 100 | 36 | 158 | 64 |
| 44 | vca-miR396-5p | 82 | 71 | 127 | 54 | 97 |
| 45 | vvi-miR396b | 82 | 71 | 127 | 54 | 97 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|---------|---------|--------|---------|--------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | bta-let-7d | 116 | 139 | 52 | 122 | 61 |
| 4 | cgr-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 5 | chi-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 6 | chi-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 7 | cja-let-7d | 116 | 139 | 52 | 122 | 61 |
| 8 | cli-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 9 | cli-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 10 | cpi-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 11 | cpo-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 12 | dno-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 13 | dno-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 14 | eca-let-7d | 116 | 139 | 52 | 122 | 61 |
| 15 | hsa-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 16 | mml-let-7d | 116 | 139 | 52 | 122 | 61 |
| 17 | mml-let-7d | 116 | 139 | 52 | 122 | 61 |
| 18 | mmu-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 19 | oan-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 20 | ocu-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 21 | ocu-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 22 | oha-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 23 | pbv-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 24 | ppy-let-7d | 116 | 139 | 52 | 122 | 61 |
| 25 | ppy-let-7d | 116 | 139 | 52 | 122 | 61 |
| 26 | ptr-let-7d | 116 | 139 | 52 | 122 | 61 |
| 27 | rno-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 28 | ssc-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 29 | ssc-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 30 | tgu-let-7d-5p | 116 | 139 | 52 | 122 | 61 |
| 31 | efu-let-7d | 119 | 140 | 55 | 124 | 63 |
| 32 | pab-miR396a-5p | 84 | 74 | 132 | 57 | 101 |
| 33 | pab-miR396a-5p | 84 | 74 | 132 | 57 | 101 |
| 34 | vvi-miR396a | 84 | 74 | 132 | 57 | 101 |
| 35 | pvu-miR159a.2 | 382 | 199 | 126 | 276 | 252 |
| 36 | gma-miR319p | 306 | 182 | 302 | 270 | 172 |
| 37 | gma-miR319p | 306 | 182 | 302 | 270 | 172 |
| 38 | cfa-let-7d | 75 | 62 | 14 | 75 | 34 |
| 39 | cpo-miR-16b-5p | 580 | 450 | 216 | 583 | 251 |
| 40 | dno-miR-16b-5p | 580 | 450 | 216 | 583 | 251 |
| 41 | dno-miR-16b-5p | 580 | 450 | 216 | 583 | 251 |
| 42 | efu-miR-16 | 580 | 450 | 216 | 583 | 251 |
| 43 | ocu-miR-16b-5p | 580 | 450 | 216 | 583 | 251 |
| 44 | ocu-miR-16b-5p | 580 | 450 | 216 | 583 | 251 |
| 45 | ccr-miR-181a | 114 | 4 | 73 | 73 | 54 |
| 46 | xla-miR-181a-5p | 114 | 4 | 73 | 73 | 54 |
| 47 | ahy-miR159 | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 48 | aly-miR159a-3p | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 49 | aly-miR159a-3p | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 50 | aof-miR159 | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 51 | ath-miR159a | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 52 | atr-miR159 | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 53 | atr-miR159 | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 54 | bna-miR159 | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 55 | bra-miR159a | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 56 | cme-miR159a | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 57 | cpa-miR159a | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 58 | csi-miR159a-3p | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 59 | csi-miR159a-3p | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 60 | | | | | | |

| | | | | | | |
|----|------------------|---------|---------|--------|---------|--------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | fve-miR159a-3p | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 4 | gma-miR159a-3p | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 5 | gma-miR159e-3p | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 6 | gma-miR159e-3p | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 7 | hbr-miR159a | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 8 | htu-miR159a | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 9 | htu-miR159a | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 10 | mdm-miR159d | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 11 | mdm-miR159e | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 12 | mdm-miR159e | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 13 | mdm-miR159f | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 14 | mes-miR159a-3p | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 15 | mes-miR159b | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 16 | mes-miR159b | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 17 | mtr-miR159a | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 18 | nta-miR159 | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 19 | ppe-miR159 | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 20 | ptc-miR159a | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 21 | ptc-miR159a | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 22 | ptc-miR159b | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 23 | pvu-miR159a.1 | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 24 | rco-miR159 | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 25 | rco-miR159 | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 26 | sly-miR159 | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 27 | vca-miR159-3p | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 28 | vvi-miR159c | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 29 | vvi-miR159c | 1399117 | 1317402 | 284674 | 1510032 | 995210 |
| 30 | osa-miR159f | 21111 | 20133 | 10743 | 24199 | 16704 |
| 31 | cgr-let-7d-3p | 74 | 62 | 14 | 74 | 34 |
| 32 | cgr-let-7d-3p | 74 | 62 | 14 | 74 | 34 |
| 33 | cpo-let-7d-3p | 74 | 62 | 14 | 74 | 34 |
| 34 | dno-let-7d-3p | 74 | 62 | 14 | 74 | 34 |
| 35 | hsa-let-7d-3p | 74 | 62 | 14 | 74 | 34 |
| 36 | mmu-let-7d-3p | 74 | 62 | 14 | 74 | 34 |
| 37 | mmu-let-7d-3p | 74 | 62 | 14 | 74 | 34 |
| 38 | ocu-let-7d-3p | 74 | 62 | 14 | 74 | 34 |
| 39 | rno-let-7d-3p | 74 | 62 | 14 | 74 | 34 |
| 40 | rno-let-7d-3p | 74 | 62 | 14 | 74 | 34 |
| 41 | ssc-let-7d-3p | 74 | 62 | 14 | 74 | 34 |
| 42 | bdi-miR159b-3p.1 | 43621 | 42808 | 14189 | 43362 | 35789 |
| 43 | far-miR159 | 43621 | 42808 | 14189 | 43362 | 35789 |
| 44 | far-miR159 | 43621 | 42808 | 14189 | 43362 | 35789 |
| 45 | hvu-miR159a | 43621 | 42808 | 14189 | 43362 | 35789 |
| 46 | hvu-miR159b | 43621 | 42808 | 14189 | 43362 | 35789 |
| 47 | hvu-miR159b | 43621 | 42808 | 14189 | 43362 | 35789 |
| 48 | osa-miR159a.1 | 43621 | 42808 | 14189 | 43362 | 35789 |
| 49 | osa-miR159b | 43621 | 42808 | 14189 | 43362 | 35789 |
| 50 | osa-miR159b | 43621 | 42808 | 14189 | 43362 | 35789 |
| 51 | sbi-miR159a | 43621 | 42808 | 14189 | 43362 | 35789 |
| 52 | sof-miR159a | 43621 | 42808 | 14189 | 43362 | 35789 |
| 53 | sof-miR159a | 43621 | 42808 | 14189 | 43362 | 35789 |
| 54 | sof-miR159b | 43621 | 42808 | 14189 | 43362 | 35789 |
| 55 | sof-miR159d | 43621 | 42808 | 14189 | 43362 | 35789 |
| 56 | ssp-miR159a | 43621 | 42808 | 14189 | 43362 | 35789 |
| 57 | ssp-miR159a | 43621 | 42808 | 14189 | 43362 | 35789 |
| 58 | tae-miR159a | 43621 | 42808 | 14189 | 43362 | 35789 |
| 59 | tae-miR159b | 43621 | 42808 | 14189 | 43362 | 35789 |
| 60 | zma-miR159a-3p | 43621 | 42808 | 14189 | 43362 | 35789 |

| | | | | | | |
|----|----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | zma-miR159b-3p | 43621 | 42808 | 14189 | 43362 | 35789 |
| 4 | zma-miR159f-3p | 43621 | 42808 | 14189 | 43362 | 35789 |
| 5 | zma-miR159j-3p | 43621 | 42808 | 14189 | 43362 | 35789 |
| 6 | zma-miR159k-3p | 43621 | 42808 | 14189 | 43362 | 35789 |
| 7 | zma-miR159k-3p | 43621 | 42808 | 14189 | 43362 | 35789 |
| 8 | cas-miR394 | 6054 | 4250 | 7309 | 3694 | 7125 |
| 9 | cas-miR394 | 6054 | 4250 | 7309 | 3694 | 7125 |
| 10 | ahy-miR394 | 6029 | 4235 | 7280 | 3673 | 7098 |
| 11 | aly-miR394a-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 12 | aly-miR394b-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 13 | aly-miR394b-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 14 | aof-miR394 | 6029 | 4235 | 7280 | 3673 | 7098 |
| 15 | ata-miR394-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 16 | ata-miR394-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 17 | ath-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 18 | ath-miR394b-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 19 | atr-miR394 | 6029 | 4235 | 7280 | 3673 | 7098 |
| 20 | atr-miR394 | 6029 | 4235 | 7280 | 3673 | 7098 |
| 21 | bdi-miR394 | 6029 | 4235 | 7280 | 3673 | 7098 |
| 22 | bdi-miR394 | 6029 | 4235 | 7280 | 3673 | 7098 |
| 23 | bna-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 24 | bna-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 25 | bna-miR394b | 6029 | 4235 | 7280 | 3673 | 7098 |
| 26 | bna-miR394b | 6029 | 4235 | 7280 | 3673 | 7098 |
| 27 | cca-miR394 | 6029 | 4235 | 7280 | 3673 | 7098 |
| 28 | cca-miR394 | 6029 | 4235 | 7280 | 3673 | 7098 |
| 29 | cme-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 30 | cme-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 31 | cme-miR394b | 6029 | 4235 | 7280 | 3673 | 7098 |
| 32 | cme-miR394b | 6029 | 4235 | 7280 | 3673 | 7098 |
| 33 | cpa-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 34 | cpa-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 35 | cpa-miR394b | 6029 | 4235 | 7280 | 3673 | 7098 |
| 36 | cpa-miR394b | 6029 | 4235 | 7280 | 3673 | 7098 |
| 37 | csi-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 38 | csi-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 39 | csi-miR394b-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 40 | csi-miR394b-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 41 | fve-miR394 | 6029 | 4235 | 7280 | 3673 | 7098 |
| 42 | fve-miR394 | 6029 | 4235 | 7280 | 3673 | 7098 |
| 43 | ghr-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 44 | ghr-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 45 | ghr-miR394b | 6029 | 4235 | 7280 | 3673 | 7098 |
| 46 | ghr-miR394b | 6029 | 4235 | 7280 | 3673 | 7098 |
| 47 | gma-miR394a-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 48 | gma-miR394a-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 49 | gma-miR394b-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 50 | gma-miR394b-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 51 | gma-miR394c-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 52 | gma-miR394c-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 53 | gma-miR394d | 6029 | 4235 | 7280 | 3673 | 7098 |
| 54 | gma-miR394d | 6029 | 4235 | 7280 | 3673 | 7098 |
| 55 | gma-miR394e | 6029 | 4235 | 7280 | 3673 | 7098 |
| 56 | gma-miR394e | 6029 | 4235 | 7280 | 3673 | 7098 |
| 57 | gma-miR394f | 6029 | 4235 | 7280 | 3673 | 7098 |
| 58 | gma-miR394f | 6029 | 4235 | 7280 | 3673 | 7098 |
| 59 | gma-miR394g | 6029 | 4235 | 7280 | 3673 | 7098 |
| 60 | gma-miR394g | 6029 | 4235 | 7280 | 3673 | 7098 |
| 61 | lus-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 62 | lus-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 63 | lus-miR394b | 6029 | 4235 | 7280 | 3673 | 7098 |
| 64 | lus-miR394b | 6029 | 4235 | 7280 | 3673 | 7098 |
| 65 | mdm-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 66 | mdm-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 67 | mdm-miR394b | 6029 | 4235 | 7280 | 3673 | 7098 |
| 68 | mdm-miR394b | 6029 | 4235 | 7280 | 3673 | 7098 |
| 69 | mes-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 70 | mes-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 71 | mes-miR394b | 6029 | 4235 | 7280 | 3673 | 7098 |
| 72 | mes-miR394b | 6029 | 4235 | 7280 | 3673 | 7098 |
| 73 | nta-miR394 | 6029 | 4235 | 7280 | 3673 | 7098 |
| 74 | nta-miR394 | 6029 | 4235 | 7280 | 3673 | 7098 |
| 75 | osa-miR394 | 6029 | 4235 | 7280 | 3673 | 7098 |
| 76 | osa-miR394 | 6029 | 4235 | 7280 | 3673 | 7098 |
| 77 | pab-miR394c | 6029 | 4235 | 7280 | 3673 | 7098 |
| 78 | pab-miR394c | 6029 | 4235 | 7280 | 3673 | 7098 |
| 79 | ppe-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 80 | ppe-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |

| | | | | | | |
|----|----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ppe-miR394b | 6029 | 4235 | 7280 | 3673 | 7098 |
| 4 | ptc-miR394a-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 5 | ptc-miR394b-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 6 | sbi-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 7 | sbi-miR394b | 6029 | 4235 | 7280 | 3673 | 7098 |
| 8 | sly-miR394-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 9 | ssl-miR394 | 6029 | 4235 | 7280 | 3673 | 7098 |
| 10 | stu-miR384-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 11 | tcc-miR394a | 6029 | 4235 | 7280 | 3673 | 7098 |
| 12 | tcc-miR394b | 6029 | 4235 | 7280 | 3673 | 7098 |
| 13 | vvi-miR394b | 6029 | 4235 | 7280 | 3673 | 7098 |
| 14 | zma-miR394a-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 15 | zma-miR394b-5p | 6029 | 4235 | 7280 | 3673 | 7098 |
| 16 | mes-miR394c | 6040 | 4241 | 7286 | 3676 | 7110 |
| 17 | vvi-miR394a | 6040 | 4241 | 7286 | 3676 | 7110 |
| 18 | vvi-miR394c | 6040 | 4241 | 7286 | 3676 | 7110 |
| 19 | lus-miR159b | 43789 | 43024 | 14233 | 43434 | 35919 |
| 20 | aly-miR159b-3p | 51628 | 50239 | 15411 | 50307 | 41274 |
| 21 | ath-miR159b-3p | 51628 | 50239 | 15411 | 50307 | 41274 |
| 22 | cas-miR159b-3p | 51628 | 50239 | 15411 | 50307 | 41274 |
| 23 | cas-miR159c-3p | 51628 | 50239 | 15411 | 50307 | 41274 |
| 24 | lus-miR159c | 51628 | 50239 | 15411 | 50307 | 41274 |
| 25 | aca-miR-21-5p | 481 | 200 | 352 | 368 | 215 |
| 26 | age-miR-21 | 481 | 200 | 352 | 368 | 215 |
| 27 | cfa-miR-21 | 481 | 200 | 352 | 368 | 215 |
| 28 | cgr-miR-21-5p | 481 | 200 | 352 | 368 | 215 |
| 29 | cja-miR-21 | 481 | 200 | 352 | 368 | 215 |
| 30 | cli-miR-21-5p | 481 | 200 | 352 | 368 | 215 |
| 31 | cpi-miR-21-5p | 481 | 200 | 352 | 368 | 215 |
| 32 | eca-miR-21 | 481 | 200 | 352 | 368 | 215 |
| 33 | gga-miR-21-5p | 481 | 200 | 352 | 368 | 215 |
| 34 | ggo-miR-21 | 481 | 200 | 352 | 368 | 215 |
| 35 | hsa-miR-21-5p | 481 | 200 | 352 | 368 | 215 |
| 36 | mdo-miR-21-5p | 481 | 200 | 352 | 368 | 215 |
| 37 | mml-miR-21-5p | 481 | 200 | 352 | 368 | 215 |
| 38 | mmu-miR-21a-5p | 481 | 200 | 352 | 368 | 215 |
| 39 | mne-miR-21 | 481 | 200 | 352 | 368 | 215 |
| 40 | oan-miR-21-5p | 481 | 200 | 352 | 368 | 215 |
| 41 | oha-miR-21-5p | 481 | 200 | 352 | 368 | 215 |
| 42 | pal-miR-21-5p | 481 | 200 | 352 | 368 | 215 |
| 43 | ppa-miR-21 | 481 | 200 | 352 | 368 | 215 |
| 44 | ppy-miR-21 | 481 | 200 | 352 | 368 | 215 |
| 45 | ptr-miR-21 | 481 | 200 | 352 | 368 | 215 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | rno-miR-21-5p | 481 | 200 | 352 | 368 | 215 |
| 4 | ssc-miR-21-5p | 481 | 200 | 352 | 368 | 215 |
| 5 | tch-miR-21-5p | 481 | 200 | 352 | 368 | 215 |
| 6 | tgu-miR-21-5p | 481 | 200 | 352 | 368 | 215 |
| 7 | age-miR-16 | 415 | 332 | 171 | 423 | 173 |
| 8 | cfa-miR-16 | 415 | 332 | 171 | 423 | 173 |
| 9 | cgr-miR-16-5p | 415 | 332 | 171 | 423 | 173 |
| 10 | cja-miR-16 | 415 | 332 | 171 | 423 | 173 |
| 11 | cpi-miR-16a-5p | 415 | 332 | 171 | 423 | 173 |
| 12 | dma-miR-16 | 415 | 332 | 171 | 423 | 173 |
| 13 | eca-miR-16 | 415 | 332 | 171 | 423 | 173 |
| 14 | ggo-miR-16 | 415 | 332 | 171 | 423 | 173 |
| 15 | hsa-miR-16-5p | 415 | 332 | 171 | 423 | 173 |
| 16 | lla-miR-16 | 415 | 332 | 171 | 423 | 173 |
| 17 | mdo-miR-16-5p | 415 | 332 | 171 | 423 | 173 |
| 18 | mml-miR-16-5p | 415 | 332 | 171 | 423 | 173 |
| 19 | mmu-miR-16-5p | 415 | 332 | 171 | 423 | 173 |
| 20 | mne-miR-16 | 415 | 332 | 171 | 423 | 173 |
| 21 | mze-miR-16a | 415 | 332 | 171 | 423 | 173 |
| 22 | nle-miR-16 | 415 | 332 | 171 | 423 | 173 |
| 23 | oan-miR-16a-5p | 415 | 332 | 171 | 423 | 173 |
| 24 | oga-miR-16 | 415 | 332 | 171 | 423 | 173 |
| 25 | oni-miR-16a | 415 | 332 | 171 | 423 | 173 |
| 26 | pal-miR-16-5p | 415 | 332 | 171 | 423 | 173 |
| 27 | pha-miR-16 | 415 | 332 | 171 | 423 | 173 |
| 28 | ppa-miR-16 | 415 | 332 | 171 | 423 | 173 |
| 29 | ptr-miR-16 | 415 | 332 | 171 | 423 | 173 |
| 30 | rno-miR-16-5p | 415 | 332 | 171 | 423 | 173 |
| 31 | sbo-miR-16 | 415 | 332 | 171 | 423 | 173 |
| 32 | sla-miR-16 | 415 | 332 | 171 | 423 | 173 |
| 33 | ssa-miR-16c-5p | 415 | 332 | 171 | 423 | 173 |
| 34 | ssc-miR-16 | 415 | 332 | 171 | 423 | 173 |
| 35 | gma-miR482c-3p | 115 | 195 | 343 | 188 | 202 |
| 36 | aof-miR171a | 18981 | 26336 | 17317 | 24117 | 23314 |
| 37 | aqc-miR171a | 18981 | 26336 | 17317 | 24117 | 23314 |
| 38 | aqc-miR171b | 18981 | 26336 | 17317 | 24117 | 23314 |
| 39 | aqc-miR171d | 18981 | 26336 | 17317 | 24117 | 23314 |
| 40 | ata-miR171b-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 41 | ata-miR171d-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 42 | bdi-miR171b | 18981 | 26336 | 17317 | 24117 | 23314 |
| 43 | bdi-miR171c-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 44 | bdi-miR171d-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 45 | bdi-miR171e | 18981 | 26336 | 17317 | 24117 | 23314 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | cme-miR171c | 18981 | 26336 | 17317 | 24117 | 23314 |
| 4 | cme-miR171f | 18981 | 26336 | 17317 | 24117 | 23314 |
| 5 | cpa-miR171a | 18981 | 26336 | 17317 | 24117 | 23314 |
| 6 | cpa-miR171b | 18981 | 26336 | 17317 | 24117 | 23314 |
| 7 | cpa-miR171c | 18981 | 26336 | 17317 | 24117 | 23314 |
| 8 | cpa-miR171d | 18981 | 26336 | 17317 | 24117 | 23314 |
| 9 | crt-miR171 | 18981 | 26336 | 17317 | 24117 | 23314 |
| 10 | csi-miR171c-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 11 | csi-miR171d-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 12 | csi-miR171f-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 13 | csi-miR171h-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 14 | csi-miR171i-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 15 | far-miR171 | 18981 | 26336 | 17317 | 24117 | 23314 |
| 16 | fve-miR171a | 18981 | 26336 | 17317 | 24117 | 23314 |
| 17 | fve-miR171c-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 18 | fve-miR171d | 18981 | 26336 | 17317 | 24117 | 23314 |
| 19 | fve-miR171e | 18981 | 26336 | 17317 | 24117 | 23314 |
| 20 | fve-miR171g | 18981 | 26336 | 17317 | 24117 | 23314 |
| 21 | gma-miR171e | 18981 | 26336 | 17317 | 24117 | 23314 |
| 22 | gma-miR171f | 18981 | 26336 | 17317 | 24117 | 23314 |
| 23 | gma-miR171g | 18981 | 26336 | 17317 | 24117 | 23314 |
| 24 | gma-miR171j-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 25 | gma-miR171u | 18981 | 26336 | 17317 | 24117 | 23314 |
| 26 | hpa-miR171a | 18981 | 26336 | 17317 | 24117 | 23314 |
| 27 | htu-miR171b | 18981 | 26336 | 17317 | 24117 | 23314 |
| 28 | htu-miR171c | 18981 | 26336 | 17317 | 24117 | 23314 |
| 29 | hvu-miR171-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 30 | lja-miR171a | 18981 | 26336 | 17317 | 24117 | 23314 |
| 31 | lus-miR171b | 18981 | 26336 | 17317 | 24117 | 23314 |
| 32 | lus-miR171c | 18981 | 26336 | 17317 | 24117 | 23314 |
| 33 | lus-miR171e | 18981 | 26336 | 17317 | 24117 | 23314 |
| 34 | mdm-miR171g | 18981 | 26336 | 17317 | 24117 | 23314 |
| 35 | mdm-miR171h | 18981 | 26336 | 17317 | 24117 | 23314 |
| 36 | mes-miR171g | 18981 | 26336 | 17317 | 24117 | 23314 |
| 37 | mes-miR171h | 18981 | 26336 | 17317 | 24117 | 23314 |
| 38 | mes-miR171i | 18981 | 26336 | 17317 | 24117 | 23314 |
| 39 | mes-miR171j | 18981 | 26336 | 17317 | 24117 | 23314 |
| 40 | mes-miR171k | 18981 | 26336 | 17317 | 24117 | 23314 |
| 41 | mtr-miR171d | 18981 | 26336 | 17317 | 24117 | 23314 |
| 42 | nta-miR171c | 18981 | 26336 | 17317 | 24117 | 23314 |
| 43 | osa-miR171b | 18981 | 26336 | 17317 | 24117 | 23314 |
| 44 | osa-miR171c-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 45 | osa-miR171d-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | osa-miR171e-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 4 | osa-miR171f-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 5 | pde-miR171 | 18981 | 26336 | 17317 | 24117 | 23314 |
| 6 | ppe-miR171a | 18981 | 26336 | 17317 | 24117 | 23314 |
| 7 | ppe-miR171c | 18981 | 26336 | 17317 | 24117 | 23314 |
| 8 | ppe-miR171f | 18981 | 26336 | 17317 | 24117 | 23314 |
| 9 | ppe-miR171g | 18981 | 26336 | 17317 | 24117 | 23314 |
| 10 | ptc-miR171e | 18981 | 26336 | 17317 | 24117 | 23314 |
| 11 | ptc-miR171f | 18981 | 26336 | 17317 | 24117 | 23314 |
| 12 | ptc-miR171g-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 13 | ptc-miR171h-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 14 | ptc-miR171i | 18981 | 26336 | 17317 | 24117 | 23314 |
| 15 | rco-miR171c | 18981 | 26336 | 17317 | 24117 | 23314 |
| 16 | rco-miR171d | 18981 | 26336 | 17317 | 24117 | 23314 |
| 17 | rco-miR171e | 18981 | 26336 | 17317 | 24117 | 23314 |
| 18 | rco-miR171f | 18981 | 26336 | 17317 | 24117 | 23314 |
| 19 | sbi-miR171a | 18981 | 26336 | 17317 | 24117 | 23314 |
| 20 | sbi-miR171b | 18981 | 26336 | 17317 | 24117 | 23314 |
| 21 | sbi-miR171d | 18981 | 26336 | 17317 | 24117 | 23314 |
| 22 | sbi-miR171i | 18981 | 26336 | 17317 | 24117 | 23314 |
| 23 | sbi-miR171k | 18981 | 26336 | 17317 | 24117 | 23314 |
| 24 | sly-miR171a | 18981 | 26336 | 17317 | 24117 | 23314 |
| 25 | stu-miR171a-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 26 | stu-miR171e | 18981 | 26336 | 17317 | 24117 | 23314 |
| 27 | tae-miR171a | 18981 | 26336 | 17317 | 24117 | 23314 |
| 28 | tcc-miR171d | 18981 | 26336 | 17317 | 24117 | 23314 |
| 29 | tcc-miR171e | 18981 | 26336 | 17317 | 24117 | 23314 |
| 30 | tcc-miR171f | 18981 | 26336 | 17317 | 24117 | 23314 |
| 31 | tcc-miR171g | 18981 | 26336 | 17317 | 24117 | 23314 |
| 32 | tcc-miR171h | 18981 | 26336 | 17317 | 24117 | 23314 |
| 33 | vvi-miR171a | 18981 | 26336 | 17317 | 24117 | 23314 |
| 34 | vvi-miR171c | 18981 | 26336 | 17317 | 24117 | 23314 |
| 35 | vvi-miR171d | 18981 | 26336 | 17317 | 24117 | 23314 |
| 36 | vvi-miR171i | 18981 | 26336 | 17317 | 24117 | 23314 |
| 37 | vvi-miR171j | 18981 | 26336 | 17317 | 24117 | 23314 |
| 38 | zma-miR171d-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 39 | zma-miR171e-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 40 | zma-miR171i-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 41 | zma-miR171j-3p | 18981 | 26336 | 17317 | 24117 | 23314 |
| 42 | aly-miR159c-3p | 143 | 159 | 52 | 148 | 104 |
| 43 | ath-miR159c | 143 | 159 | 52 | 148 | 104 |
| 44 | cas-miR159a | 143 | 159 | 52 | 148 | 104 |
| 45 | zma-miR169a-3p | 3225 | 6734 | 3860 | 4745 | 5231 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|------|-------|-------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | zma-miR169b-3p | 3225 | 6734 | 3860 | 4745 | 5231 |
| 4 | gma-miR482a-3p | 6550 | 10477 | 13426 | 7472 | 7453 |
| 5 | vun-miR482 | 6550 | 10477 | 13426 | 7472 | 7453 |
| 6 | atr-miR171b | 355 | 690 | 319 | 428 | 500 |
| 7 | atr-miR171b | 355 | 690 | 319 | 428 | 500 |
| 8 | gma-miR171c-3p | 355 | 690 | 319 | 428 | 500 |
| 9 | gma-miR171c-3p | 355 | 690 | 319 | 428 | 500 |
| 10 | gma-miR171o-3p | 355 | 690 | 319 | 428 | 500 |
| 11 | gma-miR171q | 355 | 690 | 319 | 428 | 500 |
| 12 | gma-miR171q | 355 | 690 | 319 | 428 | 500 |
| 13 | mdm-miR171m | 355 | 690 | 319 | 428 | 500 |
| 14 | mdm-miR171n | 355 | 690 | 319 | 428 | 500 |
| 15 | zma-miR171f-3p | 355 | 690 | 319 | 428 | 500 |
| 16 | aca-miR-191-5p | 477 | 428 | 181 | 576 | 207 |
| 17 | aca-miR-191-5p | 477 | 428 | 181 | 576 | 207 |
| 18 | bta-miR-191 | 477 | 428 | 181 | 576 | 207 |
| 19 | cgr-miR-191-5p | 477 | 428 | 181 | 576 | 207 |
| 20 | cja-miR-191 | 477 | 428 | 181 | 576 | 207 |
| 21 | cja-miR-191 | 477 | 428 | 181 | 576 | 207 |
| 22 | cpo-miR-191-5p | 477 | 428 | 181 | 576 | 207 |
| 23 | dma-miR-191 | 477 | 428 | 181 | 576 | 207 |
| 24 | dno-miR-191-5p | 477 | 428 | 181 | 576 | 207 |
| 25 | dno-miR-191-5p | 477 | 428 | 181 | 576 | 207 |
| 26 | eca-miR-191a | 477 | 428 | 181 | 576 | 207 |
| 27 | gga-miR-191-5p | 477 | 428 | 181 | 576 | 207 |
| 28 | hsa-miR-191-5p | 477 | 428 | 181 | 576 | 207 |
| 29 | hsa-miR-191-5p | 477 | 428 | 181 | 576 | 207 |
| 30 | mml-miR-191-5p | 477 | 428 | 181 | 576 | 207 |
| 31 | mmr-miR-191 | 477 | 428 | 181 | 576 | 207 |
| 32 | mmr-miR-191 | 477 | 428 | 181 | 576 | 207 |
| 33 | mmu-miR-191-5p | 477 | 428 | 181 | 576 | 207 |
| 34 | nle-miR-191 | 477 | 428 | 181 | 576 | 207 |
| 35 | ocu-miR-191-5p | 477 | 428 | 181 | 576 | 207 |
| 36 | oga-miR-191 | 477 | 428 | 181 | 576 | 207 |
| 37 | oga-miR-191 | 477 | 428 | 181 | 576 | 207 |
| 38 | oha-miR-191-5p | 477 | 428 | 181 | 576 | 207 |
| 39 | pbv-miR-191-5p | 477 | 428 | 181 | 576 | 207 |
| 40 | pha-miR-191 | 477 | 428 | 181 | 576 | 207 |
| 41 | pha-miR-191 | 477 | 428 | 181 | 576 | 207 |
| 42 | ppa-miR-191 | 477 | 428 | 181 | 576 | 207 |
| 43 | ppy-miR-191 | 477 | 428 | 181 | 576 | 207 |
| 44 | ptr-miR-191 | 477 | 428 | 181 | 576 | 207 |
| 45 | ptr-miR-191 | 477 | 428 | 181 | 576 | 207 |
| 46 | rno-miR-191a-5p | 477 | 428 | 181 | 576 | 207 |
| 47 | sbo-miR-191 | 477 | 428 | 181 | 576 | 207 |
| 48 | ssc-miR-191 | 477 | 428 | 181 | 576 | 207 |
| 49 | ssc-miR-191 | 477 | 428 | 181 | 576 | 207 |
| 50 | gma-miR171o-5p | 84 | 80 | 19 | 34 | 90 |
| 51 | cfa-miR-29a | 75 | 30 | 84 | 70 | 34 |
| 52 | cja-miR-29a | 75 | 30 | 84 | 70 | 34 |
| 53 | cja-miR-29a | 75 | 30 | 84 | 70 | 34 |
| 54 | cpo-miR-29a-3p | 75 | 30 | 84 | 70 | 34 |
| 55 | dma-miR-29a | 75 | 30 | 84 | 70 | 34 |
| 56 | dno-miR-29a-3p | 75 | 30 | 84 | 70 | 34 |
| 57 | dno-miR-29a-3p | 75 | 30 | 84 | 70 | 34 |
| 58 | eca-miR-29a | 75 | 30 | 84 | 70 | 34 |
| 59 | hsa-miR-29a-3p | 75 | 30 | 84 | 70 | 34 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|--------|--------|-------|--------|--------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | mmr-miR-29a | 75 | 30 | 84 | 70 | 34 |
| 4 | mmu-miR-29a-3p | 75 | 30 | 84 | 70 | 34 |
| 5 | nle-miR-29a | 75 | 30 | 84 | 70 | 34 |
| 6 | ocu-miR-29a-3p | 75 | 30 | 84 | 70 | 34 |
| 7 | oga-miR-29a | 75 | 30 | 84 | 70 | 34 |
| 8 | pal-miR-29a-3p | 75 | 30 | 84 | 70 | 34 |
| 9 | pha-miR-29a | 75 | 30 | 84 | 70 | 34 |
| 10 | rno-miR-29a-3p | 75 | 30 | 84 | 70 | 34 |
| 11 | csi-miR393b-5p | 724 | 322 | 100 | 306 | 461 |
| 12 | gma-miR393h | 724 | 322 | 100 | 306 | 461 |
| 13 | gma-miR393i | 724 | 322 | 100 | 306 | 461 |
| 14 | gma-miR393j | 724 | 322 | 100 | 306 | 461 |
| 15 | gma-miR393k | 724 | 322 | 100 | 306 | 461 |
| 16 | ami-miR-191-5p | 194 | 181 | 119 | 234 | 96 |
| 17 | cfa-miR-191 | 194 | 181 | 119 | 234 | 96 |
| 18 | chi-miR-191-5p | 194 | 181 | 119 | 234 | 96 |
| 19 | cpi-miR-191-5p | 194 | 181 | 119 | 234 | 96 |
| 20 | mdo-miR-191-5p | 194 | 181 | 119 | 234 | 96 |
| 21 | oan-miR-191-5p | 194 | 181 | 119 | 234 | 96 |
| 22 | oar-miR-191 | 194 | 181 | 119 | 234 | 96 |
| 23 | pal-miR-191-5p | 194 | 181 | 119 | 234 | 96 |
| 24 | tch-miR-191-5p | 194 | 181 | 119 | 234 | 96 |
| 25 | xla-miR-191-5p | 194 | 181 | 119 | 234 | 96 |
| 26 | xtr-miR-191 | 194 | 181 | 119 | 234 | 96 |
| 27 | aly-miR169b-5p | 146961 | 237557 | 30977 | 164185 | 155727 |
| 28 | aly-miR169c-5p | 146961 | 237557 | 30977 | 164185 | 155727 |
| 29 | aqc-miR169c | 146961 | 237557 | 30977 | 164185 | 155727 |
| 30 | ata-miR169d-5p | 146961 | 237557 | 30977 | 164185 | 155727 |
| 31 | ath-miR169b-5p | 146961 | 237557 | 30977 | 164185 | 155727 |
| 32 | ath-miR169c | 146961 | 237557 | 30977 | 164185 | 155727 |
| 33 | bdi-miR169c-5p | 146961 | 237557 | 30977 | 164185 | 155727 |
| 34 | bdi-miR169f | 146961 | 237557 | 30977 | 164185 | 155727 |
| 35 | bna-miR169n | 146961 | 237557 | 30977 | 164185 | 155727 |
| 36 | cas-miR169b | 146961 | 237557 | 30977 | 164185 | 155727 |
| 37 | cme-miR169f | 146961 | 237557 | 30977 | 164185 | 155727 |
| 38 | cme-miR169h | 146961 | 237557 | 30977 | 164185 | 155727 |
| 39 | csi-miR169g-5p | 146961 | 237557 | 30977 | 164185 | 155727 |
| 40 | csi-miR169k-5p | 146961 | 237557 | 30977 | 164185 | 155727 |
| 41 | csi-miR169m-5p | 146961 | 237557 | 30977 | 164185 | 155727 |
| 42 | csi-miR169n-5p | 146961 | 237557 | 30977 | 164185 | 155727 |
| 43 | csi-miR169o-5p | 146961 | 237557 | 30977 | 164185 | 155727 |
| 44 | csi-miR169r-5p | 146961 | 237557 | 30977 | 164185 | 155727 |
| 45 | gma-miR169a | 146961 | 237557 | 30977 | 164185 | 155727 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|--------|--------|-------|--------|--------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | gma-miR169f | 146961 | 237557 | 30977 | 164185 | 155727 |
| 4 | gma-miR169g | 146961 | 237557 | 30977 | 164185 | 155727 |
| 5 | gma-miR169m | 146961 | 237557 | 30977 | 164185 | 155727 |
| 6 | gma-miR169m | 146961 | 237557 | 30977 | 164185 | 155727 |
| 7 | lus-miR169f | 146961 | 237557 | 30977 | 164185 | 155727 |
| 8 | lus-miR169h | 146961 | 237557 | 30977 | 164185 | 155727 |
| 9 | lus-miR169j | 146961 | 237557 | 30977 | 164185 | 155727 |
| 10 | lus-miR169j | 146961 | 237557 | 30977 | 164185 | 155727 |
| 11 | mdm-miR169a | 146961 | 237557 | 30977 | 164185 | 155727 |
| 12 | mdm-miR169g | 146961 | 237557 | 30977 | 164185 | 155727 |
| 13 | mdm-miR169g | 146961 | 237557 | 30977 | 164185 | 155727 |
| 14 | mdm-miR169h | 146961 | 237557 | 30977 | 164185 | 155727 |
| 15 | mdm-miR169i | 146961 | 237557 | 30977 | 164185 | 155727 |
| 16 | mdm-miR169j | 146961 | 237557 | 30977 | 164185 | 155727 |
| 17 | mdm-miR169j | 146961 | 237557 | 30977 | 164185 | 155727 |
| 18 | mes-miR169a | 146961 | 237557 | 30977 | 164185 | 155727 |
| 19 | mes-miR169b | 146961 | 237557 | 30977 | 164185 | 155727 |
| 20 | mes-miR169b | 146961 | 237557 | 30977 | 164185 | 155727 |
| 21 | mes-miR169c | 146961 | 237557 | 30977 | 164185 | 155727 |
| 22 | mes-miR169d | 146961 | 237557 | 30977 | 164185 | 155727 |
| 23 | mes-miR169e | 146961 | 237557 | 30977 | 164185 | 155727 |
| 24 | mes-miR169e | 146961 | 237557 | 30977 | 164185 | 155727 |
| 25 | mtr-miR169b | 146961 | 237557 | 30977 | 164185 | 155727 |
| 26 | mtr-miR169g | 146961 | 237557 | 30977 | 164185 | 155727 |
| 27 | mtr-miR169l-5p | 146961 | 237557 | 30977 | 164185 | 155727 |
| 28 | nta-miR169q | 146961 | 237557 | 30977 | 164185 | 155727 |
| 29 | nta-miR169q | 146961 | 237557 | 30977 | 164185 | 155727 |
| 30 | nta-miR169r | 146961 | 237557 | 30977 | 164185 | 155727 |
| 31 | nta-miR169s | 146961 | 237557 | 30977 | 164185 | 155727 |
| 32 | nta-miR169s | 146961 | 237557 | 30977 | 164185 | 155727 |
| 33 | osa-miR169b | 146961 | 237557 | 30977 | 164185 | 155727 |
| 34 | osa-miR169c | 146961 | 237557 | 30977 | 164185 | 155727 |
| 35 | ppe-miR169a | 146961 | 237557 | 30977 | 164185 | 155727 |
| 36 | ppe-miR169b | 146961 | 237557 | 30977 | 164185 | 155727 |
| 37 | ppe-miR169b | 146961 | 237557 | 30977 | 164185 | 155727 |
| 38 | ppe-miR169c | 146961 | 237557 | 30977 | 164185 | 155727 |
| 39 | ptc-miR169d | 146961 | 237557 | 30977 | 164185 | 155727 |
| 40 | ptc-miR169d | 146961 | 237557 | 30977 | 164185 | 155727 |
| 41 | ptc-miR169e | 146961 | 237557 | 30977 | 164185 | 155727 |
| 42 | ptc-miR169f | 146961 | 237557 | 30977 | 164185 | 155727 |
| 43 | ptc-miR169g | 146961 | 237557 | 30977 | 164185 | 155727 |
| 44 | ptc-miR169g | 146961 | 237557 | 30977 | 164185 | 155727 |
| 45 | ptc-miR169h | 146961 | 237557 | 30977 | 164185 | 155727 |
| 46 | ptc-miR169p | 146961 | 237557 | 30977 | 164185 | 155727 |
| 47 | rco-miR169a | 146961 | 237557 | 30977 | 164185 | 155727 |
| 48 | rco-miR169b | 146961 | 237557 | 30977 | 164185 | 155727 |
| 49 | rco-miR169b | 146961 | 237557 | 30977 | 164185 | 155727 |
| 50 | sbi-miR169b | 146961 | 237557 | 30977 | 164185 | 155727 |
| 51 | sbi-miR169k | 146961 | 237557 | 30977 | 164185 | 155727 |
| 52 | sbi-miR169k | 146961 | 237557 | 30977 | 164185 | 155727 |
| 53 | sly-miR169a | 146961 | 237557 | 30977 | 164185 | 155727 |
| 54 | tcc-miR169b | 146961 | 237557 | 30977 | 164185 | 155727 |
| 55 | tcc-miR169k | 146961 | 237557 | 30977 | 164185 | 155727 |
| 56 | tcc-miR169l | 146961 | 237557 | 30977 | 164185 | 155727 |
| 57 | tcc-miR169l | 146961 | 237557 | 30977 | 164185 | 155727 |
| 58 | vun-miR169 | 146961 | 237557 | 30977 | 164185 | 155727 |
| 59 | vvi-miR169a | 146961 | 237557 | 30977 | 164185 | 155727 |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|--------|--------|-------|--------|--------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | vvi-miR169c | 146961 | 237557 | 30977 | 164185 | 155727 |
| 4 | vvi-miR169j | 146961 | 237557 | 30977 | 164185 | 155727 |
| 5 | vvi-miR169k | 146961 | 237557 | 30977 | 164185 | 155727 |
| 6 | vvi-miR169s | 146961 | 237557 | 30977 | 164185 | 155727 |
| 7 | vvi-miR169w | 146961 | 237557 | 30977 | 164185 | 155727 |
| 8 | | | | | | |
| 9 | | | | | | |
| 10 | zma-miR169c-5p | 146961 | 237557 | 30977 | 164185 | 155727 |
| 11 | zma-miR169r-5p | 146961 | 237557 | 30977 | 164185 | 155727 |
| 12 | | | | | | |
| 13 | aly-miR170-3p | 15308 | 25886 | 3466 | 19075 | 16163 |
| 14 | ath-miR170-3p | 15308 | 25886 | 3466 | 19075 | 16163 |
| 15 | stu-miR171c-3p | 15308 | 25886 | 3466 | 19075 | 16163 |
| 16 | | | | | | |
| 17 | cli-miR-146a-5p | 343 | 393 | 170 | 459 | 165 |
| 18 | cpo-miR-146a-5p | 343 | 393 | 170 | 459 | 165 |
| 19 | ocu-miR-146a-5p | 343 | 393 | 170 | 459 | 165 |
| 20 | | | | | | |
| 21 | dno-miR-146a-5p | 390 | 443 | 190 | 506 | 189 |
| 22 | gma-miR319d | 4472 | 2104 | 493 | 3426 | 1420 |
| 23 | gma-miR319o | 4472 | 2104 | 493 | 3426 | 1420 |
| 24 | gma-miR319i | 4536 | 2115 | 515 | 3463 | 1429 |
| 25 | | | | | | |
| 26 | cfa-miR-146a | 341 | 392 | 170 | 457 | 164 |
| 27 | cgr-miR-146a | 341 | 392 | 170 | 457 | 164 |
| 28 | cja-miR-146a | 341 | 392 | 170 | 457 | 164 |
| 29 | | | | | | |
| 30 | eca-miR-146a | 341 | 392 | 170 | 457 | 164 |
| 31 | gga-miR-146a-5p | 341 | 392 | 170 | 457 | 164 |
| 32 | hsa-miR-146a-5p | 341 | 392 | 170 | 457 | 164 |
| 33 | | | | | | |
| 34 | mdo-miR-146a-5p | 341 | 392 | 170 | 457 | 164 |
| 35 | mml-miR-146a-5p | 341 | 392 | 170 | 457 | 164 |
| 36 | mmr-miR-146a | 341 | 392 | 170 | 457 | 164 |
| 37 | | | | | | |
| 38 | mmu-miR-146a-5p | 341 | 392 | 170 | 457 | 164 |
| 39 | nle-miR-146a | 341 | 392 | 170 | 457 | 164 |
| 40 | pal-miR-146a-5p | 341 | 392 | 170 | 457 | 164 |
| 41 | | | | | | |
| 42 | pha-miR-146a | 341 | 392 | 170 | 457 | 164 |
| 43 | ppy-miR-146a | 341 | 392 | 170 | 457 | 164 |
| 44 | ptr-miR-146a | 341 | 392 | 170 | 457 | 164 |
| 45 | | | | | | |
| 46 | rno-miR-146a-5p | 341 | 392 | 170 | 457 | 164 |
| 47 | ssc-miR-146a-5p | 341 | 392 | 170 | 457 | 164 |
| 48 | tch-miR-146a-5p | 341 | 392 | 170 | 457 | 164 |
| 49 | | | | | | |
| 50 | tgu-miR-146c | 341 | 392 | 170 | 457 | 164 |
| 51 | efu-miR-22 | 731 | 372 | 963 | 618 | 328 |
| 52 | xla-miR-22-3p | 731 | 372 | 963 | 618 | 328 |
| 53 | | | | | | |
| 54 | aly-miR171b-3p | 424 | 544 | 1350 | 408 | 747 |
| 55 | aly-miR171c-3p | 424 | 544 | 1350 | 408 | 747 |
| 56 | ata-miR171c-3p | 424 | 544 | 1350 | 408 | 747 |
| 57 | | | | | | |
| 58 | ath-miR171b-3p | 424 | 544 | 1350 | 408 | 747 |
| 59 | ath-miR171c-3p | 424 | 544 | 1350 | 408 | 747 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-----|-----|------|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | bna-miR171a | 424 | 544 | 1350 | 408 | 747 |
| 4 | bna-miR171b | 424 | 544 | 1350 | 408 | 747 |
| 5 | bna-miR171c | 424 | 544 | 1350 | 408 | 747 |
| 6 | bna-miR171d | 424 | 544 | 1350 | 408 | 747 |
| 7 | bna-miR171e | 424 | 544 | 1350 | 408 | 747 |
| 8 | bol-miR171a | 424 | 544 | 1350 | 408 | 747 |
| 9 | bra-miR171a | 424 | 544 | 1350 | 408 | 747 |
| 10 | bra-miR171b | 424 | 544 | 1350 | 408 | 747 |
| 11 | bra-miR171c | 424 | 544 | 1350 | 408 | 747 |
| 12 | bra-miR171d | 424 | 544 | 1350 | 408 | 747 |
| 13 | cas-miR171b | 424 | 544 | 1350 | 408 | 747 |
| 14 | cas-miR171c-3p | 424 | 544 | 1350 | 408 | 747 |
| 15 | cme-miR171b | 424 | 544 | 1350 | 408 | 747 |
| 16 | cme-miR171d | 424 | 544 | 1350 | 408 | 747 |
| 17 | gma-miR171i-3p | 424 | 544 | 1350 | 408 | 747 |
| 18 | lus-miR171i | 424 | 544 | 1350 | 408 | 747 |
| 19 | mdm-miR171f-3p | 424 | 544 | 1350 | 408 | 747 |
| 20 | mes-miR171b | 424 | 544 | 1350 | 408 | 747 |
| 21 | mes-miR171c | 424 | 544 | 1350 | 408 | 747 |
| 22 | mtr-miR171f | 424 | 544 | 1350 | 408 | 747 |
| 23 | ptc-miR171a-3p | 424 | 544 | 1350 | 408 | 747 |
| 24 | ptc-miR171b | 424 | 544 | 1350 | 408 | 747 |
| 25 | rco-miR171a | 424 | 544 | 1350 | 408 | 747 |
| 26 | rco-miR171b | 424 | 544 | 1350 | 408 | 747 |
| 27 | sly-miR171b-3p | 424 | 544 | 1350 | 408 | 747 |
| 28 | ssl-miR171a | 424 | 544 | 1350 | 408 | 747 |
| 29 | stu-miR171d-3p | 424 | 544 | 1350 | 408 | 747 |
| 30 | tae-miR171b | 424 | 544 | 1350 | 408 | 747 |
| 31 | age-miR-22 | 709 | 369 | 937 | 608 | 319 |
| 32 | aja-miR-22 | 709 | 369 | 937 | 608 | 319 |
| 33 | cfa-miR-22 | 709 | 369 | 937 | 608 | 319 |
| 34 | cgr-miR-22-3p | 709 | 369 | 937 | 608 | 319 |
| 35 | cja-miR-22 | 709 | 369 | 937 | 608 | 319 |
| 36 | cli-miR-22-3p | 709 | 369 | 937 | 608 | 319 |
| 37 | cpi-miR-22-3p | 709 | 369 | 937 | 608 | 319 |
| 38 | cpo-miR-22-3p | 709 | 369 | 937 | 608 | 319 |
| 39 | dma-miR-22 | 709 | 369 | 937 | 608 | 319 |
| 40 | dno-miR-22-3p | 709 | 369 | 937 | 608 | 319 |
| 41 | eca-miR-22 | 709 | 369 | 937 | 608 | 319 |
| 42 | gga-miR-22-3p | 709 | 369 | 937 | 608 | 319 |
| 43 | hsa-miR-22-3p | 709 | 369 | 937 | 608 | 319 |
| 44 | lca-miR-22 | 709 | 369 | 937 | 608 | 319 |
| 45 | lla-miR-22 | 709 | 369 | 937 | 608 | 319 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | mml-miR-22 | 709 | 369 | 937 | 608 | 319 |
| 4 | mmr-miR-22 | 709 | 369 | 937 | 608 | 319 |
| 5 | mmu-miR-22-3p | 709 | 369 | 937 | 608 | 319 |
| 6 | mne-miR-22 | 709 | 369 | 937 | 608 | 319 |
| 7 | nle-miR-22 | 709 | 369 | 937 | 608 | 319 |
| 8 | oan-miR-22-3p | 709 | 369 | 937 | 608 | 319 |
| 9 | ocu-miR-22-3p | 709 | 369 | 937 | 608 | 319 |
| 10 | oga-miR-22 | 709 | 369 | 937 | 608 | 319 |
| 11 | oha-miR-22a | 709 | 369 | 937 | 608 | 319 |
| 12 | pal-miR-22-3p | 709 | 369 | 937 | 608 | 319 |
| 13 | pbv-miR-22-3p | 709 | 369 | 937 | 608 | 319 |
| 14 | pha-miR-22 | 709 | 369 | 937 | 608 | 319 |
| 15 | ppa-miR-22 | 709 | 369 | 937 | 608 | 319 |
| 16 | ppy-miR-22 | 709 | 369 | 937 | 608 | 319 |
| 17 | ptr-miR-22 | 709 | 369 | 937 | 608 | 319 |
| 18 | rno-miR-22-3p | 709 | 369 | 937 | 608 | 319 |
| 19 | sbo-miR-22 | 709 | 369 | 937 | 608 | 319 |
| 20 | sla-miR-22 | 709 | 369 | 937 | 608 | 319 |
| 21 | ssc-miR-22-3p | 709 | 369 | 937 | 608 | 319 |
| 22 | tch-miR-22-3p | 709 | 369 | 937 | 608 | 319 |
| 23 | xtr-miR-22-3p | 709 | 369 | 937 | 608 | 319 |
| 24 | gma-miR319g | 72394 | 42723 | 7142 | 58789 | 26709 |
| 25 | gma-miR319l | 72394 | 42723 | 7142 | 58789 | 26709 |
| 26 | gma-miR319q | 71606 | 42408 | 6869 | 58263 | 26449 |
| 27 | aly-miR393a-5p | 306 | 138 | 44 | 193 | 134 |
| 28 | aly-miR393b-5p | 306 | 138 | 44 | 193 | 134 |
| 29 | ath-miR393a-5p | 306 | 138 | 44 | 193 | 134 |
| 30 | ath-miR393b-5p | 306 | 138 | 44 | 193 | 134 |
| 31 | atr-miR393 | 306 | 138 | 44 | 193 | 134 |
| 32 | cas-miR393-5p | 306 | 138 | 44 | 193 | 134 |
| 33 | cpa-miR393 | 306 | 138 | 44 | 193 | 134 |
| 34 | gma-miR393c-5p | 306 | 138 | 44 | 193 | 134 |
| 35 | gma-miR393d | 306 | 138 | 44 | 193 | 134 |
| 36 | gma-miR393e | 306 | 138 | 44 | 193 | 134 |
| 37 | gma-miR393f | 306 | 138 | 44 | 193 | 134 |
| 38 | gma-miR393g | 306 | 138 | 44 | 193 | 134 |
| 39 | htu-miR393a | 306 | 138 | 44 | 193 | 134 |
| 40 | htu-miR393b | 306 | 138 | 44 | 193 | 134 |
| 41 | htu-miR393c | 306 | 138 | 44 | 193 | 134 |
| 42 | mes-miR393b | 306 | 138 | 44 | 193 | 134 |
| 43 | stu-miR393-5p | 306 | 138 | 44 | 193 | 134 |
| 44 | tcc-miR393a | 306 | 138 | 44 | 193 | 134 |
| 45 | zma-miR393b-5p | 306 | 138 | 44 | 193 | 134 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | aof-miR393b | 174 | 86 | 26 | 102 | 86 |
| 4 | fve-miR393b | 174 | 86 | 26 | 102 | 86 |
| 5 | ghr-miR393 | 174 | 86 | 26 | 102 | 86 |
| 6 | mdm-miR393a | 174 | 86 | 26 | 102 | 86 |
| 7 | mdm-miR393b | 174 | 86 | 26 | 102 | 86 |
| 8 | mdm-miR393c | 174 | 86 | 26 | 102 | 86 |
| 9 | mes-miR393c | 174 | 86 | 26 | 102 | 86 |
| 10 | mes-miR393d | 174 | 86 | 26 | 102 | 86 |
| 11 | osa-miR393b-5p | 174 | 86 | 26 | 102 | 86 |
| 12 | zma-miR393a-5p | 174 | 86 | 26 | 102 | 86 |
| 13 | zma-miR393c-5p | 174 | 86 | 26 | 102 | 86 |
| 14 | zma-miR393d-5p | 174 | 86 | 26 | 102 | 86 |
| 15 | zma-miR393e-5p | 174 | 86 | 26 | 102 | 86 |
| 16 | zma-miR393f-5p | 174 | 86 | 26 | 102 | 86 |
| 17 | zma-miR393g-5p | 174 | 86 | 26 | 102 | 86 |
| 18 | smo-miR171a | 54 | 99 | 106 | 64 | 80 |
| 19 | atr-miR319a | 10552 | 5675 | 5926 | 6787 | 3696 |
| 20 | atr-miR319c | 10552 | 5675 | 5926 | 6787 | 3696 |
| 21 | cme-miR319a | 10552 | 5675 | 5926 | 6787 | 3696 |
| 22 | cme-miR319b | 10552 | 5675 | 5926 | 6787 | 3696 |
| 23 | ctr-miR319 | 10552 | 5675 | 5926 | 6787 | 3696 |
| 24 | gma-miR319a | 10552 | 5675 | 5926 | 6787 | 3696 |
| 25 | gma-miR319b | 10552 | 5675 | 5926 | 6787 | 3696 |
| 26 | gma-miR319c | 10552 | 5675 | 5926 | 6787 | 3696 |
| 27 | gma-miR319d | 10552 | 5675 | 5926 | 6787 | 3696 |
| 28 | gma-miR319e | 10552 | 5675 | 5926 | 6787 | 3696 |
| 29 | gma-miR319f | 10552 | 5675 | 5926 | 6787 | 3696 |
| 30 | gma-miR319g | 10552 | 5675 | 5926 | 6787 | 3696 |
| 31 | gma-miR319h | 10552 | 5675 | 5926 | 6787 | 3696 |
| 32 | gma-miR319i | 10552 | 5675 | 5926 | 6787 | 3696 |
| 33 | gma-miR319j | 10552 | 5675 | 5926 | 6787 | 3696 |
| 34 | gma-miR319k | 10552 | 5675 | 5926 | 6787 | 3696 |
| 35 | gma-miR319l | 10552 | 5675 | 5926 | 6787 | 3696 |
| 36 | gma-miR319m | 10552 | 5675 | 5926 | 6787 | 3696 |
| 37 | gma-miR319n | 10552 | 5675 | 5926 | 6787 | 3696 |
| 38 | gma-miR319o | 10552 | 5675 | 5926 | 6787 | 3696 |
| 39 | gma-miR319p | 10552 | 5675 | 5926 | 6787 | 3696 |
| 40 | gma-miR319q | 10552 | 5675 | 5926 | 6787 | 3696 |
| 41 | gma-miR319r | 10552 | 5675 | 5926 | 6787 | 3696 |
| 42 | gma-miR319s | 10552 | 5675 | 5926 | 6787 | 3696 |
| 43 | gma-miR319t | 10552 | 5675 | 5926 | 6787 | 3696 |
| 44 | gma-miR319u | 10552 | 5675 | 5926 | 6787 | 3696 |
| 45 | gma-miR319v | 10552 | 5675 | 5926 | 6787 | 3696 |
| 46 | gma-miR319w | 10552 | 5675 | 5926 | 6787 | 3696 |
| 47 | gma-miR319x | 10552 | 5675 | 5926 | 6787 | 3696 |
| 48 | gma-miR319y | 10552 | 5675 | 5926 | 6787 | 3696 |
| 49 | gma-miR319z | 10552 | 5675 | 5926 | 6787 | 3696 |
| 50 | gma-miR319aa | 10552 | 5675 | 5926 | 6787 | 3696 |
| 51 | gma-miR319ab | 10552 | 5675 | 5926 | 6787 | 3696 |
| 52 | gma-miR319ac | 10552 | 5675 | 5926 | 6787 | 3696 |
| 53 | gma-miR319ad | 10552 | 5675 | 5926 | 6787 | 3696 |
| 54 | gma-miR319ae | 10552 | 5675 | 5926 | 6787 | 3696 |
| 55 | gma-miR319af | 10552 | 5675 | 5926 | 6787 | 3696 |
| 56 | gma-miR319ag | 10552 | 5675 | 5926 | 6787 | 3696 |
| 57 | gma-miR319ah | 10552 | 5675 | 5926 | 6787 | 3696 |
| 58 | gma-miR319ai | 10552 | 5675 | 5926 | 6787 | 3696 |
| 59 | gma-miR319aj | 10552 | 5675 | 5926 | 6787 | 3696 |
| 60 | gma-miR319ak | 10552 | 5675 | 5926 | 6787 | 3696 |

| | | | | | | |
|----|-----------------|-------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ppt-miR319e | 10896 | 5940 | 5944 | 7003 | 3829 |
| 4 | ath-miR8175 | 15 | 20 | 96 | 15 | 27 |
| 5 | abu-miR-200a | 0 | 2 | 202 | 0 | 0 |
| 6 | bta-miR-200a | 0 | 2 | 202 | 0 | 0 |
| 7 | cgr-miR-200a | 0 | 2 | 202 | 0 | 0 |
| 8 | cli-miR-200a-3p | 0 | 2 | 202 | 0 | 0 |
| 9 | cpi-miR-200a-3p | 0 | 2 | 202 | 0 | 0 |
| 10 | cpi-miR-200a-3p | 0 | 2 | 202 | 0 | 0 |
| 11 | cpi-miR-200a-3p | 0 | 2 | 202 | 0 | 0 |
| 12 | cpi-miR-200a-3p | 0 | 2 | 202 | 0 | 0 |
| 13 | cpo-miR-200a-3p | 0 | 2 | 202 | 0 | 0 |
| 14 | efu-miR-200a | 0 | 2 | 202 | 0 | 0 |
| 15 | mze-miR-200a | 0 | 2 | 202 | 0 | 0 |
| 16 | nbr-miR-200a | 0 | 2 | 202 | 0 | 0 |
| 17 | oan-miR-200a-3p | 0 | 2 | 202 | 0 | 0 |
| 18 | oha-miR-200a | 0 | 2 | 202 | 0 | 0 |
| 19 | oha-miR-200a | 0 | 2 | 202 | 0 | 0 |
| 20 | oni-miR-200a | 0 | 2 | 202 | 0 | 0 |
| 21 | oni-miR-200a | 0 | 2 | 202 | 0 | 0 |
| 22 | pal-miR-200a-3p | 0 | 2 | 202 | 0 | 0 |
| 23 | pal-miR-200a-3p | 0 | 2 | 202 | 0 | 0 |
| 24 | pbv-miR-200a-3p | 0 | 2 | 202 | 0 | 0 |
| 25 | pbv-miR-200a-3p | 0 | 2 | 202 | 0 | 0 |
| 26 | pnv-miR-200a | 0 | 2 | 202 | 0 | 0 |
| 27 | ssa-miR-200b-3p | 0 | 2 | 202 | 0 | 0 |
| 28 | tch-miR-200a-3p | 0 | 2 | 202 | 0 | 0 |
| 29 | tgu-miR-200a-3p | 0 | 2 | 202 | 0 | 0 |
| 30 | xla-miR-200a-3p | 0 | 2 | 202 | 0 | 0 |
| 31 | aaui-miR162 | 2516 | 1966 | 8709 | 2401 | 1344 |
| 32 | aly-miR162a-3p | 2516 | 1966 | 8709 | 2401 | 1344 |
| 33 | aly-miR162a-3p | 2516 | 1966 | 8709 | 2401 | 1344 |
| 34 | aly-miR162b-3p | 2516 | 1966 | 8709 | 2401 | 1344 |
| 35 | ath-miR162a-3p | 2516 | 1966 | 8709 | 2401 | 1344 |
| 36 | ath-miR162a-3p | 2516 | 1966 | 8709 | 2401 | 1344 |
| 37 | ath-miR162b-3p | 2516 | 1966 | 8709 | 2401 | 1344 |
| 38 | bra-miR162-3p | 2516 | 1966 | 8709 | 2401 | 1344 |
| 39 | cme-miR162 | 2516 | 1966 | 8709 | 2401 | 1344 |
| 40 | cpa-miR162a | 2516 | 1966 | 8709 | 2401 | 1344 |
| 41 | cpa-miR162a | 2516 | 1966 | 8709 | 2401 | 1344 |
| 42 | csi-miR162-3p | 2516 | 1966 | 8709 | 2401 | 1344 |
| 43 | eun-miR162-3p | 2516 | 1966 | 8709 | 2401 | 1344 |
| 44 | fve-miR162-3p | 2516 | 1966 | 8709 | 2401 | 1344 |
| 45 | fve-miR162-3p | 2516 | 1966 | 8709 | 2401 | 1344 |
| 46 | ghr-miR162a | 2516 | 1966 | 8709 | 2401 | 1344 |
| 47 | gma-miR162b | 2516 | 1966 | 8709 | 2401 | 1344 |
| 48 | gma-miR162b | 2516 | 1966 | 8709 | 2401 | 1344 |
| 49 | gma-miR162c | 2516 | 1966 | 8709 | 2401 | 1344 |
| 50 | hpe-miR162a | 2516 | 1966 | 8709 | 2401 | 1344 |
| 51 | htu-miR162a | 2516 | 1966 | 8709 | 2401 | 1344 |
| 52 | lus-miR162a | 2516 | 1966 | 8709 | 2401 | 1344 |
| 53 | lus-miR162a | 2516 | 1966 | 8709 | 2401 | 1344 |
| 54 | lus-miR162b | 2516 | 1966 | 8709 | 2401 | 1344 |
| 55 | mdm-miR162a | 2516 | 1966 | 8709 | 2401 | 1344 |
| 56 | mdm-miR162a | 2516 | 1966 | 8709 | 2401 | 1344 |
| 57 | mdm-miR162b | 2516 | 1966 | 8709 | 2401 | 1344 |
| 58 | mes-miR162 | 2516 | 1966 | 8709 | 2401 | 1344 |
| 59 | mtr-miR162 | 2516 | 1966 | 8709 | 2401 | 1344 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | nta-miR162a | 2516 | 1966 | 8709 | 2401 | 1344 |
| 4 | nta-miR162b | 2516 | 1966 | 8709 | 2401 | 1344 |
| 5 | osa-miR162a | 2516 | 1966 | 8709 | 2401 | 1344 |
| 6 | osa-miR162a | 2516 | 1966 | 8709 | 2401 | 1344 |
| 7 | pde-miR162 | 2516 | 1966 | 8709 | 2401 | 1344 |
| 8 | pde-miR162 | 2516 | 1966 | 8709 | 2401 | 1344 |
| 9 | ppe-miR162 | 2516 | 1966 | 8709 | 2401 | 1344 |
| 10 | ptc-miR162a | 2516 | 1966 | 8709 | 2401 | 1344 |
| 11 | ptc-miR162b | 2516 | 1966 | 8709 | 2401 | 1344 |
| 12 | ptc-miR162b | 2516 | 1966 | 8709 | 2401 | 1344 |
| 13 | rco-miR162 | 2516 | 1966 | 8709 | 2401 | 1344 |
| 14 | sbi-miR162 | 2516 | 1966 | 8709 | 2401 | 1344 |
| 15 | sly-miR162 | 2516 | 1966 | 8709 | 2401 | 1344 |
| 16 | stu-miR162a-3p | 2516 | 1966 | 8709 | 2401 | 1344 |
| 17 | stu-miR162a-3p | 2516 | 1966 | 8709 | 2401 | 1344 |
| 18 | stu-miR162b-3p | 2516 | 1966 | 8709 | 2401 | 1344 |
| 19 | tcc-miR162 | 2516 | 1966 | 8709 | 2401 | 1344 |
| 20 | tcc-miR162 | 2516 | 1966 | 8709 | 2401 | 1344 |
| 21 | vun-miR162 | 2516 | 1966 | 8709 | 2401 | 1344 |
| 22 | vvi-miR162 | 2516 | 1966 | 8709 | 2401 | 1344 |
| 23 | vvi-miR162 | 2516 | 1966 | 8709 | 2401 | 1344 |
| 24 | gma-miR169s-5p | 3996 | 5895 | 1244 | 4675 | 3356 |
| 25 | mtr-miR169d-5p | 3996 | 5895 | 1244 | 4675 | 3356 |
| 26 | gma-miR169d | 3762 | 5773 | 1252 | 4542 | 3103 |
| 27 | aau-miR319 | 15967 | 7907 | 7713 | 9478 | 4930 |
| 28 | aly-miR319a-3p | 15967 | 7907 | 7713 | 9478 | 4930 |
| 29 | aly-miR319a-3p | 15967 | 7907 | 7713 | 9478 | 4930 |
| 30 | aly-miR319b-3p | 15967 | 7907 | 7713 | 9478 | 4930 |
| 31 | amg-miR319 | 15967 | 7907 | 7713 | 9478 | 4930 |
| 32 | aof-miR319a | 15967 | 7907 | 7713 | 9478 | 4930 |
| 33 | aof-miR319a | 15967 | 7907 | 7713 | 9478 | 4930 |
| 34 | aqc-miR319 | 15967 | 7907 | 7713 | 9478 | 4930 |
| 35 | ath-miR319a | 15967 | 7907 | 7713 | 9478 | 4930 |
| 36 | ath-miR319a | 15967 | 7907 | 7713 | 9478 | 4930 |
| 37 | ath-miR319b | 15967 | 7907 | 7713 | 9478 | 4930 |
| 38 | bra-miR319-3p | 15967 | 7907 | 7713 | 9478 | 4930 |
| 39 | cca-miR319 | 15967 | 7907 | 7713 | 9478 | 4930 |
| 40 | gma-miR319h | 15967 | 7907 | 7713 | 9478 | 4930 |
| 41 | gma-miR319h | 15967 | 7907 | 7713 | 9478 | 4930 |
| 42 | gma-miR319j | 15967 | 7907 | 7713 | 9478 | 4930 |
| 43 | gma-miR319k | 15967 | 7907 | 7713 | 9478 | 4930 |
| 44 | gma-miR319k | 15967 | 7907 | 7713 | 9478 | 4930 |
| 45 | gma-miR319m | 15967 | 7907 | 7713 | 9478 | 4930 |
| 46 | hbr-miR319 | 15967 | 7907 | 7713 | 9478 | 4930 |
| 47 | lus-miR319a | 15967 | 7907 | 7713 | 9478 | 4930 |
| 48 | mdm-miR319a | 15967 | 7907 | 7713 | 9478 | 4930 |
| 49 | mdm-miR319a | 15967 | 7907 | 7713 | 9478 | 4930 |
| 50 | mdm-miR319b-3p | 15967 | 7907 | 7713 | 9478 | 4930 |
| 51 | mes-miR319a | 15967 | 7907 | 7713 | 9478 | 4930 |
| 52 | mes-miR319a | 15967 | 7907 | 7713 | 9478 | 4930 |
| 53 | mes-miR319b | 15967 | 7907 | 7713 | 9478 | 4930 |
| 54 | mes-miR319c | 15967 | 7907 | 7713 | 9478 | 4930 |
| 55 | mes-miR319d | 15967 | 7907 | 7713 | 9478 | 4930 |
| 56 | mes-miR319e | 15967 | 7907 | 7713 | 9478 | 4930 |
| 57 | mes-miR319e | 15967 | 7907 | 7713 | 9478 | 4930 |
| 58 | mtr-miR319d-3p | 15967 | 7907 | 7713 | 9478 | 4930 |
| 59 | nta-miR319a | 15967 | 7907 | 7713 | 9478 | 4930 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | nta-miR319b | 15967 | 7907 | 7713 | 9478 | 4930 |
| 4 | rco-miR319a | 15967 | 7907 | 7713 | 9478 | 4930 |
| 5 | rco-miR319b | 15967 | 7907 | 7713 | 9478 | 4930 |
| 6 | rco-miR319c | 15967 | 7907 | 7713 | 9478 | 4930 |
| 7 | rco-miR319c | 15967 | 7907 | 7713 | 9478 | 4930 |
| 8 | sly-miR319b | 15967 | 7907 | 7713 | 9478 | 4930 |
| 9 | sly-miR319b | 15967 | 7907 | 7713 | 9478 | 4930 |
| 10 | stu-miR319a-3p | 15967 | 7907 | 7713 | 9478 | 4930 |
| 11 | tae-miR319 | 15967 | 7907 | 7713 | 9478 | 4930 |
| 12 | tae-miR319 | 15967 | 7907 | 7713 | 9478 | 4930 |
| 13 | vun-miR319a | 15967 | 7907 | 7713 | 9478 | 4930 |
| 14 | vvi-miR319b | 15967 | 7907 | 7713 | 9478 | 4930 |
| 15 | vvi-miR319c | 15967 | 7907 | 7713 | 9478 | 4930 |
| 16 | vvi-miR319c | 15967 | 7907 | 7713 | 9478 | 4930 |
| 17 | vvi-miR319f | 15967 | 7907 | 7713 | 9478 | 4930 |
| 18 | mtr-miR169e-5p | 3708 | 5721 | 1198 | 4514 | 3024 |
| 19 | vvi-miR169m | 3708 | 5721 | 1198 | 4514 | 3024 |
| 20 | vvi-miR169n | 3708 | 5721 | 1198 | 4514 | 3024 |
| 21 | vvi-miR169n | 3708 | 5721 | 1198 | 4514 | 3024 |
| 22 | vvi-miR169p | 3708 | 5721 | 1198 | 4514 | 3024 |
| 23 | vvi-miR169q | 3708 | 5721 | 1198 | 4514 | 3024 |
| 24 | vvi-miR169q | 3708 | 5721 | 1198 | 4514 | 3024 |
| 25 | csi-miR171a | 52 | 95 | 103 | 56 | 74 |
| 26 | zma-miR171b-3p | 52 | 95 | 103 | 56 | 74 |
| 27 | gma-miR166u | 1208 | 580 | 1158 | 920 | 659 |
| 28 | ami-miR-27b-3p | 74 | 16 | 91 | 56 | 31 |
| 29 | ami-miR-27b-3p | 74 | 16 | 91 | 56 | 31 |
| 30 | dma-miR-27b | 74 | 16 | 91 | 56 | 31 |
| 31 | gmo-miR-27b-3p | 74 | 16 | 91 | 56 | 31 |
| 32 | nle-miR-27b | 74 | 16 | 91 | 56 | 31 |
| 33 | nle-miR-27b | 74 | 16 | 91 | 56 | 31 |
| 34 | oga-miR-27b | 74 | 16 | 91 | 56 | 31 |
| 35 | pha-miR-27b | 74 | 16 | 91 | 56 | 31 |
| 36 | cme-miR156j | 21180 | 34742 | 3642 | 21446 | 16004 |
| 37 | cme-miR156j | 21180 | 34742 | 3642 | 21446 | 16004 |
| 38 | fve-miR156a | 21179 | 34742 | 3642 | 21446 | 16004 |
| 39 | fve-miR156b | 21179 | 34742 | 3642 | 21446 | 16004 |
| 40 | fve-miR156c | 21179 | 34742 | 3642 | 21446 | 16004 |
| 41 | fve-miR156c | 21179 | 34742 | 3642 | 21446 | 16004 |
| 42 | fve-miR156e | 21179 | 34742 | 3642 | 21446 | 16004 |
| 43 | gma-miR156k | 21179 | 34742 | 3642 | 21446 | 16004 |
| 44 | gma-miR156n | 21179 | 34742 | 3642 | 21446 | 16004 |
| 45 | gma-miR156n | 21179 | 34742 | 3642 | 21446 | 16004 |
| 46 | gma-miR156o | 21179 | 34742 | 3642 | 21446 | 16004 |
| 47 | aly-miR156a-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 48 | aly-miR156b-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 49 | aly-miR156c-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 50 | aly-miR156c-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 51 | aly-miR156d-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 52 | aly-miR156e-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 53 | aly-miR156e-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 54 | aly-miR156f-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 55 | aof-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| 56 | ata-miR156a-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 57 | ata-miR156a-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 58 | ata-miR156b-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 59 | ata-miR156c-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 60 | ata-miR156c-5p | 20768 | 34227 | 3548 | 21110 | 15698 |

| | | | | | | |
|----|----------------|-------|-------|------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ata-miR156d-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 4 | ata-miR156e-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 5 | ath-miR156a-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 6 | ath-miR156b-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 7 | ath-miR156c-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 8 | ath-miR156d-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 9 | ath-miR156e | 20768 | 34227 | 3548 | 21110 | 15698 |
| 10 | ath-miR156f-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 11 | atr-miR156b | 20768 | 34227 | 3548 | 21110 | 15698 |
| 12 | atr-miR156d | 20768 | 34227 | 3548 | 21110 | 15698 |
| 13 | bdi-miR156b-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 14 | bdi-miR156c | 20768 | 34227 | 3548 | 21110 | 15698 |
| 15 | bdi-miR156d-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 16 | bdi-miR156e-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 17 | bdi-miR156f-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 18 | bdi-miR156g-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 19 | bdi-miR156h-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 20 | bdi-miR156i-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 21 | bna-miR156d | 20768 | 34227 | 3548 | 21110 | 15698 |
| 22 | bna-miR156e | 20768 | 34227 | 3548 | 21110 | 15698 |
| 23 | bna-miR156f | 20768 | 34227 | 3548 | 21110 | 15698 |
| 24 | bra-miR156a-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 25 | bra-miR156b-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 26 | bra-miR156c-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 27 | bra-miR156d-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 28 | bra-miR156e-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 29 | bra-miR156f-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 30 | bra-miR156g-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 31 | cas-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| 32 | cas-miR156b-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 33 | cas-miR156c-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 34 | cas-miR156d-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 35 | cas-miR156e-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 36 | cas-miR156f-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 37 | cas-miR156k-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 38 | cca-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| 39 | cme-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| 40 | cme-miR156c | 20768 | 34227 | 3548 | 21110 | 15698 |
| 41 | cme-miR156d | 20768 | 34227 | 3548 | 21110 | 15698 |
| 42 | cme-miR156i | 20768 | 34227 | 3548 | 21110 | 15698 |
| 43 | cpa-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| 44 | cpa-miR156b | 20768 | 34227 | 3548 | 21110 | 15698 |
| 45 | cpa-miR156c | 20768 | 34227 | 3548 | 21110 | 15698 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | cpa-miR156d | 20768 | 34227 | 3548 | 21110 | 15698 |
| 4 | csi-miR156a-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 5 | csi-miR156b-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 6 | csi-miR156c-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 7 | csi-miR156c-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 8 | ctr-miR156 | 20768 | 34227 | 3548 | 21110 | 15698 |
| 9 | ctr-miR156 | 20768 | 34227 | 3548 | 21110 | 15698 |
| 10 | dpr-miR156b | 20768 | 34227 | 3548 | 21110 | 15698 |
| 11 | fve-miR156d | 20768 | 34227 | 3548 | 21110 | 15698 |
| 12 | fve-miR156d | 20768 | 34227 | 3548 | 21110 | 15698 |
| 13 | ghr-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| 14 | ghr-miR156b | 20768 | 34227 | 3548 | 21110 | 15698 |
| 15 | ghr-miR156d | 20768 | 34227 | 3548 | 21110 | 15698 |
| 16 | ghr-miR156d | 20768 | 34227 | 3548 | 21110 | 15698 |
| 17 | gma-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| 18 | gma-miR156h | 20768 | 34227 | 3548 | 21110 | 15698 |
| 19 | gma-miR156u | 20768 | 34227 | 3548 | 21110 | 15698 |
| 20 | gma-miR156v | 20768 | 34227 | 3548 | 21110 | 15698 |
| 21 | gma-miR156v | 20768 | 34227 | 3548 | 21110 | 15698 |
| 22 | gma-miR156w | 20768 | 34227 | 3548 | 21110 | 15698 |
| 23 | gma-miR156x | 20768 | 34227 | 3548 | 21110 | 15698 |
| 24 | gma-miR156y | 20768 | 34227 | 3548 | 21110 | 15698 |
| 25 | gma-miR156y | 20768 | 34227 | 3548 | 21110 | 15698 |
| 26 | han-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| 27 | han-miR156b | 20768 | 34227 | 3548 | 21110 | 15698 |
| 28 | han-miR156b | 20768 | 34227 | 3548 | 21110 | 15698 |
| 29 | har-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| 30 | htu-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| 31 | htu-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| 32 | lus-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| 33 | lus-miR156g | 20768 | 34227 | 3548 | 21110 | 15698 |
| 34 | mdm-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| 35 | mdm-miR156b | 20768 | 34227 | 3548 | 21110 | 15698 |
| 36 | mdm-miR156b | 20768 | 34227 | 3548 | 21110 | 15698 |
| 37 | mdm-miR156c | 20768 | 34227 | 3548 | 21110 | 15698 |
| 38 | mdm-miR156d | 20768 | 34227 | 3548 | 21110 | 15698 |
| 39 | mdm-miR156e | 20768 | 34227 | 3548 | 21110 | 15698 |
| 40 | mdm-miR156e | 20768 | 34227 | 3548 | 21110 | 15698 |
| 41 | mdm-miR156f | 20768 | 34227 | 3548 | 21110 | 15698 |
| 42 | mdm-miR156g | 20768 | 34227 | 3548 | 21110 | 15698 |
| 43 | mdm-miR156h | 20768 | 34227 | 3548 | 21110 | 15698 |
| 44 | mdm-miR156h | 20768 | 34227 | 3548 | 21110 | 15698 |
| 45 | mdm-miR156i | 20768 | 34227 | 3548 | 21110 | 15698 |
| 46 | mdm-miR156j | 20768 | 34227 | 3548 | 21110 | 15698 |
| 47 | mdm-miR156k | 20768 | 34227 | 3548 | 21110 | 15698 |
| 48 | mdm-miR156k | 20768 | 34227 | 3548 | 21110 | 15698 |
| 49 | mdm-miR156l | 20768 | 34227 | 3548 | 21110 | 15698 |
| 50 | mdm-miR156m | 20768 | 34227 | 3548 | 21110 | 15698 |
| 51 | mdm-miR156n | 20768 | 34227 | 3548 | 21110 | 15698 |
| 52 | mdm-miR156n | 20768 | 34227 | 3548 | 21110 | 15698 |
| 53 | mdm-miR156o | 20768 | 34227 | 3548 | 21110 | 15698 |
| 54 | mes-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| 55 | mes-miR156b | 20768 | 34227 | 3548 | 21110 | 15698 |
| 56 | mes-miR156b | 20768 | 34227 | 3548 | 21110 | 15698 |
| 57 | mes-miR156c | 20768 | 34227 | 3548 | 21110 | 15698 |
| 58 | mes-miR156d | 20768 | 34227 | 3548 | 21110 | 15698 |
| 59 | mes-miR156e | 20768 | 34227 | 3548 | 21110 | 15698 |
| 60 | | | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | | | |
|----------------|-------|-------|------|-------|-------|
| mes-miR156f | 20768 | 34227 | 3548 | 21110 | 15698 |
| mes-miR156g | 20768 | 34227 | 3548 | 21110 | 15698 |
| mtr-miR156b-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| mtr-miR156c-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| mtr-miR156d-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| mtr-miR156i-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| nta-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| nta-miR156b | 20768 | 34227 | 3548 | 21110 | 15698 |
| nta-miR156c | 20768 | 34227 | 3548 | 21110 | 15698 |
| nta-miR156d | 20768 | 34227 | 3548 | 21110 | 15698 |
| nta-miR156e | 20768 | 34227 | 3548 | 21110 | 15698 |
| osa-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| osa-miR156b-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| osa-miR156c-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| osa-miR156d | 20768 | 34227 | 3548 | 21110 | 15698 |
| osa-miR156e | 20768 | 34227 | 3548 | 21110 | 15698 |
| osa-miR156f-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| osa-miR156g-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| osa-miR156h-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| osa-miR156i | 20768 | 34227 | 3548 | 21110 | 15698 |
| osa-miR156j-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| pab-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| pab-miR156l | 20768 | 34227 | 3548 | 21110 | 15698 |
| ppe-miR156c | 20768 | 34227 | 3548 | 21110 | 15698 |
| ppe-miR156d | 20768 | 34227 | 3548 | 21110 | 15698 |
| ppe-miR156e | 20768 | 34227 | 3548 | 21110 | 15698 |
| ppt-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| ppt-miR156b | 20768 | 34227 | 3548 | 21110 | 15698 |
| ppt-miR156c | 20768 | 34227 | 3548 | 21110 | 15698 |
| ptc-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| ptc-miR156b | 20768 | 34227 | 3548 | 21110 | 15698 |
| ptc-miR156c | 20768 | 34227 | 3548 | 21110 | 15698 |
| ptc-miR156d | 20768 | 34227 | 3548 | 21110 | 15698 |
| ptc-miR156e | 20768 | 34227 | 3548 | 21110 | 15698 |
| ptc-miR156f | 20768 | 34227 | 3548 | 21110 | 15698 |
| sbi-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| sbi-miR156b | 20768 | 34227 | 3548 | 21110 | 15698 |
| sbi-miR156c | 20768 | 34227 | 3548 | 21110 | 15698 |
| sbi-miR156f | 20768 | 34227 | 3548 | 21110 | 15698 |
| sbi-miR156g | 20768 | 34227 | 3548 | 21110 | 15698 |
| sbi-miR156h | 20768 | 34227 | 3548 | 21110 | 15698 |
| sbi-miR156i | 20768 | 34227 | 3548 | 21110 | 15698 |
| sly-miR156d-5p | 20768 | 34227 | 3548 | 21110 | 15698 |

| | | | | | | |
|----|----------------|-------|-------|------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | sof-miR156 | 20768 | 34227 | 3548 | 21110 | 15698 |
| 4 | stu-miR156e | 20768 | 34227 | 3548 | 21110 | 15698 |
| 5 | stu-miR156g-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 6 | stu-miR156h-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 7 | stu-miR156i-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 8 | stu-miR156j-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 9 | stu-miR156k-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 10 | tcc-miR156b | 20768 | 34227 | 3548 | 21110 | 15698 |
| 11 | tcc-miR156c | 20768 | 34227 | 3548 | 21110 | 15698 |
| 12 | tcc-miR156d | 20768 | 34227 | 3548 | 21110 | 15698 |
| 13 | tcc-miR156g | 20768 | 34227 | 3548 | 21110 | 15698 |
| 14 | vca-miR156a-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 15 | vun-miR156a | 20768 | 34227 | 3548 | 21110 | 15698 |
| 16 | vvi-miR156b | 20768 | 34227 | 3548 | 21110 | 15698 |
| 17 | vvi-miR156c | 20768 | 34227 | 3548 | 21110 | 15698 |
| 18 | vvi-miR156d | 20768 | 34227 | 3548 | 21110 | 15698 |
| 19 | zma-miR156a-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 20 | zma-miR156b-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 21 | zma-miR156c | 20768 | 34227 | 3548 | 21110 | 15698 |
| 22 | zma-miR156d-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 23 | zma-miR156e-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 24 | zma-miR156f-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 25 | zma-miR156g-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 26 | zma-miR156h-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 27 | zma-miR156i-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 28 | zma-miR156l-5p | 20768 | 34227 | 3548 | 21110 | 15698 |
| 29 | ama-miR156 | 20779 | 34249 | 3551 | 21127 | 15700 |
| 30 | gma-miR169e | 3672 | 5706 | 1196 | 4464 | 2983 |
| 31 | gma-miR156q | 20887 | 34400 | 3565 | 21195 | 15776 |
| 32 | gma-miR156s | 20887 | 34400 | 3565 | 21195 | 15776 |
| 33 | ata-miR169h-5p | 3720 | 5831 | 1223 | 4517 | 3047 |
| 34 | bdi-miR169b | 3720 | 5831 | 1223 | 4517 | 3047 |
| 35 | mes-miR169f | 3720 | 5831 | 1223 | 4517 | 3047 |
| 36 | osa-miR169e | 3720 | 5831 | 1223 | 4517 | 3047 |
| 37 | sbi-miR169e | 3720 | 5831 | 1223 | 4517 | 3047 |
| 38 | sbi-miR169j | 3720 | 5831 | 1223 | 4517 | 3047 |
| 39 | ssp-miR169 | 3720 | 5831 | 1223 | 4517 | 3047 |
| 40 | zma-miR169p-5p | 3720 | 5831 | 1223 | 4517 | 3047 |
| 41 | bna-miR156a | 20891 | 34481 | 3564 | 21215 | 15781 |
| 42 | hvu-miR156a | 20891 | 34481 | 3564 | 21215 | 15781 |
| 43 | hvu-miR156b | 20891 | 34481 | 3564 | 21215 | 15781 |
| 44 | rco-miR156a | 20891 | 34481 | 3564 | 21215 | 15781 |
| 45 | rco-miR156b | 20891 | 34481 | 3564 | 21215 | 15781 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|--------|--------|--------|--------|--------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | rco-miR156c | 20891 | 34481 | 3564 | 21215 | 15781 |
| 4 | rco-miR156d | 20891 | 34481 | 3564 | 21215 | 15781 |
| 5 | ssl-miR156 | 20891 | 34481 | 3564 | 21215 | 15781 |
| 6 | ssl-miR156 | 20891 | 34481 | 3564 | 21215 | 15781 |
| 7 | ssp-miR156 | 20891 | 34481 | 3564 | 21215 | 15781 |
| 8 | tae-miR156 | 20891 | 34481 | 3564 | 21215 | 15781 |
| 9 | tae-miR156 | 20891 | 34481 | 3564 | 21215 | 15781 |
| 10 | gso-miR2218 | 212283 | 470943 | 271083 | 300516 | 243499 |
| 11 | pvu-miR2118 | 212283 | 470943 | 271083 | 300516 | 243499 |
| 12 | pvu-miR2118 | 212283 | 470943 | 271083 | 300516 | 243499 |
| 13 | vun-miR2118 | 212283 | 470943 | 271083 | 300516 | 243499 |
| 14 | aof-miR166b | 1357 | 657 | 1354 | 1043 | 722 |
| 15 | ahy-miR156a | 187 | 211 | 101 | 167 | 113 |
| 16 | aof-miR156c | 187 | 211 | 101 | 167 | 113 |
| 17 | aof-miR156c | 187 | 211 | 101 | 167 | 113 |
| 18 | ath-miR156j | 187 | 211 | 101 | 167 | 113 |
| 19 | bdi-miR156j | 187 | 211 | 101 | 167 | 113 |
| 20 | cas-miR156j | 187 | 211 | 101 | 167 | 113 |
| 21 | cas-miR156j | 187 | 211 | 101 | 167 | 113 |
| 22 | hpa-miR156a | 187 | 211 | 101 | 167 | 113 |
| 23 | ahy-miR167-3p | 4463 | 5492 | 1307 | 2236 | 4610 |
| 24 | ptc-miR167f-3p | 4463 | 5492 | 1307 | 2236 | 4610 |
| 25 | ptc-miR167f-3p | 4463 | 5492 | 1307 | 2236 | 4610 |
| 26 | ptc-miR167g-3p | 4463 | 5492 | 1307 | 2236 | 4610 |
| 27 | ptc-miR167g-3p | 4463 | 5492 | 1307 | 2236 | 4610 |
| 28 | ptc-miR167h-3p | 4463 | 5492 | 1307 | 2236 | 4610 |
| 29 | bdi-miR156a | 193 | 211 | 103 | 169 | 114 |
| 30 | far-miR156a | 193 | 211 | 103 | 169 | 114 |
| 31 | gma-miR156b | 193 | 211 | 103 | 169 | 114 |
| 32 | mtr-miR156a | 193 | 211 | 103 | 169 | 114 |
| 33 | mtr-miR156a | 193 | 211 | 103 | 169 | 114 |
| 34 | osa-miR156k | 193 | 211 | 103 | 169 | 114 |
| 35 | rco-miR156e | 193 | 211 | 103 | 169 | 114 |
| 36 | sbi-miR156d | 193 | 211 | 103 | 169 | 114 |
| 37 | sbi-miR156d | 193 | 211 | 103 | 169 | 114 |
| 38 | tcc-miR156a | 193 | 211 | 103 | 169 | 114 |
| 39 | zma-miR156j-5p | 193 | 211 | 103 | 169 | 114 |
| 40 | gma-miR2118a-3p | 2919 | 4326 | 7841 | 4325 | 3577 |
| 41 | gma-miR2118a-3p | 2919 | 4326 | 7841 | 4325 | 3577 |
| 42 | gma-miR2118b-3p | 2919 | 4326 | 7841 | 4325 | 3577 |
| 43 | aqc-miR159 | 110 | 106 | 100 | 90 | 52 |
| 44 | mtr-miR2118 | 77 | 252 | 70 | 111 | 89 |
| 45 | gma-miR1515a | 6869 | 8641 | 20282 | 4539 | 11745 |
| 46 | gma-miR1515a | 6869 | 8641 | 20282 | 4539 | 11745 |
| 47 | gma-miR1515b | 6869 | 8641 | 20282 | 4539 | 11745 |
| 48 | aof-miR166a | 15790 | 7474 | 18107 | 11179 | 9533 |
| 49 | atr-miR166b | 15790 | 7474 | 18107 | 11179 | 9533 |
| 50 | atr-miR166b | 15790 | 7474 | 18107 | 11179 | 9533 |
| 51 | bdi-miR166f | 15790 | 7474 | 18107 | 11179 | 9533 |
| 52 | csi-miR166b-3p | 15790 | 7474 | 18107 | 11179 | 9533 |
| 53 | csi-miR166d-3p | 15790 | 7474 | 18107 | 11179 | 9533 |
| 54 | csi-miR166d-3p | 15790 | 7474 | 18107 | 11179 | 9533 |
| 55 | csi-miR166g-3p | 15790 | 7474 | 18107 | 11179 | 9533 |
| 56 | gma-miR166h-3p | 15790 | 7474 | 18107 | 11179 | 9533 |
| 57 | gma-miR166k | 15790 | 7474 | 18107 | 11179 | 9533 |
| 58 | gma-miR166k | 15790 | 7474 | 18107 | 11179 | 9533 |
| 59 | pab-miR166e | 15790 | 7474 | 18107 | 11179 | 9533 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|-------|-------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | sly-miR156e-3p | 9056 | 10012 | 17656 | 9528 | 9902 |
| 4 | stu-miR156g-3p | 9056 | 10012 | 17656 | 9528 | 9902 |
| 5 | cas-miR156k-3p | 9076 | 10019 | 17678 | 9536 | 9910 |
| 6 | mtr-miR156c-3p | 9076 | 10019 | 17678 | 9536 | 9910 |
| 7 | | | | | | |
| 8 | pvu-miR1514a | 13941 | 9159 | 16954 | 12770 | 7637 |
| 9 | | | | | | |
| 10 | aly-miR397a-5p | 13 | 14 | 140 | 50 | 28 |
| 11 | aly-miR397b-5p | 13 | 14 | 140 | 50 | 28 |
| 12 | | | | | | |
| 13 | ath-miR397a | 13 | 14 | 140 | 50 | 28 |
| 14 | bdi-miR397a | 13 | 14 | 140 | 50 | 28 |
| 15 | bna-miR397a | 13 | 14 | 140 | 50 | 28 |
| 16 | bna-miR397b | 13 | 14 | 140 | 50 | 28 |
| 17 | | | | | | |
| 18 | cas-miR397 | 13 | 14 | 140 | 50 | 28 |
| 19 | cme-miR397 | 13 | 14 | 140 | 50 | 28 |
| 20 | csi-miR397-5p | 13 | 14 | 140 | 50 | 28 |
| 21 | | | | | | |
| 22 | fve-miR397 | 13 | 14 | 140 | 50 | 28 |
| 23 | gma-miR397a | 13 | 14 | 140 | 50 | 28 |
| 24 | gma-miR397b-5p | 13 | 14 | 140 | 50 | 28 |
| 25 | | | | | | |
| 26 | lus-miR397b | 13 | 14 | 140 | 50 | 28 |
| 27 | mes-miR397b | 13 | 14 | 140 | 50 | 28 |
| 28 | mtr-miR397-5p | 13 | 14 | 140 | 50 | 28 |
| 29 | | | | | | |
| 30 | osa-miR397a | 13 | 14 | 140 | 50 | 28 |
| 31 | ppe-miR397 | 13 | 14 | 140 | 50 | 28 |
| 32 | ptc-miR397a | 13 | 14 | 140 | 50 | 28 |
| 33 | | | | | | |
| 34 | rco-miR397 | 13 | 14 | 140 | 50 | 28 |
| 35 | sbi-miR397-5p | 13 | 14 | 140 | 50 | 28 |
| 36 | ssl-miR397 | 13 | 14 | 140 | 50 | 28 |
| 37 | | | | | | |
| 38 | tcc-miR397 | 13 | 14 | 140 | 50 | 28 |
| 39 | vca-miR397-5p | 13 | 14 | 140 | 50 | 28 |
| 40 | vvi-miR397a | 13 | 14 | 140 | 50 | 28 |
| 41 | | | | | | |
| 42 | pvu-miR482-3p | 53 | 84 | 281 | 74 | 63 |
| 43 | bdi-miR393a | 133 | 78 | 12 | 81 | 58 |
| 44 | bdi-miR393b-5p | 133 | 78 | 12 | 81 | 58 |
| 45 | | | | | | |
| 46 | bna-miR393 | 133 | 78 | 12 | 81 | 58 |
| 47 | cme-miR393a | 133 | 78 | 12 | 81 | 58 |
| 48 | cme-miR393b | 133 | 78 | 12 | 81 | 58 |
| 49 | | | | | | |
| 50 | cme-miR393c | 133 | 78 | 12 | 81 | 58 |
| 51 | csi-miR393c-5p | 133 | 78 | 12 | 81 | 58 |
| 52 | fve-miR393a | 133 | 78 | 12 | 81 | 58 |
| 53 | | | | | | |
| 54 | gma-miR393a | 133 | 78 | 12 | 81 | 58 |
| 55 | lus-miR393a | 133 | 78 | 12 | 81 | 58 |
| 56 | lus-miR393b | 133 | 78 | 12 | 81 | 58 |
| 57 | | | | | | |
| 58 | lus-miR393c | 133 | 78 | 12 | 81 | 58 |
| 59 | lus-miR393d | 133 | 78 | 12 | 81 | 58 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|-----|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | mes-miR393a | 133 | 78 | 12 | 81 | 58 |
| 4 | mtr-miR393a | 133 | 78 | 12 | 81 | 58 |
| 5 | mtr-miR393b-5p | 133 | 78 | 12 | 81 | 58 |
| 6 | osa-miR393a | 133 | 78 | 12 | 81 | 58 |
| 7 | ppe-miR393b | 133 | 78 | 12 | 81 | 58 |
| 8 | ptc-miR393a-5p | 133 | 78 | 12 | 81 | 58 |
| 9 | ptc-miR393b-5p | 133 | 78 | 12 | 81 | 58 |
| 10 | ptc-miR393c | 133 | 78 | 12 | 81 | 58 |
| 11 | rco-miR393 | 133 | 78 | 12 | 81 | 58 |
| 12 | sbi-miR393a | 133 | 78 | 12 | 81 | 58 |
| 13 | sbi-miR393b | 133 | 78 | 12 | 81 | 58 |
| 14 | tcc-miR393b | 133 | 78 | 12 | 81 | 58 |
| 15 | vca-miR393-5p | 133 | 78 | 12 | 81 | 58 |
| 16 | vvi-miR393a | 133 | 78 | 12 | 81 | 58 |
| 17 | vvi-miR393b | 133 | 78 | 12 | 81 | 58 |
| 18 | sly-miR171e | 218 | 358 | 269 | 153 | 276 |
| 19 | stu-miR171b-3p | 218 | 358 | 269 | 153 | 276 |
| 20 | aof-miR171c | 212 | 347 | 248 | 146 | 267 |
| 21 | csi-miR171e-3p | 212 | 347 | 248 | 146 | 267 |
| 22 | csi-miR171g-3p | 212 | 347 | 248 | 146 | 267 |
| 23 | ctr-miR171 | 212 | 347 | 248 | 146 | 267 |
| 24 | fve-miR171h | 212 | 347 | 248 | 146 | 267 |
| 25 | mdm-miR171a | 212 | 347 | 248 | 146 | 267 |
| 26 | mdm-miR171b | 212 | 347 | 248 | 146 | 267 |
| 27 | mdm-miR171p | 212 | 347 | 248 | 146 | 267 |
| 28 | mes-miR171a | 212 | 347 | 248 | 146 | 267 |
| 29 | ppe-miR171h | 212 | 347 | 248 | 146 | 267 |
| 30 | efu-miR-126 | 173 | 35 | 497 | 123 | 79 |
| 31 | bdi-miR160f | 269 | 267 | 351 | 221 | 234 |
| 32 | cas-miR160a | 269 | 267 | 351 | 221 | 234 |
| 33 | cas-miR160b-5p | 269 | 267 | 351 | 221 | 234 |
| 34 | gma-miR160b | 269 | 267 | 351 | 221 | 234 |
| 35 | gma-miR160c | 269 | 267 | 351 | 221 | 234 |
| 36 | gma-miR160d | 269 | 267 | 351 | 221 | 234 |
| 37 | gma-miR160e | 269 | 267 | 351 | 221 | 234 |
| 38 | htu-miR160a | 269 | 267 | 351 | 221 | 234 |
| 39 | pab-miR160c | 269 | 267 | 351 | 221 | 234 |
| 40 | pab-miR160e | 269 | 267 | 351 | 221 | 234 |
| 41 | pab-miR160f | 269 | 267 | 351 | 221 | 234 |
| 42 | gma-miR159e-5p | 1346 | 1115 | 1126 | 751 | 1072 |
| 43 | aca-miR-126-3p | 165 | 35 | 490 | 120 | 78 |
| 44 | ami-miR-126-3p | 165 | 35 | 490 | 120 | 78 |
| 45 | cgr-miR-126a | 165 | 35 | 490 | 120 | 78 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | cja-miR-126 | 165 | 35 | 490 | 120 | 78 |
| 4 | cli-miR-126-3p | 165 | 35 | 490 | 120 | 78 |
| 5 | cpi-miR-126-3p | 165 | 35 | 490 | 120 | 78 |
| 6 | cpi-miR-126-3p | 165 | 35 | 490 | 120 | 78 |
| 7 | cpo-miR-126-3p | 165 | 35 | 490 | 120 | 78 |
| 8 | dno-miR-126-3p | 165 | 35 | 490 | 120 | 78 |
| 9 | dno-miR-126-3p | 165 | 35 | 490 | 120 | 78 |
| 10 | eca-miR-126-3p | 165 | 35 | 490 | 120 | 78 |
| 11 | gga-miR-126-3p | 165 | 35 | 490 | 120 | 78 |
| 12 | gga-miR-126-3p | 165 | 35 | 490 | 120 | 78 |
| 13 | hsa-miR-126-3p | 165 | 35 | 490 | 120 | 78 |
| 14 | mdo-miR-126-3p | 165 | 35 | 490 | 120 | 78 |
| 15 | mml-miR-126 | 165 | 35 | 490 | 120 | 78 |
| 16 | mmu-miR-126a-3p | 165 | 35 | 490 | 120 | 78 |
| 17 | mmu-miR-126a-3p | 165 | 35 | 490 | 120 | 78 |
| 18 | oan-miR-126-3p | 165 | 35 | 490 | 120 | 78 |
| 19 | pbv-miR-126-3p | 165 | 35 | 490 | 120 | 78 |
| 20 | ppy-miR-126 | 165 | 35 | 490 | 120 | 78 |
| 21 | ppy-miR-126 | 165 | 35 | 490 | 120 | 78 |
| 22 | ptr-miR-126 | 165 | 35 | 490 | 120 | 78 |
| 23 | rno-miR-126a-3p | 165 | 35 | 490 | 120 | 78 |
| 24 | ssc-miR-126-3p | 165 | 35 | 490 | 120 | 78 |
| 25 | ssc-miR-126-3p | 165 | 35 | 490 | 120 | 78 |
| 26 | tgu-miR-126-3p | 165 | 35 | 490 | 120 | 78 |
| 27 | cme-miR168 | 1102 | 1956 | 779 | 1355 | 812 |
| 28 | bra-miR168b-5p | 1151 | 2054 | 812 | 1449 | 839 |
| 29 | bra-miR168b-5p | 1151 | 2054 | 812 | 1449 | 839 |
| 30 | bra-miR168c-5p | 1151 | 2054 | 812 | 1449 | 839 |
| 31 | nta-miR168a | 1151 | 2054 | 812 | 1449 | 839 |
| 32 | nta-miR168b | 1151 | 2054 | 812 | 1449 | 839 |
| 33 | nta-miR168b | 1151 | 2054 | 812 | 1449 | 839 |
| 34 | nta-miR168c | 1151 | 2054 | 812 | 1449 | 839 |
| 35 | sly-miR168a-5p | 1151 | 2054 | 812 | 1449 | 839 |
| 36 | sly-miR168b-5p | 1151 | 2054 | 812 | 1449 | 839 |
| 37 | sly-miR168b-5p | 1151 | 2054 | 812 | 1449 | 839 |
| 38 | csi-miR160b-5p | 270 | 268 | 359 | 222 | 234 |
| 39 | mes-miR160c | 270 | 268 | 359 | 222 | 234 |
| 40 | osa-miR160e-5p | 270 | 268 | 359 | 222 | 234 |
| 41 | osa-miR160e-5p | 270 | 268 | 359 | 222 | 234 |
| 42 | zma-miR160f-5p | 270 | 268 | 359 | 222 | 234 |
| 43 | aly-miR167d-5p | 52986 | 43732 | 40946 | 44083 | 24763 |
| 44 | ath-miR167d | 52986 | 43732 | 40946 | 44083 | 24763 |
| 45 | ath-miR167d | 52986 | 43732 | 40946 | 44083 | 24763 |
| 46 | cca-miR167 | 52986 | 43732 | 40946 | 44083 | 24763 |
| 47 | eun-miR167b-5p | 52986 | 43732 | 40946 | 44083 | 24763 |
| 48 | nta-miR167a | 52986 | 43732 | 40946 | 44083 | 24763 |
| 49 | nta-miR167a | 52986 | 43732 | 40946 | 44083 | 24763 |
| 50 | nta-miR167b | 52986 | 43732 | 40946 | 44083 | 24763 |
| 51 | nta-miR167c | 52986 | 43732 | 40946 | 44083 | 24763 |
| 52 | pab-miR167b | 52986 | 43732 | 40946 | 44083 | 24763 |
| 53 | pab-miR167b | 52986 | 43732 | 40946 | 44083 | 24763 |
| 54 | rco-miR167c | 52986 | 43732 | 40946 | 44083 | 24763 |
| 55 | csi-miR393a | 135 | 83 | 12 | 81 | 58 |
| 56 | ghr-miR169b | 72 | 100 | 50 | 52 | 73 |
| 57 | aly-miR170-5p | 6950 | 14810 | 10511 | 9105 | 8883 |
| 58 | aly-miR170-5p | 6950 | 14810 | 10511 | 9105 | 8883 |
| 59 | aly-miR171a-5p | 6950 | 14810 | 10511 | 9105 | 8883 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|-------|-------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ath-miR170-5p | 6950 | 14810 | 10511 | 9105 | 8883 |
| 4 | ath-miR171a-5p | 6950 | 14810 | 10511 | 9105 | 8883 |
| 5 | cas-miR170 | 6950 | 14810 | 10511 | 9105 | 8883 |
| 6 | cas-miR171a-5p | 6950 | 14810 | 10511 | 9105 | 8883 |
| 7 | csi-miR171f-5p | 6950 | 14810 | 10511 | 9105 | 8883 |
| 8 | gma-miR171j-5p | 6950 | 14810 | 10511 | 9105 | 8883 |
| 9 | sly-miR171f | 6950 | 14810 | 10511 | 9105 | 8883 |
| 10 | stu-miR171a-5p | 6950 | 14810 | 10511 | 9105 | 8883 |
| 11 | stu-miR171c-5p | 6950 | 14810 | 10511 | 9105 | 8883 |
| 12 | gma-miR482b-3p | 2853 | 6453 | 1543 | 3760 | 1637 |
| 13 | gma-miR482d-3p | 2853 | 6453 | 1543 | 3760 | 1637 |
| 14 | gma-miR159a-5p | 1844 | 1295 | 2005 | 1030 | 1335 |
| 15 | ptc-miR396e-3p | 432 | 620 | 184 | 245 | 397 |
| 16 | gma-miR319f | 103 | 34 | 139 | 68 | 43 |
| 17 | age-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 18 | bta-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 19 | cgr-miR-19b-3p | 57 | 49 | 84 | 90 | 22 |
| 20 | chi-miR-19b-3p | 57 | 49 | 84 | 90 | 22 |
| 21 | cja-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 22 | cli-miR-19b-3p | 57 | 49 | 84 | 90 | 22 |
| 23 | cpo-miR-19b-3p | 57 | 49 | 84 | 90 | 22 |
| 24 | dno-miR-19b-3p | 57 | 49 | 84 | 90 | 22 |
| 25 | dre-miR-19b-3p | 57 | 49 | 84 | 90 | 22 |
| 26 | eca-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 27 | fru-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 28 | gga-miR-19b-3p | 57 | 49 | 84 | 90 | 22 |
| 29 | ggo-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 30 | gmo-miR-19b-3p | 57 | 49 | 84 | 90 | 22 |
| 31 | hsa-miR-19b-3p | 57 | 49 | 84 | 90 | 22 |
| 32 | lca-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 33 | lla-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 34 | mdo-miR-19b-3p | 57 | 49 | 84 | 90 | 22 |
| 35 | mml-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 36 | mmu-miR-19b-3p | 57 | 49 | 84 | 90 | 22 |
| 37 | mne-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 38 | oan-miR-19b-3p | 57 | 49 | 84 | 90 | 22 |
| 39 | oar-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 40 | ocu-miR-19b-3p | 57 | 49 | 84 | 90 | 22 |
| 41 | oha-miR-19b-3p | 57 | 49 | 84 | 90 | 22 |
| 42 | pal-miR-19-3p | 57 | 49 | 84 | 90 | 22 |
| 43 | pma-miR-19b-3p | 57 | 49 | 84 | 90 | 22 |
| 44 | ppa-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 45 | ppy-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|-------|-------|------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ptr-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 4 | rno-miR-19b-3p | 57 | 49 | 84 | 90 | 22 |
| 5 | sha-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 6 | sla-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 7 | ssc-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 8 | tch-miR-19b-3p | 57 | 49 | 84 | 90 | 22 |
| 9 | tgu-miR-19b-3p | 57 | 49 | 84 | 90 | 22 |
| 10 | tni-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 11 | xla-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 12 | xtr-miR-19b | 57 | 49 | 84 | 90 | 22 |
| 13 | efu-miR-378 | 200 | 224 | 143 | 216 | 102 |
| 14 | ggo-miR-378a | 199 | 224 | 143 | 216 | 102 |
| 15 | bta-miR-378 | 195 | 224 | 143 | 215 | 102 |
| 16 | cfa-miR-378 | 195 | 224 | 143 | 215 | 102 |
| 17 | cgr-miR-378-3p | 195 | 224 | 143 | 215 | 102 |
| 18 | chi-miR-378-3p | 195 | 224 | 143 | 215 | 102 |
| 19 | cja-miR-378 | 195 | 224 | 143 | 215 | 102 |
| 20 | cpo-miR-378-3p | 195 | 224 | 143 | 215 | 102 |
| 21 | dno-miR-378-3p | 195 | 224 | 143 | 215 | 102 |
| 22 | hsa-miR-378a-3p | 195 | 224 | 143 | 215 | 102 |
| 23 | nle-miR-378a | 195 | 224 | 143 | 215 | 102 |
| 24 | ocu-miR-378-3p | 195 | 224 | 143 | 215 | 102 |
| 25 | oga-miR-378 | 195 | 224 | 143 | 215 | 102 |
| 26 | pal-miR-378-3p | 195 | 224 | 143 | 215 | 102 |
| 27 | pha-miR-378 | 195 | 224 | 143 | 215 | 102 |
| 28 | ppa-miR-378a | 195 | 224 | 143 | 215 | 102 |
| 29 | ssc-miR-378 | 195 | 224 | 143 | 215 | 102 |
| 30 | tch-miR-378a-3p | 195 | 224 | 143 | 215 | 102 |
| 31 | efu-miR-19 | 58 | 50 | 84 | 91 | 22 |
| 32 | xla-miR-19b-3p | 58 | 50 | 84 | 91 | 22 |
| 33 | gma-miR156f | 12431 | 14883 | 2848 | 9875 | 6181 |
| 34 | ahy-miR156c | 12339 | 14785 | 2836 | 9790 | 6132 |
| 35 | far-miR156b | 12339 | 14785 | 2836 | 9790 | 6132 |
| 36 | mdm-miR156t | 12339 | 14785 | 2836 | 9790 | 6132 |
| 37 | mdm-miR156u | 12339 | 14785 | 2836 | 9790 | 6132 |
| 38 | mdm-miR156v | 12339 | 14785 | 2836 | 9790 | 6132 |
| 39 | mdm-miR156w | 12339 | 14785 | 2836 | 9790 | 6132 |
| 40 | mes-miR156k | 12339 | 14785 | 2836 | 9790 | 6132 |
| 41 | gma-miR390b-5p | 304 | 338 | 292 | 199 | 164 |
| 42 | gma-miR390d | 304 | 338 | 292 | 199 | 164 |
| 43 | nta-miR390a | 304 | 338 | 292 | 199 | 164 |
| 44 | sly-miR390a-5p | 304 | 338 | 292 | 199 | 164 |
| 45 | stu-miR390-5p | 304 | 338 | 292 | 199 | 164 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | csi-miR396f-3p | 468 | 659 | 204 | 252 | 413 |
| 4 | gma-miR396b-3p | 468 | 659 | 204 | 252 | 413 |
| 5 | gma-miR396k-3p | 468 | 659 | 204 | 252 | 413 |
| 6 | mtr-miR396a-3p | 468 | 659 | 204 | 252 | 413 |
| 7 | ahy-miR160-5p | 95 | 80 | 217 | 96 | 42 |
| 8 | aof-miR160a | 95 | 80 | 217 | 96 | 42 |
| 9 | bdi-miR160e-5p | 95 | 80 | 217 | 96 | 42 |
| 10 | cme-miR160d | 95 | 80 | 217 | 96 | 42 |
| 11 | cpa-miR160d | 95 | 80 | 217 | 96 | 42 |
| 12 | mes-miR160e | 95 | 80 | 217 | 96 | 42 |
| 13 | mes-miR160f | 95 | 80 | 217 | 96 | 42 |
| 14 | mtr-miR160c | 95 | 80 | 217 | 96 | 42 |
| 15 | osa-miR160f-5p | 95 | 80 | 217 | 96 | 42 |
| 16 | ptc-miR160e-5p | 95 | 80 | 217 | 96 | 42 |
| 17 | ptc-miR160f | 95 | 80 | 217 | 96 | 42 |
| 18 | rco-miR160c | 95 | 80 | 217 | 96 | 42 |
| 19 | sbi-miR160f | 95 | 80 | 217 | 96 | 42 |
| 20 | tcc-miR160a | 95 | 80 | 217 | 96 | 42 |
| 21 | vca-miR160-5p | 95 | 80 | 217 | 96 | 42 |
| 22 | vvi-miR160a | 95 | 80 | 217 | 96 | 42 |
| 23 | vvi-miR160b | 95 | 80 | 217 | 96 | 42 |
| 24 | lja-miR166-3p | 41108 | 35806 | 93852 | 26586 | 32868 |
| 25 | aly-miR166a-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 26 | aly-miR166b-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 27 | aly-miR166c-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 28 | aly-miR166d-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 29 | aly-miR166e-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 30 | aly-miR166f-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 31 | aly-miR166g-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 32 | aly-miR166h-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 33 | aof-miR166d | 39290 | 34477 | 91739 | 25385 | 31490 |
| 34 | aqc-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 35 | aqc-miR166e | 39290 | 34477 | 91739 | 25385 | 31490 |
| 36 | ata-miR166a-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 37 | ata-miR166b-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 38 | ata-miR166d-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 39 | ata-miR166e-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 40 | ath-miR166a-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 41 | ath-miR166b-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 42 | ath-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 43 | ath-miR166d | 39290 | 34477 | 91739 | 25385 | 31490 |
| 44 | ath-miR166e-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 45 | ath-miR166f | 39290 | 34477 | 91739 | 25385 | 31490 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ath-miR166g | 39290 | 34477 | 91739 | 25385 | 31490 |
| 4 | atr-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 5 | atr-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 6 | atr-miR166d | 39290 | 34477 | 91739 | 25385 | 31490 |
| 7 | atr-miR166d | 39290 | 34477 | 91739 | 25385 | 31490 |
| 8 | bdi-miR166a-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 9 | bdi-miR166b-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 10 | bdi-miR166c-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 11 | bdi-miR166c-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 12 | bdi-miR166d-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 13 | bdi-miR166d-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 14 | bdi-miR166i-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 15 | bna-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 16 | bna-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 17 | bna-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 18 | bna-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 19 | bna-miR166d | 39290 | 34477 | 91739 | 25385 | 31490 |
| 20 | bna-miR166e | 39290 | 34477 | 91739 | 25385 | 31490 |
| 21 | bna-miR166e | 39290 | 34477 | 91739 | 25385 | 31490 |
| 22 | cme-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 23 | cme-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 24 | cme-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 25 | cme-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 26 | cme-miR166d | 39290 | 34477 | 91739 | 25385 | 31490 |
| 27 | cme-miR166f | 39290 | 34477 | 91739 | 25385 | 31490 |
| 28 | cme-miR166h | 39290 | 34477 | 91739 | 25385 | 31490 |
| 29 | cme-miR166h | 39290 | 34477 | 91739 | 25385 | 31490 |
| 30 | cpa-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 31 | cpa-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 32 | cpa-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 33 | cpa-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 34 | csi-miR166e-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 35 | dpr-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 36 | eun-miR166-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 37 | eun-miR166-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 38 | fve-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 39 | fve-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 40 | fve-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 41 | fve-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 42 | fve-miR166d-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 43 | fve-miR166e | 39290 | 34477 | 91739 | 25385 | 31490 |
| 44 | fve-miR166e | 39290 | 34477 | 91739 | 25385 | 31490 |
| 45 | fve-miR166f | 39290 | 34477 | 91739 | 25385 | 31490 |
| 46 | ghr-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 47 | gma-miR166a-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 48 | gma-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 49 | gma-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 50 | gma-miR166c-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 51 | gma-miR166d | 39290 | 34477 | 91739 | 25385 | 31490 |
| 52 | gma-miR166d | 39290 | 34477 | 91739 | 25385 | 31490 |
| 53 | gma-miR166e | 39290 | 34477 | 91739 | 25385 | 31490 |
| 54 | gma-miR166e | 39290 | 34477 | 91739 | 25385 | 31490 |
| 55 | gma-miR166f | 39290 | 34477 | 91739 | 25385 | 31490 |
| 56 | gma-miR166g | 39290 | 34477 | 91739 | 25385 | 31490 |
| 57 | gma-miR166g | 39290 | 34477 | 91739 | 25385 | 31490 |
| 58 | gma-miR166i-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 59 | gma-miR166n | 39290 | 34477 | 91739 | 25385 | 31490 |
| 60 | gma-miR166o | 39290 | 34477 | 91739 | 25385 | 31490 |

| | | | | | | |
|----|----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | hpa-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 4 | hpe-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 5 | hvu-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 6 | hvu-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 7 | hvu-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 8 | lus-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 9 | lus-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 10 | lus-miR166d | 39290 | 34477 | 91739 | 25385 | 31490 |
| 11 | lus-miR166g | 39290 | 34477 | 91739 | 25385 | 31490 |
| 12 | lus-miR166h | 39290 | 34477 | 91739 | 25385 | 31490 |
| 13 | lus-miR166j | 39290 | 34477 | 91739 | 25385 | 31490 |
| 14 | mdm-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 15 | mdm-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 16 | mdm-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 17 | mdm-miR166d | 39290 | 34477 | 91739 | 25385 | 31490 |
| 18 | mdm-miR166e | 39290 | 34477 | 91739 | 25385 | 31490 |
| 19 | mdm-miR166f | 39290 | 34477 | 91739 | 25385 | 31490 |
| 20 | mdm-miR166g | 39290 | 34477 | 91739 | 25385 | 31490 |
| 21 | mdm-miR166h | 39290 | 34477 | 91739 | 25385 | 31490 |
| 22 | mdm-miR166i | 39290 | 34477 | 91739 | 25385 | 31490 |
| 23 | mdm-miR166j | 39290 | 34477 | 91739 | 25385 | 31490 |
| 24 | mes-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 25 | mes-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 26 | mes-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 27 | mes-miR166d | 39290 | 34477 | 91739 | 25385 | 31490 |
| 28 | mes-miR166e | 39290 | 34477 | 91739 | 25385 | 31490 |
| 29 | mes-miR166f | 39290 | 34477 | 91739 | 25385 | 31490 |
| 30 | mes-miR166g | 39290 | 34477 | 91739 | 25385 | 31490 |
| 31 | mtr-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 32 | mtr-miR166e-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 33 | mtr-miR166g-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 34 | nta-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 35 | nta-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 36 | nta-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 37 | nta-miR166d | 39290 | 34477 | 91739 | 25385 | 31490 |
| 38 | nta-miR166e | 39290 | 34477 | 91739 | 25385 | 31490 |
| 39 | nta-miR166f | 39290 | 34477 | 91739 | 25385 | 31490 |
| 40 | nta-miR166g | 39290 | 34477 | 91739 | 25385 | 31490 |
| 41 | nta-miR166h | 39290 | 34477 | 91739 | 25385 | 31490 |
| 42 | osa-miR166a-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 43 | osa-miR166b-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 44 | osa-miR166c-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 45 | osa-miR166d-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | osa-miR166f | 39290 | 34477 | 91739 | 25385 | 31490 |
| 4 | osa-miR166j-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 5 | pab-miR166f | 39290 | 34477 | 91739 | 25385 | 31490 |
| 6 | pab-miR166g | 39290 | 34477 | 91739 | 25385 | 31490 |
| 7 | pab-miR166h | 39290 | 34477 | 91739 | 25385 | 31490 |
| 8 | pab-miR166i | 39290 | 34477 | 91739 | 25385 | 31490 |
| 9 | ppe-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 10 | ppe-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 11 | ppe-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 12 | ppe-miR166d | 39290 | 34477 | 91739 | 25385 | 31490 |
| 13 | ppe-miR166e | 39290 | 34477 | 91739 | 25385 | 31490 |
| 14 | ppt-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 15 | ppt-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 16 | ppt-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 17 | ppt-miR166d | 39290 | 34477 | 91739 | 25385 | 31490 |
| 18 | ppt-miR166e | 39290 | 34477 | 91739 | 25385 | 31490 |
| 19 | ppt-miR166f | 39290 | 34477 | 91739 | 25385 | 31490 |
| 20 | ppt-miR166g | 39290 | 34477 | 91739 | 25385 | 31490 |
| 21 | ppt-miR166h | 39290 | 34477 | 91739 | 25385 | 31490 |
| 22 | ppt-miR166i | 39290 | 34477 | 91739 | 25385 | 31490 |
| 23 | pta-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 24 | pta-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 25 | ptc-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 26 | ptc-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 27 | ptc-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 28 | ptc-miR166d | 39290 | 34477 | 91739 | 25385 | 31490 |
| 29 | ptc-miR166e | 39290 | 34477 | 91739 | 25385 | 31490 |
| 30 | ptc-miR166f | 39290 | 34477 | 91739 | 25385 | 31490 |
| 31 | ptc-miR166g | 39290 | 34477 | 91739 | 25385 | 31490 |
| 32 | ptc-miR166h | 39290 | 34477 | 91739 | 25385 | 31490 |
| 33 | ptc-miR166i | 39290 | 34477 | 91739 | 25385 | 31490 |
| 34 | ptc-miR166j | 39290 | 34477 | 91739 | 25385 | 31490 |
| 35 | ptc-miR166k | 39290 | 34477 | 91739 | 25385 | 31490 |
| 36 | ptc-miR166l | 39290 | 34477 | 91739 | 25385 | 31490 |
| 37 | ptc-miR166m | 39290 | 34477 | 91739 | 25385 | 31490 |
| 38 | pvu-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 39 | rco-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 40 | rco-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 41 | rco-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 42 | rco-miR166d | 39290 | 34477 | 91739 | 25385 | 31490 |
| 43 | rco-miR166e | 39290 | 34477 | 91739 | 25385 | 31490 |
| 44 | sly-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 45 | sly-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|--------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | smo-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 4 | smo-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 5 | smo-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 6 | ssl-miR166b | 39290 | 34477 | 91739 | 25385 | 31490 |
| 7 | ssp-miR166 | 39290 | 34477 | 91739 | 25385 | 31490 |
| 8 | stu-miR166a-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 9 | stu-miR166c-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 10 | stu-miR166d-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 11 | tcc-miR166a | 39290 | 34477 | 91739 | 25385 | 31490 |
| 12 | tcc-miR166d | 39290 | 34477 | 91739 | 25385 | 31490 |
| 13 | vca-miR166a-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 14 | vca-miR166b-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 15 | vca-miR166c-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 16 | vvi-miR166c | 39290 | 34477 | 91739 | 25385 | 31490 |
| 17 | vvi-miR166d | 39290 | 34477 | 91739 | 25385 | 31490 |
| 18 | vvi-miR166e | 39290 | 34477 | 91739 | 25385 | 31490 |
| 19 | vvi-miR166f | 39290 | 34477 | 91739 | 25385 | 31490 |
| 20 | vvi-miR166g | 39290 | 34477 | 91739 | 25385 | 31490 |
| 21 | vvi-miR166h | 39290 | 34477 | 91739 | 25385 | 31490 |
| 22 | zma-miR166a-3p | 39290 | 34477 | 91739 | 25385 | 31490 |
| 23 | csi-miR166a-3p | 39295 | 34481 | 91787 | 25387 | 31492 |
| 24 | ctr-miR166 | 39295 | 34481 | 91787 | 25387 | 31492 |
| 25 | hbr-miR166b | 39295 | 34481 | 91787 | 25387 | 31492 |
| 26 | lus-miR166i | 39295 | 34481 | 91787 | 25387 | 31492 |
| 27 | lus-miR166k | 39295 | 34481 | 91787 | 25387 | 31492 |
| 28 | cas-miR166c-3p | 39375 | 34575 | 92370 | 25450 | 31533 |
| 29 | cas-miR166d | 39375 | 34575 | 92370 | 25450 | 31533 |
| 30 | cas-miR166f-3p | 39375 | 34575 | 92370 | 25450 | 31533 |
| 31 | lja-miR168-5p | 64684 | 135916 | 28128 | 81069 | 38549 |
| 32 | aly-miR168a-5p | 64535 | 135686 | 28082 | 80905 | 38434 |
| 33 | aly-miR168b-5p | 64535 | 135686 | 28082 | 80905 | 38434 |
| 34 | aof-miR168a | 64535 | 135686 | 28082 | 80905 | 38434 |
| 35 | ath-miR168a-5p | 64535 | 135686 | 28082 | 80905 | 38434 |
| 36 | ath-miR168b-5p | 64535 | 135686 | 28082 | 80905 | 38434 |
| 37 | atr-miR168 | 64535 | 135686 | 28082 | 80905 | 38434 |
| 38 | bna-miR168a | 64535 | 135686 | 28082 | 80905 | 38434 |
| 39 | bra-miR168a-5p | 64535 | 135686 | 28082 | 80905 | 38434 |
| 40 | cca-miR168a | 64535 | 135686 | 28082 | 80905 | 38434 |
| 41 | ccl-miR168 | 64535 | 135686 | 28082 | 80905 | 38434 |
| 42 | crt-miR168 | 64535 | 135686 | 28082 | 80905 | 38434 |
| 43 | csi-miR168-5p | 64535 | 135686 | 28082 | 80905 | 38434 |
| 44 | fve-miR168-5p | 64535 | 135686 | 28082 | 80905 | 38434 |
| 45 | gma-miR168a | 64535 | 135686 | 28082 | 80905 | 38434 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|--------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | lus-miR168a | 64535 | 135686 | 28082 | 80905 | 38434 |
| 4 | lus-miR168b | 64535 | 135686 | 28082 | 80905 | 38434 |
| 5 | mdm-miR168a | 64535 | 135686 | 28082 | 80905 | 38434 |
| 6 | mdm-miR168b | 64535 | 135686 | 28082 | 80905 | 38434 |
| 7 | mes-miR168a | 64535 | 135686 | 28082 | 80905 | 38434 |
| 8 | mes-miR168b | 64535 | 135686 | 28082 | 80905 | 38434 |
| 9 | mtr-miR168b | 64535 | 135686 | 28082 | 80905 | 38434 |
| 10 | mtr-miR168c-5p | 64535 | 135686 | 28082 | 80905 | 38434 |
| 11 | nta-miR168d | 64535 | 135686 | 28082 | 80905 | 38434 |
| 12 | nta-miR168e | 64535 | 135686 | 28082 | 80905 | 38434 |
| 13 | pab-miR168a | 64535 | 135686 | 28082 | 80905 | 38434 |
| 14 | ppe-miR168 | 64535 | 135686 | 28082 | 80905 | 38434 |
| 15 | ptc-miR168a-5p | 64535 | 135686 | 28082 | 80905 | 38434 |
| 16 | ptc-miR168b-5p | 64535 | 135686 | 28082 | 80905 | 38434 |
| 17 | rco-miR168 | 64535 | 135686 | 28082 | 80905 | 38434 |
| 18 | tcc-miR168 | 64535 | 135686 | 28082 | 80905 | 38434 |
| 19 | vca-miR168a-5p | 64535 | 135686 | 28082 | 80905 | 38434 |
| 20 | vca-miR168b-5p | 64535 | 135686 | 28082 | 80905 | 38434 |
| 21 | vun-miR168 | 64535 | 135686 | 28082 | 80905 | 38434 |
| 22 | vvi-miR168 | 64535 | 135686 | 28082 | 80905 | 38434 |
| 23 | ahy-miR167-5p | 32592 | 40851 | 39761 | 19815 | 28085 |
| 24 | cme-miR167c | 32592 | 40851 | 39761 | 19815 | 28085 |
| 25 | cpa-miR167c | 32592 | 40851 | 39761 | 19815 | 28085 |
| 26 | csi-miR167b-5p | 32592 | 40851 | 39761 | 19815 | 28085 |
| 27 | gma-miR167e | 32592 | 40851 | 39761 | 19815 | 28085 |
| 28 | gma-miR167f | 32592 | 40851 | 39761 | 19815 | 28085 |
| 29 | lus-miR167b | 32592 | 40851 | 39761 | 19815 | 28085 |
| 30 | mes-miR167g | 32592 | 40851 | 39761 | 19815 | 28085 |
| 31 | mes-miR167h | 32592 | 40851 | 39761 | 19815 | 28085 |
| 32 | ptc-miR167f-5p | 32592 | 40851 | 39761 | 19815 | 28085 |
| 33 | ptc-miR167g-5p | 32592 | 40851 | 39761 | 19815 | 28085 |
| 34 | tcc-miR167c | 32592 | 40851 | 39761 | 19815 | 28085 |
| 35 | gma-miR403a | 5565 | 3750 | 30300 | 4887 | 2458 |
| 36 | gma-miR403b | 5565 | 3750 | 30300 | 4887 | 2458 |
| 37 | aly-miR396b-5p | 1143 | 1233 | 2696 | 688 | 841 |
| 38 | ama-miR396-5p | 1143 | 1233 | 2696 | 688 | 841 |
| 39 | aqc-miR396b | 1143 | 1233 | 2696 | 688 | 841 |
| 40 | ata-miR396c-5p | 1143 | 1233 | 2696 | 688 | 841 |
| 41 | ath-miR396b-5p | 1143 | 1233 | 2696 | 688 | 841 |
| 42 | atr-miR396b | 1143 | 1233 | 2696 | 688 | 841 |
| 43 | atr-miR396c | 1143 | 1233 | 2696 | 688 | 841 |
| 44 | atr-miR396e | 1143 | 1233 | 2696 | 688 | 841 |
| 45 | bcy-miR396b | 1143 | 1233 | 2696 | 688 | 841 |
| 46 | bdi-miR396e-5p | 1143 | 1233 | 2696 | 688 | 841 |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|-----|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | bgj-miR396b | 1143 | 1233 | 2696 | 688 | 841 |
| 4 | bnj-miR396a | 1143 | 1233 | 2696 | 688 | 841 |
| 5 | brj-miR396-5p | 1143 | 1233 | 2696 | 688 | 841 |
| 6 | cas-miR396b | 1143 | 1233 | 2696 | 688 | 841 |
| 7 | cca-miR396a-5p | 1143 | 1233 | 2696 | 688 | 841 |
| 8 | ccl-miR396 | 1143 | 1233 | 2696 | 688 | 841 |
| 9 | cme-miR396a | 1143 | 1233 | 2696 | 688 | 841 |
| 10 | cme-miR396c | 1143 | 1233 | 2696 | 688 | 841 |
| 11 | cme-miR396d | 1143 | 1233 | 2696 | 688 | 841 |
| 12 | csi-miR396f-5p | 1143 | 1233 | 2696 | 688 | 841 |
| 13 | fve-miR396b-5p | 1143 | 1233 | 2696 | 688 | 841 |
| 14 | gma-miR396b-5p | 1143 | 1233 | 2696 | 688 | 841 |
| 15 | gma-miR396c | 1143 | 1233 | 2696 | 688 | 841 |
| 16 | gma-miR396k-5p | 1143 | 1233 | 2696 | 688 | 841 |
| 17 | lus-miR396b | 1143 | 1233 | 2696 | 688 | 841 |
| 18 | lus-miR396e | 1143 | 1233 | 2696 | 688 | 841 |
| 19 | mdm-miR396c | 1143 | 1233 | 2696 | 688 | 841 |
| 20 | mdm-miR396d | 1143 | 1233 | 2696 | 688 | 841 |
| 21 | mdm-miR396e | 1143 | 1233 | 2696 | 688 | 841 |
| 22 | mes-miR396c | 1143 | 1233 | 2696 | 688 | 841 |
| 23 | mes-miR396d | 1143 | 1233 | 2696 | 688 | 841 |
| 24 | mes-miR396e | 1143 | 1233 | 2696 | 688 | 841 |
| 25 | mes-miR396f | 1143 | 1233 | 2696 | 688 | 841 |
| 26 | mtr-miR396a-5p | 1143 | 1233 | 2696 | 688 | 841 |
| 27 | nta-miR396b | 1143 | 1233 | 2696 | 688 | 841 |
| 28 | nta-miR396c | 1143 | 1233 | 2696 | 688 | 841 |
| 29 | osa-miR396c-5p | 1143 | 1233 | 2696 | 688 | 841 |
| 30 | pab-miR396g | 1143 | 1233 | 2696 | 688 | 841 |
| 31 | pab-miR396h | 1143 | 1233 | 2696 | 688 | 841 |
| 32 | ppe-miR396b | 1143 | 1233 | 2696 | 688 | 841 |
| 33 | pta-miR396 | 1143 | 1233 | 2696 | 688 | 841 |
| 34 | ptc-miR396c | 1143 | 1233 | 2696 | 688 | 841 |
| 35 | ptc-miR396d | 1143 | 1233 | 2696 | 688 | 841 |
| 36 | ptc-miR396e-5p | 1143 | 1233 | 2696 | 688 | 841 |
| 37 | rco-miR396 | 1143 | 1233 | 2696 | 688 | 841 |
| 38 | sbi-miR396c | 1143 | 1233 | 2696 | 688 | 841 |
| 39 | sly-miR396b | 1143 | 1233 | 2696 | 688 | 841 |
| 40 | stu-miR396-5p | 1143 | 1233 | 2696 | 688 | 841 |
| 41 | tcc-miR396c | 1143 | 1233 | 2696 | 688 | 841 |
| 42 | tcc-miR396e | 1143 | 1233 | 2696 | 688 | 841 |
| 43 | zma-miR396e-5p | 1143 | 1233 | 2696 | 688 | 841 |
| 44 | zma-miR396f-5p | 1143 | 1233 | 2696 | 688 | 841 |
| 45 | gma-miR1511 | 1103 | 618 | 4493 | 521 | 1150 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|-------|------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | gma-miR5374-5p | 554 | 502 | 295 | 428 | 210 |
| 4 | mtr-miR171c | 28 | 60 | 103 | 47 | 25 |
| 5 | aly-miR166a-5p | 15363 | 15709 | 1648 | 5141 | 10013 |
| 6 | aly-miR166c-5p | 15363 | 15709 | 1648 | 5141 | 10013 |
| 7 | aly-miR166d-5p | 15363 | 15709 | 1648 | 5141 | 10013 |
| 8 | bdi-miR166e-5p | 15363 | 15709 | 1648 | 5141 | 10013 |
| 9 | cas-miR166a | 15363 | 15709 | 1648 | 5141 | 10013 |
| 10 | csi-miR166a-5p | 15363 | 15709 | 1648 | 5141 | 10013 |
| 11 | csi-miR166e-5p | 15363 | 15709 | 1648 | 5141 | 10013 |
| 12 | eun-miR166-5p | 15363 | 15709 | 1648 | 5141 | 10013 |
| 13 | gma-miR166a-5p | 15363 | 15709 | 1648 | 5141 | 10013 |
| 14 | gma-miR166c-5p | 15363 | 15709 | 1648 | 5141 | 10013 |
| 15 | gma-miR166l | 15363 | 15709 | 1648 | 5141 | 10013 |
| 16 | mtr-miR166g-5p | 15363 | 15709 | 1648 | 5141 | 10013 |
| 17 | osa-miR166d-5p | 15363 | 15709 | 1648 | 5141 | 10013 |
| 18 | stu-miR166a-5p | 15363 | 15709 | 1648 | 5141 | 10013 |
| 19 | vca-miR166b-5p | 15363 | 15709 | 1648 | 5141 | 10013 |
| 20 | zma-miR166c-5p | 15363 | 15709 | 1648 | 5141 | 10013 |
| 21 | gma-miR391-5p | 85 | 61 | 167 | 59 | 39 |
| 22 | gma-miR171m | 9514 | 18038 | 18276 | 8015 | 9536 |
| 23 | gma-miR171t | 9514 | 18038 | 18276 | 8015 | 9536 |
| 24 | aly-miR169a-5p | 491 | 981 | 621 | 460 | 423 |
| 25 | ata-miR169e-5p | 491 | 981 | 621 | 460 | 423 |
| 26 | ata-miR169f-5p | 491 | 981 | 621 | 460 | 423 |
| 27 | ata-miR169g-5p | 491 | 981 | 621 | 460 | 423 |
| 28 | ath-miR169a-5p | 491 | 981 | 621 | 460 | 423 |
| 29 | bdi-miR169a-5p | 491 | 981 | 621 | 460 | 423 |
| 30 | bna-miR169a | 491 | 981 | 621 | 460 | 423 |
| 31 | bna-miR169b | 491 | 981 | 621 | 460 | 423 |
| 32 | cas-miR169a | 491 | 981 | 621 | 460 | 423 |
| 33 | gma-miR169b | 491 | 981 | 621 | 460 | 423 |
| 34 | lus-miR169g | 491 | 981 | 621 | 460 | 423 |
| 35 | lus-miR169l | 491 | 981 | 621 | 460 | 423 |
| 36 | mes-miR169g | 491 | 981 | 621 | 460 | 423 |
| 37 | mtr-miR169a | 491 | 981 | 621 | 460 | 423 |
| 38 | nta-miR169a | 491 | 981 | 621 | 460 | 423 |
| 39 | nta-miR169b | 491 | 981 | 621 | 460 | 423 |
| 40 | nta-miR169c | 491 | 981 | 621 | 460 | 423 |
| 41 | nta-miR169d | 491 | 981 | 621 | 460 | 423 |
| 42 | nta-miR169e | 491 | 981 | 621 | 460 | 423 |
| 43 | nta-miR169f | 491 | 981 | 621 | 460 | 423 |
| 44 | nta-miR169g | 491 | 981 | 621 | 460 | 423 |
| 45 | nta-miR169h | 491 | 981 | 621 | 460 | 423 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|-------|-------|-------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | nta-miR169i | 491 | 981 | 621 | 460 | 423 |
| 4 | nta-miR169j | 491 | 981 | 621 | 460 | 423 |
| 5 | nta-miR169k | 491 | 981 | 621 | 460 | 423 |
| 6 | nta-miR169l | 491 | 981 | 621 | 460 | 423 |
| 7 | nta-miR169m | 491 | 981 | 621 | 460 | 423 |
| 8 | nta-miR169n | 491 | 981 | 621 | 460 | 423 |
| 9 | nta-miR169o | 491 | 981 | 621 | 460 | 423 |
| 10 | nta-miR169p | 491 | 981 | 621 | 460 | 423 |
| 11 | osa-miR169a | 491 | 981 | 621 | 460 | 423 |
| 12 | ptc-miR169a | 491 | 981 | 621 | 460 | 423 |
| 13 | ptc-miR169b-5p | 491 | 981 | 621 | 460 | 423 |
| 14 | ptc-miR169c | 491 | 981 | 621 | 460 | 423 |
| 15 | sbi-miR169a | 491 | 981 | 621 | 460 | 423 |
| 16 | sly-miR169c | 491 | 981 | 621 | 460 | 423 |
| 17 | tcc-miR169a | 491 | 981 | 621 | 460 | 423 |
| 18 | tcc-miR169c | 491 | 981 | 621 | 460 | 423 |
| 19 | tcc-miR169e | 491 | 981 | 621 | 460 | 423 |
| 20 | vvi-miR169f | 491 | 981 | 621 | 460 | 423 |
| 21 | vvi-miR169g | 491 | 981 | 621 | 460 | 423 |
| 22 | zma-miR169a-5p | 491 | 981 | 621 | 460 | 423 |
| 23 | zma-miR169b-5p | 491 | 981 | 621 | 460 | 423 |
| 24 | gma-miR169u | 487 | 966 | 649 | 440 | 429 |
| 25 | mdm-miR167h | 68755 | 87811 | 93911 | 40687 | 54233 |
| 26 | mdm-miR167i | 68755 | 87811 | 93911 | 40687 | 54233 |
| 27 | mdm-miR167j | 68755 | 87811 | 93911 | 40687 | 54233 |
| 28 | ppe-miR167d | 68755 | 87811 | 93911 | 40687 | 54233 |
| 29 | ppe-miR398b | 60 | 51 | 339 | 61 | 58 |
| 30 | bnm-miR167a | 5635 | 8853 | 15331 | 4957 | 5190 |
| 31 | bnm-miR167b | 5635 | 8853 | 15331 | 4957 | 5190 |
| 32 | aly-miR167a-5p | 5632 | 8844 | 15323 | 4951 | 5186 |
| 33 | aly-miR167b-5p | 5632 | 8844 | 15323 | 4951 | 5186 |
| 34 | aof-miR167a | 5632 | 8844 | 15323 | 4951 | 5186 |
| 35 | ata-miR167a-5p | 5632 | 8844 | 15323 | 4951 | 5186 |
| 36 | ata-miR167c-5p | 5632 | 8844 | 15323 | 4951 | 5186 |
| 37 | ata-miR167e-5p | 5632 | 8844 | 15323 | 4951 | 5186 |
| 38 | ath-miR167a-5p | 5632 | 8844 | 15323 | 4951 | 5186 |
| 39 | ath-miR167b | 5632 | 8844 | 15323 | 4951 | 5186 |
| 40 | bdi-miR167a | 5632 | 8844 | 15323 | 4951 | 5186 |
| 41 | bdi-miR167b | 5632 | 8844 | 15323 | 4951 | 5186 |
| 42 | bdi-miR167f | 5632 | 8844 | 15323 | 4951 | 5186 |
| 43 | bnm-miR167c | 5632 | 8844 | 15323 | 4951 | 5186 |
| 44 | bra-miR167a | 5632 | 8844 | 15323 | 4951 | 5186 |
| 45 | bra-miR167b | 5632 | 8844 | 15323 | 4951 | 5186 |
| 46 | bra-miR167c | 5632 | 8844 | 15323 | 4951 | 5186 |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|-------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | bra-miR167d | 5632 | 8844 | 15323 | 4951 | 5186 |
| 4 | cme-miR167a | 5632 | 8844 | 15323 | 4951 | 5186 |
| 5 | cme-miR167b | 5632 | 8844 | 15323 | 4951 | 5186 |
| 6 | cpa-miR167a | 5632 | 8844 | 15323 | 4951 | 5186 |
| 7 | cpa-miR167b | 5632 | 8844 | 15323 | 4951 | 5186 |
| 8 | csi-miR167d-5p | 5632 | 8844 | 15323 | 4951 | 5186 |
| 9 | csi-miR167e-5p | 5632 | 8844 | 15323 | 4951 | 5186 |
| 10 | dpr-miR167a | 5632 | 8844 | 15323 | 4951 | 5186 |
| 11 | dpr-miR167b | 5632 | 8844 | 15323 | 4951 | 5186 |
| 12 | ghr-miR167a | 5632 | 8844 | 15323 | 4951 | 5186 |
| 13 | ghr-miR167b | 5632 | 8844 | 15323 | 4951 | 5186 |
| 14 | gma-miR167a | 5632 | 8844 | 15323 | 4951 | 5186 |
| 15 | gma-miR167b | 5632 | 8844 | 15323 | 4951 | 5186 |
| 16 | gma-miR167d | 5632 | 8844 | 15323 | 4951 | 5186 |
| 17 | lus-miR167c | 5632 | 8844 | 15323 | 4951 | 5186 |
| 18 | lus-miR167d | 5632 | 8844 | 15323 | 4951 | 5186 |
| 19 | lus-miR167e | 5632 | 8844 | 15323 | 4951 | 5186 |
| 20 | lus-miR167h | 5632 | 8844 | 15323 | 4951 | 5186 |
| 21 | mdm-miR167b | 5632 | 8844 | 15323 | 4951 | 5186 |
| 22 | mdm-miR167c | 5632 | 8844 | 15323 | 4951 | 5186 |
| 23 | mdm-miR167d | 5632 | 8844 | 15323 | 4951 | 5186 |
| 24 | mdm-miR167e | 5632 | 8844 | 15323 | 4951 | 5186 |
| 25 | mdm-miR167f | 5632 | 8844 | 15323 | 4951 | 5186 |
| 26 | mdm-miR167g | 5632 | 8844 | 15323 | 4951 | 5186 |
| 27 | mes-miR167c | 5632 | 8844 | 15323 | 4951 | 5186 |
| 28 | mtr-miR167a | 5632 | 8844 | 15323 | 4951 | 5186 |
| 29 | nta-miR167d | 5632 | 8844 | 15323 | 4951 | 5186 |
| 30 | nta-miR167e | 5632 | 8844 | 15323 | 4951 | 5186 |
| 31 | osa-miR167a-5p | 5632 | 8844 | 15323 | 4951 | 5186 |
| 32 | osa-miR167b | 5632 | 8844 | 15323 | 4951 | 5186 |
| 33 | osa-miR167c-5p | 5632 | 8844 | 15323 | 4951 | 5186 |
| 34 | ppe-miR167a | 5632 | 8844 | 15323 | 4951 | 5186 |
| 35 | ppe-miR167b | 5632 | 8844 | 15323 | 4951 | 5186 |
| 36 | ptc-miR167a | 5632 | 8844 | 15323 | 4951 | 5186 |
| 37 | ptc-miR167b | 5632 | 8844 | 15323 | 4951 | 5186 |
| 38 | ptc-miR167c | 5632 | 8844 | 15323 | 4951 | 5186 |
| 39 | ptc-miR167d | 5632 | 8844 | 15323 | 4951 | 5186 |
| 40 | rco-miR167a | 5632 | 8844 | 15323 | 4951 | 5186 |
| 41 | rco-miR167b | 5632 | 8844 | 15323 | 4951 | 5186 |
| 42 | sbi-miR167a | 5632 | 8844 | 15323 | 4951 | 5186 |
| 43 | sbi-miR167b | 5632 | 8844 | 15323 | 4951 | 5186 |
| 44 | sbi-miR167i | 5632 | 8844 | 15323 | 4951 | 5186 |
| 45 | sly-miR167a | 5632 | 8844 | 15323 | 4951 | 5186 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|-------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | stu-miR167a-5p | 5632 | 8844 | 15323 | 4951 | 5186 |
| 4 | stu-miR167b-5p | 5632 | 8844 | 15323 | 4951 | 5186 |
| 5 | stu-miR167c-5p | 5632 | 8844 | 15323 | 4951 | 5186 |
| 6 | stu-miR167d-5p | 5632 | 8844 | 15323 | 4951 | 5186 |
| 7 | tae-miR167a | 5632 | 8844 | 15323 | 4951 | 5186 |
| 8 | tcc-miR167a | 5632 | 8844 | 15323 | 4951 | 5186 |
| 9 | tcc-miR167b | 5632 | 8844 | 15323 | 4951 | 5186 |
| 10 | vvi-miR167b | 5632 | 8844 | 15323 | 4951 | 5186 |
| 11 | vvi-miR167d | 5632 | 8844 | 15323 | 4951 | 5186 |
| 12 | vvi-miR167e | 5632 | 8844 | 15323 | 4951 | 5186 |
| 13 | zma-miR167a-5p | 5632 | 8844 | 15323 | 4951 | 5186 |
| 14 | zma-miR167b-5p | 5632 | 8844 | 15323 | 4951 | 5186 |
| 15 | zma-miR167c-5p | 5632 | 8844 | 15323 | 4951 | 5186 |
| 16 | zma-miR167d-5p | 5632 | 8844 | 15323 | 4951 | 5186 |
| 17 | ppt-miR160b | 33 | 24 | 341 | 30 | 17 |
| 18 | ppt-miR160i | 33 | 24 | 341 | 30 | 17 |
| 19 | lus-miR398f | 59 | 52 | 334 | 59 | 55 |
| 20 | gma-miR159d | 3954 | 2175 | 751 | 1985 | 1102 |
| 21 | aof-miR398 | 6176 | 8152 | 22550 | 5826 | 6562 |
| 22 | aqc-miR398b | 6176 | 8152 | 22550 | 5826 | 6562 |
| 23 | bdi-miR398a | 6176 | 8152 | 22550 | 5826 | 6562 |
| 24 | cca-miR398 | 6176 | 8152 | 22550 | 5826 | 6562 |
| 25 | cme-miR398a | 6176 | 8152 | 22550 | 5826 | 6562 |
| 26 | csi-miR398b-3p | 6176 | 8152 | 22550 | 5826 | 6562 |
| 27 | gma-miR398c | 6176 | 8152 | 22550 | 5826 | 6562 |
| 28 | gma-miR398d | 6176 | 8152 | 22550 | 5826 | 6562 |
| 29 | lus-miR398a | 6176 | 8152 | 22550 | 5826 | 6562 |
| 30 | mdm-miR398b | 6176 | 8152 | 22550 | 5826 | 6562 |
| 31 | mdm-miR398c | 6176 | 8152 | 22550 | 5826 | 6562 |
| 32 | mes-miR398 | 6176 | 8152 | 22550 | 5826 | 6562 |
| 33 | mtr-miR398b | 6176 | 8152 | 22550 | 5826 | 6562 |
| 34 | mtr-miR398c | 6176 | 8152 | 22550 | 5826 | 6562 |
| 35 | nta-miR398 | 6176 | 8152 | 22550 | 5826 | 6562 |
| 36 | osa-miR398b | 6176 | 8152 | 22550 | 5826 | 6562 |
| 37 | ppe-miR398a-3p | 6176 | 8152 | 22550 | 5826 | 6562 |
| 38 | ptc-miR398b | 6176 | 8152 | 22550 | 5826 | 6562 |
| 39 | ptc-miR398c-3p | 6176 | 8152 | 22550 | 5826 | 6562 |
| 40 | rco-miR398b | 6176 | 8152 | 22550 | 5826 | 6562 |
| 41 | tcc-miR398a | 6176 | 8152 | 22550 | 5826 | 6562 |
| 42 | vvi-miR398b | 6176 | 8152 | 22550 | 5826 | 6562 |
| 43 | vvi-miR398c | 6176 | 8152 | 22550 | 5826 | 6562 |
| 44 | bdi-miR166e-3p | 380 | 323 | 1408 | 247 | 290 |
| 45 | ptc-miR169s | 400 | 865 | 603 | 371 | 338 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|-------|-------|-------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | aof-miR171b | 202 | 402 | 561 | 162 | 158 |
| 4 | fve-miR171f-3p | 202 | 402 | 561 | 162 | 158 |
| 5 | gma-miR171k-3p | 202 | 402 | 561 | 162 | 158 |
| 6 | lja-miR171d-5p | 202 | 402 | 561 | 162 | 158 |
| 7 | mdm-miR171j | 202 | 402 | 561 | 162 | 158 |
| 8 | mdm-miR171k | 202 | 402 | 561 | 162 | 158 |
| 9 | mdm-miR171l | 202 | 402 | 561 | 162 | 158 |
| 10 | mes-miR171e | 202 | 402 | 561 | 162 | 158 |
| 11 | nta-miR171b | 202 | 402 | 561 | 162 | 158 |
| 12 | pab-miR171b | 202 | 402 | 561 | 162 | 158 |
| 13 | pab-miR171c | 202 | 402 | 561 | 162 | 158 |
| 14 | ppe-miR171b | 202 | 402 | 561 | 162 | 158 |
| 15 | ssl-miR171b | 202 | 402 | 561 | 162 | 158 |
| 16 | vvi-miR171f | 202 | 402 | 561 | 162 | 158 |
| 17 | lja-miR1511-3p | 12708 | 10343 | 28977 | 6523 | 8375 |
| 18 | htu-miR171a | 21 | 50 | 99 | 36 | 17 |
| 19 | fve-miR167d | 1734 | 2867 | 4223 | 1487 | 1553 |
| 20 | lus-miR167a | 1609 | 2734 | 4204 | 1417 | 1469 |
| 21 | vvi-miR167c | 1609 | 2734 | 4204 | 1417 | 1469 |
| 22 | bna-miR167d | 1547 | 2691 | 4152 | 1384 | 1420 |
| 23 | fve-miR167a | 1547 | 2691 | 4152 | 1384 | 1420 |
| 24 | fve-miR167b | 1547 | 2691 | 4152 | 1384 | 1420 |
| 25 | fve-miR167c | 1547 | 2691 | 4152 | 1384 | 1420 |
| 26 | gma-miR167l | 1547 | 2691 | 4152 | 1384 | 1420 |
| 27 | lja-miR167a | 1547 | 2691 | 4152 | 1384 | 1420 |
| 28 | lja-miR167b | 1547 | 2691 | 4152 | 1384 | 1420 |
| 29 | lja-miR167c | 1547 | 2691 | 4152 | 1384 | 1420 |
| 30 | mes-miR167b | 1547 | 2691 | 4152 | 1384 | 1420 |
| 31 | ptc-miR390d-3p | 69 | 72 | 127 | 26 | 49 |
| 32 | sly-miR390a-3p | 69 | 72 | 127 | 26 | 49 |
| 33 | cme-miR166g | 322 | 277 | 935 | 199 | 221 |
| 34 | csi-miR166c-3p | 322 | 277 | 935 | 199 | 221 |
| 35 | gma-miR166p | 322 | 277 | 935 | 199 | 221 |
| 36 | gma-miR166q | 322 | 277 | 935 | 199 | 221 |
| 37 | gma-miR166r | 322 | 277 | 935 | 199 | 221 |
| 38 | gma-miR166s | 322 | 277 | 935 | 199 | 221 |
| 39 | gma-miR166t | 322 | 277 | 935 | 199 | 221 |
| 40 | sbi-miR166a | 322 | 277 | 935 | 199 | 221 |
| 41 | sbi-miR166b | 322 | 277 | 935 | 199 | 221 |
| 42 | sbi-miR166c | 322 | 277 | 935 | 199 | 221 |
| 43 | sbi-miR166d | 322 | 277 | 935 | 199 | 221 |
| 44 | sbi-miR166h | 322 | 277 | 935 | 199 | 221 |
| 45 | sbi-miR166i | 322 | 277 | 935 | 199 | 221 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|-----------------|------|------|-------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | sbi-miR166j | 322 | 277 | 935 | 199 | 221 |
| 4 | tcc-miR166b | 322 | 277 | 935 | 199 | 221 |
| 5 | zma-miR166b-3p | 322 | 277 | 935 | 199 | 221 |
| 6 | zma-miR166c-3p | 322 | 277 | 935 | 199 | 221 |
| 7 | zma-miR166d-3p | 322 | 277 | 935 | 199 | 221 |
| 8 | zma-miR166e | 322 | 277 | 935 | 199 | 221 |
| 9 | zma-miR166f | 322 | 277 | 935 | 199 | 221 |
| 10 | zma-miR166g-3p | 322 | 277 | 935 | 199 | 221 |
| 11 | zma-miR166h-3p | 322 | 277 | 935 | 199 | 221 |
| 12 | zma-miR166i-3p | 322 | 277 | 935 | 199 | 221 |
| 13 | eun-miR167b-3p | 464 | 825 | 474 | 344 | 315 |
| 14 | csi-miR167c-3p | 2180 | 2342 | 4079 | 1257 | 1598 |
| 15 | ppt-miR390c-5p | 244 | 380 | 768 | 230 | 183 |
| 16 | csi-miR390b-5p | 244 | 380 | 767 | 230 | 183 |
| 17 | gma-miR390e | 244 | 380 | 767 | 230 | 183 |
| 18 | eca-miR-378 | 53 | 77 | 105 | 70 | 35 |
| 19 | mml-miR-378a | 53 | 77 | 105 | 70 | 35 |
| 20 | mmu-miR-378a-3p | 53 | 77 | 105 | 70 | 35 |
| 21 | ptr-miR-378a | 53 | 77 | 105 | 70 | 35 |
| 22 | rno-miR-378a-3p | 53 | 77 | 105 | 70 | 35 |
| 23 | aof-miR167b | 4141 | 6388 | 13239 | 3318 | 3696 |
| 24 | ata-miR167b-5p | 4141 | 6388 | 13239 | 3318 | 3696 |
| 25 | ata-miR167d-5p | 4141 | 6388 | 13239 | 3318 | 3696 |
| 26 | bdi-miR167c-5p | 4141 | 6388 | 13239 | 3318 | 3696 |
| 27 | bdi-miR167d-5p | 4141 | 6388 | 13239 | 3318 | 3696 |
| 28 | bdi-miR167e-5p | 4141 | 6388 | 13239 | 3318 | 3696 |
| 29 | bdi-miR167g | 4141 | 6388 | 13239 | 3318 | 3696 |
| 30 | ccl-miR167a | 4141 | 6388 | 13239 | 3318 | 3696 |
| 31 | ccl-miR167b | 4141 | 6388 | 13239 | 3318 | 3696 |
| 32 | cpa-miR167d | 4141 | 6388 | 13239 | 3318 | 3696 |
| 33 | ctr-miR167 | 4141 | 6388 | 13239 | 3318 | 3696 |
| 34 | eun-miR167a-5p | 4141 | 6388 | 13239 | 3318 | 3696 |
| 35 | gma-miR167g | 4141 | 6388 | 13239 | 3318 | 3696 |
| 36 | mes-miR167d | 4141 | 6388 | 13239 | 3318 | 3696 |
| 37 | mes-miR167e | 4141 | 6388 | 13239 | 3318 | 3696 |
| 38 | mes-miR167f | 4141 | 6388 | 13239 | 3318 | 3696 |
| 39 | ppe-miR167c | 4141 | 6388 | 13239 | 3318 | 3696 |
| 40 | vca-miR167a-5p | 4141 | 6388 | 13239 | 3318 | 3696 |
| 41 | vca-miR167b-5p | 4141 | 6388 | 13239 | 3318 | 3696 |
| 42 | cpa-miR166d | 2329 | 1741 | 8028 | 1495 | 1533 |
| 43 | gma-miR166j-3p | 2329 | 1741 | 8028 | 1495 | 1533 |
| 44 | mes-miR160h | 8719 | 7677 | 23410 | 5160 | 4684 |
| 45 | crt-miR166a | 2333 | 1741 | 8038 | 1495 | 1535 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|-------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | mes-miR166h | 2333 | 1741 | 8038 | 1495 | 1535 |
| 4 | gma-miR390a-3p | 3229 | 3523 | 12001 | 2369 | 3052 |
| 5 | gma-miR390c | 3229 | 3523 | 12001 | 2369 | 3052 |
| 6 | mes-miR390 | 3229 | 3523 | 12001 | 2369 | 3052 |
| 7 | aly-miR390a-3p | 3489 | 3760 | 12662 | 2457 | 3259 |
| 8 | ath-miR390a-3p | 3489 | 3760 | 12662 | 2457 | 3259 |
| 9 | cas-miR390a-3p | 3489 | 3760 | 12662 | 2457 | 3259 |
| 10 | csi-miR390a-3p | 3489 | 3760 | 12662 | 2457 | 3259 |
| 11 | lja-miR390a-3p | 3489 | 3760 | 12662 | 2457 | 3259 |
| 12 | lja-miR390b-3p | 3489 | 3760 | 12662 | 2457 | 3259 |
| 13 | sly-miR390b-3p | 3489 | 3760 | 12662 | 2457 | 3259 |
| 14 | aly-miR160a-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 15 | aly-miR160b-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 16 | aly-miR160c-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 17 | aof-miR160c | 8586 | 7490 | 23233 | 5057 | 4547 |
| 18 | aqc-miR160b | 8586 | 7490 | 23233 | 5057 | 4547 |
| 19 | ata-miR160a-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 20 | ata-miR160b-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 21 | ata-miR160c-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 22 | ath-miR160a-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 23 | ath-miR160b | 8586 | 7490 | 23233 | 5057 | 4547 |
| 24 | ath-miR160c-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 25 | atr-miR160 | 8586 | 7490 | 23233 | 5057 | 4547 |
| 26 | bdi-miR160a-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 27 | bdi-miR160b-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 28 | bdi-miR160c-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 29 | bdi-miR160d-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 30 | bna-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 31 | bna-miR160b | 8586 | 7490 | 23233 | 5057 | 4547 |
| 32 | bna-miR160c | 8586 | 7490 | 23233 | 5057 | 4547 |
| 33 | bna-miR160d | 8586 | 7490 | 23233 | 5057 | 4547 |
| 34 | bra-miR160a-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 35 | cca-miR160b | 8586 | 7490 | 23233 | 5057 | 4547 |
| 36 | cme-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 37 | cme-miR160b | 8586 | 7490 | 23233 | 5057 | 4547 |
| 38 | cme-miR160c | 8586 | 7490 | 23233 | 5057 | 4547 |
| 39 | cpa-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 40 | cpa-miR160b | 8586 | 7490 | 23233 | 5057 | 4547 |
| 41 | cpa-miR160c-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 42 | cpa-miR160e | 8586 | 7490 | 23233 | 5057 | 4547 |
| 43 | cpa-miR160f-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 44 | eun-miR160-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 45 | far-miR160 | 8586 | 7490 | 23233 | 5057 | 4547 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|-------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | fve-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 4 | fve-miR160b | 8586 | 7490 | 23233 | 5057 | 4547 |
| 5 | gma-miR160a-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 6 | gma-miR160f | 8586 | 7490 | 23233 | 5057 | 4547 |
| 7 | gma-miR160f | 8586 | 7490 | 23233 | 5057 | 4547 |
| 8 | lus-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 9 | lus-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 10 | lus-miR160b | 8586 | 7490 | 23233 | 5057 | 4547 |
| 11 | lus-miR160d | 8586 | 7490 | 23233 | 5057 | 4547 |
| 12 | lus-miR160d | 8586 | 7490 | 23233 | 5057 | 4547 |
| 13 | lus-miR160e | 8586 | 7490 | 23233 | 5057 | 4547 |
| 14 | lus-miR160f | 8586 | 7490 | 23233 | 5057 | 4547 |
| 15 | lus-miR160h | 8586 | 7490 | 23233 | 5057 | 4547 |
| 16 | lus-miR160i | 8586 | 7490 | 23233 | 5057 | 4547 |
| 17 | lus-miR160i | 8586 | 7490 | 23233 | 5057 | 4547 |
| 18 | lus-miR160j | 8586 | 7490 | 23233 | 5057 | 4547 |
| 19 | mdm-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 20 | mdm-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 21 | mdm-miR160b | 8586 | 7490 | 23233 | 5057 | 4547 |
| 22 | mdm-miR160c | 8586 | 7490 | 23233 | 5057 | 4547 |
| 23 | mdm-miR160d | 8586 | 7490 | 23233 | 5057 | 4547 |
| 24 | mdm-miR160d | 8586 | 7490 | 23233 | 5057 | 4547 |
| 25 | mdm-miR160e | 8586 | 7490 | 23233 | 5057 | 4547 |
| 26 | mes-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 27 | mes-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 28 | mes-miR160b | 8586 | 7490 | 23233 | 5057 | 4547 |
| 29 | mes-miR160d | 8586 | 7490 | 23233 | 5057 | 4547 |
| 30 | mtr-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 31 | mtr-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 32 | mtr-miR160b | 8586 | 7490 | 23233 | 5057 | 4547 |
| 33 | mtr-miR160d | 8586 | 7490 | 23233 | 5057 | 4547 |
| 34 | mtr-miR160d | 8586 | 7490 | 23233 | 5057 | 4547 |
| 35 | mtr-miR160e | 8586 | 7490 | 23233 | 5057 | 4547 |
| 36 | nta-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 37 | nta-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 38 | nta-miR160b | 8586 | 7490 | 23233 | 5057 | 4547 |
| 39 | nta-miR160c | 8586 | 7490 | 23233 | 5057 | 4547 |
| 40 | osa-miR160a-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 41 | osa-miR160b-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 42 | osa-miR160c-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 43 | osa-miR160d-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 44 | osa-miR160d-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 45 | pab-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 46 | pab-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 47 | pab-miR160b | 8586 | 7490 | 23233 | 5057 | 4547 |
| 48 | pab-miR160d | 8586 | 7490 | 23233 | 5057 | 4547 |
| 49 | ppe-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 50 | ppe-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 51 | ppe-miR160b | 8586 | 7490 | 23233 | 5057 | 4547 |
| 52 | ppt-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 53 | ppt-miR160e | 8586 | 7490 | 23233 | 5057 | 4547 |
| 54 | ppt-miR160e | 8586 | 7490 | 23233 | 5057 | 4547 |
| 55 | ppt-miR160f | 8586 | 7490 | 23233 | 5057 | 4547 |
| 56 | ptc-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 57 | ptc-miR160b-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 58 | ptc-miR160c-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 59 | ptc-miR160d | 8586 | 7490 | 23233 | 5057 | 4547 |
| 60 | ptc-miR160d | 8586 | 7490 | 23233 | 5057 | 4547 |

| | | | | | | |
|----|----------------|------|------|-------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | rco-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 4 | rco-miR160b | 8586 | 7490 | 23233 | 5057 | 4547 |
| 5 | sbi-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 6 | sbi-miR160b | 8586 | 7490 | 23233 | 5057 | 4547 |
| 7 | sbi-miR160c | 8586 | 7490 | 23233 | 5057 | 4547 |
| 8 | sbi-miR160d | 8586 | 7490 | 23233 | 5057 | 4547 |
| 9 | sbi-miR160e | 8586 | 7490 | 23233 | 5057 | 4547 |
| 10 | sly-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 11 | smo-miR160a | 8586 | 7490 | 23233 | 5057 | 4547 |
| 12 | smo-miR160b | 8586 | 7490 | 23233 | 5057 | 4547 |
| 13 | stu-miR160a-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 14 | stu-miR160b | 8586 | 7490 | 23233 | 5057 | 4547 |
| 15 | tae-miR160 | 8586 | 7490 | 23233 | 5057 | 4547 |
| 16 | tcc-miR160b | 8586 | 7490 | 23233 | 5057 | 4547 |
| 17 | ttu-miR160 | 8586 | 7490 | 23233 | 5057 | 4547 |
| 18 | vun-miR160 | 8586 | 7490 | 23233 | 5057 | 4547 |
| 19 | vvi-miR160c | 8586 | 7490 | 23233 | 5057 | 4547 |
| 20 | vvi-miR160d | 8586 | 7490 | 23233 | 5057 | 4547 |
| 21 | vvi-miR160e | 8586 | 7490 | 23233 | 5057 | 4547 |
| 22 | zma-miR160a-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 23 | zma-miR160b-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 24 | zma-miR160c-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 25 | zma-miR160d-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 26 | zma-miR160e | 8586 | 7490 | 23233 | 5057 | 4547 |
| 27 | zma-miR160g-5p | 8586 | 7490 | 23233 | 5057 | 4547 |
| 28 | mes-miR160g | 8613 | 7512 | 23314 | 5065 | 4566 |
| 29 | cas-miR166e | 450 | 435 | 1699 | 337 | 287 |
| 30 | csi-miR166f-3p | 450 | 435 | 1699 | 337 | 287 |
| 31 | osa-miR166m | 450 | 435 | 1699 | 337 | 287 |
| 32 | crt-miR166b | 450 | 439 | 1702 | 337 | 288 |
| 33 | ata-miR167f-5p | 3638 | 5641 | 12623 | 2961 | 3288 |
| 34 | tae-miR167c-5p | 3638 | 5641 | 12623 | 2961 | 3288 |
| 35 | aof-miR167c | 3574 | 5613 | 12595 | 2914 | 3256 |
| 36 | atr-miR167 | 3574 | 5613 | 12595 | 2914 | 3256 |
| 37 | cme-miR167d | 3574 | 5613 | 12595 | 2914 | 3256 |
| 38 | cme-miR167f | 3574 | 5613 | 12595 | 2914 | 3256 |
| 39 | csi-miR167a-5p | 3574 | 5613 | 12595 | 2914 | 3256 |
| 40 | csi-miR167c-5p | 3574 | 5613 | 12595 | 2914 | 3256 |
| 41 | dpr-miR167c | 3574 | 5613 | 12595 | 2914 | 3256 |
| 42 | gma-miR167c | 3574 | 5613 | 12595 | 2914 | 3256 |
| 43 | gma-miR167j | 3574 | 5613 | 12595 | 2914 | 3256 |
| 44 | gso-miR167a | 3574 | 5613 | 12595 | 2914 | 3256 |
| 45 | lja-miR167 | 3574 | 5613 | 12595 | 2914 | 3256 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|-------|------|------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | lus-miR167f | 3574 | 5613 | 12595 | 2914 | 3256 |
| 4 | lus-miR167g | 3574 | 5613 | 12595 | 2914 | 3256 |
| 5 | lus-miR167i | 3574 | 5613 | 12595 | 2914 | 3256 |
| 6 | mes-miR167a | 3574 | 5613 | 12595 | 2914 | 3256 |
| 7 | mes-miR167a | 3574 | 5613 | 12595 | 2914 | 3256 |
| 8 | mtr-miR167b-5p | 3574 | 5613 | 12595 | 2914 | 3256 |
| 9 | mtr-miR167b-5p | 3574 | 5613 | 12595 | 2914 | 3256 |
| 10 | osa-miR167d-5p | 3574 | 5613 | 12595 | 2914 | 3256 |
| 11 | osa-miR167e-5p | 3574 | 5613 | 12595 | 2914 | 3256 |
| 12 | osa-miR167e-5p | 3574 | 5613 | 12595 | 2914 | 3256 |
| 13 | osa-miR167f | 3574 | 5613 | 12595 | 2914 | 3256 |
| 14 | osa-miR167g | 3574 | 5613 | 12595 | 2914 | 3256 |
| 15 | osa-miR167h-5p | 3574 | 5613 | 12595 | 2914 | 3256 |
| 16 | osa-miR167i-5p | 3574 | 5613 | 12595 | 2914 | 3256 |
| 17 | osa-miR167i-5p | 3574 | 5613 | 12595 | 2914 | 3256 |
| 18 | osa-miR167j | 3574 | 5613 | 12595 | 2914 | 3256 |
| 19 | ptc-miR167e | 3574 | 5613 | 12595 | 2914 | 3256 |
| 20 | ptc-miR167e | 3574 | 5613 | 12595 | 2914 | 3256 |
| 21 | sbi-miR167c | 3574 | 5613 | 12595 | 2914 | 3256 |
| 22 | sbi-miR167d | 3574 | 5613 | 12595 | 2914 | 3256 |
| 23 | sbi-miR167e | 3574 | 5613 | 12595 | 2914 | 3256 |
| 24 | sbi-miR167e | 3574 | 5613 | 12595 | 2914 | 3256 |
| 25 | sbi-miR167f | 3574 | 5613 | 12595 | 2914 | 3256 |
| 26 | sbi-miR167g | 3574 | 5613 | 12595 | 2914 | 3256 |
| 27 | sbi-miR167g | 3574 | 5613 | 12595 | 2914 | 3256 |
| 28 | sbi-miR167h | 3574 | 5613 | 12595 | 2914 | 3256 |
| 29 | sof-miR167a | 3574 | 5613 | 12595 | 2914 | 3256 |
| 30 | sof-miR167b | 3574 | 5613 | 12595 | 2914 | 3256 |
| 31 | sof-miR167b | 3574 | 5613 | 12595 | 2914 | 3256 |
| 32 | ssp-miR167b | 3574 | 5613 | 12595 | 2914 | 3256 |
| 33 | vvi-miR167a | 3574 | 5613 | 12595 | 2914 | 3256 |
| 34 | zma-miR167e-5p | 3574 | 5613 | 12595 | 2914 | 3256 |
| 35 | zma-miR167f-5p | 3574 | 5613 | 12595 | 2914 | 3256 |
| 36 | zma-miR167g-5p | 3574 | 5613 | 12595 | 2914 | 3256 |
| 37 | zma-miR167g-5p | 3574 | 5613 | 12595 | 2914 | 3256 |
| 38 | zma-miR167h-5p | 3574 | 5613 | 12595 | 2914 | 3256 |
| 39 | zma-miR167i-5p | 3574 | 5613 | 12595 | 2914 | 3256 |
| 40 | zma-miR167j-5p | 3574 | 5613 | 12595 | 2914 | 3256 |
| 41 | zma-miR167j-5p | 3574 | 5613 | 12595 | 2914 | 3256 |
| 42 | aly-miR166g-5p | 700 | 800 | 69 | 148 | 435 |
| 43 | cas-miR166f-5p | 700 | 800 | 69 | 148 | 435 |
| 44 | cas-miR166f-5p | 700 | 800 | 69 | 148 | 435 |
| 45 | csi-miR166b-5p | 700 | 800 | 69 | 148 | 435 |
| 46 | gma-miR166h-5p | 700 | 800 | 69 | 148 | 435 |
| 47 | gma-miR166j-5p | 700 | 800 | 69 | 148 | 435 |
| 48 | gma-miR166j-5p | 700 | 800 | 69 | 148 | 435 |
| 49 | stu-miR166c-5p | 700 | 800 | 69 | 148 | 435 |
| 50 | aly-miR390a-5p | 1490 | 1960 | 3675 | 965 | 866 |
| 51 | aly-miR390b-5p | 1490 | 1960 | 3675 | 965 | 866 |
| 52 | aof-miR390 | 1490 | 1960 | 3675 | 965 | 866 |
| 53 | ata-miR390-5p | 1490 | 1960 | 3675 | 965 | 866 |
| 54 | ata-miR390-5p | 1490 | 1960 | 3675 | 965 | 866 |
| 55 | ath-miR390a-5p | 1490 | 1960 | 3675 | 965 | 866 |
| 56 | ath-miR390b-5p | 1490 | 1960 | 3675 | 965 | 866 |
| 57 | ath-miR390b-5p | 1490 | 1960 | 3675 | 965 | 866 |
| 58 | atr-miR390.2 | 1490 | 1960 | 3675 | 965 | 866 |
| 59 | bdi-miR390a-5p | 1490 | 1960 | 3675 | 965 | 866 |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | bna-miR390a | 1490 | 1960 | 3675 | 965 | 866 |
| 4 | bna-miR390b | 1490 | 1960 | 3675 | 965 | 866 |
| 5 | bna-miR390c | 1490 | 1960 | 3675 | 965 | 866 |
| 6 | bra-miR390-5p | 1490 | 1960 | 3675 | 965 | 866 |
| 7 | cas-miR390a-5p | 1490 | 1960 | 3675 | 965 | 866 |
| 8 | cas-miR390b | 1490 | 1960 | 3675 | 965 | 866 |
| 9 | cme-miR390a | 1490 | 1960 | 3675 | 965 | 866 |
| 10 | cme-miR390b | 1490 | 1960 | 3675 | 965 | 866 |
| 11 | cme-miR390c | 1490 | 1960 | 3675 | 965 | 866 |
| 12 | cme-miR390d | 1490 | 1960 | 3675 | 965 | 866 |
| 13 | cpa-miR390a | 1490 | 1960 | 3675 | 965 | 866 |
| 14 | cpa-miR390b | 1490 | 1960 | 3675 | 965 | 866 |
| 15 | csi-miR390a-5p | 1490 | 1960 | 3675 | 965 | 866 |
| 16 | fve-miR390a | 1490 | 1960 | 3675 | 965 | 866 |
| 17 | fve-miR390b | 1490 | 1960 | 3675 | 965 | 866 |
| 18 | ghr-miR390a | 1490 | 1960 | 3675 | 965 | 866 |
| 19 | ghr-miR390b | 1490 | 1960 | 3675 | 965 | 866 |
| 20 | ghr-miR390c | 1490 | 1960 | 3675 | 965 | 866 |
| 21 | gma-miR390a-5p | 1490 | 1960 | 3675 | 965 | 866 |
| 22 | gma-miR390f | 1490 | 1960 | 3675 | 965 | 866 |
| 23 | gma-miR390g | 1490 | 1960 | 3675 | 965 | 866 |
| 24 | hex-miR390a | 1490 | 1960 | 3675 | 965 | 866 |
| 25 | hex-miR390b | 1490 | 1960 | 3675 | 965 | 866 |
| 26 | lja-miR390a-5p | 1490 | 1960 | 3675 | 965 | 866 |
| 27 | lja-miR390b-5p | 1490 | 1960 | 3675 | 965 | 866 |
| 28 | lus-miR390a | 1490 | 1960 | 3675 | 965 | 866 |
| 29 | lus-miR390b | 1490 | 1960 | 3675 | 965 | 866 |
| 30 | lus-miR390c | 1490 | 1960 | 3675 | 965 | 866 |
| 31 | lus-miR390d | 1490 | 1960 | 3675 | 965 | 866 |
| 32 | mdm-miR390a | 1490 | 1960 | 3675 | 965 | 866 |
| 33 | mdm-miR390b | 1490 | 1960 | 3675 | 965 | 866 |
| 34 | mdm-miR390c | 1490 | 1960 | 3675 | 965 | 866 |
| 35 | mdm-miR390d | 1490 | 1960 | 3675 | 965 | 866 |
| 36 | mdm-miR390e | 1490 | 1960 | 3675 | 965 | 866 |
| 37 | mdm-miR390f | 1490 | 1960 | 3675 | 965 | 866 |
| 38 | mes-miR390b | 1490 | 1960 | 3675 | 965 | 866 |
| 39 | mtr-miR390 | 1490 | 1960 | 3675 | 965 | 866 |
| 40 | nta-miR390b | 1490 | 1960 | 3675 | 965 | 866 |
| 41 | nta-miR390c | 1490 | 1960 | 3675 | 965 | 866 |
| 42 | osa-miR390-5p | 1490 | 1960 | 3675 | 965 | 866 |
| 43 | pab-miR390a | 1490 | 1960 | 3675 | 965 | 866 |
| 44 | pab-miR390b | 1490 | 1960 | 3675 | 965 | 866 |
| 45 | ppe-miR390 | 1490 | 1960 | 3675 | 965 | 866 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|------|------|------|-----|-----|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | ppt-miR390a | 1490 | 1960 | 3675 | 965 | 866 |
| 4 | ppt-miR390b | 1490 | 1960 | 3675 | 965 | 866 |
| 5 | ptc-miR390a | 1490 | 1960 | 3675 | 965 | 866 |
| 6 | ptc-miR390b | 1490 | 1960 | 3675 | 965 | 866 |
| 7 | ptc-miR390c | 1490 | 1960 | 3675 | 965 | 866 |
| 8 | ptc-miR390d-5p | 1490 | 1960 | 3675 | 965 | 866 |
| 9 | rco-miR390a | 1490 | 1960 | 3675 | 965 | 866 |
| 10 | rco-miR390b | 1490 | 1960 | 3675 | 965 | 866 |
| 11 | sbi-miR390 | 1490 | 1960 | 3675 | 965 | 866 |
| 12 | sly-miR390b-5p | 1490 | 1960 | 3675 | 965 | 866 |
| 13 | tcc-miR390a | 1490 | 1960 | 3675 | 965 | 866 |
| 14 | tcc-miR390b | 1490 | 1960 | 3675 | 965 | 866 |
| 15 | vvi-miR390 | 1490 | 1960 | 3675 | 965 | 866 |
| 16 | zma-miR390a-5p | 1490 | 1960 | 3675 | 965 | 866 |
| 17 | zma-miR390b-5p | 1490 | 1960 | 3675 | 965 | 866 |
| 18 | csi-miR160a-5p | 35 | 24 | 336 | 24 | 15 |
| 19 | pab-miR166j | 76 | 50 | 1329 | 38 | 57 |
| 20 | mes-miR166i | 15 | 10 | 174 | 5 | 15 |
| 21 | gma-miR166m | 69 | 36 | 1299 | 29 | 44 |
| 22 | mtr-miR166e-5p | 206 | 672 | 52 | 93 | 201 |
| 23 | osa-miR166h-5p | 206 | 672 | 52 | 93 | 201 |
| 24 | zma-miR166m-5p | 206 | 672 | 52 | 93 | 201 |
| 25 | aly-miR168a-3p | 434 | 484 | 5046 | 334 | 647 |
| 26 | ath-miR168a-3p | 434 | 484 | 5046 | 334 | 647 |
| 27 | bra-miR168b-3p | 434 | 484 | 5046 | 334 | 647 |
| 28 | bra-miR168c-3p | 434 | 484 | 5046 | 334 | 647 |
| 29 | cas-miR168 | 434 | 484 | 5046 | 334 | 647 |
| 30 | csi-miR168-3p | 434 | 484 | 5046 | 334 | 647 |
| 31 | fve-miR168-3p | 434 | 484 | 5046 | 334 | 647 |
| 32 | mtr-miR168c-3p | 434 | 484 | 5046 | 334 | 647 |
| 33 | ptc-miR168a-3p | 434 | 484 | 5046 | 334 | 647 |
| 34 | ptc-miR168b-3p | 434 | 484 | 5046 | 334 | 647 |
| 35 | sly-miR168b-3p | 434 | 484 | 5046 | 334 | 647 |
| 36 | lja-miR168-3p | 436 | 488 | 5067 | 335 | 648 |
| 37 | aof-miR166c | 5 | 6 | 1623 | 3 | 11 |
| 38 | ath-miR165a-3p | 5 | 6 | 1623 | 3 | 11 |
| 39 | ath-miR165b | 5 | 6 | 1623 | 3 | 11 |
| 40 | bna-miR166f | 5 | 6 | 1623 | 3 | 11 |
| 41 | cas-miR165a | 5 | 6 | 1623 | 3 | 11 |
| 42 | lus-miR166b | 5 | 6 | 1623 | 3 | 11 |
| 43 | gmo-miR-451-5p | 12 | 192 | 761 | 11 | 7 |
| 44 | cfa-miR-375 | 0 | 0 | 477 | 0 | 0 |
| 45 | cpo-miR-375-3p | 0 | 0 | 477 | 0 | 0 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | |
|----|----------------|---|-----|-----|---|---|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | dno-miR-375-3p | 0 | 0 | 477 | 0 | 0 |
| 4 | ggo-miR-375 | 0 | 0 | 477 | 0 | 0 |
| 5 | hsa-miR-375-3p | 0 | 0 | 477 | 0 | 0 |
| 6 | mml-miR-375 | 0 | 0 | 477 | 0 | 0 |
| 7 | mmu-miR-375-3p | 0 | 0 | 477 | 0 | 0 |
| 8 | ocu-miR-375-3p | 0 | 0 | 477 | 0 | 0 |
| 9 | pal-miR-375-3p | 0 | 0 | 477 | 0 | 0 |
| 10 | ppy-miR-375 | 0 | 0 | 477 | 0 | 0 |
| 11 | ptr-miR-375 | 0 | 0 | 477 | 0 | 0 |
| 12 | rno-miR-375-3p | 0 | 0 | 477 | 0 | 0 |
| 13 | ssc-miR-375 | 0 | 0 | 477 | 0 | 0 |
| 14 | bta-miR-375 | 0 | 0 | 486 | 0 | 0 |
| 15 | efu-miR-375 | 0 | 0 | 486 | 0 | 0 |
| 16 | mdo-miR-375 | 0 | 0 | 486 | 0 | 0 |
| 17 | aae-miR-184 | 1 | 352 | 0 | 0 | 1 |
| 18 | abu-miR-184a | 1 | 352 | 0 | 0 | 1 |
| 19 | ame-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| 20 | api-miR-184a | 1 | 352 | 0 | 0 | 1 |
| 21 | bbe-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| 22 | bdo-miR-184 | 1 | 352 | 0 | 0 | 1 |
| 23 | bmo-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| 24 | ccr-miR-184 | 1 | 352 | 0 | 0 | 1 |
| 25 | cin-miR-184 | 1 | 352 | 0 | 0 | 1 |
| 26 | cqu-miR-184 | 1 | 352 | 0 | 0 | 1 |
| 27 | cte-miR-184a | 1 | 352 | 0 | 0 | 1 |
| 28 | dan-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| 29 | der-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| 30 | dgr-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| 31 | dme-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| 32 | dmo-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| 33 | dpe-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| 34 | dps-miR-184 | 1 | 352 | 0 | 0 | 1 |
| 35 | dre-miR-184 | 1 | 352 | 0 | 0 | 1 |
| 36 | dse-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| 37 | dsi-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| 38 | dvi-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| 39 | dwi-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| 40 | dya-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| 41 | hme-miR-184 | 1 | 352 | 0 | 0 | 1 |
| 42 | ipu-miR-184 | 1 | 352 | 0 | 0 | 1 |
| 43 | isc-miR-184 | 1 | 352 | 0 | 0 | 1 |
| 44 | lgi-miR-184 | 1 | 352 | 0 | 0 | 1 |
| 45 | lva-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | | | |
|-----------------|---|-----|---|---|---|
| mle-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| mse-miR-184 | 1 | 352 | 0 | 0 | 1 |
| mze-miR-184a | 1 | 352 | 0 | 0 | 1 |
| nbr-miR-184a | 1 | 352 | 0 | 0 | 1 |
| ngi-miR-184 | 1 | 352 | 0 | 0 | 1 |
| nlo-miR-184 | 1 | 352 | 0 | 0 | 1 |
| nvi-miR-184 | 1 | 352 | 0 | 0 | 1 |
| oni-miR-184a | 1 | 352 | 0 | 0 | 1 |
| pca-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| pmi-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| pony-miR-184a | 1 | 352 | 0 | 0 | 1 |
| pte-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| sko-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| spu-miR-184 | 1 | 352 | 0 | 0 | 1 |
| tca-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| tcf-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| tur-miR-184-3p | 1 | 352 | 0 | 0 | 1 |
| aae-miR-2940-3p | 0 | 673 | 2 | 0 | 0 |

Do not distribute

| | | | | | | | |
|----|-----|-----|-----|-----|----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 4 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 5 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 6 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 7 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 8 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 9 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 10 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 11 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 12 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 13 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 14 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 15 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 16 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 17 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 18 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 19 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 20 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 21 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 22 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 23 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 24 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 25 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 26 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 27 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 28 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 29 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 30 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 31 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 32 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 33 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 34 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 35 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 36 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 37 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 38 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 39 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 40 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 41 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 42 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 43 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 44 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 45 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 46 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 47 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 48 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 49 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 50 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 51 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 52 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 53 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 54 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 55 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 56 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 57 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 58 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 59 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-----|-----|------|----|-----|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 4 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 5 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 6 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 7 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 8 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 9 | 390 | 430 | 793 | 198 | 53 | 135 | 184 |
| 10 | 391 | 434 | 793 | 201 | 53 | 135 | 184 |
| 11 | 779 | 77 | 366 | 3498 | 86 | 89 | 367 |
| 12 | 779 | 77 | 366 | 3498 | 86 | 89 | 367 |
| 13 | 779 | 77 | 366 | 3498 | 86 | 89 | 367 |
| 14 | 779 | 77 | 366 | 3498 | 86 | 89 | 367 |
| 15 | 779 | 77 | 366 | 3498 | 86 | 89 | 367 |
| 16 | 779 | 77 | 366 | 3498 | 86 | 89 | 367 |
| 17 | 779 | 77 | 366 | 3498 | 86 | 89 | 367 |
| 18 | 779 | 77 | 366 | 3498 | 86 | 89 | 367 |
| 19 | 779 | 77 | 366 | 3498 | 86 | 89 | 367 |
| 20 | 779 | 77 | 366 | 3498 | 86 | 89 | 367 |
| 21 | 779 | 77 | 366 | 3498 | 86 | 89 | 367 |
| 22 | 779 | 77 | 366 | 3498 | 86 | 89 | 367 |
| 23 | 574 | 30 | 346 | 2036 | 31 | 24 | 271 |
| 24 | 574 | 30 | 346 | 2036 | 31 | 24 | 271 |
| 25 | 574 | 30 | 346 | 2036 | 31 | 24 | 271 |
| 26 | 574 | 30 | 346 | 2036 | 31 | 24 | 271 |
| 27 | 574 | 30 | 346 | 2036 | 31 | 24 | 271 |
| 28 | 574 | 30 | 346 | 2036 | 31 | 24 | 271 |
| 29 | 574 | 30 | 346 | 2036 | 31 | 24 | 271 |
| 30 | 574 | 30 | 346 | 2036 | 31 | 24 | 271 |
| 31 | 574 | 30 | 346 | 2036 | 31 | 24 | 271 |
| 32 | 574 | 30 | 346 | 2036 | 31 | 24 | 271 |
| 33 | 574 | 30 | 346 | 2036 | 31 | 24 | 271 |
| 34 | 574 | 30 | 346 | 2036 | 31 | 24 | 271 |
| 35 | 574 | 30 | 346 | 2036 | 31 | 24 | 271 |
| 36 | 574 | 30 | 346 | 2036 | 31 | 24 | 271 |
| 37 | 574 | 30 | 346 | 2036 | 31 | 24 | 271 |
| 38 | 574 | 30 | 346 | 2036 | 31 | 24 | 271 |
| 39 | 5568 | 0 | 0 | 1 | 0 | 0 | 2627 |
| 40 | 5136 | 0 | 0 | 1 | 0 | 0 | 2423 |
| 41 | 2181 | 0 | 0 | 1 | 0 | 0 | 1029 |
| 42 | 1803 | 0 | 0 | 0 | 0 | 0 | 850 |
| 43 | 1599 | 0 | 0 | 0 | 0 | 0 | 754 |
| 44 | 1591 | 0 | 0 | 0 | 0 | 0 | 750 |
| 45 | 1294 | 0 | 0 | 1 | 0 | 0 | 610 |
| 46 | 1102 | 0 | 0 | 0 | 0 | 0 | 520 |
| 47 | 396 | 0 | 0 | 0 | 0 | 0 | 187 |
| 48 | 393 | 0 | 0 | 0 | 0 | 0 | 185 |
| 49 | 336 | 0 | 0 | 1 | 0 | 0 | 158 |
| 50 | 308 | 0 | 0 | 1 | 0 | 0 | 145 |
| 51 | 9770 | 0 | 0 | 2 | 0 | 0 | 4609 |
| 52 | 16301 | 0 | 0 | 6 | 0 | 0 | 7689 |
| 53 | 26912 | 0 | 0 | 12 | 0 | 0 | 12695 |
| 54 | 6438 | 0 | 0 | 2 | 0 | 0 | 3037 |
| 55 | | | | | | | |
| 56 | | | | | | | |
| 57 | | | | | | | |
| 58 | | | | | | | |
| 59 | | | | | | | |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|---|---|----|---|----|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 4629 | 0 | 0 | 2 | 0 | 0 | 2184 |
| 4 | 3487 | 0 | 0 | 2 | 0 | 0 | 1645 |
| 5 | 1308 | 0 | 0 | 3 | 0 | 0 | 617 |
| 6 | 1809 | 3 | 7 | 10 | 5 | 3 | 853 |
| 7 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 8 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 9 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 10 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 11 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 12 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 13 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 14 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 15 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 16 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 17 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 18 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 19 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 20 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 21 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 22 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 23 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 24 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 25 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 26 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 27 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 28 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 29 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 30 | 422 | 0 | 3 | 3 | 2 | 2 | 199 |
| 31 | 615 | 3 | 7 | 6 | 4 | 3 | 290 |
| 32 | 483 | 2 | 5 | 4 | 3 | 3 | 228 |
| 33 | 1613 | 5 | 3 | 44 | 5 | 10 | 761 |
| 34 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 35 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 36 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 37 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 38 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 39 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 40 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 41 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 42 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 43 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 44 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 45 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 46 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 47 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 48 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 49 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 50 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 51 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 52 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 53 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 54 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 55 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 56 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 57 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 58 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 59 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|----|----|----|----|----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 4 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 5 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 6 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 7 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 8 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 9 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 10 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 11 | 1612 | 5 | 3 | 44 | 5 | 10 | 760 |
| 12 | 1618 | 5 | 3 | 45 | 5 | 10 | 763 |
| 13 | 1759 | 13 | 37 | 17 | 10 | 10 | 830 |
| 14 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 15 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 16 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 17 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 18 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 19 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 20 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 21 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 22 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 23 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 24 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 25 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 26 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 27 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 28 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 29 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 30 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 31 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 32 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 33 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 34 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 35 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 36 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 37 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 38 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 39 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 40 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 41 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 42 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 43 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 44 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 45 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 46 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 47 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 48 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 49 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 50 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 51 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 52 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 53 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 54 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 55 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 56 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 57 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 58 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 59 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|----|----|----|----|----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 4 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 5 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 6 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 7 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 8 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 9 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 10 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 11 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 12 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 13 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 14 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 15 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 16 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 17 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 18 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 19 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 20 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 21 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 22 | 1758 | 13 | 37 | 17 | 10 | 10 | 829 |
| 23 | 442 | 5 | 1 | 23 | 8 | 3 | 208 |
| 24 | 442 | 5 | 1 | 23 | 8 | 3 | 208 |
| 25 | 442 | 5 | 1 | 23 | 8 | 3 | 208 |
| 26 | 442 | 5 | 1 | 23 | 8 | 3 | 208 |
| 27 | 442 | 5 | 1 | 23 | 8 | 3 | 208 |
| 28 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 29 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 30 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 31 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 32 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 33 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 34 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 35 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 36 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 37 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 38 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 39 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 40 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 41 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 42 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 43 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 44 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 45 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 46 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 47 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 48 | 305 | 5 | 1 | 16 | 6 | 2 | 144 |
| 49 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 50 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 51 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 52 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 53 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 54 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 55 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 56 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 57 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 58 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 59 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|----|-----|----|-----|----|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 4 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 5 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 6 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 7 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 8 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 9 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 10 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 11 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 12 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 13 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 14 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 15 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 16 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 17 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 18 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 19 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 20 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 21 | 401 | 7 | 7 | 17 | 4 | 8 | 189 |
| 22 | 431 | 7 | 7 | 18 | 4 | 8 | 203 |
| 23 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 24 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 25 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 26 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 27 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 28 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 29 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 30 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 31 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 32 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 33 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 34 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 35 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 36 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 37 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 38 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 39 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 40 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 41 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 42 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 43 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 44 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 45 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 46 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 47 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 48 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 49 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 50 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 51 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 52 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 53 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 54 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 55 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 56 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 57 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 58 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 59 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|-----|-----|-----|-----|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 4609 | 87 | 248 | 39 | 109 | 80 | 2174 |
| 4 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 5 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 6 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 7 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 8 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 9 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 10 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 11 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 12 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 13 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 14 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 15 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 16 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 17 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 18 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 19 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 20 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 21 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 22 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 23 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 24 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 25 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 26 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 27 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 28 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 29 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 30 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 31 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 32 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 33 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 34 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 35 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 36 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 37 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 38 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 39 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 40 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 41 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 42 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 43 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 44 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 45 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 46 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 47 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 48 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 49 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 50 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 51 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 52 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 53 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 54 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 55 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 56 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 57 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 58 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 59 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|-----|-----|-----|-----|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 4 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 5 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 6 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 7 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 8 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 9 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 10 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 11 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 12 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 13 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 14 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 15 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 16 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 17 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 18 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 19 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 20 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 21 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 22 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 23 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 24 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 25 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 26 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 27 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 28 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 29 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 30 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 31 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 32 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 33 | 7427 | 235 | 288 | 237 | 256 | 224 | 3503 |
| 34 | 7549 | 238 | 292 | 245 | 263 | 229 | 3561 |
| 35 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 36 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 37 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 38 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 39 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 40 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 41 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 42 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 43 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 44 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 45 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 46 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 47 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 48 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 49 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 50 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 51 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 52 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 53 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 54 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 55 | 314 | 35 | 4 | 4 | 19 | 44 | 148 |
| 56 | 1722 | 62 | 13 | 111 | 60 | 54 | 812 |
| 57 | 1714 | 62 | 13 | 111 | 60 | 54 | 809 |
| 58 | 1714 | 62 | 13 | 111 | 60 | 54 | 809 |
| 59 | 1714 | 62 | 13 | 111 | 60 | 54 | 809 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|-----|-----|-----|-----|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 1714 | 62 | 13 | 111 | 60 | 54 | 809 |
| 4 | 1714 | 62 | 13 | 111 | 60 | 54 | 809 |
| 5 | 1714 | 62 | 13 | 111 | 60 | 54 | 809 |
| 6 | 1714 | 62 | 13 | 111 | 60 | 54 | 809 |
| 7 | 1714 | 62 | 13 | 111 | 60 | 54 | 809 |
| 8 | 1714 | 62 | 13 | 111 | 60 | 54 | 809 |
| 9 | 1714 | 62 | 13 | 111 | 60 | 54 | 809 |
| 10 | 370 | 41 | 5 | 4 | 28 | 50 | 175 |
| 11 | 370 | 41 | 5 | 4 | 28 | 50 | 175 |
| 12 | 370 | 41 | 5 | 4 | 28 | 50 | 175 |
| 13 | 370 | 41 | 5 | 4 | 28 | 50 | 175 |
| 14 | 370 | 41 | 5 | 4 | 28 | 50 | 175 |
| 15 | 370 | 41 | 5 | 4 | 28 | 50 | 175 |
| 16 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 17 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 18 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 19 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 20 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 21 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 22 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 23 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 24 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 25 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 26 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 27 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 28 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 29 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 30 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 31 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 32 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 33 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 34 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 35 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 36 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 37 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 38 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 39 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 40 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 41 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 42 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 43 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 44 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 45 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 46 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 47 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 48 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 49 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 50 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 51 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 52 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 53 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 54 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 55 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 56 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 57 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 58 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 59 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|-----|-----|-----|-----|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 4 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 5 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 6 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 7 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 8 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 9 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 10 | 5779 | 236 | 214 | 211 | 210 | 220 | 2726 |
| 11 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 12 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 13 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 14 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 15 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 16 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 17 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 18 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 19 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 20 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 21 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 22 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 23 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 24 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 25 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 26 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 27 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 28 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 29 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 30 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 31 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 32 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 33 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 34 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 35 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 36 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 37 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 38 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 39 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 40 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 41 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 42 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 43 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 44 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 45 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 46 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 47 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 48 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 49 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 50 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 51 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 52 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 53 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 54 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 55 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 56 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 57 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 58 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 59 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|-----|-----|-----|----|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 1311 | 52 | 12 | 95 | 44 | 47 | 618 |
| 4 | 714 | 25 | 27 | 37 | 34 | 23 | 337 |
| 5 | 714 | 25 | 27 | 37 | 34 | 23 | 337 |
| 6 | 714 | 25 | 27 | 37 | 34 | 23 | 337 |
| 7 | 714 | 25 | 27 | 37 | 34 | 23 | 337 |
| 8 | 714 | 25 | 27 | 37 | 34 | 23 | 337 |
| 9 | 714 | 25 | 27 | 37 | 34 | 23 | 337 |
| 10 | 714 | 25 | 27 | 37 | 34 | 23 | 337 |
| 11 | 714 | 25 | 27 | 37 | 34 | 23 | 337 |
| 12 | 597 | 28 | 0 | 45 | 11 | 13 | 282 |
| 13 | 597 | 28 | 0 | 45 | 11 | 13 | 282 |
| 14 | 597 | 28 | 0 | 45 | 11 | 13 | 282 |
| 15 | 597 | 28 | 0 | 45 | 11 | 13 | 282 |
| 16 | 597 | 28 | 0 | 45 | 11 | 13 | 282 |
| 17 | 597 | 28 | 0 | 45 | 11 | 13 | 282 |
| 18 | 597 | 28 | 0 | 45 | 11 | 13 | 282 |
| 19 | 597 | 28 | 0 | 45 | 11 | 13 | 282 |
| 20 | 597 | 28 | 0 | 45 | 11 | 13 | 282 |
| 21 | 597 | 28 | 0 | 45 | 11 | 13 | 282 |
| 22 | 597 | 28 | 0 | 45 | 11 | 13 | 282 |
| 23 | 597 | 28 | 0 | 45 | 11 | 13 | 282 |
| 24 | 597 | 28 | 0 | 45 | 11 | 13 | 282 |
| 25 | 597 | 28 | 0 | 45 | 11 | 13 | 282 |
| 26 | 1471 | 77 | 54 | 85 | 66 | 72 | 694 |
| 27 | 1471 | 77 | 54 | 85 | 66 | 72 | 694 |
| 28 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 29 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 30 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 31 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 32 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 33 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 34 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 35 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 36 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 37 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 38 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 39 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 40 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 41 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 42 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 43 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 44 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 45 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 46 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 47 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 48 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 49 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 50 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 51 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 52 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 53 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 54 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 55 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 56 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 57 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 58 | 1463 | 77 | 54 | 85 | 66 | 70 | 690 |
| 59 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|-----|-----|-----|-----|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 4 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 5 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 6 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 7 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 8 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 9 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 10 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 11 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 12 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 13 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 14 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 15 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 16 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 17 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 18 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 19 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 20 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 21 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 22 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 23 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 24 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 25 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 26 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 27 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 28 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 29 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 30 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 31 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 32 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 33 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 34 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 35 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 36 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 37 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 38 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 39 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 40 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 41 | 2739 | 111 | 141 | 207 | 159 | 86 | 1292 |
| 42 | 2311 | 181 | 149 | 128 | 194 | 203 | 1090 |
| 43 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 44 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 45 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 46 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 47 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 48 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 49 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 50 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 51 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 52 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 53 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 54 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 55 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 56 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 57 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 58 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 59 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|-----|-----|-----|-----|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 4 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 5 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 6 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 7 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 8 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 9 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 10 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 11 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 12 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 13 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 14 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 15 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 16 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 17 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 18 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 19 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 20 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 21 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 22 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 23 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 24 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 25 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 26 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 27 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 28 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 29 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 30 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 31 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 32 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 33 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 34 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 35 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 36 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 37 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 38 | 2291 | 179 | 149 | 128 | 193 | 203 | 1081 |
| 39 | 2444 | 51 | 3 | 336 | 37 | 33 | 1153 |
| 40 | 2444 | 51 | 3 | 336 | 37 | 33 | 1153 |
| 41 | 2444 | 51 | 3 | 336 | 37 | 33 | 1153 |
| 42 | 2444 | 51 | 3 | 336 | 37 | 33 | 1153 |
| 43 | 2444 | 51 | 3 | 336 | 37 | 33 | 1153 |
| 44 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 45 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 46 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 47 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 48 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 49 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 50 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 51 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 52 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 53 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 54 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 55 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 56 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 57 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 58 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 59 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|-----|-----|-----|-----|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 4 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 5 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 6 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 7 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 8 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 9 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 10 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 11 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 12 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 13 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 14 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 15 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 16 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 17 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 18 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 19 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 20 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 21 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 22 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 23 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 24 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 25 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 26 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 27 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 28 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 29 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 30 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 31 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 32 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 33 | 2976 | 275 | 215 | 136 | 268 | 268 | 1404 |
| 34 | 2986 | 278 | 215 | 137 | 271 | 268 | 1409 |
| 35 | 2454 | 51 | 4 | 347 | 37 | 33 | 1158 |
| 36 | 2454 | 51 | 4 | 347 | 37 | 33 | 1158 |
| 37 | 2142 | 42 | 3 | 322 | 34 | 26 | 1010 |
| 38 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 39 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 40 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 41 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 42 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 43 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 44 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 45 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 46 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 47 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 48 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 49 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 50 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 51 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 52 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 53 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 54 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 55 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 56 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 57 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 58 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 59 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|----|----|-----|----|----|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 4 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 5 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 6 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 7 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 8 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 9 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 10 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 11 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 12 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 13 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 14 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 15 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 16 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 17 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 18 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 19 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 20 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 21 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 22 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 23 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 24 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 25 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 26 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 27 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 28 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 29 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 30 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 31 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 32 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 33 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 34 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 35 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 36 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 37 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 38 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 39 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 40 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 41 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 42 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 43 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 44 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 45 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 46 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 47 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 48 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 49 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 50 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 51 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 52 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 53 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 54 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 55 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 56 | 2139 | 42 | 3 | 322 | 33 | 26 | 1009 |
| 57 | 2143 | 42 | 3 | 324 | 33 | 26 | 1011 |
| 58 | 436 | 49 | 21 | 44 | 54 | 59 | 206 |
| 59 | | | | | | | |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 436 | 49 | 21 | 44 | 54 | 59 | 206 |
| 4 | 436 | 49 | 21 | 44 | 54 | 59 | 206 |
| 5 | 436 | 49 | 21 | 44 | 54 | 59 | 206 |
| 6 | 1253 | 405 | 21 | 127 | 426 | 394 | 591 |
| 7 | 1253 | 405 | 21 | 127 | 426 | 394 | 591 |
| 8 | 1224 | 384 | 20 | 124 | 397 | 369 | 577 |
| 9 | 1224 | 384 | 20 | 124 | 397 | 369 | 577 |
| 10 | 1224 | 384 | 20 | 124 | 397 | 369 | 577 |
| 11 | 1224 | 384 | 20 | 124 | 397 | 369 | 577 |
| 12 | 1224 | 384 | 20 | 124 | 397 | 369 | 577 |
| 13 | 1224 | 384 | 20 | 124 | 397 | 369 | 577 |
| 14 | 1061 | 341 | 16 | 117 | 354 | 325 | 500 |
| 15 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 16 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 17 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 18 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 19 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 20 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 21 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 22 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 23 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 24 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 25 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 26 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 27 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 28 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 29 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 30 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 31 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 32 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 33 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 34 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 35 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 36 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 37 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 38 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 39 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 40 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 41 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 42 | 1060 | 341 | 16 | 117 | 354 | 325 | 500 |
| 43 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 44 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 45 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 46 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 47 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 48 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 49 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 50 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 51 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 52 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 53 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 54 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 55 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 56 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 57 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 58 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 59 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 4 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 5 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 6 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 7 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 8 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 9 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 10 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 11 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 12 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 13 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 14 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 15 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 16 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 17 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 18 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 19 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 20 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 21 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 22 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 23 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 24 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 25 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 26 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 27 | 1031 | 323 | 15 | 114 | 327 | 301 | 486 |
| 28 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 29 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 30 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 31 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 32 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 33 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 34 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 35 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 36 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 37 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 38 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 39 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 40 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 41 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 42 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 43 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 44 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 45 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 46 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 47 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 48 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 49 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 50 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 51 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 52 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 53 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 54 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 55 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 56 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 57 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 58 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 59 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|----|---|----|----|----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 4 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 5 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 6 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 7 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 8 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 9 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 10 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 11 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 12 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 13 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 14 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 15 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 16 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 17 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 18 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 19 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 20 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 21 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 22 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 23 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 24 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 25 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 26 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 27 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 28 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 29 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 30 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 31 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 32 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 33 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 34 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 35 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 36 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 37 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 38 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 39 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 40 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 41 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 42 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 43 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 44 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 45 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 46 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 47 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 48 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 49 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 50 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 51 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 52 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 53 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 54 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 55 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 56 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 57 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 58 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 59 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|----|----|----|----|----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 4 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 5 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 6 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 7 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 8 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 9 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 10 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 11 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 12 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 13 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 14 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 15 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 16 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 17 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 18 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 19 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 20 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 21 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 22 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 23 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 24 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 25 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 26 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 27 | 567 | 68 | 7 | 69 | 41 | 36 | 267 |
| 28 | 743 | 59 | 46 | 83 | 44 | 49 | 350 |
| 29 | 743 | 59 | 46 | 83 | 44 | 49 | 350 |
| 30 | 743 | 59 | 46 | 83 | 44 | 49 | 350 |
| 31 | 743 | 59 | 46 | 83 | 44 | 49 | 350 |
| 32 | 743 | 59 | 46 | 83 | 44 | 49 | 350 |
| 33 | 743 | 59 | 46 | 83 | 44 | 49 | 350 |
| 34 | 743 | 59 | 46 | 83 | 44 | 49 | 350 |
| 35 | 220 | 39 | 3 | 26 | 28 | 29 | 104 |
| 36 | 220 | 39 | 3 | 26 | 28 | 29 | 104 |
| 37 | 220 | 39 | 3 | 26 | 28 | 29 | 104 |
| 38 | 220 | 39 | 3 | 26 | 28 | 29 | 104 |
| 39 | 220 | 39 | 3 | 26 | 28 | 29 | 104 |
| 40 | 220 | 39 | 3 | 26 | 28 | 29 | 104 |
| 41 | 220 | 39 | 3 | 26 | 28 | 29 | 104 |
| 42 | 220 | 39 | 3 | 26 | 28 | 29 | 104 |
| 43 | 220 | 39 | 3 | 26 | 28 | 29 | 104 |
| 44 | 220 | 39 | 3 | 26 | 28 | 29 | 104 |
| 45 | 220 | 39 | 3 | 26 | 28 | 29 | 104 |
| 46 | 220 | 39 | 3 | 26 | 28 | 29 | 104 |
| 47 | 220 | 39 | 3 | 26 | 28 | 29 | 104 |
| 48 | 459 | 38 | 1 | 85 | 18 | 29 | 217 |
| 49 | 458 | 38 | 1 | 85 | 18 | 29 | 216 |
| 50 | 458 | 38 | 1 | 85 | 18 | 29 | 216 |
| 51 | 458 | 38 | 1 | 85 | 18 | 29 | 216 |
| 52 | 458 | 38 | 1 | 85 | 18 | 29 | 216 |
| 53 | 458 | 38 | 1 | 85 | 18 | 29 | 216 |
| 54 | 458 | 38 | 1 | 85 | 18 | 29 | 216 |
| 55 | 458 | 38 | 1 | 85 | 18 | 29 | 216 |
| 56 | 458 | 38 | 1 | 85 | 18 | 29 | 216 |
| 57 | 458 | 38 | 1 | 85 | 18 | 29 | 216 |
| 58 | 458 | 38 | 1 | 85 | 18 | 29 | 216 |
| 59 | 458 | 38 | 1 | 85 | 18 | 29 | 216 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|----|-----|-----|-----|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 458 | 38 | 1 | 85 | 18 | 29 | 216 |
| 4 | 458 | 38 | 1 | 85 | 18 | 29 | 216 |
| 5 | 458 | 38 | 1 | 85 | 18 | 29 | 216 |
| 6 | 458 | 38 | 1 | 85 | 18 | 29 | 216 |
| 7 | 458 | 38 | 1 | 85 | 18 | 29 | 216 |
| 8 | 458 | 38 | 1 | 85 | 18 | 29 | 216 |
| 9 | 458 | 38 | 1 | 85 | 18 | 29 | 216 |
| 10 | 458 | 38 | 1 | 85 | 18 | 29 | 216 |
| 11 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 12 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 13 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 14 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 15 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 16 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 17 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 18 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 19 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 20 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 21 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 22 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 23 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 24 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 25 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 26 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 27 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 28 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 29 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 30 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 31 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 32 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 33 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 34 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 35 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 36 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 37 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 38 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 39 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 40 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 41 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 42 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 43 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 44 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 45 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 46 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 47 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 48 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 49 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 50 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 51 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 52 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 53 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 54 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 55 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 56 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 57 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 58 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 59 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|------|------|------|------|------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 4 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 5 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 6 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 7 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 8 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 9 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 10 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 11 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 12 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 13 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 14 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 15 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 16 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 17 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 18 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 19 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 20 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 21 | 2564 | 554 | 65 | 389 | 466 | 451 | 1209 |
| 22 | 2566 | 557 | 65 | 392 | 473 | 452 | 1210 |
| 23 | 2566 | 557 | 65 | 392 | 473 | 452 | 1210 |
| 24 | 21884 | 2135 | 2640 | 2345 | 2392 | 1919 | 10323 |
| 25 | 21884 | 2135 | 2640 | 2345 | 2392 | 1919 | 10323 |
| 26 | 21884 | 2135 | 2640 | 2345 | 2392 | 1919 | 10323 |
| 27 | 21884 | 2135 | 2640 | 2345 | 2392 | 1919 | 10323 |
| 28 | 21884 | 2135 | 2640 | 2345 | 2392 | 1919 | 10323 |
| 29 | 21884 | 2135 | 2640 | 2345 | 2392 | 1919 | 10323 |
| 30 | 21884 | 2135 | 2640 | 2345 | 2392 | 1919 | 10323 |
| 31 | 21707 | 2121 | 2620 | 2329 | 2373 | 1898 | 10239 |
| 32 | 21707 | 2121 | 2620 | 2329 | 2373 | 1898 | 10239 |
| 33 | 21707 | 2121 | 2620 | 2329 | 2373 | 1898 | 10239 |
| 34 | 21707 | 2121 | 2620 | 2329 | 2373 | 1898 | 10239 |
| 35 | 21707 | 2121 | 2620 | 2329 | 2373 | 1898 | 10239 |
| 36 | 21707 | 2121 | 2620 | 2329 | 2373 | 1898 | 10239 |
| 37 | 21707 | 2121 | 2620 | 2329 | 2373 | 1898 | 10239 |
| 38 | 21707 | 2121 | 2620 | 2329 | 2373 | 1898 | 10239 |
| 39 | 21707 | 2121 | 2620 | 2329 | 2373 | 1898 | 10239 |
| 40 | 21707 | 2121 | 2620 | 2329 | 2373 | 1898 | 10239 |
| 41 | 21707 | 2121 | 2620 | 2329 | 2373 | 1898 | 10239 |
| 42 | 21707 | 2121 | 2620 | 2329 | 2373 | 1898 | 10239 |
| 43 | 21707 | 2121 | 2620 | 2329 | 2373 | 1898 | 10239 |
| 44 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 45 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 46 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 47 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 48 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 49 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 50 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 51 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 52 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 53 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 54 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 55 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 56 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 57 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 58 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 59 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|-------|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 4 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 5 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 6 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 7 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 8 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 9 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 10 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 11 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 12 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 13 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 14 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 15 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 16 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 17 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 18 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 19 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 20 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 21 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 22 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 23 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 24 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 25 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 26 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 27 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 28 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 29 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 30 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 31 | 1411 | 478 | 32 | 228 | 385 | 457 | 666 |
| 32 | 1682 | 4014 | 5998 | 1233 | 5014 | 17068 | 793 |
| 33 | 1682 | 4014 | 5998 | 1233 | 5014 | 17068 | 793 |
| 34 | 1682 | 4014 | 5998 | 1233 | 5014 | 17068 | 793 |
| 35 | 1682 | 4014 | 5998 | 1233 | 5014 | 17068 | 793 |
| 36 | 1682 | 4014 | 5998 | 1233 | 5014 | 17068 | 793 |
| 37 | 1517 | 516 | 36 | 263 | 412 | 490 | 716 |
| 38 | 1517 | 516 | 36 | 263 | 412 | 490 | 716 |
| 39 | 1517 | 516 | 36 | 263 | 412 | 490 | 716 |
| 40 | 1517 | 516 | 36 | 263 | 412 | 490 | 716 |
| 41 | 1517 | 516 | 36 | 263 | 412 | 490 | 716 |
| 42 | 1517 | 516 | 36 | 263 | 412 | 490 | 716 |
| 43 | 1517 | 516 | 36 | 263 | 412 | 490 | 716 |
| 44 | 1517 | 516 | 36 | 263 | 412 | 490 | 716 |
| 45 | 1517 | 516 | 36 | 263 | 412 | 490 | 716 |
| 46 | 1517 | 516 | 36 | 263 | 412 | 490 | 716 |
| 47 | 1517 | 516 | 36 | 263 | 412 | 490 | 716 |
| 48 | 1517 | 516 | 36 | 263 | 412 | 490 | 716 |
| 49 | 281 | 37 | 23 | 51 | 42 | 44 | 133 |
| 50 | 281 | 37 | 23 | 51 | 42 | 44 | 133 |
| 51 | 281 | 37 | 23 | 51 | 42 | 44 | 133 |
| 52 | 281 | 37 | 23 | 51 | 42 | 44 | 133 |
| 53 | 281 | 37 | 23 | 51 | 42 | 44 | 133 |
| 54 | 281 | 37 | 23 | 51 | 42 | 44 | 133 |
| 55 | 281 | 37 | 23 | 51 | 42 | 44 | 133 |
| 56 | 281 | 37 | 23 | 51 | 42 | 44 | 133 |
| 57 | 281 | 37 | 23 | 51 | 42 | 44 | 133 |
| 58 | 281 | 37 | 23 | 51 | 42 | 44 | 133 |
| 59 | 281 | 37 | 23 | 51 | 42 | 44 | 133 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|-----|-----|-----|-----|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 4 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 5 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 6 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 7 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 8 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 9 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 10 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 11 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 12 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 13 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 14 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 15 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 16 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 17 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 18 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 19 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 20 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 21 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 22 | 348 | 41 | 37 | 42 | 42 | 23 | 164 |
| 23 | 355 | 42 | 40 | 44 | 43 | 23 | 167 |
| 24 | 2995 | 457 | 417 | 407 | 569 | 387 | 1413 |
| 25 | 2995 | 457 | 417 | 407 | 569 | 387 | 1413 |
| 26 | 2995 | 457 | 417 | 407 | 569 | 387 | 1413 |
| 27 | 2995 | 457 | 417 | 407 | 569 | 387 | 1413 |
| 28 | 2995 | 457 | 417 | 407 | 569 | 387 | 1413 |
| 29 | 2995 | 457 | 417 | 407 | 569 | 387 | 1413 |
| 30 | 2995 | 457 | 417 | 407 | 569 | 387 | 1413 |
| 31 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 32 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 33 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 34 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 35 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 36 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 37 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 38 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 39 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 40 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 41 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 42 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 43 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 44 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 45 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 46 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 47 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 48 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 49 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 50 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 51 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 52 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 53 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 54 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 55 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 56 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 57 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 58 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 59 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|-----|-----|-----|-----|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 4 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 5 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 6 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 7 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 8 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 9 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 10 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 11 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 12 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 13 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 14 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 15 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 16 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 17 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 18 | 2977 | 455 | 417 | 407 | 569 | 386 | 1404 |
| 19 | 168 | 58 | 20 | 31 | 44 | 73 | 79 |
| 20 | 168 | 58 | 20 | 31 | 44 | 73 | 79 |
| 21 | 168 | 58 | 20 | 31 | 44 | 73 | 79 |
| 22 | 168 | 58 | 20 | 31 | 44 | 73 | 79 |
| 23 | 168 | 58 | 20 | 31 | 44 | 73 | 79 |
| 24 | 168 | 58 | 20 | 31 | 44 | 73 | 79 |
| 25 | 168 | 58 | 20 | 31 | 44 | 73 | 79 |
| 26 | 168 | 58 | 20 | 31 | 44 | 73 | 79 |
| 27 | 168 | 58 | 20 | 31 | 44 | 73 | 79 |
| 28 | 168 | 58 | 20 | 31 | 44 | 73 | 79 |
| 29 | 168 | 58 | 20 | 31 | 44 | 73 | 79 |
| 30 | 168 | 58 | 20 | 31 | 44 | 73 | 79 |
| 31 | 168 | 58 | 20 | 31 | 44 | 73 | 79 |
| 32 | 119 | 308 | 203 | 49 | 403 | 537 | 56 |
| 33 | 254 | 138 | 23 | 40 | 126 | 104 | 120 |
| 34 | 242 | 140 | 23 | 39 | 125 | 104 | 114 |
| 35 | 242 | 140 | 23 | 39 | 125 | 104 | 114 |
| 36 | 242 | 140 | 23 | 39 | 125 | 104 | 114 |
| 37 | 242 | 140 | 23 | 39 | 125 | 104 | 114 |
| 38 | 242 | 140 | 23 | 39 | 125 | 104 | 114 |
| 39 | 350 | 10 | 13 | 84 | 10 | 8 | 165 |
| 40 | 350 | 10 | 13 | 84 | 10 | 8 | 165 |
| 41 | 282 | 30 | 23 | 63 | 32 | 33 | 133 |
| 42 | 282 | 30 | 23 | 63 | 32 | 33 | 133 |
| 43 | 282 | 30 | 23 | 63 | 32 | 33 | 133 |
| 44 | 282 | 30 | 23 | 63 | 32 | 33 | 133 |
| 45 | 282 | 30 | 23 | 63 | 32 | 33 | 133 |
| 46 | 282 | 30 | 23 | 63 | 32 | 33 | 133 |
| 47 | 282 | 30 | 23 | 63 | 32 | 33 | 133 |
| 48 | 246 | 140 | 24 | 39 | 126 | 102 | 116 |
| 49 | 242 | 141 | 23 | 40 | 125 | 106 | 114 |
| 50 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 51 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 52 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 53 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 54 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 55 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 56 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 57 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 58 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 59 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 4 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 5 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 6 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 7 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 8 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 9 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 10 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 11 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 12 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 13 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 14 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 15 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 16 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 17 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 18 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 19 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 20 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 21 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 22 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 23 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 24 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 25 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 26 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 27 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 28 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 29 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 30 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 31 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 32 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 33 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 34 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 35 | 938 | 89 | 106 | 170 | 96 | 78 | 442 |
| 36 | 235 | 138 | 23 | 39 | 123 | 102 | 111 |
| 37 | 235 | 138 | 23 | 39 | 123 | 102 | 111 |
| 38 | 235 | 138 | 23 | 39 | 123 | 102 | 111 |
| 39 | 235 | 138 | 23 | 39 | 123 | 102 | 111 |
| 40 | 235 | 138 | 23 | 39 | 123 | 102 | 111 |
| 41 | 235 | 138 | 23 | 39 | 123 | 102 | 111 |
| 42 | 235 | 138 | 23 | 39 | 123 | 102 | 111 |
| 43 | 235 | 138 | 23 | 39 | 123 | 102 | 111 |
| 44 | 235 | 138 | 23 | 39 | 123 | 102 | 111 |
| 45 | 235 | 138 | 23 | 39 | 123 | 102 | 111 |
| 46 | 235 | 138 | 23 | 39 | 123 | 102 | 111 |
| 47 | 235 | 138 | 23 | 39 | 123 | 102 | 111 |
| 48 | 235 | 138 | 23 | 39 | 123 | 102 | 111 |
| 49 | 235 | 138 | 23 | 39 | 123 | 102 | 111 |
| 50 | 235 | 138 | 23 | 39 | 123 | 102 | 111 |
| 51 | 235 | 138 | 23 | 39 | 123 | 102 | 111 |
| 52 | 235 | 138 | 23 | 39 | 123 | 102 | 111 |
| 53 | 235 | 138 | 23 | 39 | 123 | 102 | 111 |
| 54 | 235 | 138 | 23 | 39 | 123 | 102 | 111 |
| 55 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 56 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 57 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 58 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 59 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 4 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 5 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 6 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 7 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 8 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 9 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 10 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 11 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 12 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 13 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 14 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 15 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 16 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 17 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 18 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 19 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 20 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 21 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 22 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 23 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 24 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 25 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 26 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 27 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 28 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 29 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 30 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 31 | 806 | 363 | 149 | 143 | 362 | 337 | 380 |
| 32 | 359 | 13 | 21 | 85 | 14 | 13 | 169 |
| 33 | | | | | | | |
| 34 | 207 | 34 | 60 | 27 | 51 | 44 | 98 |
| 35 | 207 | 34 | 60 | 27 | 51 | 44 | 98 |
| 36 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 37 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 38 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 39 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 40 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 41 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 42 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 43 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 44 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 45 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 46 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 47 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 48 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 49 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 50 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 51 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 52 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 53 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 54 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 55 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 56 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 57 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 58 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 59 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|----|----|----|----|----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 4 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 5 | 249 | 86 | 36 | 56 | 70 | 96 | 117 |
| 6 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 7 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 8 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 9 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 10 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 11 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 12 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 13 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 14 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 15 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 16 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 17 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 18 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 19 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 20 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 21 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 22 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 23 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 24 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 25 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 26 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 27 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 28 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 29 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 30 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 31 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 32 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 33 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 34 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 35 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 36 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 37 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 38 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 39 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 40 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 41 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 42 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 43 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 44 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 45 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 46 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 47 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 48 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 49 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 50 | 250 | 31 | 28 | 44 | 24 | 18 | 118 |
| 51 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 52 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 53 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 54 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 55 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 56 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 57 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 58 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 59 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 4 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 5 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 6 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 7 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 8 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 9 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 10 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 11 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 12 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 13 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 14 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 15 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 16 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 17 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 18 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 19 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 20 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 21 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 22 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 23 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 24 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 25 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 26 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 27 | 130 | 96 | 8 | 26 | 71 | 68 | 61 |
| 28 | 1258 | 624 | 328 | 209 | 663 | 545 | 593 |
| 29 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 30 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 31 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 32 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 33 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 34 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 35 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 36 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 37 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 38 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 39 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 40 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 41 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 42 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 43 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 44 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 45 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 46 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 47 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 48 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 49 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 50 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 51 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 52 | 319 | 51 | 37 | 77 | 66 | 36 | 150 |
| 53 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 54 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 55 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 56 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 57 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 58 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 59 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|------|-----|------|-----|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 4 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 5 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 6 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 7 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 8 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 9 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 10 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 11 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 12 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 13 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 14 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 15 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 16 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 17 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 18 | 263 | 81 | 42 | 49 | 71 | 67 | 124 |
| 19 | 148 | 124 | 12 | 36 | 103 | 88 | 70 |
| 20 | 148 | 124 | 12 | 36 | 103 | 88 | 70 |
| 21 | 148 | 124 | 12 | 36 | 103 | 88 | 70 |
| 22 | 148 | 124 | 12 | 36 | 103 | 88 | 70 |
| 23 | 148 | 124 | 12 | 36 | 103 | 88 | 70 |
| 24 | 148 | 124 | 12 | 36 | 103 | 88 | 70 |
| 25 | 148 | 124 | 12 | 36 | 103 | 88 | 70 |
| 26 | 148 | 124 | 12 | 36 | 103 | 88 | 70 |
| 27 | 148 | 124 | 12 | 36 | 103 | 88 | 70 |
| 28 | 1117 | 605 | 302 | 206 | 643 | 527 | 527 |
| 29 | 1117 | 605 | 302 | 206 | 643 | 527 | 527 |
| 30 | 469 | 117 | 171 | 31 | 148 | 115 | 221 |
| 31 | 469 | 117 | 171 | 31 | 148 | 115 | 221 |
| 32 | 469 | 117 | 171 | 31 | 148 | 115 | 221 |
| 33 | 469 | 117 | 171 | 31 | 148 | 115 | 221 |
| 34 | 264 | 82 | 42 | 49 | 71 | 68 | 125 |
| 35 | 3632 | 871 | 1477 | 109 | 1230 | 773 | 1713 |
| 36 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 37 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 38 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 39 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 40 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 41 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 42 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 43 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 44 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 45 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 46 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 47 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 48 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 49 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 50 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 51 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 52 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 53 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 54 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 55 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 56 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 57 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 58 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 59 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|------|-----|------|-----|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 4 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 5 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 6 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 7 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 8 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 9 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 10 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 11 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 12 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 13 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 14 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 15 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 16 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 17 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 18 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 19 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 20 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 21 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 22 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 23 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 24 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 25 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 26 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 27 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 28 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 29 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 30 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 31 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 32 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 33 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 34 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 35 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 36 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 37 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 38 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 39 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 40 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 41 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 42 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 43 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 44 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 45 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 46 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 47 | 3630 | 871 | 1477 | 108 | 1229 | 773 | 1712 |
| 48 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 49 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 50 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 51 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 52 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 53 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 54 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 55 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 56 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 57 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 58 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 59 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|-----|-----|-----|------|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 4 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 5 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 6 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 7 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 8 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 9 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 10 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 11 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 12 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 13 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 14 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 15 | 1068 | 587 | 289 | 202 | 618 | 503 | 504 |
| 16 | 1149 | 550 | 374 | 390 | 402 | 1033 | 542 |
| 17 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 18 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 19 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 20 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 21 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 22 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 23 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 24 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 25 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 26 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 27 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 28 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 29 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 30 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 31 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 32 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 33 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 34 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 35 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 36 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 37 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 38 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 39 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 40 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 41 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 42 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 43 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 44 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 45 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 46 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 47 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 48 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 49 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 50 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 51 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 52 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 53 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 54 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 55 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 56 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 57 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 58 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 59 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|-----|-----|-----|------|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 4 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 5 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 6 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 7 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 8 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 9 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 10 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 11 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 12 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 13 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 14 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 15 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 16 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 17 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 18 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 19 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 20 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 21 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 22 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 23 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 24 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 25 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 26 | 1149 | 550 | 374 | 389 | 402 | 1033 | 542 |
| 27 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 28 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 29 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 30 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 31 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 32 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 33 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 34 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 35 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 36 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 37 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 38 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 39 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 40 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 41 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 42 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 43 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 44 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 45 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 46 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 47 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 48 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 49 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 50 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 51 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 52 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 53 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 54 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 55 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 56 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 57 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 58 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 59 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 4 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 5 | 20 | 135 | 23 | 4 | 114 | 120 | 9 |
| 6 | 22 | 137 | 24 | 4 | 116 | 120 | 10 |
| 7 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 8 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 9 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 10 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 11 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 12 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 13 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 14 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 15 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 16 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 17 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 18 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 19 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 20 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 21 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 22 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 23 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 24 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 25 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 26 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 27 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 28 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 29 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 30 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 31 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 32 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 33 | 433 | 111 | 161 | 30 | 142 | 102 | 204 |
| 34 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 35 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 36 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 37 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 38 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 39 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 40 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 41 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 42 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 43 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 44 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 45 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 46 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 47 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 48 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 49 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 50 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 51 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 52 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 53 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 54 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 55 | 65 | 34 | 53 | 48 | 76 | 85 | 31 |
| 56 | 1689 | 474 | 403 | 395 | 551 | 416 | 797 |
| 57 | 1689 | 474 | 403 | 395 | 551 | 416 | 797 |
| 58 | 1689 | 474 | 403 | 395 | 551 | 416 | 797 |
| 59 | 1689 | 474 | 403 | 395 | 551 | 416 | 797 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 110 | 114 | 135 | 101 | 100 | 327 | 52 |
| 4 | 110 | 114 | 135 | 101 | 100 | 327 | 52 |
| 5 | 110 | 114 | 135 | 101 | 100 | 327 | 52 |
| 6 | 110 | 114 | 135 | 101 | 100 | 327 | 52 |
| 7 | 110 | 114 | 135 | 101 | 100 | 327 | 52 |
| 8 | 110 | 114 | 135 | 101 | 100 | 327 | 52 |
| 9 | 110 | 114 | 135 | 101 | 100 | 327 | 52 |
| 10 | 110 | 114 | 135 | 101 | 100 | 327 | 52 |
| 11 | 110 | 114 | 135 | 101 | 100 | 327 | 52 |
| 12 | 110 | 114 | 135 | 101 | 100 | 327 | 52 |
| 13 | 110 | 114 | 135 | 101 | 100 | 327 | 52 |
| 14 | 110 | 114 | 135 | 101 | 100 | 327 | 52 |
| 15 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 16 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 17 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 18 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 19 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 20 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 21 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 22 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 23 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 24 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 25 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 26 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 27 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 28 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 29 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 30 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 31 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 32 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 33 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 34 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 35 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 36 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 37 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 38 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 39 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 40 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 41 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 42 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 43 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 44 | 1551 | 420 | 383 | 380 | 510 | 368 | 732 |
| 45 | 1552 | 420 | 385 | 380 | 511 | 368 | 732 |
| 46 | 1552 | 420 | 385 | 380 | 511 | 368 | 732 |
| 47 | 1552 | 420 | 385 | 380 | 511 | 368 | 732 |
| 48 | 1552 | 420 | 385 | 380 | 511 | 368 | 732 |
| 49 | 1552 | 420 | 385 | 380 | 511 | 368 | 732 |
| 50 | 1552 | 420 | 385 | 380 | 511 | 368 | 732 |
| 51 | 1552 | 420 | 385 | 380 | 511 | 368 | 732 |
| 52 | 1552 | 420 | 385 | 380 | 511 | 368 | 732 |
| 53 | 1552 | 420 | 385 | 380 | 511 | 368 | 732 |
| 54 | 1552 | 420 | 385 | 380 | 511 | 368 | 732 |
| 55 | 1552 | 420 | 385 | 380 | 511 | 368 | 732 |
| 56 | 1552 | 420 | 385 | 380 | 511 | 368 | 732 |
| 57 | 1552 | 420 | 385 | 380 | 511 | 368 | 732 |
| 58 | 1552 | 420 | 385 | 380 | 511 | 368 | 732 |
| 59 | 984 | 160 | 122 | 351 | 192 | 177 | 464 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 984 | 160 | 122 | 351 | 192 | 177 | 464 |
| 4 | 441 | 47 | 113 | 97 | 75 | 57 | 208 |
| 5 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 6 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 7 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 8 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 9 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 10 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 11 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 12 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 13 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 14 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 15 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 16 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 17 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 18 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 19 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 20 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 21 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 22 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 23 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 24 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 25 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 26 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 27 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 28 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 29 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 30 | 418 | 43 | 99 | 95 | 67 | 46 | 197 |
| 31 | 6023 | 1939 | 4936 | 8493 | 2488 | 14611 | 2841 |
| 32 | 2257 | 3949 | 6752 | 779 | 3256 | 10511 | 1065 |
| 33 | | | | | | | |
| 34 | 369 | 192 | 53 | 151 | 182 | 142 | 174 |
| 35 | 369 | 192 | 53 | 151 | 182 | 142 | 174 |
| 36 | 369 | 192 | 53 | 151 | 182 | 142 | 174 |
| 37 | 369 | 192 | 53 | 151 | 182 | 142 | 174 |
| 38 | 369 | 192 | 53 | 151 | 182 | 142 | 174 |
| 39 | 369 | 192 | 53 | 151 | 182 | 142 | 174 |
| 40 | 369 | 192 | 53 | 151 | 182 | 142 | 174 |
| 41 | 369 | 192 | 53 | 151 | 182 | 142 | 174 |
| 42 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 43 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 44 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 45 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 46 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 47 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 48 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 49 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 50 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 51 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 52 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 53 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 54 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 55 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 56 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 57 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 58 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 59 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 4 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 5 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 6 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 7 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 8 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 9 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 10 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 11 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 12 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 13 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 14 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 15 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 16 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 17 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 18 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 19 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 20 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 21 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 22 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 23 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 24 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 25 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 26 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 27 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 28 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 29 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 30 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 31 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 32 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 33 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 34 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 35 | 345 | 154 | 44 | 146 | 142 | 124 | 163 |
| 36 | 372 | 196 | 56 | 153 | 182 | 142 | 175 |
| 37 | 25 | 86 | 42 | 32 | 95 | 89 | 12 |
| 38 | 25 | 86 | 42 | 32 | 95 | 89 | 12 |
| 39 | 25 | 86 | 42 | 32 | 95 | 89 | 12 |
| 40 | 647 | 182 | 142 | 221 | 212 | 153 | 305 |
| 41 | 647 | 182 | 142 | 221 | 212 | 153 | 305 |
| 42 | 647 | 182 | 142 | 221 | 212 | 153 | 305 |
| 43 | 980 | 448 | 383 | 199 | 274 | 516 | 462 |
| 44 | 980 | 448 | 383 | 199 | 274 | 516 | 462 |
| 45 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 46 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 47 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 48 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 49 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 50 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 51 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 52 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 53 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 54 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 55 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 56 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 57 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 58 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 59 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 4 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 5 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 6 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 7 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 8 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 9 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 10 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 11 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 12 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 13 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 14 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 15 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 16 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 17 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 18 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 19 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 20 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 21 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 22 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 23 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 24 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 25 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 26 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 27 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 28 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 29 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 30 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 31 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 32 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 33 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 34 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 35 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 36 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 37 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 38 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 39 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 40 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 41 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 42 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 43 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 44 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 45 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 46 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 47 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 48 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 49 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 50 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 51 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 52 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 53 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 54 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 55 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 56 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 57 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 58 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 59 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 4 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 5 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 6 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 7 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 8 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 9 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 10 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 11 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 12 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 13 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 14 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 15 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 16 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 17 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 18 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 19 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 20 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 21 | 978 | 448 | 383 | 198 | 274 | 516 | 461 |
| 22 | 22 | 193 | 195 | 6 | 249 | 218 | 10 |
| 23 | 22 | 199 | 200 | 7 | 250 | 224 | 10 |
| 24 | 6547 | 3929 | 2251 | 3498 | 4372 | 3919 | 3088 |
| 25 | 6547 | 3929 | 2251 | 3498 | 4372 | 3919 | 3088 |
| 26 | 6547 | 3929 | 2251 | 3498 | 4372 | 3919 | 3088 |
| 27 | 6547 | 3929 | 2251 | 3498 | 4372 | 3919 | 3088 |
| 28 | 6547 | 3929 | 2251 | 3498 | 4372 | 3919 | 3088 |
| 29 | 6547 | 3929 | 2251 | 3498 | 4372 | 3919 | 3088 |
| 30 | 6547 | 3929 | 2251 | 3498 | 4372 | 3919 | 3088 |
| 31 | 6547 | 3929 | 2251 | 3498 | 4372 | 3919 | 3088 |
| 32 | 6547 | 3929 | 2251 | 3498 | 4372 | 3919 | 3088 |
| 33 | 6547 | 3929 | 2251 | 3498 | 4372 | 3919 | 3088 |
| 34 | 6547 | 3929 | 2251 | 3498 | 4372 | 3919 | 3088 |
| 35 | 6547 | 3929 | 2251 | 3498 | 4372 | 3919 | 3088 |
| 36 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 37 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 38 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 39 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 40 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 41 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 42 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 43 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 44 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 45 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 46 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 47 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 48 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 49 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 50 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 51 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 52 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 53 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 54 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 55 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 56 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 57 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 58 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 59 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | | | | | | | |
| 4 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 5 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 6 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 7 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 8 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 9 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 10 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 11 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 12 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 13 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 14 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 15 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 16 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 17 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 18 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 19 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 20 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 21 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 22 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 23 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 24 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 25 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 26 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 27 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 28 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 29 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 30 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 31 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 32 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 33 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 34 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 35 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 36 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 37 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 38 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 39 | 270 | 392 | 267 | 113 | 396 | 382 | 127 |
| 40 | 280 | 404 | 277 | 124 | 408 | 402 | 132 |
| 41 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 42 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 43 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 44 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 45 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 46 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 47 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 48 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 49 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 50 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 51 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 52 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 53 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 54 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 55 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 56 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 57 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 58 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 59 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|------|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 4 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 5 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 6 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 7 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 8 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 9 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 10 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 11 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 12 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 13 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 14 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 15 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 16 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 17 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 18 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 19 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 20 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 21 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 22 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 23 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 24 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 25 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 26 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 27 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 28 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 29 | 957 | 104 | 5 | 366 | 54 | 49 | 451 |
| 30 | 963 | 104 | 5 | 368 | 54 | 49 | 454 |
| 31 | 429 | 214 | 110 | 226 | 222 | 211 | 202 |
| 32 | 429 | 214 | 110 | 226 | 222 | 211 | 202 |
| 33 | 403 | 196 | 102 | 221 | 213 | 198 | 190 |
| 34 | 403 | 196 | 102 | 221 | 213 | 198 | 190 |
| 35 | 403 | 196 | 102 | 221 | 213 | 198 | 190 |
| 36 | 403 | 196 | 102 | 221 | 213 | 198 | 190 |
| 37 | 403 | 196 | 102 | 221 | 213 | 198 | 190 |
| 38 | 403 | 196 | 102 | 221 | 213 | 198 | 190 |
| 39 | 403 | 196 | 102 | 221 | 213 | 198 | 190 |
| 40 | 403 | 196 | 102 | 221 | 213 | 198 | 190 |
| 41 | 403 | 196 | 102 | 221 | 213 | 198 | 190 |
| 42 | 403 | 196 | 102 | 221 | 213 | 198 | 190 |
| 43 | 403 | 196 | 102 | 221 | 213 | 198 | 190 |
| 44 | 171 | 567 | 13 | 333 | 448 | 522 | 81 |
| 45 | 166 | 554 | 12 | 321 | 439 | 504 | 78 |
| 46 | 567 | 633 | 394 | 464 | 401 | 1041 | 267 |
| 47 | 567 | 633 | 394 | 464 | 401 | 1041 | 267 |
| 48 | 567 | 633 | 394 | 464 | 401 | 1041 | 267 |
| 49 | 163 | 527 | 12 | 317 | 420 | 480 | 77 |
| 50 | 163 | 527 | 12 | 317 | 420 | 480 | 77 |
| 51 | 163 | 527 | 12 | 317 | 420 | 480 | 77 |
| 52 | 163 | 527 | 12 | 317 | 420 | 480 | 77 |
| 53 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 54 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 55 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 56 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 57 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 58 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 59 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 4 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 5 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 6 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 7 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 8 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 9 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 10 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 11 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 12 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 13 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 14 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 15 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 16 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 17 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 18 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 19 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 20 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 21 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 22 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 23 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 24 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 25 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 26 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 27 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 28 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 29 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 30 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 31 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 32 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 33 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 34 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 35 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 36 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 37 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 38 | 163 | 527 | 12 | 317 | 419 | 478 | 77 |
| 39 | 79 | 90 | 157 | 78 | 68 | 262 | 37 |
| 40 | 79 | 90 | 157 | 78 | 68 | 262 | 37 |
| 41 | | | | | | | |
| 42 | 470 | 222 | 111 | 255 | 231 | 205 | 222 |
| 43 | 470 | 222 | 111 | 255 | 231 | 205 | 222 |
| 44 | 470 | 222 | 111 | 255 | 231 | 205 | 222 |
| 45 | 470 | 222 | 111 | 255 | 231 | 205 | 222 |
| 46 | 470 | 222 | 111 | 255 | 231 | 205 | 222 |
| 47 | 470 | 222 | 111 | 255 | 231 | 205 | 222 |
| 48 | 470 | 222 | 111 | 255 | 231 | 205 | 222 |
| 49 | 470 | 222 | 111 | 255 | 231 | 205 | 222 |
| 50 | 470 | 222 | 111 | 255 | 231 | 205 | 222 |
| 51 | 976 | 110 | 8 | 403 | 59 | 59 | 460 |
| 52 | 976 | 110 | 8 | 403 | 59 | 59 | 460 |
| 53 | 976 | 110 | 8 | 403 | 59 | 59 | 460 |
| 54 | 976 | 110 | 8 | 403 | 59 | 59 | 460 |
| 55 | 976 | 110 | 8 | 403 | 59 | 59 | 460 |
| 56 | 976 | 110 | 8 | 403 | 59 | 59 | 460 |
| 57 | 976 | 110 | 8 | 403 | 59 | 59 | 460 |
| 58 | 976 | 110 | 8 | 403 | 59 | 59 | 460 |
| 59 | 976 | 110 | 8 | 403 | 59 | 59 | 460 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 976 | 110 | 8 | 403 | 59 | 59 | 460 |
| 4 | 623 | 123 | 86 | 302 | 145 | 124 | 294 |
| 5 | 623 | 123 | 86 | 302 | 145 | 124 | 294 |
| 6 | 623 | 123 | 86 | 302 | 145 | 124 | 294 |
| 7 | 623 | 123 | 86 | 302 | 145 | 124 | 294 |
| 8 | 623 | 123 | 86 | 302 | 145 | 124 | 294 |
| 9 | 623 | 123 | 86 | 302 | 145 | 124 | 294 |
| 10 | 623 | 123 | 86 | 302 | 145 | 124 | 294 |
| 11 | 623 | 123 | 86 | 302 | 145 | 124 | 294 |
| 12 | 623 | 123 | 86 | 302 | 145 | 124 | 294 |
| 13 | 623 | 123 | 86 | 302 | 145 | 124 | 294 |
| 14 | 623 | 123 | 86 | 302 | 145 | 124 | 294 |
| 15 | 108 | 147 | 8 | 117 | 111 | 138 | 51 |
| 16 | 108 | 147 | 8 | 117 | 111 | 138 | 51 |
| 17 | 108 | 147 | 8 | 117 | 111 | 138 | 51 |
| 18 | 108 | 147 | 8 | 117 | 111 | 138 | 51 |
| 19 | 108 | 147 | 8 | 117 | 111 | 138 | 51 |
| 20 | 108 | 147 | 8 | 117 | 111 | 138 | 51 |
| 21 | 108 | 147 | 8 | 117 | 111 | 138 | 51 |
| 22 | 260 | 95 | 52 | 133 | 102 | 81 | 123 |
| 23 | 260 | 95 | 52 | 133 | 102 | 81 | 123 |
| 24 | 267 | 98 | 54 | 136 | 103 | 85 | 126 |
| 25 | 227 | 59 | 31 | 107 | 61 | 47 | 107 |
| 26 | 227 | 59 | 31 | 107 | 61 | 47 | 107 |
| 27 | 227 | 59 | 31 | 107 | 61 | 47 | 107 |
| 28 | 227 | 59 | 31 | 107 | 61 | 47 | 107 |
| 29 | 227 | 59 | 31 | 107 | 61 | 47 | 107 |
| 30 | 227 | 59 | 31 | 107 | 61 | 47 | 107 |
| 31 | 227 | 59 | 31 | 107 | 61 | 47 | 107 |
| 32 | 227 | 59 | 31 | 107 | 61 | 47 | 107 |
| 33 | 227 | 59 | 31 | 107 | 61 | 47 | 107 |
| 34 | 227 | 59 | 31 | 107 | 61 | 47 | 107 |
| 35 | 227 | 59 | 31 | 107 | 61 | 47 | 107 |
| 36 | 227 | 59 | 31 | 107 | 61 | 47 | 107 |
| 37 | 227 | 59 | 31 | 107 | 61 | 47 | 107 |
| 38 | 227 | 59 | 31 | 107 | 61 | 47 | 107 |
| 39 | 98 | 330 | 1 | 206 | 253 | 286 | 46 |
| 40 | 98 | 330 | 1 | 206 | 253 | 286 | 46 |
| 41 | 98 | 330 | 1 | 206 | 253 | 286 | 46 |
| 42 | 98 | 330 | 1 | 206 | 253 | 286 | 46 |
| 43 | 98 | 330 | 1 | 206 | 253 | 286 | 46 |
| 44 | 98 | 330 | 1 | 206 | 253 | 286 | 46 |
| 45 | 98 | 330 | 1 | 206 | 253 | 286 | 46 |
| 46 | 98 | 330 | 1 | 206 | 253 | 286 | 46 |
| 47 | 98 | 330 | 1 | 206 | 253 | 286 | 46 |
| 48 | 98 | 330 | 1 | 206 | 253 | 286 | 46 |
| 49 | 98 | 330 | 1 | 206 | 253 | 286 | 46 |
| 50 | 98 | 330 | 1 | 206 | 253 | 286 | 46 |
| 51 | 98 | 330 | 1 | 206 | 253 | 286 | 46 |
| 52 | 98 | 330 | 1 | 206 | 253 | 286 | 46 |
| 53 | 98 | 330 | 1 | 206 | 253 | 286 | 46 |
| 54 | 98 | 330 | 1 | 206 | 253 | 286 | 46 |
| 55 | 98 | 330 | 1 | 206 | 253 | 286 | 46 |
| 56 | 21 | 91 | 133 | 40 | 167 | 104 | 10 |
| 57 | 242 | 74 | 94 | 142 | 57 | 158 | 114 |
| 58 | 242 | 74 | 94 | 142 | 57 | 158 | 114 |
| 59 | 242 | 74 | 94 | 142 | 57 | 158 | 114 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|---------|---------|--------|---------|---------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 4 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 5 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 6 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 7 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 8 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 9 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 10 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 11 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 12 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 13 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 14 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 15 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 16 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 17 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 18 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 19 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 20 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 21 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 22 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 23 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 24 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 25 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 26 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 27 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 28 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 29 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 30 | 296 | 105 | 184 | 58 | 129 | 99 | 140 |
| 31 | 302 | 107 | 186 | 61 | 131 | 102 | 142 |
| 32 | 246 | 76 | 98 | 147 | 60 | 164 | 116 |
| 33 | 246 | 76 | 98 | 147 | 60 | 164 | 116 |
| 34 | 246 | 76 | 98 | 147 | 60 | 164 | 116 |
| 35 | 188 | 344 | 264 | 141 | 292 | 410 | 89 |
| 36 | 702 | 276 | 241 | 337 | 286 | 280 | 331 |
| 37 | 77 | 68 | 82 | 16 | 79 | 55 | 36 |
| 38 | 814 | 523 | 597 | 241 | 617 | 408 | 384 |
| 39 | 814 | 523 | 597 | 241 | 617 | 408 | 384 |
| 40 | 814 | 523 | 597 | 241 | 617 | 408 | 384 |
| 41 | 814 | 523 | 597 | 241 | 617 | 408 | 384 |
| 42 | 814 | 523 | 597 | 241 | 617 | 408 | 384 |
| 43 | 814 | 523 | 597 | 241 | 617 | 408 | 384 |
| 44 | 62 | 103 | 5 | 82 | 77 | 88 | 29 |
| 45 | 62 | 103 | 5 | 82 | 77 | 88 | 29 |
| 46 | 62 | 103 | 5 | 82 | 77 | 88 | 29 |
| 47 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 48 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 49 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 50 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 51 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 52 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 53 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 54 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 55 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 56 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 57 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 58 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 59 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 60 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |

| | | | | | | | |
|----|--------|---------|---------|--------|---------|---------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 4 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 5 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 6 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 7 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 8 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 9 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 10 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 11 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 12 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 13 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 14 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 15 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 16 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 17 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 18 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 19 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 20 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 21 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 22 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 23 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 24 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 25 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 26 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 27 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 28 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 29 | 424371 | 1260625 | 1747674 | 318033 | 1598398 | 1618861 | 200182 |
| 30 | 13412 | 19021 | 26709 | 12002 | 25615 | 27172 | 6327 |
| 31 | 77 | 67 | 82 | 16 | 78 | 55 | 36 |
| 32 | 77 | 67 | 82 | 16 | 78 | 55 | 36 |
| 33 | 77 | 67 | 82 | 16 | 78 | 55 | 36 |
| 34 | 77 | 67 | 82 | 16 | 78 | 55 | 36 |
| 35 | 77 | 67 | 82 | 16 | 78 | 55 | 36 |
| 36 | 77 | 67 | 82 | 16 | 78 | 55 | 36 |
| 37 | 77 | 67 | 82 | 16 | 78 | 55 | 36 |
| 38 | 77 | 67 | 82 | 16 | 78 | 55 | 36 |
| 39 | 77 | 67 | 82 | 16 | 78 | 55 | 36 |
| 40 | 77 | 67 | 82 | 16 | 78 | 55 | 36 |
| 41 | | | | | | | |
| 42 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 43 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 44 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 45 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 46 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 47 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 48 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 49 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 50 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 51 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 52 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 53 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 54 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 55 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 56 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 57 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 58 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 59 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|-------|-------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 4 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 5 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 6 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 7 | 19799 | 39303 | 56789 | 15852 | 45900 | 58216 | 9339 |
| 8 | 8491 | 5455 | 5638 | 8165 | 3910 | 11590 | 4005 |
| 9 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 10 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 11 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 12 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 13 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 14 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 15 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 16 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 17 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 18 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 19 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 20 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 21 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 22 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 23 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 24 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 25 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 26 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 27 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 28 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 29 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 30 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 31 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 32 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 33 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 34 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 35 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 36 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 37 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 38 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 39 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 40 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 41 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 42 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 43 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 44 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 45 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 46 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 47 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 48 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 49 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 50 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 51 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 52 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 53 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 54 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 55 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 56 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 57 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 58 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 59 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|-------|-------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 4 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 5 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 6 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 7 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 8 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 9 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 10 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 11 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 12 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 13 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 14 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 15 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 16 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 17 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 18 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 19 | 8449 | 5432 | 5618 | 8133 | 3888 | 11546 | 3986 |
| 20 | 8459 | 5442 | 5626 | 8140 | 3891 | 11565 | 3990 |
| 21 | 8459 | 5442 | 5626 | 8140 | 3891 | 11565 | 3990 |
| 22 | 8459 | 5442 | 5626 | 8140 | 3891 | 11565 | 3990 |
| 23 | 8459 | 5442 | 5626 | 8140 | 3891 | 11565 | 3990 |
| 24 | 19847 | 39455 | 57076 | 15901 | 45976 | 58428 | 9362 |
| 25 | 21486 | 46518 | 66647 | 17217 | 53251 | 67138 | 10135 |
| 26 | 21486 | 46518 | 66647 | 17217 | 53251 | 67138 | 10135 |
| 27 | 21486 | 46518 | 66647 | 17217 | 53251 | 67138 | 10135 |
| 28 | 21486 | 46518 | 66647 | 17217 | 53251 | 67138 | 10135 |
| 29 | 21486 | 46518 | 66647 | 17217 | 53251 | 67138 | 10135 |
| 30 | 21486 | 46518 | 66647 | 17217 | 53251 | 67138 | 10135 |
| 31 | 21486 | 46518 | 66647 | 17217 | 53251 | 67138 | 10135 |
| 32 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 33 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 34 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 35 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 36 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 37 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 38 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 39 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 40 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 41 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 42 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 43 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 44 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 45 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 46 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 47 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 48 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 49 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 50 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 51 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 52 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 53 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 54 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 55 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 56 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 57 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 58 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 59 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|-------|-------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 4 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 5 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 6 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 7 | 744 | 433 | 265 | 393 | 390 | 350 | 351 |
| 8 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 9 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 10 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 11 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 12 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 13 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 14 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 15 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 16 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 17 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 18 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 19 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 20 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 21 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 22 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 23 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 24 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 25 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 26 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 27 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 28 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 29 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 30 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 31 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 32 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 33 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 34 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 35 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 36 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 37 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 38 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 39 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 40 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 41 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 42 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 43 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 44 | 585 | 374 | 440 | 191 | 448 | 281 | 276 |
| 45 | 451 | 104 | 259 | 383 | 199 | 329 | 213 |
| 46 | | | | | | | |
| 47 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 48 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 49 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 50 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 51 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 52 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 53 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 54 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 55 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 56 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 57 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 58 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 59 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|-------|-------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 4 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 5 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 6 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 7 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 8 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 9 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 10 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 11 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 12 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 13 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 14 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 15 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 16 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 17 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 18 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 19 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 20 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 21 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 22 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 23 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 24 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 25 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 26 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 27 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 28 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 29 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 30 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 31 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 32 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 33 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 34 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 35 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 36 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 37 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 38 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 39 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 40 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 41 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 42 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 43 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 44 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 45 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 46 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 47 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 48 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 49 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 50 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 51 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 52 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 53 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 54 | 14781 | 17102 | 34938 | 19346 | 25528 | 37924 | 6972 |
| 55 | 129 | 129 | 211 | 58 | 157 | 169 | 61 |
| 56 | 129 | 129 | 211 | 58 | 157 | 169 | 61 |
| 57 | 129 | 129 | 211 | 58 | 157 | 169 | 61 |
| 58 | 129 | 129 | 211 | 58 | 157 | 169 | 61 |
| 59 | 4486 | 2906 | 8933 | 4312 | 5023 | 8509 | 2116 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|------|-------|-------|------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 4486 | 2906 | 8933 | 4312 | 5023 | 8509 | 2116 |
| 4 | 28101 | 5902 | 13899 | 14999 | 7909 | 12123 | 13256 |
| 5 | 28101 | 5902 | 13899 | 14999 | 7909 | 12123 | 13256 |
| 6 | 509 | 320 | 915 | 356 | 453 | 813 | 240 |
| 7 | 509 | 320 | 915 | 356 | 453 | 813 | 240 |
| 8 | 509 | 320 | 915 | 356 | 453 | 813 | 240 |
| 9 | 509 | 320 | 915 | 356 | 453 | 813 | 240 |
| 10 | 509 | 320 | 915 | 356 | 453 | 813 | 240 |
| 11 | 509 | 320 | 915 | 356 | 453 | 813 | 240 |
| 12 | 509 | 320 | 915 | 356 | 453 | 813 | 240 |
| 13 | 509 | 320 | 915 | 356 | 453 | 813 | 240 |
| 14 | 509 | 320 | 915 | 356 | 453 | 813 | 240 |
| 15 | 509 | 320 | 915 | 356 | 453 | 813 | 240 |
| 16 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 17 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 18 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 19 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 20 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 21 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 22 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 23 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 24 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 25 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 26 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 27 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 28 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 29 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 30 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 31 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 32 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 33 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 34 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 35 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 36 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 37 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 38 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 39 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 40 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 41 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 42 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 43 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 44 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 45 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 46 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 47 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 48 | 394 | 430 | 568 | 202 | 610 | 337 | 186 |
| 49 | 24 | 76 | 106 | 21 | 36 | 146 | 11 |
| 50 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 51 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 52 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 53 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 54 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 55 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 56 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 57 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 58 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 59 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|--------|--------|-------|--------|--------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 4 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 5 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 6 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 7 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 8 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 9 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 10 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 11 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 12 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 13 | 129 | 68 | 40 | 94 | 74 | 55 | 61 |
| 14 | 96 | 652 | 427 | 112 | 324 | 750 | 45 |
| 15 | 96 | 652 | 427 | 112 | 324 | 750 | 45 |
| 16 | 96 | 652 | 427 | 112 | 324 | 750 | 45 |
| 17 | 96 | 652 | 427 | 112 | 324 | 750 | 45 |
| 18 | 96 | 652 | 427 | 112 | 324 | 750 | 45 |
| 19 | 96 | 652 | 427 | 112 | 324 | 750 | 45 |
| 20 | 224 | 175 | 240 | 133 | 248 | 156 | 106 |
| 21 | 224 | 175 | 240 | 133 | 248 | 156 | 106 |
| 22 | 224 | 175 | 240 | 133 | 248 | 156 | 106 |
| 23 | 224 | 175 | 240 | 133 | 248 | 156 | 106 |
| 24 | 224 | 175 | 240 | 133 | 248 | 156 | 106 |
| 25 | 224 | 175 | 240 | 133 | 248 | 156 | 106 |
| 26 | 224 | 175 | 240 | 133 | 248 | 156 | 106 |
| 27 | 224 | 175 | 240 | 133 | 248 | 156 | 106 |
| 28 | 224 | 175 | 240 | 133 | 248 | 156 | 106 |
| 29 | 224 | 175 | 240 | 133 | 248 | 156 | 106 |
| 30 | 224 | 175 | 240 | 133 | 248 | 156 | 106 |
| 31 | 224 | 175 | 240 | 133 | 248 | 156 | 106 |
| 32 | 224 | 175 | 240 | 133 | 248 | 156 | 106 |
| 33 | 224 | 175 | 240 | 133 | 248 | 156 | 106 |
| 34 | 224 | 175 | 240 | 133 | 248 | 156 | 106 |
| 35 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 36 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 37 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 38 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 39 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 40 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 41 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 42 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 43 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 44 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 45 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 46 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 47 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 48 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 49 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 50 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 51 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 52 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 53 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 54 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 55 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 56 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 57 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 58 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 59 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|--------|--------|-------|--------|--------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 4 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 5 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 6 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 7 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 8 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 9 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 10 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 11 | 39532 | 132414 | 315145 | 34607 | 173793 | 253314 | 18648 |
| 12 | 2985 | 13793 | 34341 | 3872 | 20191 | 26292 | 1408 |
| 13 | 2985 | 13793 | 34341 | 3872 | 20191 | 26292 | 1408 |
| 14 | 2985 | 13793 | 34341 | 3872 | 20191 | 26292 | 1408 |
| 15 | 2985 | 13793 | 34341 | 3872 | 20191 | 26292 | 1408 |
| 16 | 377 | 309 | 521 | 190 | 486 | 268 | 178 |
| 17 | 377 | 309 | 521 | 190 | 486 | 268 | 178 |
| 18 | 377 | 309 | 521 | 190 | 486 | 268 | 178 |
| 19 | 377 | 309 | 521 | 190 | 486 | 268 | 178 |
| 20 | 447 | 351 | 588 | 212 | 536 | 307 | 211 |
| 21 | 1680 | 4029 | 2791 | 551 | 3626 | 2310 | 792 |
| 22 | 1680 | 4029 | 2791 | 551 | 3626 | 2310 | 792 |
| 23 | 1680 | 4029 | 2791 | 551 | 3626 | 2310 | 792 |
| 24 | 1734 | 4087 | 2806 | 575 | 3666 | 2324 | 818 |
| 25 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 26 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 27 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 28 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 29 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 30 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 31 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 32 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 33 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 34 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 35 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 36 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 37 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 38 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 39 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 40 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 41 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 42 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 43 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 44 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 45 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 46 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 47 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 48 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 49 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 50 | 351 | 307 | 520 | 190 | 484 | 267 | 166 |
| 51 | 1731 | 659 | 493 | 1076 | 654 | 534 | 817 |
| 52 | 1731 | 659 | 493 | 1076 | 654 | 534 | 817 |
| 53 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 54 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 55 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 56 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 57 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 58 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 59 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-----|-----|------|-----|------|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 4 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 5 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 6 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 7 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 8 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 9 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 10 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 11 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 12 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 13 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 14 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 15 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 16 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 17 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 18 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 19 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 20 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 21 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 22 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 23 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 24 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 25 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 26 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 27 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 28 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 29 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 30 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 31 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 32 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 33 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 34 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 35 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 36 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 37 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 38 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 39 | 1489 | 382 | 722 | 1508 | 432 | 1215 | 702 |
| 40 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 41 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 42 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 43 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 44 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 45 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 46 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 47 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 48 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 49 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 50 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 51 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 52 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 53 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 54 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 55 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 56 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 57 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 58 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 59 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|------|-------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 4 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 5 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 6 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 7 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 8 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 9 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 10 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 11 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 12 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 13 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 14 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 15 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 16 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 17 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 18 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 19 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 20 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 21 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 22 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 23 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 24 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 25 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 26 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 27 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 28 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 29 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 30 | 1674 | 639 | 490 | 1047 | 644 | 519 | 790 |
| 31 | 20564 | 65228 | 56677 | 7979 | 62229 | 43446 | 9700 |
| 32 | 20564 | 65228 | 56677 | 7979 | 62229 | 43446 | 9700 |
| 33 | | | | | | | |
| 34 | 19920 | 64518 | 56259 | 7674 | 61673 | 43023 | 9397 |
| 35 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 36 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 37 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 38 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 39 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 40 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 41 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 42 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 43 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 44 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 45 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 46 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 47 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 48 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 49 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 50 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 51 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 52 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 53 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 54 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 55 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 56 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 57 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 58 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 59 | 60 | 276 | 183 | 49 | 204 | 218 | 28 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 34 | 157 | 114 | 29 | 108 | 140 | 16 |
| 4 | 34 | 157 | 114 | 29 | 108 | 140 | 16 |
| 5 | 34 | 157 | 114 | 29 | 108 | 140 | 16 |
| 6 | 34 | 157 | 114 | 29 | 108 | 140 | 16 |
| 7 | 34 | 157 | 114 | 29 | 108 | 140 | 16 |
| 8 | 34 | 157 | 114 | 29 | 108 | 140 | 16 |
| 9 | 34 | 157 | 114 | 29 | 108 | 140 | 16 |
| 10 | 34 | 157 | 114 | 29 | 108 | 140 | 16 |
| 11 | 34 | 157 | 114 | 29 | 108 | 140 | 16 |
| 12 | 34 | 157 | 114 | 29 | 108 | 140 | 16 |
| 13 | 34 | 157 | 114 | 29 | 108 | 140 | 16 |
| 14 | 34 | 157 | 114 | 29 | 108 | 140 | 16 |
| 15 | 34 | 157 | 114 | 29 | 108 | 140 | 16 |
| 16 | 34 | 157 | 114 | 29 | 108 | 140 | 16 |
| 17 | 34 | 157 | 114 | 29 | 108 | 140 | 16 |
| 18 | 130 | 49 | 131 | 118 | 68 | 130 | 61 |
| 19 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 20 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 21 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 22 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 23 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 24 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 25 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 26 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 27 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 28 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 29 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 30 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 31 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 32 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 33 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 34 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 35 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 36 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 37 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 38 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 39 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 40 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 41 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 42 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 43 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 44 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 45 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 46 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 47 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 48 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 49 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 50 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 51 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 52 | 15445 | 9508 | 7528 | 6620 | 7184 | 6012 | 7286 |
| 53 | 15492 | 9613 | 7576 | 6647 | 7235 | 6058 | 7308 |
| 54 | 15492 | 9613 | 7576 | 6647 | 7235 | 6058 | 7308 |
| 55 | 15492 | 9613 | 7576 | 6647 | 7235 | 6058 | 7308 |
| 56 | 15506 | 9817 | 7880 | 6641 | 7413 | 6228 | 7314 |
| 57 | 15506 | 9817 | 7880 | 6641 | 7413 | 6228 | 7314 |
| 58 | 15506 | 9817 | 7880 | 6641 | 7413 | 6228 | 7314 |
| 59 | 15506 | 9817 | 7880 | 6641 | 7413 | 6228 | 7314 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 15506 | 9817 | 7880 | 6641 | 7413 | 6228 | 7314 |
| 4 | 139 | 14 | 27 | 107 | 16 | 44 | 66 |
| 5 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 6 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 7 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 8 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 9 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 10 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 11 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 12 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 13 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 14 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 15 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 16 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 17 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 18 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 19 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 20 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 21 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 22 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 23 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 24 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 25 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 26 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 27 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 28 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 29 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 30 | 416 | 0 | 3 | 226 | 0 | 0 | 196 |
| 31 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 32 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 33 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 34 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 35 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 36 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 37 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 38 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 39 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 40 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 41 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 42 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 43 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 44 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 45 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 46 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 47 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 48 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 49 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 50 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 51 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 52 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 53 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 54 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 55 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 56 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 57 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 58 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 59 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|------|-------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 4 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 5 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 6 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 7 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 8 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 9 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 10 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 11 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 12 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 13 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 14 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 15 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 16 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 17 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 18 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 19 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 20 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 21 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 22 | 16286 | 2267 | 2608 | 9730 | 2542 | 2186 | 7682 |
| 23 | 993 | 3600 | 7820 | 1390 | 4949 | 5459 | 468 |
| 24 | 993 | 3600 | 7820 | 1390 | 4949 | 5459 | 468 |
| 25 | 1259 | 3390 | 7658 | 1399 | 4808 | 5048 | 594 |
| 26 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 27 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 28 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 29 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 30 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 31 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 32 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 33 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 34 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 35 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 36 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 37 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 38 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 39 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 40 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 41 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 42 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 43 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 44 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 45 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 46 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 47 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 48 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 49 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 50 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 51 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 52 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 53 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 54 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 55 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 56 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 57 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 58 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 59 | 21047 | 14387 | 10489 | 8617 | 10033 | 8019 | 9928 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|------|-------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 4 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 5 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 6 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 7 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 8 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 9 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 10 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 11 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 12 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 13 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 14 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 15 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 16 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 17 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 18 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 19 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 20 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 21 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 22 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 23 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 24 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 25 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 26 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 27 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 28 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 29 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 30 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 31 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 32 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 33 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 34 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 35 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 36 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 37 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 38 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 39 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 40 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 41 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 42 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 43 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 44 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 45 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 46 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 47 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 48 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 49 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 50 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 51 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 52 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 53 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 54 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 55 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 56 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 57 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 58 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 59 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|------|-------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 4 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 5 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 6 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 7 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 8 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 9 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 10 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 11 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 12 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 13 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 14 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 15 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 16 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 17 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 18 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 19 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 20 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 21 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 22 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 23 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 24 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 25 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 26 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 27 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 28 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 29 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 30 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 31 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 32 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 33 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 34 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 35 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 36 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 37 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 38 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 39 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 40 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 41 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 42 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 43 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 44 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 45 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 46 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 47 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 48 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 49 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 50 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 51 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 52 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 53 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 54 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 55 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 56 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 57 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 58 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 59 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|------|-------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 4 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 5 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 6 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 7 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 8 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 9 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 10 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 11 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 12 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 13 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 14 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 15 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 16 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 17 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 18 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 19 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 20 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 21 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 22 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 23 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 24 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 25 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 26 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 27 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 28 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 29 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 30 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 31 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 32 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 33 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 34 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 35 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 36 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 37 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 38 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 39 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 40 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 41 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 42 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 43 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 44 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 45 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 46 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 47 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 48 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 49 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 50 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 51 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 52 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 53 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 54 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 55 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 56 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 57 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 58 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 59 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|------|-------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 4 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 5 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 6 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 7 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 8 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 9 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 10 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 11 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 12 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 13 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 14 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 15 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 16 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 17 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 18 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 19 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 20 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 21 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 22 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 23 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 24 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 25 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 26 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 27 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 28 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 29 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 30 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 31 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 32 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 33 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 34 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 35 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 36 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 37 | 16656 | 18712 | 45406 | 3964 | 22345 | 25535 | 7857 |
| 38 | 16658 | 18722 | 45435 | 3967 | 22363 | 25538 | 7858 |
| 39 | 889 | 3309 | 7750 | 1336 | 4725 | 4852 | 419 |
| 40 | 16732 | 18820 | 45635 | 3983 | 22435 | 25662 | 7893 |
| 41 | 16732 | 18820 | 45635 | 3983 | 22435 | 25662 | 7893 |
| 42 | 16732 | 18820 | 45635 | 3983 | 22435 | 25662 | 7893 |
| 43 | 937 | 3352 | 7735 | 1366 | 4781 | 4956 | 442 |
| 44 | 937 | 3352 | 7735 | 1366 | 4781 | 4956 | 442 |
| 45 | 937 | 3352 | 7735 | 1366 | 4781 | 4956 | 442 |
| 46 | 937 | 3352 | 7735 | 1366 | 4781 | 4956 | 442 |
| 47 | 937 | 3352 | 7735 | 1366 | 4781 | 4956 | 442 |
| 48 | 937 | 3352 | 7735 | 1366 | 4781 | 4956 | 442 |
| 49 | 937 | 3352 | 7735 | 1366 | 4781 | 4956 | 442 |
| 50 | 937 | 3352 | 7735 | 1366 | 4781 | 4956 | 442 |
| 51 | 937 | 3352 | 7735 | 1366 | 4781 | 4956 | 442 |
| 52 | 937 | 3352 | 7735 | 1366 | 4781 | 4956 | 442 |
| 53 | 16732 | 18823 | 45743 | 3982 | 22456 | 25670 | 7893 |
| 54 | 16732 | 18823 | 45743 | 3982 | 22456 | 25670 | 7893 |
| 55 | 16732 | 18823 | 45743 | 3982 | 22456 | 25670 | 7893 |
| 56 | 16732 | 18823 | 45743 | 3982 | 22456 | 25670 | 7893 |
| 57 | 16732 | 18823 | 45743 | 3982 | 22456 | 25670 | 7893 |
| 58 | 16732 | 18823 | 45743 | 3982 | 22456 | 25670 | 7893 |
| 59 | 16732 | 18823 | 45743 | 3982 | 22456 | 25670 | 7893 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|--------|--------|--------|--------|--------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 16732 | 18823 | 45743 | 3982 | 22456 | 25670 | 7893 |
| 4 | 16732 | 18823 | 45743 | 3982 | 22456 | 25670 | 7893 |
| 5 | 16732 | 18823 | 45743 | 3982 | 22456 | 25670 | 7893 |
| 6 | 16732 | 18823 | 45743 | 3982 | 22456 | 25670 | 7893 |
| 7 | 16732 | 18823 | 45743 | 3982 | 22456 | 25670 | 7893 |
| 8 | 16732 | 18823 | 45743 | 3982 | 22456 | 25670 | 7893 |
| 9 | 16732 | 18823 | 45743 | 3982 | 22456 | 25670 | 7893 |
| 10 | 421740 | 191270 | 624756 | 302850 | 318102 | 396088 | 198941 |
| 11 | 421740 | 191270 | 624756 | 302850 | 318102 | 396088 | 198941 |
| 12 | 421740 | 191270 | 624756 | 302850 | 318102 | 396088 | 198941 |
| 13 | 421740 | 191270 | 624756 | 302850 | 318102 | 396088 | 198941 |
| 14 | 1391 | 1223 | 872 | 1513 | 1104 | 1174 | 656 |
| 15 | 204 | 168 | 280 | 113 | 177 | 184 | 96 |
| 16 | 204 | 168 | 280 | 113 | 177 | 184 | 96 |
| 17 | 204 | 168 | 280 | 113 | 177 | 184 | 96 |
| 18 | 204 | 168 | 280 | 113 | 177 | 184 | 96 |
| 19 | 204 | 168 | 280 | 113 | 177 | 184 | 96 |
| 20 | 204 | 168 | 280 | 113 | 177 | 184 | 96 |
| 21 | 204 | 168 | 280 | 113 | 177 | 184 | 96 |
| 22 | 204 | 168 | 280 | 113 | 177 | 184 | 96 |
| 23 | 1078 | 4021 | 7286 | 1460 | 2367 | 7499 | 509 |
| 24 | 1078 | 4021 | 7286 | 1460 | 2367 | 7499 | 509 |
| 25 | 1078 | 4021 | 7286 | 1460 | 2367 | 7499 | 509 |
| 26 | 1078 | 4021 | 7286 | 1460 | 2367 | 7499 | 509 |
| 27 | 1078 | 4021 | 7286 | 1460 | 2367 | 7499 | 509 |
| 28 | 208 | 174 | 280 | 115 | 179 | 185 | 98 |
| 29 | 208 | 174 | 280 | 115 | 179 | 185 | 98 |
| 30 | 208 | 174 | 280 | 115 | 179 | 185 | 98 |
| 31 | 208 | 174 | 280 | 115 | 179 | 185 | 98 |
| 32 | 208 | 174 | 280 | 115 | 179 | 185 | 98 |
| 33 | 208 | 174 | 280 | 115 | 179 | 185 | 98 |
| 34 | 208 | 174 | 280 | 115 | 179 | 185 | 98 |
| 35 | 208 | 174 | 280 | 115 | 179 | 185 | 98 |
| 36 | 208 | 174 | 280 | 115 | 179 | 185 | 98 |
| 37 | 208 | 174 | 280 | 115 | 179 | 185 | 98 |
| 38 | 208 | 174 | 280 | 115 | 179 | 185 | 98 |
| 39 | 208 | 174 | 280 | 115 | 179 | 185 | 98 |
| 40 | 7184 | 2630 | 5739 | 8760 | 4578 | 5819 | 3389 |
| 41 | 7184 | 2630 | 5739 | 8760 | 4578 | 5819 | 3389 |
| 42 | 7184 | 2630 | 5739 | 8760 | 4578 | 5819 | 3389 |
| 43 | 214 | 99 | 141 | 112 | 95 | 85 | 101 |
| 44 | 259 | 69 | 334 | 78 | 117 | 145 | 122 |
| 45 | 17109 | 6189 | 11463 | 22659 | 4805 | 19105 | 8071 |
| 46 | 17109 | 6189 | 11463 | 22659 | 4805 | 19105 | 8071 |
| 47 | 17109 | 6189 | 11463 | 22659 | 4805 | 19105 | 8071 |
| 48 | 16226 | 14227 | 9915 | 20229 | 11833 | 15507 | 7654 |
| 49 | 16226 | 14227 | 9915 | 20229 | 11833 | 15507 | 7654 |
| 50 | 16226 | 14227 | 9915 | 20229 | 11833 | 15507 | 7654 |
| 51 | 16226 | 14227 | 9915 | 20229 | 11833 | 15507 | 7654 |
| 52 | 16226 | 14227 | 9915 | 20229 | 11833 | 15507 | 7654 |
| 53 | 16226 | 14227 | 9915 | 20229 | 11833 | 15507 | 7654 |
| 54 | 16226 | 14227 | 9915 | 20229 | 11833 | 15507 | 7654 |
| 55 | 16226 | 14227 | 9915 | 20229 | 11833 | 15507 | 7654 |
| 56 | 16226 | 14227 | 9915 | 20229 | 11833 | 15507 | 7654 |
| 57 | 16226 | 14227 | 9915 | 20229 | 11833 | 15507 | 7654 |
| 58 | 16226 | 14227 | 9915 | 20229 | 11833 | 15507 | 7654 |
| 59 | 16226 | 14227 | 9915 | 20229 | 11833 | 15507 | 7654 |
| 60 | 16226 | 14227 | 9915 | 20229 | 11833 | 15507 | 7654 |

| | | | | | | | |
|----|-------|-------|-------|-------|-------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 13116 | 8160 | 13282 | 19725 | 10086 | 16107 | 6187 |
| 4 | 13116 | 8160 | 13282 | 19725 | 10086 | 16107 | 6187 |
| 5 | 13116 | 8160 | 13282 | 19725 | 10086 | 16107 | 6187 |
| 6 | 13138 | 8178 | 13291 | 19750 | 10094 | 16120 | 6197 |
| 7 | 13138 | 8178 | 13291 | 19750 | 10094 | 16120 | 6197 |
| 8 | 13138 | 8178 | 13291 | 19750 | 10094 | 16120 | 6197 |
| 9 | 17672 | 12561 | 12150 | 18941 | 13517 | 12423 | 8336 |
| 10 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 11 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 12 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 13 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 14 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 15 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 16 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 17 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 18 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 19 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 20 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 21 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 22 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 23 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 24 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 25 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 26 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 27 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 28 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 29 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 30 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 31 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 32 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 33 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 34 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 35 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 36 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 37 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 38 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 39 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 40 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 41 | 97 | 12 | 19 | 156 | 53 | 46 | 46 |
| 42 | 397 | 48 | 111 | 314 | 78 | 102 | 187 |
| 43 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 44 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 45 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 46 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 47 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 48 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 49 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 50 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 51 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 52 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 53 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 54 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 55 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 56 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 57 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 58 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 59 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|------|------|------|-----|------|-----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 4 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 5 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 6 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 7 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 8 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 9 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 10 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 11 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 12 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 13 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 14 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 15 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 16 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 17 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 18 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 19 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 20 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 21 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 22 | 9 | 120 | 103 | 13 | 86 | 94 | 4 |
| 23 | 287 | 196 | 475 | 301 | 162 | 449 | 135 |
| 24 | 287 | 196 | 475 | 301 | 162 | 449 | 135 |
| 25 | 258 | 191 | 460 | 277 | 155 | 434 | 122 |
| 26 | 258 | 191 | 460 | 277 | 155 | 434 | 122 |
| 27 | 258 | 191 | 460 | 277 | 155 | 434 | 122 |
| 28 | 258 | 191 | 460 | 277 | 155 | 434 | 122 |
| 29 | 258 | 191 | 460 | 277 | 155 | 434 | 122 |
| 30 | 258 | 191 | 460 | 277 | 155 | 434 | 122 |
| 31 | 258 | 191 | 460 | 277 | 155 | 434 | 122 |
| 32 | 258 | 191 | 460 | 277 | 155 | 434 | 122 |
| 33 | 258 | 191 | 460 | 277 | 155 | 434 | 122 |
| 34 | 258 | 191 | 460 | 277 | 155 | 434 | 122 |
| 35 | 258 | 191 | 460 | 277 | 155 | 434 | 122 |
| 36 | 258 | 191 | 460 | 277 | 155 | 434 | 122 |
| 37 | 258 | 191 | 460 | 277 | 155 | 434 | 122 |
| 38 | 258 | 191 | 460 | 277 | 155 | 434 | 122 |
| 39 | 674 | 156 | 46 | 555 | 130 | 129 | 318 |
| 40 | 284 | 242 | 354 | 392 | 234 | 381 | 134 |
| 41 | 284 | 242 | 354 | 392 | 234 | 381 | 134 |
| 42 | 284 | 242 | 354 | 392 | 234 | 381 | 134 |
| 43 | 284 | 242 | 354 | 392 | 234 | 381 | 134 |
| 44 | 284 | 242 | 354 | 392 | 234 | 381 | 134 |
| 45 | 284 | 242 | 354 | 392 | 234 | 381 | 134 |
| 46 | 284 | 242 | 354 | 392 | 234 | 381 | 134 |
| 47 | 284 | 242 | 354 | 392 | 234 | 381 | 134 |
| 48 | 284 | 242 | 354 | 392 | 234 | 381 | 134 |
| 49 | 284 | 242 | 354 | 392 | 234 | 381 | 134 |
| 50 | 284 | 242 | 354 | 392 | 234 | 381 | 134 |
| 51 | 284 | 242 | 354 | 392 | 234 | 381 | 134 |
| 52 | 284 | 242 | 354 | 392 | 234 | 381 | 134 |
| 53 | 284 | 242 | 354 | 392 | 234 | 381 | 134 |
| 54 | 284 | 242 | 354 | 392 | 234 | 381 | 134 |
| 55 | 963 | 1213 | 1479 | 1258 | 795 | 1744 | 454 |
| 56 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 57 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 58 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 59 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|-------|-------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 4 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 5 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 6 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 7 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 8 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 9 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 10 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 11 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 12 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 13 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 14 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 15 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 16 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 17 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 18 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 19 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 20 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 21 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 22 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 23 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 24 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 25 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 26 | 646 | 149 | 46 | 547 | 127 | 127 | 305 |
| 27 | 1262 | 993 | 2595 | 870 | 1434 | 1321 | 595 |
| 28 | 1290 | 1037 | 2725 | 907 | 1534 | 1365 | 609 |
| 29 | 1290 | 1037 | 2725 | 907 | 1534 | 1365 | 609 |
| 30 | 1290 | 1037 | 2725 | 907 | 1534 | 1365 | 609 |
| 31 | 1290 | 1037 | 2725 | 907 | 1534 | 1365 | 609 |
| 32 | 1290 | 1037 | 2725 | 907 | 1534 | 1365 | 609 |
| 33 | 1290 | 1037 | 2725 | 907 | 1534 | 1365 | 609 |
| 34 | 1290 | 1037 | 2725 | 907 | 1534 | 1365 | 609 |
| 35 | 1290 | 1037 | 2725 | 907 | 1534 | 1365 | 609 |
| 36 | 1290 | 1037 | 2725 | 907 | 1534 | 1365 | 609 |
| 37 | 287 | 243 | 356 | 401 | 235 | 381 | 135 |
| 38 | 287 | 243 | 356 | 401 | 235 | 381 | 135 |
| 39 | 287 | 243 | 356 | 401 | 235 | 381 | 135 |
| 40 | 287 | 243 | 356 | 401 | 235 | 381 | 135 |
| 41 | 287 | 243 | 356 | 401 | 235 | 381 | 135 |
| 42 | 287 | 243 | 356 | 401 | 235 | 381 | 135 |
| 43 | 56638 | 47741 | 58015 | 45744 | 46663 | 40281 | 26717 |
| 44 | 56638 | 47741 | 58015 | 45744 | 46663 | 40281 | 26717 |
| 45 | 56638 | 47741 | 58015 | 45744 | 46663 | 40281 | 26717 |
| 46 | 56638 | 47741 | 58015 | 45744 | 46663 | 40281 | 26717 |
| 47 | 56638 | 47741 | 58015 | 45744 | 46663 | 40281 | 26717 |
| 48 | 56638 | 47741 | 58015 | 45744 | 46663 | 40281 | 26717 |
| 49 | 56638 | 47741 | 58015 | 45744 | 46663 | 40281 | 26717 |
| 50 | 56638 | 47741 | 58015 | 45744 | 46663 | 40281 | 26717 |
| 51 | 56638 | 47741 | 58015 | 45744 | 46663 | 40281 | 26717 |
| 52 | 56638 | 47741 | 58015 | 45744 | 46663 | 40281 | 26717 |
| 53 | 56638 | 47741 | 58015 | 45744 | 46663 | 40281 | 26717 |
| 54 | 56638 | 47741 | 58015 | 45744 | 46663 | 40281 | 26717 |
| 55 | 9 | 122 | 110 | 13 | 86 | 94 | 4 |
| 56 | 29 | 65 | 133 | 56 | 55 | 119 | 14 |
| 57 | 7902 | 6262 | 19647 | 11743 | 9638 | 14450 | 3727 |
| 58 | 7902 | 6262 | 19647 | 11743 | 9638 | 14450 | 3727 |
| 59 | 7902 | 6262 | 19647 | 11743 | 9638 | 14450 | 3727 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|-------|-------|------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 7902 | 6262 | 19647 | 11743 | 9638 | 14450 | 3727 |
| 4 | 7902 | 6262 | 19647 | 11743 | 9638 | 14450 | 3727 |
| 5 | 7902 | 6262 | 19647 | 11743 | 9638 | 14450 | 3727 |
| 6 | 7902 | 6262 | 19647 | 11743 | 9638 | 14450 | 3727 |
| 7 | 7902 | 6262 | 19647 | 11743 | 9638 | 14450 | 3727 |
| 8 | 7902 | 6262 | 19647 | 11743 | 9638 | 14450 | 3727 |
| 9 | 7902 | 6262 | 19647 | 11743 | 9638 | 14450 | 3727 |
| 10 | 7902 | 6262 | 19647 | 11743 | 9638 | 14450 | 3727 |
| 11 | 7902 | 6262 | 19647 | 11743 | 9638 | 14450 | 3727 |
| 12 | 7902 | 6262 | 19647 | 11743 | 9638 | 14450 | 3727 |
| 13 | 7902 | 6262 | 19647 | 11743 | 9638 | 14450 | 3727 |
| 14 | 7902 | 6262 | 19647 | 11743 | 9638 | 14450 | 3727 |
| 15 | 5736 | 2571 | 8561 | 1724 | 3980 | 2663 | 2706 |
| 16 | 5736 | 2571 | 8561 | 1724 | 3980 | 2663 | 2706 |
| 17 | 1744 | 1661 | 1718 | 2240 | 1090 | 2172 | 823 |
| 18 | 230 | 389 | 822 | 206 | 259 | 646 | 108 |
| 19 | 145 | 93 | 45 | 155 | 72 | 70 | 68 |
| 20 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 21 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 22 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 23 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 24 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 25 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 26 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 27 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 28 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 29 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 30 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 31 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 32 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 33 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 34 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 35 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 36 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 37 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 38 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 39 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 40 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 41 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 42 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 43 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 44 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 45 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 46 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 47 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 48 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 49 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 50 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 51 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 52 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 53 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 54 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 55 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 56 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 57 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 58 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 59 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|-------|-------|------|-------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 4 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 5 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 6 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 7 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 8 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 9 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 10 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 11 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 12 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 13 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 14 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 15 | 39 | 51 | 65 | 94 | 95 | 36 | 18 |
| 16 | 122 | 180 | 297 | 160 | 229 | 166 | 58 |
| 17 | 121 | 179 | 297 | 160 | 229 | 166 | 57 |
| 18 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 19 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 20 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 21 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 22 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 23 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 24 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 25 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 26 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 27 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 28 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 29 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 30 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 31 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 32 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 33 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 34 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 35 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 36 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 37 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 38 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 39 | 121 | 176 | 297 | 160 | 228 | 166 | 57 |
| 40 | 39 | 52 | 66 | 94 | 96 | 36 | 18 |
| 41 | 39 | 52 | 66 | 94 | 96 | 36 | 18 |
| 42 | 6760 | 11201 | 19744 | 3182 | 10453 | 10054 | 3189 |
| 43 | 6719 | 11118 | 19614 | 3168 | 10363 | 9975 | 3169 |
| 44 | 6719 | 11118 | 19614 | 3168 | 10363 | 9975 | 3169 |
| 45 | 6719 | 11118 | 19614 | 3168 | 10363 | 9975 | 3169 |
| 46 | 6719 | 11118 | 19614 | 3168 | 10363 | 9975 | 3169 |
| 47 | 6719 | 11118 | 19614 | 3168 | 10363 | 9975 | 3169 |
| 48 | 6719 | 11118 | 19614 | 3168 | 10363 | 9975 | 3169 |
| 49 | 6719 | 11118 | 19614 | 3168 | 10363 | 9975 | 3169 |
| 50 | 6719 | 11118 | 19614 | 3168 | 10363 | 9975 | 3169 |
| 51 | 6719 | 11118 | 19614 | 3168 | 10363 | 9975 | 3169 |
| 52 | 6719 | 11118 | 19614 | 3168 | 10363 | 9975 | 3169 |
| 53 | 526 | 274 | 448 | 326 | 211 | 267 | 248 |
| 54 | 526 | 274 | 448 | 326 | 211 | 267 | 248 |
| 55 | 526 | 274 | 448 | 326 | 211 | 267 | 248 |
| 56 | 526 | 274 | 448 | 326 | 211 | 267 | 248 |
| 57 | 526 | 274 | 448 | 326 | 211 | 267 | 248 |
| 58 | 526 | 274 | 448 | 326 | 211 | 267 | 248 |
| 59 | 526 | 274 | 448 | 326 | 211 | 267 | 248 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|--------|-------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 249 | 422 | 874 | 228 | 267 | 672 | 117 |
| 4 | 249 | 422 | 874 | 228 | 267 | 672 | 117 |
| 5 | 249 | 422 | 874 | 228 | 267 | 672 | 117 |
| 6 | 249 | 422 | 874 | 228 | 267 | 672 | 117 |
| 7 | 249 | 422 | 874 | 228 | 267 | 672 | 117 |
| 8 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 9 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 10 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 11 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 12 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 13 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 14 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 15 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 16 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 17 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 18 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 19 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 20 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 21 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 22 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 23 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 24 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 25 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 26 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 27 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 28 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 29 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 30 | 262 | 86 | 106 | 242 | 102 | 68 | 124 |
| 31 | 94131 | 37039 | 47500 | 104850 | 28142 | 53465 | 44403 |
| 32 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 33 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 34 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 35 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 36 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 37 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 38 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 39 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 40 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 41 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 42 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 43 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 44 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 45 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 46 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 47 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 48 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 49 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 50 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 51 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 52 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 53 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 54 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 55 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 56 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 57 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 58 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 59 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|--------|--------|-------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 4 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 5 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 6 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 7 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 8 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 9 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 10 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 11 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 12 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 13 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 14 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 15 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 16 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 17 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 18 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 19 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 20 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 21 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 22 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 23 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 24 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 25 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 26 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 27 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 28 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 29 | 92154 | 35401 | 45737 | 102489 | 26871 | 51223 | 43470 |
| 30 | 92217 | 35405 | 45743 | 102543 | 26873 | 51227 | 43500 |
| 31 | 92217 | 35405 | 45743 | 102543 | 26873 | 51227 | 43500 |
| 32 | 92217 | 35405 | 45743 | 102543 | 26873 | 51227 | 43500 |
| 33 | 92217 | 35405 | 45743 | 102543 | 26873 | 51227 | 43500 |
| 34 | 92217 | 35405 | 45743 | 102543 | 26873 | 51227 | 43500 |
| 35 | 92217 | 35405 | 45743 | 102543 | 26873 | 51227 | 43500 |
| 36 | 92660 | 35477 | 45867 | 103194 | 26939 | 51293 | 43709 |
| 37 | 92660 | 35477 | 45867 | 103194 | 26939 | 51293 | 43709 |
| 38 | 92660 | 35477 | 45867 | 103194 | 26939 | 51293 | 43709 |
| 39 | 92660 | 35477 | 45867 | 103194 | 26939 | 51293 | 43709 |
| 40 | 54636 | 58281 | 180307 | 31424 | 85813 | 62706 | 25773 |
| 41 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 42 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 43 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 44 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 45 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 46 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 47 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 48 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 49 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 50 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 51 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 52 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 53 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 54 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 55 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 56 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 57 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 58 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 59 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|--------|-------|-------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 4 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 5 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 6 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 7 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 8 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 9 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 10 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 11 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 12 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 13 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 14 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 15 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 16 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 17 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 18 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 19 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 20 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 21 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 22 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 23 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 24 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 25 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 26 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 27 | 54545 | 58147 | 180002 | 31373 | 85640 | 62519 | 25730 |
| 28 | 32525 | 29366 | 54193 | 44420 | 20975 | 45685 | 15342 |
| 29 | 32525 | 29366 | 54193 | 44420 | 20975 | 45685 | 15342 |
| 30 | 32525 | 29366 | 54193 | 44420 | 20975 | 45685 | 15342 |
| 31 | 32525 | 29366 | 54193 | 44420 | 20975 | 45685 | 15342 |
| 32 | 32525 | 29366 | 54193 | 44420 | 20975 | 45685 | 15342 |
| 33 | 32525 | 29366 | 54193 | 44420 | 20975 | 45685 | 15342 |
| 34 | 32525 | 29366 | 54193 | 44420 | 20975 | 45685 | 15342 |
| 35 | 32525 | 29366 | 54193 | 44420 | 20975 | 45685 | 15342 |
| 36 | 32525 | 29366 | 54193 | 44420 | 20975 | 45685 | 15342 |
| 37 | 32525 | 29366 | 54193 | 44420 | 20975 | 45685 | 15342 |
| 38 | 32525 | 29366 | 54193 | 44420 | 20975 | 45685 | 15342 |
| 39 | 32525 | 29366 | 54193 | 44420 | 20975 | 45685 | 15342 |
| 40 | 32525 | 29366 | 54193 | 44420 | 20975 | 45685 | 15342 |
| 41 | 32525 | 29366 | 54193 | 44420 | 20975 | 45685 | 15342 |
| 42 | 32525 | 29366 | 54193 | 44420 | 20975 | 45685 | 15342 |
| 43 | 32525 | 29366 | 54193 | 44420 | 20975 | 45685 | 15342 |
| 44 | 39568 | 5014 | 4975 | 33851 | 5173 | 3998 | 18665 |
| 45 | 39568 | 5014 | 4975 | 33851 | 5173 | 3998 | 18665 |
| 46 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 47 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 48 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 49 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 50 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 51 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 52 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 53 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 54 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 55 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 56 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 57 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 58 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 59 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|-----|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 4 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 5 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 6 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 7 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 8 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 9 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 10 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 11 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 12 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 13 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 14 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 15 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 16 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 17 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 18 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 19 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 20 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 21 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 22 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 23 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 24 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 25 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 26 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 27 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 28 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 29 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 30 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 31 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 32 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 33 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 34 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 35 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 36 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 37 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 38 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 39 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 40 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 41 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 42 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 43 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 44 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 45 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 46 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 47 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 48 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 49 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 50 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 51 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 52 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 53 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 54 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 55 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 56 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 57 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 58 | 3055 | 1030 | 1636 | 3012 | 728 | 1368 | 1441 |
| 59 | 3833 | 994 | 820 | 5020 | 551 | 1871 | 1808 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|-------|------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 266 | 499 | 666 | 330 | 453 | 342 | 125 |
| 4 | 94 | 25 | 80 | 115 | 50 | 41 | 44 |
| 5 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 6 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 7 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 8 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 9 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 10 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 11 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 12 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 13 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 14 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 15 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 16 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 17 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 18 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 19 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 20 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 21 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 22 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 23 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 24 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 25 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 26 | 1637 | 13842 | 20840 | 1841 | 5442 | 16288 | 772 |
| 27 | 181 | 77 | 81 | 187 | 62 | 63 | 85 |
| 28 | 17057 | 8572 | 23929 | 20418 | 8484 | 15512 | 8046 |
| 29 | 17057 | 8572 | 23929 | 20418 | 8484 | 15512 | 8046 |
| 30 | 17057 | 8572 | 23929 | 20418 | 8484 | 15512 | 8046 |
| 31 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 32 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 33 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 34 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 35 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 36 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 37 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 38 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 39 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 40 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 41 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 42 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 43 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 44 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 45 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 46 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 47 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 48 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 49 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 50 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 51 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 52 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 53 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 54 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 55 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 56 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 57 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 58 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 59 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|--------|--------|-------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 4 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 5 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 6 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 7 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 8 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 9 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 10 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 11 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 12 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 13 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 14 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 15 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 16 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 17 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 18 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 19 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 20 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 21 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 22 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 23 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 24 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 25 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 26 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 27 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 28 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 29 | 622 | 442 | 1301 | 694 | 487 | 688 | 293 |
| 30 | 632 | 439 | 1282 | 725 | 466 | 698 | 298 |
| 31 | 77969 | 61949 | 116491 | 104916 | 43068 | 88218 | 36779 |
| 32 | 77969 | 61949 | 116491 | 104916 | 43068 | 88218 | 36779 |
| 33 | 77969 | 61949 | 116491 | 104916 | 43068 | 88218 | 36779 |
| 34 | 77969 | 61949 | 116491 | 104916 | 43068 | 88218 | 36779 |
| 35 | 77969 | 61949 | 116491 | 104916 | 43068 | 88218 | 36779 |
| 36 | 280 | 54 | 68 | 379 | 65 | 94 | 132 |
| 37 | 12436 | 5077 | 11744 | 17128 | 5247 | 8442 | 5866 |
| 38 | 12436 | 5077 | 11744 | 17128 | 5247 | 8442 | 5866 |
| 39 | 12436 | 5077 | 11744 | 17128 | 5247 | 8442 | 5866 |
| 40 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 41 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 42 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 43 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 44 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 45 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 46 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 47 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 48 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 49 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 50 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 51 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 52 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 53 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 54 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 55 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 56 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 57 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 58 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 59 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|------|-------|-------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 4 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 5 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 6 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 7 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 8 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 9 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 10 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 11 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 12 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 13 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 14 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 15 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 16 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 17 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 18 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 19 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 20 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 21 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 22 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 23 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 24 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 25 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 26 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 27 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 28 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 29 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 30 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 31 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 32 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 33 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 34 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 35 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 36 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 37 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 38 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 39 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 40 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 41 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 42 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 43 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 44 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 45 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 46 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 47 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 48 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 49 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 50 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 51 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 52 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 53 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 54 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 55 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 56 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 57 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 58 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 59 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|------|-------|-------|------|-------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 4 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 5 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 6 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 7 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 8 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 9 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 10 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 11 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 12 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 13 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 14 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 15 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 16 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 17 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 18 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 19 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 20 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 21 | 12429 | 5075 | 11733 | 17119 | 5241 | 8436 | 5863 |
| 22 | 413 | 30 | 32 | 381 | 32 | 28 | 195 |
| 23 | 413 | 30 | 32 | 381 | 32 | 28 | 195 |
| 24 | 280 | 53 | 69 | 373 | 62 | 89 | 132 |
| 25 | 538 | 3563 | 2885 | 839 | 2101 | 1793 | 254 |
| 26 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 27 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 28 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 29 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 30 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 31 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 32 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 33 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 34 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 35 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 36 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 37 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 38 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 39 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 40 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 41 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 42 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 43 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 44 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 45 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 46 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 47 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 48 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 49 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 50 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 51 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 52 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 53 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 54 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 55 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 56 | 14380 | 5565 | 10814 | 25193 | 6167 | 10674 | 6783 |
| 57 | 1248 | 342 | 428 | 1573 | 261 | 472 | 589 |
| 58 | 593 | 360 | 1148 | 674 | 393 | 550 | 280 |
| 59 | | | | | | | |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|-------|-------|-------|------|-------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 684 | 182 | 533 | 627 | 171 | 257 | 323 |
| 4 | 684 | 182 | 533 | 627 | 171 | 257 | 323 |
| 5 | 684 | 182 | 533 | 627 | 171 | 257 | 323 |
| 6 | 684 | 182 | 533 | 627 | 171 | 257 | 323 |
| 7 | 684 | 182 | 533 | 627 | 171 | 257 | 323 |
| 8 | 684 | 182 | 533 | 627 | 171 | 257 | 323 |
| 9 | 684 | 182 | 533 | 627 | 171 | 257 | 323 |
| 10 | 684 | 182 | 533 | 627 | 171 | 257 | 323 |
| 11 | 684 | 182 | 533 | 627 | 171 | 257 | 323 |
| 12 | 684 | 182 | 533 | 627 | 171 | 257 | 323 |
| 13 | 684 | 182 | 533 | 627 | 171 | 257 | 323 |
| 14 | 684 | 182 | 533 | 627 | 171 | 257 | 323 |
| 15 | 684 | 182 | 533 | 627 | 171 | 257 | 323 |
| 16 | 684 | 182 | 533 | 627 | 171 | 257 | 323 |
| 17 | 684 | 182 | 533 | 627 | 171 | 257 | 323 |
| 18 | 684 | 182 | 533 | 627 | 171 | 257 | 323 |
| 19 | 684 | 182 | 533 | 627 | 171 | 257 | 323 |
| 20 | 684 | 182 | 533 | 627 | 171 | 257 | 323 |
| 21 | 684 | 182 | 533 | 627 | 171 | 257 | 323 |
| 22 | 24282 | 11450 | 13721 | 32373 | 6905 | 13623 | 11454 |
| 23 | 88 | 19 | 66 | 111 | 38 | 28 | 42 |
| 24 | 3097 | 1562 | 3803 | 4718 | 1574 | 2526 | 1461 |
| 25 | 3068 | 1450 | 3627 | 4697 | 1500 | 2390 | 1447 |
| 26 | 3068 | 1450 | 3627 | 4697 | 1500 | 2390 | 1447 |
| 27 | 3068 | 1450 | 3627 | 4697 | 1500 | 2390 | 1447 |
| 28 | 3031 | 1394 | 3570 | 4639 | 1465 | 2310 | 1430 |
| 29 | 3031 | 1394 | 3570 | 4639 | 1465 | 2310 | 1430 |
| 30 | 3031 | 1394 | 3570 | 4639 | 1465 | 2310 | 1430 |
| 31 | 3031 | 1394 | 3570 | 4639 | 1465 | 2310 | 1430 |
| 32 | 3031 | 1394 | 3570 | 4639 | 1465 | 2310 | 1430 |
| 33 | 3031 | 1394 | 3570 | 4639 | 1465 | 2310 | 1430 |
| 34 | 3031 | 1394 | 3570 | 4639 | 1465 | 2310 | 1430 |
| 35 | 3031 | 1394 | 3570 | 4639 | 1465 | 2310 | 1430 |
| 36 | 3031 | 1394 | 3570 | 4639 | 1465 | 2310 | 1430 |
| 37 | 3031 | 1394 | 3570 | 4639 | 1465 | 2310 | 1430 |
| 38 | 3031 | 1394 | 3570 | 4639 | 1465 | 2310 | 1430 |
| 39 | 3031 | 1394 | 3570 | 4639 | 1465 | 2310 | 1430 |
| 40 | 112 | 62 | 96 | 142 | 28 | 80 | 53 |
| 41 | 112 | 62 | 96 | 142 | 28 | 80 | 53 |
| 42 | 112 | 62 | 96 | 142 | 28 | 80 | 53 |
| 43 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 44 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 45 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 46 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 47 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 48 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 49 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 50 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 51 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 52 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 53 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 54 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 55 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 56 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 57 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 58 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 59 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|------|-------|-------|------|------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 4 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 5 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 6 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 7 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 8 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 9 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 10 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 11 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 12 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 13 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 14 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 15 | 736 | 290 | 367 | 1045 | 211 | 359 | 347 |
| 16 | 468 | 418 | 1094 | 530 | 364 | 512 | 221 |
| 17 | 2614 | 1964 | 3107 | 4557 | 1331 | 2599 | 1233 |
| 18 | 641 | 220 | 504 | 858 | 243 | 298 | 302 |
| 19 | 637 | 220 | 504 | 857 | 243 | 298 | 300 |
| 20 | 637 | 220 | 504 | 857 | 243 | 298 | 300 |
| 21 | 23 | 48 | 102 | 117 | 74 | 57 | 11 |
| 22 | 23 | 48 | 102 | 117 | 74 | 57 | 11 |
| 23 | 23 | 48 | 102 | 117 | 74 | 57 | 11 |
| 24 | 23 | 48 | 102 | 117 | 74 | 57 | 11 |
| 25 | 23 | 48 | 102 | 117 | 74 | 57 | 11 |
| 26 | 23 | 48 | 102 | 117 | 74 | 57 | 11 |
| 27 | 23 | 48 | 102 | 117 | 74 | 57 | 11 |
| 28 | 23 | 48 | 102 | 117 | 74 | 57 | 11 |
| 29 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 30 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 31 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 32 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 33 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 34 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 35 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 36 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 37 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 38 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 39 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 40 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 41 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 42 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 43 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 44 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 45 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 46 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 47 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 48 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 49 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 50 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 51 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 52 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 53 | 9805 | 3731 | 8474 | 14790 | 3512 | 6012 | 4625 |
| 54 | 6209 | 2098 | 2310 | 8969 | 1582 | 2494 | 2929 |
| 55 | 6209 | 2098 | 2310 | 8969 | 1582 | 2494 | 2929 |
| 56 | 21313 | 7856 | 10184 | 26153 | 5462 | 7619 | 10054 |
| 57 | 6215 | 2102 | 2310 | 8980 | 1582 | 2497 | 2932 |
| 58 | | | | | | | |
| 59 | | | | | | | |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|------|------|-------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 6215 | 2102 | 2310 | 8980 | 1582 | 2497 | 2932 |
| 4 | 7425 | 2909 | 4674 | 13407 | 2508 | 4965 | 3502 |
| 5 | 7425 | 2909 | 4674 | 13407 | 2508 | 4965 | 3502 |
| 6 | 7425 | 2909 | 4674 | 13407 | 2508 | 4965 | 3502 |
| 7 | 7425 | 2909 | 4674 | 13407 | 2508 | 4965 | 3502 |
| 8 | 7880 | 3144 | 4988 | 14146 | 2601 | 5301 | 3717 |
| 9 | 7880 | 3144 | 4988 | 14146 | 2601 | 5301 | 3717 |
| 10 | 7880 | 3144 | 4988 | 14146 | 2601 | 5301 | 3717 |
| 11 | 7880 | 3144 | 4988 | 14146 | 2601 | 5301 | 3717 |
| 12 | 7880 | 3144 | 4988 | 14146 | 2601 | 5301 | 3717 |
| 13 | 7880 | 3144 | 4988 | 14146 | 2601 | 5301 | 3717 |
| 14 | 7880 | 3144 | 4988 | 14146 | 2601 | 5301 | 3717 |
| 15 | 7880 | 3144 | 4988 | 14146 | 2601 | 5301 | 3717 |
| 16 | 7880 | 3144 | 4988 | 14146 | 2601 | 5301 | 3717 |
| 17 | 7880 | 3144 | 4988 | 14146 | 2601 | 5301 | 3717 |
| 18 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 19 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 20 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 21 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 22 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 23 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 24 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 25 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 26 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 27 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 28 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 29 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 30 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 31 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 32 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 33 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 34 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 35 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 36 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 37 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 38 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 39 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 40 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 41 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 42 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 43 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 44 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 45 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 46 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 47 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 48 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 49 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 50 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 51 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 52 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 53 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 54 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 55 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 56 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 57 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 58 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 59 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|------|------|-------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 4 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 5 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 6 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 7 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 8 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 9 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 10 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 11 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 12 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 13 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 14 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 15 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 16 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 17 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 18 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 19 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 20 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 21 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 22 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 23 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 24 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 25 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 26 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 27 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 28 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 29 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 30 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 31 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 32 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 33 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 34 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 35 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 36 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 37 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 38 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 39 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 40 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 41 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 42 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 43 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 44 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 45 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 46 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 47 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 48 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 49 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 50 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 51 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 52 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 53 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 54 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 55 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 56 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 57 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 58 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 59 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|------|------|-------|------|------|-------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 4 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 5 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 6 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 7 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 8 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 9 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 10 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 11 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 12 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 13 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 14 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 15 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 16 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 17 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 18 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 19 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 20 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 21 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 22 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 23 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 24 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 25 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 26 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 27 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 28 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 29 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 30 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 31 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 32 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 33 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 34 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 35 | 21169 | 7736 | 9936 | 25956 | 5353 | 7396 | 9986 |
| 36 | 21220 | 7760 | 9965 | 26046 | 5361 | 7427 | 10010 |
| 37 | 1432 | 405 | 577 | 1898 | 357 | 467 | 675 |
| 38 | 1432 | 405 | 577 | 1898 | 357 | 467 | 675 |
| 39 | 1432 | 405 | 577 | 1898 | 357 | 467 | 675 |
| 40 | 1432 | 405 | 577 | 1898 | 357 | 467 | 675 |
| 41 | 1436 | 405 | 582 | 1901 | 357 | 468 | 677 |
| 42 | 9277 | 3278 | 7483 | 14102 | 3134 | 5348 | 4376 |
| 43 | 9277 | 3278 | 7483 | 14102 | 3134 | 5348 | 4376 |
| 44 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 45 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 46 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 47 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 48 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 49 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 50 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 51 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 52 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 53 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 54 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 55 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 56 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 57 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 58 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 59 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|-------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 4 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 5 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 6 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 7 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 8 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 9 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 10 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 11 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 12 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 13 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 14 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 15 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 16 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 17 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 18 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 19 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 20 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 21 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 22 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 23 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 24 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 25 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 26 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 27 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 28 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 29 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 30 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 31 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 32 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 33 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 34 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 35 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 36 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 37 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 38 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 39 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 40 | 9212 | 3220 | 7446 | 14071 | 3085 | 5296 | 4345 |
| 41 | | | | | | | |
| 42 | 85 | 631 | 1061 | 77 | 157 | 708 | 40 |
| 43 | 85 | 631 | 1061 | 77 | 157 | 708 | 40 |
| 44 | 85 | 631 | 1061 | 77 | 157 | 708 | 40 |
| 45 | 85 | 631 | 1061 | 77 | 157 | 708 | 40 |
| 46 | 85 | 631 | 1061 | 77 | 157 | 708 | 40 |
| 47 | 85 | 631 | 1061 | 77 | 157 | 708 | 40 |
| 48 | 85 | 631 | 1061 | 77 | 157 | 708 | 40 |
| 49 | | | | | | | |
| 50 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 51 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 52 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 53 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 54 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 55 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 56 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 57 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 58 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 59 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 4 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 5 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 6 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 7 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 8 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 9 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 10 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 11 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 12 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 13 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 14 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 15 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 16 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 17 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 18 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 19 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 20 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 21 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 22 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 23 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 24 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 25 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 26 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 27 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 28 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 29 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 30 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 31 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 32 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 33 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 34 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 35 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 36 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 37 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 38 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 39 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 40 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 41 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 42 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 43 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 44 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 45 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 46 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 47 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 48 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 49 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 50 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 51 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 52 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 53 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 54 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 55 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 56 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 57 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 58 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 59 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------|------|------|------|------|------|------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 4 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 5 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 6 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 7 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 8 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 9 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 10 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 11 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 12 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 13 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 14 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 15 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 16 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 17 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 18 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 19 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 20 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 21 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 22 | 3509 | 1343 | 2600 | 4106 | 1021 | 1409 | 1655 |
| 23 | 353 | 32 | 32 | 375 | 25 | 24 | 167 |
| 24 | 1333 | 68 | 66 | 1485 | 40 | 93 | 629 |
| 25 | 139 | 14 | 13 | 194 | 5 | 24 | 66 |
| 26 | 1135 | 62 | 48 | 1451 | 31 | 72 | 535 |
| 27 | 80 | 186 | 891 | 58 | 98 | 327 | 38 |
| 28 | 80 | 186 | 891 | 58 | 98 | 327 | 38 |
| 29 | 80 | 186 | 891 | 58 | 98 | 327 | 38 |
| 30 | 80 | 186 | 891 | 58 | 98 | 327 | 38 |
| 31 | 80 | 186 | 891 | 58 | 98 | 327 | 38 |
| 32 | 2726 | 391 | 642 | 5637 | 354 | 1052 | 1286 |
| 33 | 2726 | 391 | 642 | 5637 | 354 | 1052 | 1286 |
| 34 | 2726 | 391 | 642 | 5637 | 354 | 1052 | 1286 |
| 35 | 2726 | 391 | 642 | 5637 | 354 | 1052 | 1286 |
| 36 | 2726 | 391 | 642 | 5637 | 354 | 1052 | 1286 |
| 37 | 2726 | 391 | 642 | 5637 | 354 | 1052 | 1286 |
| 38 | 2726 | 391 | 642 | 5637 | 354 | 1052 | 1286 |
| 39 | 2726 | 391 | 642 | 5637 | 354 | 1052 | 1286 |
| 40 | 2726 | 391 | 642 | 5637 | 354 | 1052 | 1286 |
| 41 | 2726 | 391 | 642 | 5637 | 354 | 1052 | 1286 |
| 42 | 2726 | 391 | 642 | 5637 | 354 | 1052 | 1286 |
| 43 | 2726 | 391 | 642 | 5637 | 354 | 1052 | 1286 |
| 44 | 2726 | 391 | 642 | 5637 | 354 | 1052 | 1286 |
| 45 | 2726 | 391 | 642 | 5637 | 354 | 1052 | 1286 |
| 46 | 2726 | 391 | 642 | 5637 | 354 | 1052 | 1286 |
| 47 | 2737 | 393 | 647 | 5661 | 355 | 1054 | 1291 |
| 48 | 1235 | 5 | 8 | 1813 | 3 | 18 | 583 |
| 49 | 1235 | 5 | 8 | 1813 | 3 | 18 | 583 |
| 50 | 1235 | 5 | 8 | 1813 | 3 | 18 | 583 |
| 51 | 1235 | 5 | 8 | 1813 | 3 | 18 | 583 |
| 52 | 1235 | 5 | 8 | 1813 | 3 | 18 | 583 |
| 53 | 1235 | 5 | 8 | 1813 | 3 | 18 | 583 |
| 54 | 1235 | 5 | 8 | 1813 | 3 | 18 | 583 |
| 55 | 1235 | 5 | 8 | 1813 | 3 | 18 | 583 |
| 56 | 330 | 11 | 255 | 850 | 12 | 11 | 156 |
| 57 | 146 | 0 | 0 | 533 | 0 | 0 | 69 |
| 58 | 146 | 0 | 0 | 533 | 0 | 0 | 69 |
| 59 | 146 | 0 | 0 | 533 | 0 | 0 | 69 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----|---|-----|-----|---|---|----|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 146 | 0 | 0 | 533 | 0 | 0 | 69 |
| 4 | 146 | 0 | 0 | 533 | 0 | 0 | 69 |
| 5 | 146 | 0 | 0 | 533 | 0 | 0 | 69 |
| 6 | 146 | 0 | 0 | 533 | 0 | 0 | 69 |
| 7 | 146 | 0 | 0 | 533 | 0 | 0 | 69 |
| 8 | 146 | 0 | 0 | 533 | 0 | 0 | 69 |
| 9 | 146 | 0 | 0 | 533 | 0 | 0 | 69 |
| 10 | 146 | 0 | 0 | 533 | 0 | 0 | 69 |
| 11 | 146 | 0 | 0 | 533 | 0 | 0 | 69 |
| 12 | 146 | 0 | 0 | 533 | 0 | 0 | 69 |
| 13 | 146 | 0 | 0 | 533 | 0 | 0 | 69 |
| 14 | 146 | 0 | 0 | 533 | 0 | 0 | 69 |
| 15 | 146 | 0 | 0 | 533 | 0 | 0 | 69 |
| 16 | 146 | 0 | 0 | 533 | 0 | 0 | 69 |
| 17 | 146 | 0 | 0 | 533 | 0 | 0 | 69 |
| 18 | 147 | 0 | 0 | 543 | 0 | 0 | 69 |
| 19 | 147 | 0 | 0 | 543 | 0 | 0 | 69 |
| 20 | 147 | 0 | 0 | 543 | 0 | 0 | 69 |
| 21 | 147 | 0 | 0 | 543 | 0 | 0 | 69 |
| 22 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 23 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 24 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 25 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 26 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 27 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 28 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 29 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 30 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 31 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 32 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 33 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 34 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 35 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 36 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 37 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 38 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 39 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 40 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 41 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 42 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 43 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 44 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 45 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 46 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 47 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 48 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 49 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 50 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 51 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 52 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 53 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 54 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 55 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 56 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 57 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 58 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 59 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----|---|-----|---|---|---|---|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 4 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 5 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 6 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 7 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 8 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 9 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 10 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 11 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 12 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 13 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 14 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 15 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 16 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 17 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 18 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 19 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 20 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 21 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 22 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 23 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 24 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 25 | 14 | 1 | 467 | 0 | 0 | 2 | 7 |
| 26 | 7 | 0 | 893 | 2 | 0 | 0 | 3 |
| 27 | | | | | | | |
| 28 | | | | | | | |
| 29 | | | | | | | |
| 30 | | | | | | | |
| 31 | | | | | | | |
| 32 | | | | | | | |
| 33 | | | | | | | |
| 34 | | | | | | | |
| 35 | | | | | | | |
| 36 | | | | | | | |
| 37 | | | | | | | |
| 38 | | | | | | | |
| 39 | | | | | | | |
| 40 | | | | | | | |
| 41 | | | | | | | |
| 42 | | | | | | | |
| 43 | | | | | | | |
| 44 | | | | | | | |
| 45 | | | | | | | |
| 46 | | | | | | | |
| 47 | | | | | | | |
| 48 | | | | | | | |
| 49 | | | | | | | |
| 50 | | | | | | | |
| 51 | | | | | | | |
| 52 | | | | | | | |
| 53 | | | | | | | |
| 54 | | | | | | | |
| 55 | | | | | | | |
| 56 | | | | | | | |
| 57 | | | | | | | |
| 58 | | | | | | | |
| 59 | | | | | | | |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|------------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 298.79 | 474 | 124 | 0.99 | -1.9345469 | -2.058 | 0.03956937 |
| 4 | 298.79 | 474 | 124 | 0.99 | -1.9345469 | -2.058 | 0.03956937 |
| 5 | 298.79 | 474 | 124 | 0.99 | -1.9345469 | -2.058 | 0.03956937 |
| 6 | 298.79 | 474 | 124 | 0.99 | -1.9345469 | -2.058 | 0.03956937 |
| 7 | 298.79 | 474 | 124 | 0.99 | -1.9345469 | -2.058 | 0.03956937 |
| 8 | 298.79 | 474 | 124 | 0.99 | -1.9345469 | -2.058 | 0.03956937 |
| 9 | 298.79 | 474 | 124 | 0.99 | -1.9345469 | -2.058 | 0.03956937 |
| 10 | 300.18 | 476 | 124 | 0.99 | -1.9406215 | -2.069 | 0.03858368 |
| 11 | 747.37 | 1314 | 181 | 0.985 | -2.8599037 | -2.221 | 0.02635303 |
| 12 | 747.37 | 1314 | 181 | 0.985 | -2.8599037 | -2.221 | 0.02635303 |
| 13 | 747.37 | 1314 | 181 | 0.985 | -2.8599037 | -2.221 | 0.02635303 |
| 14 | 747.37 | 1314 | 181 | 0.985 | -2.8599037 | -2.221 | 0.02635303 |
| 15 | 747.37 | 1314 | 181 | 0.985 | -2.8599037 | -2.221 | 0.02635303 |
| 16 | 747.37 | 1314 | 181 | 0.985 | -2.8599037 | -2.221 | 0.02635303 |
| 17 | 747.37 | 1314 | 181 | 0.985 | -2.8599037 | -2.221 | 0.02635303 |
| 18 | 747.37 | 1314 | 181 | 0.985 | -2.8599037 | -2.221 | 0.02635303 |
| 19 | 747.37 | 1314 | 181 | 0.985 | -2.8599037 | -2.221 | 0.02635303 |
| 20 | 747.37 | 1314 | 181 | 0.985 | -2.8599037 | -2.221 | 0.02635303 |
| 21 | 747.37 | 1314 | 181 | 0.985 | -2.8599037 | -2.221 | 0.02635303 |
| 22 | 747.37 | 1314 | 181 | 0.985 | -2.8599037 | -2.221 | 0.02635303 |
| 23 | 456.22 | 804 | 109 | 0.988 | -2.8828674 | -2.082 | 0.03737477 |
| 24 | 456.22 | 804 | 109 | 0.988 | -2.8828674 | -2.082 | 0.03737477 |
| 25 | 456.22 | 804 | 109 | 0.988 | -2.8828674 | -2.082 | 0.03737477 |
| 26 | 456.22 | 804 | 109 | 0.988 | -2.8828674 | -2.082 | 0.03737477 |
| 27 | 456.22 | 804 | 109 | 0.988 | -2.8828674 | -2.082 | 0.03737477 |
| 28 | 456.22 | 804 | 109 | 0.988 | -2.8828674 | -2.082 | 0.03737477 |
| 29 | 456.22 | 804 | 109 | 0.988 | -2.8828674 | -2.082 | 0.03737477 |
| 30 | 456.22 | 804 | 109 | 0.988 | -2.8828674 | -2.082 | 0.03737477 |
| 31 | 456.22 | 804 | 109 | 0.988 | -2.8828674 | -2.082 | 0.03737477 |
| 32 | 456.22 | 804 | 109 | 0.988 | -2.8828674 | -2.082 | 0.03737477 |
| 33 | 456.22 | 804 | 109 | 0.988 | -2.8828674 | -2.082 | 0.03737477 |
| 34 | 456.22 | 804 | 109 | 0.988 | -2.8828674 | -2.082 | 0.03737477 |
| 35 | 456.22 | 804 | 109 | 0.988 | -2.8828674 | -2.082 | 0.03737477 |
| 36 | 456.22 | 804 | 109 | 0.988 | -2.8828674 | -2.082 | 0.03737477 |
| 37 | 456.22 | 804 | 109 | 0.988 | -2.8828674 | -2.082 | 0.03737477 |
| 38 | 456.22 | 804 | 109 | 0.988 | -2.8828674 | -2.082 | 0.03737477 |
| 39 | 437.94 | 0 | 876 | 1.567 | #DIV/0! | 2.867 | NA |
| 40 | 403.97 | 0 | 808 | 1.51 | #DIV/0! | 2.837 | NA |
| 41 | 171.65 | 0 | 343 | 1.186 | #DIV/0! | 2.521 | NA |
| 42 | 141.75 | 0 | 283 | 3691349.76 | #DIV/0! | 5.902 | NA |
| 43 | 125.71 | 0 | 251 | 4829582.72 | #DIV/0! | 6.007 | NA |
| 44 | 125.08 | 0 | 250 | 4228034 | #DIV/0! | 5.955 | NA |
| 45 | 101.92 | 0 | 203 | 1.108 | #DIV/0! | 2.328 | NA |
| 46 | 86.64 | 0 | 173 | 3621108.59 | #DIV/0! | 5.894 | NA |
| 47 | 31.13 | 0 | 62 | 1416934 | #DIV/0! | 5.529 | NA |
| 48 | 30.9 | 0 | 62 | 1402888.26 | #DIV/0! | 5.525 | NA |
| 49 | 26.6 | 0 | 53 | 1.276 | #DIV/0! | 2.901 | NA |
| 50 | 24.4 | 0 | 48 | 1.229 | #DIV/0! | 2.845 | NA |
| 51 | 768.48 | 1 | 1536 | 1.526 | 10.5849625 | 2.851 | NA |
| 52 | 1282.5 | 2 | 2563 | 1.369 | 10.3236178 | 2.758 | NA |
| 53 | 2117.84 | 4 | 4232 | 1.273 | 10.0471239 | 2.67 | NA |
| 54 | 506.52 | 1 | 1012 | 1.311 | 9.98299357 | 2.696 | NA |
| 55 | | | | | | | |
| 56 | | | | | | | |
| 57 | | | | | | | |
| 58 | | | | | | | |
| 59 | | | | | | | |
| 60 | | | | | | | |

| | | | | | | |
|----|--------|----|-----|-------|------------|----------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | 364.3 | 1 | 728 | 1.213 | 9.50779464 | 2.572 NA |
| 4 | 274.52 | 1 | 548 | 1.156 | 9.09803208 | 2.467 NA |
| 5 | 103.39 | 1 | 206 | 1.043 | 7.68650053 | 1.971 NA |
| 6 | 146.88 | 7 | 287 | 1.685 | 5.357552 | 3.378 NA |
| 7 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 8 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 9 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 10 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 11 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 12 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 13 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 14 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 15 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 16 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 17 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 18 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 19 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 20 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 21 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 22 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 23 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 24 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 25 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 26 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 27 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 28 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 29 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 30 | 34.8 | 2 | 68 | 1.121 | 5.08746284 | 2.828 NA |
| 31 | 52.09 | 5 | 99 | 1.085 | 4.30742853 | 2.804 NA |
| 32 | 40.97 | 4 | 78 | 1.08 | 4.28540222 | 2.774 NA |
| 33 | 137.78 | 17 | 259 | 1.032 | 3.92934545 | 2.42 NA |
| 34 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 35 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 36 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 37 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 38 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 39 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 40 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 41 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 42 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 43 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 44 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 45 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 46 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 47 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 48 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 49 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 50 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 51 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 52 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 53 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 54 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 55 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 56 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 57 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 58 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 59 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 60 | | | | | | |

| | | | | | | |
|----|--------|----|-----|-------|------------|----------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 4 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 5 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 6 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 7 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 8 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 9 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 10 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 11 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 12 | 137.7 | 17 | 258 | 1.032 | 3.92376441 | 2.42 NA |
| 13 | 138.36 | 18 | 259 | 1.031 | 3.84688329 | 2.4 NA |
| 14 | 152.59 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 15 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 16 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 17 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 18 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 19 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 20 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 21 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 22 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 23 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 24 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 25 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 26 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 27 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 28 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 29 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 30 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 31 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 32 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 33 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 34 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 35 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 36 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 37 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 38 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 39 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 40 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 41 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 42 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 43 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 44 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 45 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 46 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 47 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 48 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 49 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 50 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 51 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 52 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 53 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 54 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 55 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 56 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 57 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 58 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 59 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 60 | | | | | | |

| | | | | | | |
|----|--------|----|-----|-------|------------|----------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 4 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 5 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 6 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 7 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 8 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 9 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 10 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 11 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 12 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 13 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 14 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 15 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 16 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 17 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 18 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 19 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 20 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 21 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 22 | 152.51 | 22 | 283 | 1.033 | 3.68522662 | 2.488 NA |
| 23 | 41.74 | 10 | 73 | 1.009 | 2.86789646 | 1.857 NA |
| 24 | 41.74 | 10 | 73 | 1.009 | 2.86789646 | 1.857 NA |
| 25 | 41.74 | 10 | 73 | 1.009 | 2.86789646 | 1.857 NA |
| 26 | 41.74 | 10 | 73 | 1.009 | 2.86789646 | 1.857 NA |
| 27 | 41.74 | 10 | 73 | 1.009 | 2.86789646 | 1.857 NA |
| 28 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 29 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 30 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 31 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 32 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 33 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 34 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 35 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 36 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 37 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 38 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 39 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 40 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 41 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 42 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 43 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 44 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 45 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 46 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 47 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 48 | 29.04 | 7 | 51 | 1.008 | 2.86507042 | 1.766 NA |
| 49 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 50 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 51 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 52 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 53 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 54 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 55 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 56 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 57 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 58 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 59 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 60 | | | | | | |

| | | | | | | |
|----|--------|-----|-----|-------|------------|----------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 4 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 5 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 6 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 7 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 8 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 9 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 10 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 11 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 12 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 13 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 14 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 15 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 16 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 17 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 18 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 19 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 20 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 21 | 38.69 | 10 | 67 | 1.01 | 2.7441611 | 1.925 NA |
| 22 | 41.23 | 11 | 72 | 1.01 | 2.71049338 | 1.946 NA |
| 23 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 24 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 25 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 26 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 27 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 28 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 29 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 30 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 31 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 32 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 33 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 34 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 35 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 36 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 37 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 38 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 39 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 40 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 41 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 42 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 43 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 44 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 45 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 46 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 47 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 48 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 49 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 50 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 51 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 52 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 53 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 54 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 55 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 56 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 57 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 58 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 59 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 60 | | | | | | |

| | | | | | | |
|----|--------|-----|------|-------|------------|----------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | 456.24 | 125 | 788 | 1.011 | 2.65626753 | 2.032 NA |
| 4 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 5 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 6 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 7 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 8 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 9 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 10 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 11 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 12 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 13 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 14 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 15 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 16 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 17 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 18 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 19 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 20 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 21 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 22 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 23 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 24 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 25 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 26 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 27 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 28 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 29 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 30 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 31 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 32 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 33 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 34 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 35 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 36 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 37 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 38 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 39 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 40 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 41 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 42 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 43 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 44 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 45 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 46 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 47 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 48 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 49 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 50 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 51 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 52 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 53 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 54 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 55 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 56 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 57 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 58 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 59 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 NA |
| 60 | | | | | | |

| | | | | | | | |
|----|--------|-----|------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 4 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 5 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 6 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 7 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 8 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 9 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 10 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 11 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 12 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 13 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 14 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 15 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 16 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 17 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 18 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 19 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 20 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 21 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 22 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 23 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 24 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 25 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 26 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 27 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 28 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 29 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 30 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 31 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 32 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 33 | 790.66 | 253 | 1328 | 1.011 | 2.39204586 | 2.076 | NA |
| 34 | 804.54 | 258 | 1351 | 1.011 | 2.3885847 | 2.076 | NA |
| 35 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 36 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 37 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 38 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 39 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 40 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 41 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 42 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 43 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 44 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 45 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 46 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 47 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 48 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 49 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 50 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 51 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 52 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 53 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 54 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 55 | 42.45 | 14 | 70 | 1.007 | 2.32192809 | 1.802 | 0.07154974 |
| 56 | 185.39 | 62 | 309 | 1.008 | 2.31726672 | 1.839 | 0.06584198 |
| 57 | 184.76 | 62 | 308 | 1.008 | 2.31259023 | 1.836 | 0.0663934 |
| 58 | 184.76 | 62 | 308 | 1.008 | 2.31259023 | 1.836 | 0.0663934 |
| 59 | 184.76 | 62 | 308 | 1.008 | 2.31259023 | 1.836 | 0.0663934 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 184.76 | 62 | 308 | 1.008 | 2.31259023 | 1.836 | 0.0663934 |
| 4 | 184.76 | 62 | 308 | 1.008 | 2.31259023 | 1.836 | 0.0663934 |
| 5 | 184.76 | 62 | 308 | 1.008 | 2.31259023 | 1.836 | 0.0663934 |
| 6 | 184.76 | 62 | 308 | 1.008 | 2.31259023 | 1.836 | 0.0663934 |
| 7 | 184.76 | 62 | 308 | 1.008 | 2.31259023 | 1.836 | 0.0663934 |
| 8 | 184.76 | 62 | 308 | 1.008 | 2.31259023 | 1.836 | 0.0663934 |
| 9 | 184.76 | 62 | 308 | 1.008 | 2.31259023 | 1.836 | 0.0663934 |
| 10 | 50.47 | 17 | 84 | 1.008 | 2.30485458 | 1.886 | 0.05930402 |
| 11 | 50.47 | 17 | 84 | 1.008 | 2.30485458 | 1.886 | 0.05930402 |
| 12 | 50.47 | 17 | 84 | 1.008 | 2.30485458 | 1.886 | 0.05930402 |
| 13 | 50.47 | 17 | 84 | 1.008 | 2.30485458 | 1.886 | 0.05930402 |
| 14 | 50.47 | 17 | 84 | 1.008 | 2.30485458 | 1.886 | 0.05930402 |
| 15 | 50.47 | 17 | 84 | 1.008 | 2.30485458 | 1.886 | 0.05930402 |
| 16 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 17 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 18 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 19 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 20 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 21 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 22 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 23 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 24 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 25 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 26 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 27 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 28 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 29 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 30 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 31 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 32 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 33 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 34 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 35 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 36 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 37 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 38 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 39 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 40 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 41 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 42 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 43 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 44 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 45 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 46 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 47 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 48 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 49 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 50 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 51 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 52 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 53 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 54 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 55 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 56 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 57 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 58 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 59 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 4 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 5 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 6 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 7 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 8 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 9 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 10 | 636 | 220 | 1052 | 1.01 | 2.25755928 | 2.002 | NA |
| 11 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 12 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 13 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 14 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 15 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 16 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 17 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 18 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 19 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 20 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 21 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 22 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 23 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 24 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 25 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 26 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 27 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 28 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 29 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 30 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 31 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 32 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 33 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 34 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 35 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 36 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 37 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 38 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 39 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 40 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 41 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 42 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 43 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 44 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 45 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 46 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 47 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 48 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 49 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 50 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 51 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 52 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 53 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 54 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 55 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 56 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 57 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 58 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 59 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 144.87 | 53 | 236 | 1.007 | 2.15472259 | 1.722 | 0.08505991 |
| 4 | 80.35 | 30 | 131 | 1.008 | 2.12653241 | 1.838 | NA |
| 5 | 80.35 | 30 | 131 | 1.008 | 2.12653241 | 1.838 | NA |
| 6 | 80.35 | 30 | 131 | 1.008 | 2.12653241 | 1.838 | NA |
| 7 | 80.35 | 30 | 131 | 1.008 | 2.12653241 | 1.838 | NA |
| 8 | 80.35 | 30 | 131 | 1.008 | 2.12653241 | 1.838 | NA |
| 9 | 80.35 | 30 | 131 | 1.008 | 2.12653241 | 1.838 | NA |
| 10 | 80.35 | 30 | 131 | 1.008 | 2.12653241 | 1.838 | NA |
| 11 | 80.35 | 30 | 131 | 1.008 | 2.12653241 | 1.838 | NA |
| 12 | 62.97 | 24 | 102 | 1.004 | 2.08746284 | 1.309 | 0.1906123 |
| 13 | 62.97 | 24 | 102 | 1.004 | 2.08746284 | 1.309 | 0.1906123 |
| 14 | 62.97 | 24 | 102 | 1.004 | 2.08746284 | 1.309 | 0.1906123 |
| 15 | 62.97 | 24 | 102 | 1.004 | 2.08746284 | 1.309 | 0.1906123 |
| 16 | 62.97 | 24 | 102 | 1.004 | 2.08746284 | 1.309 | 0.1906123 |
| 17 | 62.97 | 24 | 102 | 1.004 | 2.08746284 | 1.309 | 0.1906123 |
| 18 | 62.97 | 24 | 102 | 1.004 | 2.08746284 | 1.309 | 0.1906123 |
| 19 | 62.97 | 24 | 102 | 1.004 | 2.08746284 | 1.309 | 0.1906123 |
| 20 | 62.97 | 24 | 102 | 1.004 | 2.08746284 | 1.309 | 0.1906123 |
| 21 | 62.97 | 24 | 102 | 1.004 | 2.08746284 | 1.309 | 0.1906123 |
| 22 | 62.97 | 24 | 102 | 1.004 | 2.08746284 | 1.309 | 0.1906123 |
| 23 | 62.97 | 24 | 102 | 1.004 | 2.08746284 | 1.309 | 0.1906123 |
| 24 | 62.97 | 24 | 102 | 1.004 | 2.08746284 | 1.309 | 0.1906123 |
| 25 | 174.65 | 72 | 277 | 1.007 | 1.94381716 | 1.749 | NA |
| 26 | 174.65 | 72 | 277 | 1.007 | 1.94381716 | 1.749 | NA |
| 27 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 28 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 29 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 30 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 31 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 32 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 33 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 34 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 35 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 36 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 37 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 38 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 39 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 40 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 41 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 42 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 43 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 44 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 45 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 46 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 47 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 48 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 49 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 50 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 51 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 52 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 53 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 54 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 55 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 56 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 57 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 58 | 173.75 | 72 | 275 | 1.007 | 1.93336281 | 1.738 | NA |
| 59 | 332.52 | 153 | 512 | 1.006 | 1.74261216 | 1.558 | 0.11912555 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 4 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 5 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 6 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 7 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 8 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 9 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 10 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 11 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 12 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 13 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 14 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 15 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 16 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 17 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 18 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 19 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 20 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 21 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 22 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 23 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 24 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 25 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 26 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 27 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 28 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 29 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 30 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 31 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 32 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 33 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 34 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 35 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 36 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 37 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 38 | 322.17 | 152 | 492 | 1.007 | 1.69458699 | 1.734 | 0.08297435 |
| 39 | 268.79 | 130 | 408 | 1.003 | 1.65005753 | 1.052 | NA |
| 40 | 268.79 | 130 | 408 | 1.003 | 1.65005753 | 1.052 | NA |
| 41 | 268.79 | 130 | 408 | 1.003 | 1.65005753 | 1.052 | NA |
| 42 | 268.79 | 130 | 408 | 1.003 | 1.65005753 | 1.052 | NA |
| 43 | 268.79 | 130 | 408 | 1.003 | 1.65005753 | 1.052 | NA |
| 44 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 45 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 46 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 47 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 48 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 49 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 50 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 51 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 52 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 53 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 54 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 55 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 56 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 57 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 58 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 59 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 4 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 5 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 6 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 7 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 8 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 9 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 10 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 11 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 12 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 13 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 14 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 15 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 16 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 17 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 18 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 19 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 20 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 21 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 22 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 23 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 24 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 25 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 26 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 27 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 28 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 29 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 30 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 31 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 32 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 33 | 427.67 | 209 | 647 | 1.006 | 1.63026277 | 1.665 | 0.09598677 |
| 34 | 429.78 | 210 | 649 | 1.006 | 1.62782915 | 1.66 | 0.0969 |
| 35 | 271.66 | 134 | 409 | 1.003 | 1.60986784 | 1.04 | NA |
| 36 | 271.66 | 134 | 409 | 1.003 | 1.60986784 | 1.04 | NA |
| 37 | | | | | | | |
| 38 | 239.51 | 122 | 357 | 1.003 | 1.54904293 | 0.982 | NA |
| 39 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 40 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 41 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 42 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 43 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 44 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 45 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 46 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 47 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 48 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 49 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 50 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 51 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 52 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 53 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 54 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 55 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 56 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 57 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 58 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 59 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 4 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 5 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 6 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 7 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 8 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 9 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 10 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 11 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 12 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 13 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 14 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 15 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 16 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 17 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 18 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 19 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 20 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 21 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 22 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 23 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 24 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 25 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 26 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 27 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 28 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 29 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 30 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 31 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 32 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 33 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 34 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 35 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 36 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 37 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 38 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 39 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 40 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 41 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 42 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 43 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 44 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 45 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 46 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 47 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 48 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 49 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 50 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 51 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 52 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 53 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 54 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 55 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 56 | 239.1 | 122 | 356 | 1.003 | 1.54499609 | 0.979 | NA |
| 57 | 239.78 | 123 | 357 | 1.003 | 1.53726576 | 0.975 | NA |
| 58 | 71.94 | 38 | 106 | 1.005 | 1.47999294 | 1.516 | 0.12940383 |
| 59 | | | | | | | |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 71.94 | 38 | 106 | 1.005 | 1.47999294 | 1.516 | 0.12940383 |
| 4 | 71.94 | 38 | 106 | 1.005 | 1.47999294 | 1.516 | 0.12940383 |
| 5 | 327.38 | 184 | 470 | 1.004 | 1.35295499 | 1.251 | 0.21108201 |
| 6 | 327.38 | 184 | 470 | 1.004 | 1.35295499 | 1.251 | 0.21108201 |
| 7 | 311.89 | 176 | 448 | 1.004 | 1.3479233 | 1.249 | 0.21180156 |
| 8 | 311.89 | 176 | 448 | 1.004 | 1.3479233 | 1.249 | 0.21180156 |
| 9 | 311.89 | 176 | 448 | 1.004 | 1.3479233 | 1.249 | 0.21180156 |
| 10 | 311.89 | 176 | 448 | 1.004 | 1.3479233 | 1.249 | 0.21180156 |
| 11 | 311.89 | 176 | 448 | 1.004 | 1.3479233 | 1.249 | 0.21180156 |
| 12 | 311.89 | 176 | 448 | 1.004 | 1.3479233 | 1.249 | 0.21180156 |
| 13 | 311.89 | 176 | 448 | 1.004 | 1.3479233 | 1.249 | 0.21180156 |
| 14 | 275.68 | 158 | 393 | 1.004 | 1.31460475 | 1.205 | 0.22830595 |
| 15 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 16 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 17 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 18 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 19 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 20 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 21 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 22 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 23 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 24 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 25 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 26 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 27 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 28 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 29 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 30 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 31 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 32 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 33 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 34 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 35 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 36 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 37 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 38 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 39 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 40 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 41 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 42 | 275.6 | 158 | 393 | 1.004 | 1.31460475 | 1.204 | 0.22849876 |
| 43 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 44 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 45 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 46 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 47 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 48 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 49 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 50 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 51 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 52 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 53 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 54 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 55 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 56 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 57 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 58 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 59 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 4 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 5 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 6 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 7 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 8 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 9 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 10 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 11 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 12 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 13 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 14 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 15 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 16 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 17 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 18 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 19 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 20 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 21 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 22 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 23 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 24 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 25 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 26 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 27 | 260.91 | 151 | 371 | 1.004 | 1.29687064 | 1.192 | 0.23328097 |
| 28 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 29 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 30 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 31 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 32 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 33 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 34 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 35 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 36 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 37 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 38 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 39 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 40 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 41 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 42 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 43 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 44 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 45 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 46 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 47 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 48 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 49 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 50 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 51 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 52 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 53 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 54 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 55 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 56 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 57 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 58 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 59 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 4 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 5 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 6 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 7 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 8 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 9 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 10 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 11 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 12 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 13 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 14 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 15 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 16 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 17 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 18 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 19 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 20 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 21 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 22 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 23 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 24 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 25 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 26 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 27 | 81.33 | 48 | 115 | 1.003 | 1.26052755 | 1.05 | 0.29377339 |
| 28 | 105.39 | 63 | 148 | 1.004 | 1.23217344 | 1.154 | 0.24859571 |
| 29 | 105.39 | 63 | 148 | 1.004 | 1.23217344 | 1.154 | 0.24859571 |
| 30 | 105.39 | 63 | 148 | 1.004 | 1.23217344 | 1.154 | 0.24859571 |
| 31 | 105.39 | 63 | 148 | 1.004 | 1.23217344 | 1.154 | 0.24859571 |
| 32 | 105.39 | 63 | 148 | 1.004 | 1.23217344 | 1.154 | 0.24859571 |
| 33 | 105.39 | 63 | 148 | 1.004 | 1.23217344 | 1.154 | 0.24859571 |
| 34 | 105.39 | 63 | 148 | 1.004 | 1.23217344 | 1.154 | 0.24859571 |
| 35 | 37.95 | 23 | 54 | 1.003 | 1.23132555 | 1.058 | 0.28985108 |
| 36 | 37.95 | 23 | 54 | 1.003 | 1.23132555 | 1.058 | 0.28985108 |
| 37 | 37.95 | 23 | 54 | 1.003 | 1.23132555 | 1.058 | 0.28985108 |
| 38 | 37.95 | 23 | 54 | 1.003 | 1.23132555 | 1.058 | 0.28985108 |
| 39 | 37.95 | 23 | 54 | 1.003 | 1.23132555 | 1.058 | 0.28985108 |
| 40 | 37.95 | 23 | 54 | 1.003 | 1.23132555 | 1.058 | 0.28985108 |
| 41 | 37.95 | 23 | 54 | 1.003 | 1.23132555 | 1.058 | 0.28985108 |
| 42 | 37.95 | 23 | 54 | 1.003 | 1.23132555 | 1.058 | 0.28985108 |
| 43 | 37.95 | 23 | 54 | 1.003 | 1.23132555 | 1.058 | 0.28985108 |
| 44 | 37.95 | 23 | 54 | 1.003 | 1.23132555 | 1.058 | 0.28985108 |
| 45 | 37.95 | 23 | 54 | 1.003 | 1.23132555 | 1.058 | 0.28985108 |
| 46 | 37.95 | 23 | 54 | 1.003 | 1.23132555 | 1.058 | 0.28985108 |
| 47 | 37.95 | 23 | 54 | 1.003 | 1.23132555 | 1.058 | 0.28985108 |
| 48 | 64.64 | 41 | 88 | 1.002 | 1.10187961 | 0.788 | 0.43061147 |
| 49 | 64.57 | 41 | 88 | 1.002 | 1.10187961 | 0.786 | 0.43163334 |
| 50 | 64.57 | 41 | 88 | 1.002 | 1.10187961 | 0.786 | 0.43163334 |
| 51 | 64.57 | 41 | 88 | 1.002 | 1.10187961 | 0.786 | 0.43163334 |
| 52 | 64.57 | 41 | 88 | 1.002 | 1.10187961 | 0.786 | 0.43163334 |
| 53 | 64.57 | 41 | 88 | 1.002 | 1.10187961 | 0.786 | 0.43163334 |
| 54 | 64.57 | 41 | 88 | 1.002 | 1.10187961 | 0.786 | 0.43163334 |
| 55 | 64.57 | 41 | 88 | 1.002 | 1.10187961 | 0.786 | 0.43163334 |
| 56 | 64.57 | 41 | 88 | 1.002 | 1.10187961 | 0.786 | 0.43163334 |
| 57 | 64.57 | 41 | 88 | 1.002 | 1.10187961 | 0.786 | 0.43163334 |
| 58 | 64.57 | 41 | 88 | 1.002 | 1.10187961 | 0.786 | 0.43163334 |
| 59 | 64.57 | 41 | 88 | 1.002 | 1.10187961 | 0.786 | 0.43163334 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 522.29 | 336 | 709 | 1.003 | 1.07732439 | 1.064 | 0.28713039 |
| 4 | 522.29 | 336 | 709 | 1.003 | 1.07732439 | 1.064 | 0.28713039 |
| 5 | 522.29 | 336 | 709 | 1.003 | 1.07732439 | 1.064 | 0.28713039 |
| 6 | 522.29 | 336 | 709 | 1.003 | 1.07732439 | 1.064 | 0.28713039 |
| 7 | 522.29 | 336 | 709 | 1.003 | 1.07732439 | 1.064 | 0.28713039 |
| 8 | 522.29 | 336 | 709 | 1.003 | 1.07732439 | 1.064 | 0.28713039 |
| 9 | 522.29 | 336 | 709 | 1.003 | 1.07732439 | 1.064 | 0.28713039 |
| 10 | 522.29 | 336 | 709 | 1.003 | 1.07732439 | 1.064 | 0.28713039 |
| 11 | 522.29 | 336 | 709 | 1.003 | 1.07732439 | 1.064 | 0.28713039 |
| 12 | 522.29 | 336 | 709 | 1.003 | 1.07732439 | 1.064 | 0.28713039 |
| 13 | 522.29 | 336 | 709 | 1.003 | 1.07732439 | 1.064 | 0.28713039 |
| 14 | 522.29 | 336 | 709 | 1.003 | 1.07732439 | 1.064 | 0.28713039 |
| 15 | 522.29 | 336 | 709 | 1.003 | 1.07732439 | 1.064 | 0.28713039 |
| 16 | 522.29 | 336 | 709 | 1.003 | 1.07732439 | 1.064 | 0.28713039 |
| 17 | 522.29 | 336 | 709 | 1.003 | 1.07732439 | 1.064 | 0.28713039 |
| 18 | 522.29 | 336 | 709 | 1.003 | 1.07732439 | 1.064 | 0.28713039 |
| 19 | 522.29 | 336 | 709 | 1.003 | 1.07732439 | 1.064 | 0.28713039 |
| 20 | 522.29 | 336 | 709 | 1.003 | 1.07732439 | 1.064 | 0.28713039 |
| 21 | 522.29 | 336 | 709 | 1.003 | 1.07732439 | 1.064 | 0.28713039 |
| 22 | 524.96 | 338 | 712 | 1.003 | 1.07485399 | 1.063 | 0.28783915 |
| 23 | 524.96 | 338 | 712 | 1.003 | 1.07485399 | 1.063 | 0.28783915 |
| 24 | 3625.83 | 2373 | 4878 | 1.004 | 1.03957766 | 1.109 | 0.26755602 |
| 25 | 3625.83 | 2373 | 4878 | 1.004 | 1.03957766 | 1.109 | 0.26755602 |
| 26 | 3625.83 | 2373 | 4878 | 1.004 | 1.03957766 | 1.109 | 0.26755602 |
| 27 | 3625.83 | 2373 | 4878 | 1.004 | 1.03957766 | 1.109 | 0.26755602 |
| 28 | 3625.83 | 2373 | 4878 | 1.004 | 1.03957766 | 1.109 | 0.26755602 |
| 29 | 3625.83 | 2373 | 4878 | 1.004 | 1.03957766 | 1.109 | 0.26755602 |
| 30 | 3625.83 | 2373 | 4878 | 1.004 | 1.03957766 | 1.109 | 0.26755602 |
| 31 | 3596.89 | 2357 | 4837 | 1.004 | 1.03716078 | 1.106 | 0.26866729 |
| 32 | 3596.89 | 2357 | 4837 | 1.004 | 1.03716078 | 1.106 | 0.26866729 |
| 33 | 3596.89 | 2357 | 4837 | 1.004 | 1.03716078 | 1.106 | 0.26866729 |
| 34 | 3596.89 | 2357 | 4837 | 1.004 | 1.03716078 | 1.106 | 0.26866729 |
| 35 | 3596.89 | 2357 | 4837 | 1.004 | 1.03716078 | 1.106 | 0.26866729 |
| 36 | 3596.89 | 2357 | 4837 | 1.004 | 1.03716078 | 1.106 | 0.26866729 |
| 37 | 3596.89 | 2357 | 4837 | 1.004 | 1.03716078 | 1.106 | 0.26866729 |
| 38 | 3596.89 | 2357 | 4837 | 1.004 | 1.03716078 | 1.106 | 0.26866729 |
| 39 | 3596.89 | 2357 | 4837 | 1.004 | 1.03716078 | 1.106 | 0.26866729 |
| 40 | 3596.89 | 2357 | 4837 | 1.004 | 1.03716078 | 1.106 | 0.26866729 |
| 41 | 3596.89 | 2357 | 4837 | 1.004 | 1.03716078 | 1.106 | 0.26866729 |
| 42 | 3596.89 | 2357 | 4837 | 1.004 | 1.03716078 | 1.106 | 0.26866729 |
| 43 | 3596.89 | 2357 | 4837 | 1.004 | 1.03716078 | 1.106 | 0.26866729 |
| 44 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 45 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 46 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 47 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 48 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 49 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 50 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 51 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 52 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 53 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 54 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 55 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 56 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 57 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 58 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 59 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 4 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 5 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 6 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 7 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 8 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 9 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 10 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 11 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 12 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 13 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 14 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 15 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 16 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 17 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 18 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 19 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 20 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 21 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 22 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 23 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 24 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 25 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 26 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 27 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 28 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 29 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 30 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 31 | 374.21 | 246 | 503 | 1.003 | 1.03190008 | 0.99 | 0.32194986 |
| 32 | 5686.85 | 3748 | 7625 | 1.003 | 1.02461638 | 0.895 | 0.37066403 |
| 33 | 5686.85 | 3748 | 7625 | 1.003 | 1.02461638 | 0.895 | 0.37066403 |
| 34 | 5686.85 | 3748 | 7625 | 1.003 | 1.02461638 | 0.895 | 0.37066403 |
| 35 | 5686.85 | 3748 | 7625 | 1.003 | 1.02461638 | 0.895 | 0.37066403 |
| 36 | 5686.85 | 3748 | 7625 | 1.003 | 1.02461638 | 0.895 | 0.37066403 |
| 37 | 405.27 | 272 | 539 | 1.003 | 0.98667862 | 0.954 | 0.33999601 |
| 38 | 405.27 | 272 | 539 | 1.003 | 0.98667862 | 0.954 | 0.33999601 |
| 39 | 405.27 | 272 | 539 | 1.003 | 0.98667862 | 0.954 | 0.33999601 |
| 40 | 405.27 | 272 | 539 | 1.003 | 0.98667862 | 0.954 | 0.33999601 |
| 41 | 405.27 | 272 | 539 | 1.003 | 0.98667862 | 0.954 | 0.33999601 |
| 42 | 405.27 | 272 | 539 | 1.003 | 0.98667862 | 0.954 | 0.33999601 |
| 43 | 405.27 | 272 | 539 | 1.003 | 0.98667862 | 0.954 | 0.33999601 |
| 44 | 405.27 | 272 | 539 | 1.003 | 0.98667862 | 0.954 | 0.33999601 |
| 45 | 405.27 | 272 | 539 | 1.003 | 0.98667862 | 0.954 | 0.33999601 |
| 46 | 405.27 | 272 | 539 | 1.003 | 0.98667862 | 0.954 | 0.33999601 |
| 47 | 405.27 | 272 | 539 | 1.003 | 0.98667862 | 0.954 | 0.33999601 |
| 48 | 405.27 | 272 | 539 | 1.003 | 0.98667862 | 0.954 | 0.33999601 |
| 49 | 54.95 | 37 | 73 | 1.003 | 0.98037119 | 1.018 | 0.30886289 |
| 50 | 54.95 | 37 | 73 | 1.003 | 0.98037119 | 1.018 | 0.30886289 |
| 51 | 54.95 | 37 | 73 | 1.003 | 0.98037119 | 1.018 | 0.30886289 |
| 52 | 54.95 | 37 | 73 | 1.003 | 0.98037119 | 1.018 | 0.30886289 |
| 53 | 54.95 | 37 | 73 | 1.003 | 0.98037119 | 1.018 | 0.30886289 |
| 54 | 54.95 | 37 | 73 | 1.003 | 0.98037119 | 1.018 | 0.30886289 |
| 55 | 54.95 | 37 | 73 | 1.003 | 0.98037119 | 1.018 | 0.30886289 |
| 56 | 54.95 | 37 | 73 | 1.003 | 0.98037119 | 1.018 | 0.30886289 |
| 57 | 54.95 | 37 | 73 | 1.003 | 0.98037119 | 1.018 | 0.30886289 |
| 58 | 54.95 | 37 | 73 | 1.003 | 0.98037119 | 1.018 | 0.30886289 |
| 59 | 54.95 | 37 | 73 | 1.003 | 0.98037119 | 1.018 | 0.30886289 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 4 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 5 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 6 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 7 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 8 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 9 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 10 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 11 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 12 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 13 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 14 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 15 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 16 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 17 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 18 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 19 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 20 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 21 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 22 | 58.39 | 40 | 76 | 1.003 | 0.92599942 | 0.899 | 0.36853809 |
| 23 | 59.89 | 42 | 78 | 1.003 | 0.8930848 | 0.873 | 0.38252063 |
| 24 | 608.24 | 427 | 790 | 1.004 | 0.88761658 | 1.036 | 0.30034281 |
| 25 | 608.24 | 427 | 790 | 1.004 | 0.88761658 | 1.036 | 0.30034281 |
| 26 | 608.24 | 427 | 790 | 1.004 | 0.88761658 | 1.036 | 0.30034281 |
| 27 | 608.24 | 427 | 790 | 1.004 | 0.88761658 | 1.036 | 0.30034281 |
| 28 | 608.24 | 427 | 790 | 1.004 | 0.88761658 | 1.036 | 0.30034281 |
| 29 | 608.24 | 427 | 790 | 1.004 | 0.88761658 | 1.036 | 0.30034281 |
| 30 | 608.24 | 427 | 790 | 1.004 | 0.88761658 | 1.036 | 0.30034281 |
| 31 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 32 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 33 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 34 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 35 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 36 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 37 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 38 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 39 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 40 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 41 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 42 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 43 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 44 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 45 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 46 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 47 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 48 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 49 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 50 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 51 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 52 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 53 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 54 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 55 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 56 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 57 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 58 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 59 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 4 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 5 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 6 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 7 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 8 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 9 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 10 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 11 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 12 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 13 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 14 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 15 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 16 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 17 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 18 | 606.25 | 426 | 786 | 1.004 | 0.88367588 | 1.032 | 0.30225578 |
| 19 | 50.96 | 36 | 65 | 1.003 | 0.85244281 | 0.919 | 0.35816764 |
| 20 | 50.96 | 36 | 65 | 1.003 | 0.85244281 | 0.919 | 0.35816764 |
| 21 | 50.96 | 36 | 65 | 1.003 | 0.85244281 | 0.919 | 0.35816764 |
| 22 | 50.96 | 36 | 65 | 1.003 | 0.85244281 | 0.919 | 0.35816764 |
| 23 | 50.96 | 36 | 65 | 1.003 | 0.85244281 | 0.919 | 0.35816764 |
| 24 | 50.96 | 36 | 65 | 1.003 | 0.85244281 | 0.919 | 0.35816764 |
| 25 | 50.96 | 36 | 65 | 1.003 | 0.85244281 | 0.919 | 0.35816764 |
| 26 | 50.96 | 36 | 65 | 1.003 | 0.85244281 | 0.919 | 0.35816764 |
| 27 | 50.96 | 36 | 65 | 1.003 | 0.85244281 | 0.919 | 0.35816764 |
| 28 | 50.96 | 36 | 65 | 1.003 | 0.85244281 | 0.919 | 0.35816764 |
| 29 | 50.96 | 36 | 65 | 1.003 | 0.85244281 | 0.919 | 0.35816764 |
| 30 | 50.96 | 36 | 65 | 1.003 | 0.85244281 | 0.919 | 0.35816764 |
| 31 | 50.96 | 36 | 65 | 1.003 | 0.85244281 | 0.919 | 0.35816764 |
| 32 | 259.42 | 187 | 332 | 1.002 | 0.82814497 | 0.76 | 0.44711115 |
| 33 | 91.75 | 67 | 117 | 1.003 | 0.80427553 | 0.816 | 0.41436939 |
| 34 | 90.75 | 67 | 114 | 1.002 | 0.76680082 | 0.779 | 0.4360549 |
| 35 | 90.75 | 67 | 114 | 1.002 | 0.76680082 | 0.779 | 0.4360549 |
| 36 | 90.75 | 67 | 114 | 1.002 | 0.76680082 | 0.779 | 0.4360549 |
| 37 | 90.75 | 67 | 114 | 1.002 | 0.76680082 | 0.779 | 0.4360549 |
| 38 | 90.75 | 67 | 114 | 1.002 | 0.76680082 | 0.779 | 0.4360549 |
| 39 | 48.29 | 36 | 61 | 1.001 | 0.76081234 | 0.561 | NA |
| 40 | 48.29 | 36 | 61 | 1.001 | 0.76081234 | 0.561 | NA |
| 41 | 52.03 | 39 | 66 | 1.002 | 0.7589919 | 0.759 | 0.44794427 |
| 42 | 52.03 | 39 | 66 | 1.002 | 0.7589919 | 0.759 | 0.44794427 |
| 43 | 52.03 | 39 | 66 | 1.002 | 0.7589919 | 0.759 | 0.44794427 |
| 44 | 52.03 | 39 | 66 | 1.002 | 0.7589919 | 0.759 | 0.44794427 |
| 45 | 52.03 | 39 | 66 | 1.002 | 0.7589919 | 0.759 | 0.44794427 |
| 46 | 52.03 | 39 | 66 | 1.002 | 0.7589919 | 0.759 | 0.44794427 |
| 47 | 52.03 | 39 | 66 | 1.002 | 0.7589919 | 0.759 | 0.44794427 |
| 48 | 91.19 | 68 | 115 | 1.002 | 0.75802721 | 0.78 | 0.43556478 |
| 49 | 91.35 | 68 | 115 | 1.002 | 0.75802721 | 0.772 | 0.43997876 |
| 50 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 51 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 52 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 53 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 54 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 55 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 56 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 57 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 58 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 59 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 4 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 5 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 6 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 7 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 8 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 9 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 10 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 11 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 12 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 13 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 14 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 15 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 16 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 17 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 18 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 19 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 20 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 21 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 22 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 23 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 24 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 25 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 26 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 27 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 28 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 29 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 30 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 31 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 32 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 33 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 34 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 35 | 163.67 | 122 | 205 | 1.002 | 0.74874276 | 0.766 | 0.44342806 |
| 36 | 89.27 | 67 | 112 | 1.002 | 0.74126573 | 0.763 | 0.44559638 |
| 37 | 89.27 | 67 | 112 | 1.002 | 0.74126573 | 0.763 | 0.44559638 |
| 38 | 89.27 | 67 | 112 | 1.002 | 0.74126573 | 0.763 | 0.44559638 |
| 39 | 89.27 | 67 | 112 | 1.002 | 0.74126573 | 0.763 | 0.44559638 |
| 40 | 89.27 | 67 | 112 | 1.002 | 0.74126573 | 0.763 | 0.44559638 |
| 41 | 89.27 | 67 | 112 | 1.002 | 0.74126573 | 0.763 | 0.44559638 |
| 42 | 89.27 | 67 | 112 | 1.002 | 0.74126573 | 0.763 | 0.44559638 |
| 43 | 89.27 | 67 | 112 | 1.002 | 0.74126573 | 0.763 | 0.44559638 |
| 44 | 89.27 | 67 | 112 | 1.002 | 0.74126573 | 0.763 | 0.44559638 |
| 45 | 89.27 | 67 | 112 | 1.002 | 0.74126573 | 0.763 | 0.44559638 |
| 46 | 89.27 | 67 | 112 | 1.002 | 0.74126573 | 0.763 | 0.44559638 |
| 47 | 89.27 | 67 | 112 | 1.002 | 0.74126573 | 0.763 | 0.44559638 |
| 48 | 89.27 | 67 | 112 | 1.002 | 0.74126573 | 0.763 | 0.44559638 |
| 49 | 89.27 | 67 | 112 | 1.002 | 0.74126573 | 0.763 | 0.44559638 |
| 50 | 89.27 | 67 | 112 | 1.002 | 0.74126573 | 0.763 | 0.44559638 |
| 51 | 89.27 | 67 | 112 | 1.002 | 0.74126573 | 0.763 | 0.44559638 |
| 52 | 89.27 | 67 | 112 | 1.002 | 0.74126573 | 0.763 | 0.44559638 |
| 53 | 89.27 | 67 | 112 | 1.002 | 0.74126573 | 0.763 | 0.44559638 |
| 54 | 89.27 | 67 | 112 | 1.002 | 0.74126573 | 0.763 | 0.44559638 |
| 55 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 56 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 57 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 58 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 59 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 4 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 5 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 6 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 7 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 8 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 9 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 10 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 11 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 12 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 13 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 14 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 15 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 16 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 17 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 18 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 19 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 20 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 21 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 22 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 23 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 24 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 25 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 26 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 27 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 28 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 29 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 30 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 31 | 288.94 | 218 | 360 | 1.003 | 0.72366877 | 0.867 | 0.38601358 |
| 32 | 52.48 | 40 | 65 | 1.002 | 0.70043972 | 0.566 | NA |
| 33 | 52.19 | 40 | 64 | 1.002 | 0.67807191 | 0.738 | 0.46037501 |
| 34 | 52.19 | 40 | 64 | 1.002 | 0.67807191 | 0.738 | 0.46037501 |
| 35 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 36 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 37 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 38 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 39 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 40 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 41 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 42 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 43 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 44 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 45 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 46 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 47 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 48 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 49 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 50 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 51 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 52 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 53 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 54 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 55 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 56 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 57 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 58 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 59 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-------|----|----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 4 | 76.76 | 59 | 94 | 1.003 | 0.6719458 | 0.778 | 0.43664989 |
| 5 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 6 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 7 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 8 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 9 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 10 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 11 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 12 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 13 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 14 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 15 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 16 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 17 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 18 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 19 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 20 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 21 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 22 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 23 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 24 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 25 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 26 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 27 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 28 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 29 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 30 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 31 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 32 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 33 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 34 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 35 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 36 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 37 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 38 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 39 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 40 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 41 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 42 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 43 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 44 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 45 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 46 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 47 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 48 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 49 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 50 | 43.71 | 34 | 53 | 1.002 | 0.64045761 | 0.617 | 0.53710245 |
| 51 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 52 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 53 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 54 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 55 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 56 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 57 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 58 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 59 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | | | | | | | |
| 4 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 5 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 6 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 7 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 8 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 9 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 10 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 11 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 12 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 13 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 14 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 15 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 16 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 17 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 18 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 19 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 20 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 21 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 22 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 23 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 24 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 25 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 26 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 27 | 54.95 | 43 | 67 | 1.002 | 0.63982444 | 0.58 | 0.56203146 |
| 28 | | | | | | | |
| 29 | 493.51 | 387 | 600 | 1.003 | 0.63262893 | 0.768 | 0.44251288 |
| 30 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 31 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 32 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 33 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 34 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 35 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 36 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 37 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 38 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 39 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 40 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 41 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 42 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 43 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 44 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 45 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 46 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 47 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 48 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 49 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 50 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 51 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 52 | 69.58 | 55 | 84 | 1.002 | 0.61095771 | 0.64 | 0.52222472 |
| 53 | | | | | | | |
| 54 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 55 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 56 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 57 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 58 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 59 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|-----|------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 4 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 5 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 6 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 7 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 8 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 9 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 10 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 11 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 12 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 13 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 14 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 15 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 16 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 17 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 18 | 72.4 | 57 | 87 | 1.002 | 0.61005348 | 0.691 | 0.48947759 |
| 19 | 72.06 | 57 | 87 | 1.002 | 0.61005348 | 0.562 | 0.5739466 |
| 20 | 72.06 | 57 | 87 | 1.002 | 0.61005348 | 0.562 | 0.5739466 |
| 21 | 72.06 | 57 | 87 | 1.002 | 0.61005348 | 0.562 | 0.5739466 |
| 22 | 72.06 | 57 | 87 | 1.002 | 0.61005348 | 0.562 | 0.5739466 |
| 23 | 72.06 | 57 | 87 | 1.002 | 0.61005348 | 0.562 | 0.5739466 |
| 24 | 72.06 | 57 | 87 | 1.002 | 0.61005348 | 0.562 | 0.5739466 |
| 25 | 72.06 | 57 | 87 | 1.002 | 0.61005348 | 0.562 | 0.5739466 |
| 26 | 72.06 | 57 | 87 | 1.002 | 0.61005348 | 0.562 | 0.5739466 |
| 27 | 72.06 | 57 | 87 | 1.002 | 0.61005348 | 0.562 | 0.5739466 |
| 28 | 468.33 | 371 | 566 | 1.003 | 0.60938287 | 0.733 | 0.46350316 |
| 29 | 468.33 | 371 | 566 | 1.003 | 0.60938287 | 0.733 | 0.46350316 |
| 30 | 134.08 | 106 | 161 | 1.002 | 0.60299642 | 0.64 | 0.52193757 |
| 31 | 134.08 | 106 | 161 | 1.002 | 0.60299642 | 0.64 | 0.52193757 |
| 32 | 72.9 | 58 | 88 | 1.002 | 0.60145062 | 0.696 | 0.48653258 |
| 33 | 1028.87 | 819 | 1239 | 1.002 | 0.59724083 | 0.578 | 0.56345612 |
| 34 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 35 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 36 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 37 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 38 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 39 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 40 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 41 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 42 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 43 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 44 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 45 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 46 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 47 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 48 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 49 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 50 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 51 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 52 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 53 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 54 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 55 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 56 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 57 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 58 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 59 | 1028.35 | 819 | 1238 | 1.002 | 0.59607596 | 0.577 | 0.56398484 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|-----------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 4 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 5 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 6 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 7 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 8 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 9 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 10 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 11 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 12 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 13 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 14 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 15 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 16 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 17 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 18 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 19 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 20 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 21 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 22 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 23 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 24 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 25 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 26 | 548.28 | 438 | 659 | 1.003 | 0.5893476 | 0.721 | 0.47064478 |
| 27 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 28 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 29 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 30 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 31 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 32 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 33 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 34 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 35 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 36 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 37 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 38 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 39 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 40 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 41 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 42 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 43 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 44 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 45 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 46 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 47 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 48 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 49 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 50 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 51 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 52 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 53 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 54 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 55 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 56 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 57 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 58 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 59 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 4 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 5 | 67.72 | 54 | 81 | 1.001 | 0.5849625 | 0.437 | 0.66180834 |
| 6 | 68.75 | 55 | 82 | 1.001 | 0.57619229 | 0.433 | 0.6649149 |
| 7 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 8 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 9 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 10 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 11 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 12 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 13 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 14 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 15 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 16 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 17 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 18 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 19 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 20 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 21 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 22 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 23 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 24 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 25 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 26 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 27 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 28 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 29 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 30 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 31 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 32 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 33 | 125.01 | 101 | 149 | 1.002 | 0.56095704 | 0.61 | 0.5419706 |
| 34 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 35 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 36 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 37 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 38 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 39 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 40 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 41 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 42 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 43 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 44 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 45 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 46 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 47 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 48 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 49 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 50 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 51 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 52 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 53 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 54 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 55 | 54.47 | 45 | 64 | 1.002 | 0.5081469 | 0.545 | 0.58546446 |
| 56 | 506.22 | 424 | 588 | 1.002 | 0.47175189 | 0.61 | 0.54159641 |
| 57 | 506.22 | 424 | 588 | 1.002 | 0.47175189 | 0.61 | 0.54159641 |
| 58 | 506.22 | 424 | 588 | 1.002 | 0.47175189 | 0.61 | 0.54159641 |
| 59 | 506.22 | 424 | 588 | 1.002 | 0.47175189 | 0.61 | 0.54159641 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 138.11 | 117 | 160 | 1.001 | 0.45156338 | 0.46 | 0.64521595 |
| 4 | 138.11 | 117 | 160 | 1.001 | 0.45156338 | 0.46 | 0.64521595 |
| 5 | 138.11 | 117 | 160 | 1.001 | 0.45156338 | 0.46 | 0.64521595 |
| 6 | 138.11 | 117 | 160 | 1.001 | 0.45156338 | 0.46 | 0.64521595 |
| 7 | 138.11 | 117 | 160 | 1.001 | 0.45156338 | 0.46 | 0.64521595 |
| 8 | 138.11 | 117 | 160 | 1.001 | 0.45156338 | 0.46 | 0.64521595 |
| 9 | 138.11 | 117 | 160 | 1.001 | 0.45156338 | 0.46 | 0.64521595 |
| 10 | 138.11 | 117 | 160 | 1.001 | 0.45156338 | 0.46 | 0.64521595 |
| 11 | 138.11 | 117 | 160 | 1.001 | 0.45156338 | 0.46 | 0.64521595 |
| 12 | 138.11 | 117 | 160 | 1.001 | 0.45156338 | 0.46 | 0.64521595 |
| 13 | 138.11 | 117 | 160 | 1.001 | 0.45156338 | 0.46 | 0.64521595 |
| 14 | 138.11 | 117 | 160 | 1.001 | 0.45156338 | 0.46 | 0.64521595 |
| 15 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 16 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 17 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 18 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 19 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 20 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 21 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 22 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 23 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 24 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 25 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 26 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 27 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 28 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 29 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 30 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 31 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 32 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 33 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 34 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 35 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 36 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 37 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 38 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 39 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 40 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 41 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 42 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 43 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 44 | 465.43 | 394 | 537 | 1.002 | 0.44672646 | 0.573 | 0.56640241 |
| 45 | 465.9 | 395 | 537 | 1.002 | 0.44306943 | 0.573 | 0.56661469 |
| 46 | 465.9 | 395 | 537 | 1.002 | 0.44306943 | 0.573 | 0.56661469 |
| 47 | 465.9 | 395 | 537 | 1.002 | 0.44306943 | 0.573 | 0.56661469 |
| 48 | 465.9 | 395 | 537 | 1.002 | 0.44306943 | 0.573 | 0.56661469 |
| 49 | 465.9 | 395 | 537 | 1.002 | 0.44306943 | 0.573 | 0.56661469 |
| 50 | 465.9 | 395 | 537 | 1.002 | 0.44306943 | 0.573 | 0.56661469 |
| 51 | 465.9 | 395 | 537 | 1.002 | 0.44306943 | 0.573 | 0.56661469 |
| 52 | 465.9 | 395 | 537 | 1.002 | 0.44306943 | 0.573 | 0.56661469 |
| 53 | 465.9 | 395 | 537 | 1.002 | 0.44306943 | 0.573 | 0.56661469 |
| 54 | 465.9 | 395 | 537 | 1.002 | 0.44306943 | 0.573 | 0.56661469 |
| 55 | 465.9 | 395 | 537 | 1.002 | 0.44306943 | 0.573 | 0.56661469 |
| 56 | 465.9 | 395 | 537 | 1.002 | 0.44306943 | 0.573 | 0.56661469 |
| 57 | 465.9 | 395 | 537 | 1.002 | 0.44306943 | 0.573 | 0.56661469 |
| 58 | 465.9 | 395 | 537 | 1.002 | 0.44306943 | 0.573 | 0.56661469 |
| 59 | 244.38 | 211 | 278 | 1.001 | 0.39784188 | 0.44 | 0.65978995 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 244.38 | 211 | 278 | 1.001 | 0.39784188 | 0.44 | 0.65978995 |
| 4 | 99.49 | 86 | 113 | 1.001 | 0.39391421 | 0.436 | 0.66254595 |
| 5 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 6 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 7 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 8 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 9 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 10 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 11 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 12 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 13 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 14 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 15 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 16 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 17 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 18 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 19 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 20 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 21 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 22 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 23 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 24 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 25 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 26 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 27 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 28 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 29 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 30 | 91.19 | 79 | 103 | 1.001 | 0.38271978 | 0.401 | 0.68863385 |
| 31 | 5884.56 | 5123 | 6647 | 1.001 | 0.37571446 | 0.363 | 0.71665988 |
| 32 | 4385.39 | 3827 | 4944 | 1.001 | 0.36946484 | 0.331 | 0.74060492 |
| 33 | 148.91 | 132 | 166 | 1.001 | 0.33064531 | 0.378 | 0.70579331 |
| 34 | 148.91 | 132 | 166 | 1.001 | 0.33064531 | 0.378 | 0.70579331 |
| 35 | 148.91 | 132 | 166 | 1.001 | 0.33064531 | 0.378 | 0.70579331 |
| 36 | 148.91 | 132 | 166 | 1.001 | 0.33064531 | 0.378 | 0.70579331 |
| 37 | 148.91 | 132 | 166 | 1.001 | 0.33064531 | 0.378 | 0.70579331 |
| 38 | 148.91 | 132 | 166 | 1.001 | 0.33064531 | 0.378 | 0.70579331 |
| 39 | 148.91 | 132 | 166 | 1.001 | 0.33064531 | 0.378 | 0.70579331 |
| 40 | 148.91 | 132 | 166 | 1.001 | 0.33064531 | 0.378 | 0.70579331 |
| 41 | 148.91 | 132 | 166 | 1.001 | 0.33064531 | 0.378 | 0.70579331 |
| 42 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 43 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 44 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 45 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 46 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 47 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 48 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 49 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 50 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 51 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 52 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 53 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 54 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 55 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 56 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 57 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 58 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 59 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 4 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 5 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 6 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 7 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 8 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 9 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 10 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 11 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 12 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 13 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 14 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 15 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 16 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 17 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 18 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 19 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 20 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 21 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 22 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 23 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 24 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 25 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 26 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 27 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 28 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 29 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 30 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 31 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 32 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 33 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 34 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 35 | 128.74 | 115 | 143 | 1.001 | 0.31438129 | 0.356 | 0.72163001 |
| 36 | 150.56 | 135 | 166 | 1.001 | 0.29822383 | 0.349 | 0.727184 |
| 37 | 59.5 | 53 | 65 | 1.001 | 0.29444736 | 0.267 | 0.78983058 |
| 38 | 59.5 | 53 | 65 | 1.001 | 0.29444736 | 0.267 | 0.78983058 |
| 39 | 202.49 | 182 | 223 | 1.001 | 0.29310526 | 0.371 | 0.7103846 |
| 40 | 202.49 | 182 | 223 | 1.001 | 0.29310526 | 0.371 | 0.7103846 |
| 41 | 380.36 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73148779 |
| 42 | 380.36 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73148779 |
| 43 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 44 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 45 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 46 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 47 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 48 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 49 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 50 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 51 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 52 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 53 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 54 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 55 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 56 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 57 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 58 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 59 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 4 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 5 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 6 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 7 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 8 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 9 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 10 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 11 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 12 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 13 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 14 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 15 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 16 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 17 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 18 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 19 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 20 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 21 | 380.01 | 343 | 417 | 1.001 | 0.28183881 | 0.343 | 0.73122458 |
| 22 | 145.09 | 131 | 159 | 1.001 | 0.27945995 | 0.206 | 0.83686919 |
| 23 | 148.47 | 135 | 161 | 1 | 0.25410128 | 0.19 | 0.84922835 |
| 24 | 3509.51 | 3226 | 3793 | 1.001 | 0.23359293 | 0.306 | 0.75951581 |
| 25 | 3509.51 | 3226 | 3793 | 1.001 | 0.23359293 | 0.306 | 0.75951581 |
| 26 | 3509.51 | 3226 | 3793 | 1.001 | 0.23359293 | 0.306 | 0.75951581 |
| 27 | 3509.51 | 3226 | 3793 | 1.001 | 0.23359293 | 0.306 | 0.75951581 |
| 28 | 3509.51 | 3226 | 3793 | 1.001 | 0.23359293 | 0.306 | 0.75951581 |
| 29 | 3509.51 | 3226 | 3793 | 1.001 | 0.23359293 | 0.306 | 0.75951581 |
| 30 | 3509.51 | 3226 | 3793 | 1.001 | 0.23359293 | 0.306 | 0.75951581 |
| 31 | 3509.51 | 3226 | 3793 | 1.001 | 0.23359293 | 0.306 | 0.75951581 |
| 32 | 3509.51 | 3226 | 3793 | 1.001 | 0.23359293 | 0.306 | 0.75951581 |
| 33 | 3509.51 | 3226 | 3793 | 1.001 | 0.23359293 | 0.306 | 0.75951581 |
| 34 | 3509.51 | 3226 | 3793 | 1.001 | 0.23359293 | 0.306 | 0.75951581 |
| 35 | 3509.51 | 3226 | 3793 | 1.001 | 0.23359293 | 0.306 | 0.75951581 |
| 36 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 37 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 38 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 39 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 40 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 41 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 42 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 43 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 44 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 45 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 46 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 47 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 48 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 49 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 50 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 51 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 52 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 53 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 54 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 55 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 56 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 57 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 58 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 59 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 4 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 5 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 6 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 7 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 8 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 9 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 10 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 11 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 12 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 13 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 14 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 15 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 16 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 17 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 18 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 19 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 20 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 21 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 22 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 23 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 24 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 25 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 26 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 27 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 28 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 29 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 30 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 31 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 32 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 33 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 34 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 35 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 36 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 37 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 38 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 39 | 279.49 | 257 | 302 | 1.001 | 0.23278019 | 0.25 | 0.80277995 |
| 40 | 291.05 | 268 | 314 | 1.001 | 0.22853156 | 0.246 | 0.80573394 |
| 41 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 42 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 43 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 44 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 45 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 46 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 47 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 48 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 49 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 50 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 51 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 52 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 53 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 54 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 55 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 56 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 57 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 58 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 59 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 4 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 5 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 6 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 7 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 8 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 9 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 10 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 11 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 12 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 13 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 14 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 15 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 16 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 17 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 18 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 19 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 20 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 21 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 22 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 23 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 24 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 25 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 26 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 27 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 28 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 29 | 171.6 | 158 | 185 | 1 | 0.22760071 | 0.164 | 0.86972278 |
| 30 | 172.25 | 159 | 186 | 1 | 0.22627586 | 0.167 | 0.86753177 |
| 31 | 197.57 | 183 | 212 | 1.001 | 0.21222062 | 0.264 | 0.7918615 |
| 32 | 197.57 | 183 | 212 | 1.001 | 0.21222062 | 0.264 | 0.7918615 |
| 33 | 186.85 | 173 | 200 | 1.001 | 0.20922796 | 0.26 | 0.79454113 |
| 34 | 186.85 | 173 | 200 | 1.001 | 0.20922796 | 0.26 | 0.79454113 |
| 35 | 186.85 | 173 | 200 | 1.001 | 0.20922796 | 0.26 | 0.79454113 |
| 36 | 186.85 | 173 | 200 | 1.001 | 0.20922796 | 0.26 | 0.79454113 |
| 37 | 186.85 | 173 | 200 | 1.001 | 0.20922796 | 0.26 | 0.79454113 |
| 38 | 186.85 | 173 | 200 | 1.001 | 0.20922796 | 0.26 | 0.79454113 |
| 39 | 186.85 | 173 | 200 | 1.001 | 0.20922796 | 0.26 | 0.79454113 |
| 40 | 186.85 | 173 | 200 | 1.001 | 0.20922796 | 0.26 | 0.79454113 |
| 41 | 186.85 | 173 | 200 | 1.001 | 0.20922796 | 0.26 | 0.79454113 |
| 42 | 186.85 | 173 | 200 | 1.001 | 0.20922796 | 0.26 | 0.79454113 |
| 43 | 186.85 | 173 | 200 | 1.001 | 0.20922796 | 0.26 | 0.79454113 |
| 44 | 327.25 | 304 | 350 | 1 | 0.2032836 | 0.163 | 0.87045425 |
| 45 | 318.09 | 296 | 340 | 1 | 0.19993757 | 0.164 | 0.86992485 |
| 46 | 533.46 | 497 | 570 | 1.001 | 0.19771607 | 0.223 | 0.82382762 |
| 47 | 533.46 | 497 | 570 | 1.001 | 0.19771607 | 0.223 | 0.82382762 |
| 48 | 305.55 | 285 | 326 | 1 | 0.19391005 | 0.153 | 0.8785945 |
| 49 | 305.55 | 285 | 326 | 1 | 0.19391005 | 0.153 | 0.8785945 |
| 50 | 305.55 | 285 | 326 | 1 | 0.19391005 | 0.153 | 0.8785945 |
| 51 | 305.55 | 285 | 326 | 1 | 0.19391005 | 0.153 | 0.8785945 |
| 52 | 305.55 | 285 | 326 | 1 | 0.19391005 | 0.153 | 0.8785945 |
| 53 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 54 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 55 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 56 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 57 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 58 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 59 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 4 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 5 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 6 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 7 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 8 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 9 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 10 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 11 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 12 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 13 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 14 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 15 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 16 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 17 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 18 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 19 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 20 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 21 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 22 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 23 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 24 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 25 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 26 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 27 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 28 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 29 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 30 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 31 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 32 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 33 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 34 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 35 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 36 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 37 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 38 | 305.1 | 285 | 325 | 1 | 0.1894778 | 0.15 | 0.8811123 |
| 39 | 115.29 | 108 | 122 | 1.001 | 0.17584984 | 0.168 | 0.86626012 |
| 40 | 115.29 | 108 | 122 | 1.001 | 0.17584984 | 0.168 | 0.86626012 |
| 41 | 207.54 | 196 | 219 | 1.001 | 0.16007722 | 0.2 | 0.84177747 |
| 42 | 207.54 | 196 | 219 | 1.001 | 0.16007722 | 0.2 | 0.84177747 |
| 43 | 207.54 | 196 | 219 | 1.001 | 0.16007722 | 0.2 | 0.84177747 |
| 44 | 207.54 | 196 | 219 | 1.001 | 0.16007722 | 0.2 | 0.84177747 |
| 45 | 207.54 | 196 | 219 | 1.001 | 0.16007722 | 0.2 | 0.84177747 |
| 46 | 207.54 | 196 | 219 | 1.001 | 0.16007722 | 0.2 | 0.84177747 |
| 47 | 207.54 | 196 | 219 | 1.001 | 0.16007722 | 0.2 | 0.84177747 |
| 48 | 207.54 | 196 | 219 | 1.001 | 0.16007722 | 0.2 | 0.84177747 |
| 49 | 207.54 | 196 | 219 | 1.001 | 0.16007722 | 0.2 | 0.84177747 |
| 50 | 207.54 | 196 | 219 | 1.001 | 0.16007722 | 0.2 | 0.84177747 |
| 51 | 183.24 | 174 | 193 | 1 | 0.14951354 | 0.115 | 0.90880066 |
| 52 | 183.24 | 174 | 193 | 1 | 0.14951354 | 0.115 | 0.90880066 |
| 53 | 183.24 | 174 | 193 | 1 | 0.14951354 | 0.115 | 0.90880066 |
| 54 | 183.24 | 174 | 193 | 1 | 0.14951354 | 0.115 | 0.90880066 |
| 55 | 183.24 | 174 | 193 | 1 | 0.14951354 | 0.115 | 0.90880066 |
| 56 | 183.24 | 174 | 193 | 1 | 0.14951354 | 0.115 | 0.90880066 |
| 57 | 183.24 | 174 | 193 | 1 | 0.14951354 | 0.115 | 0.90880066 |
| 58 | 183.24 | 174 | 193 | 1 | 0.14951354 | 0.115 | 0.90880066 |
| 59 | 183.24 | 174 | 193 | 1 | 0.14951354 | 0.115 | 0.90880066 |
| 60 | | | | | | | |

| | | | | | | | |
|----|--------|-----|-----|-------|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 183.24 | 174 | 193 | 1 | 0.14951354 | 0.115 | 0.90880066 |
| 4 | 178.82 | 170 | 188 | 1.001 | 0.14519792 | 0.155 | 0.87666722 |
| 5 | 178.82 | 170 | 188 | 1.001 | 0.14519792 | 0.155 | 0.87666722 |
| 6 | 178.82 | 170 | 188 | 1.001 | 0.14519792 | 0.155 | 0.87666722 |
| 7 | 178.82 | 170 | 188 | 1.001 | 0.14519792 | 0.155 | 0.87666722 |
| 8 | 178.82 | 170 | 188 | 1.001 | 0.14519792 | 0.155 | 0.87666722 |
| 9 | 178.82 | 170 | 188 | 1.001 | 0.14519792 | 0.155 | 0.87666722 |
| 10 | 178.82 | 170 | 188 | 1.001 | 0.14519792 | 0.155 | 0.87666722 |
| 11 | 178.82 | 170 | 188 | 1.001 | 0.14519792 | 0.155 | 0.87666722 |
| 12 | 178.82 | 170 | 188 | 1.001 | 0.14519792 | 0.155 | 0.87666722 |
| 13 | 178.82 | 170 | 188 | 1.001 | 0.14519792 | 0.155 | 0.87666722 |
| 14 | 178.82 | 170 | 188 | 1.001 | 0.14519792 | 0.155 | 0.87666722 |
| 15 | 95.41 | 91 | 100 | 1 | 0.13606155 | 0.123 | 0.9020904 |
| 16 | 95.41 | 91 | 100 | 1 | 0.13606155 | 0.123 | 0.9020904 |
| 17 | 95.41 | 91 | 100 | 1 | 0.13606155 | 0.123 | 0.9020904 |
| 18 | 95.41 | 91 | 100 | 1 | 0.13606155 | 0.123 | 0.9020904 |
| 19 | 95.41 | 91 | 100 | 1 | 0.13606155 | 0.123 | 0.9020904 |
| 20 | 95.41 | 91 | 100 | 1 | 0.13606155 | 0.123 | 0.9020904 |
| 21 | 95.41 | 91 | 100 | 1 | 0.13606155 | 0.123 | 0.9020904 |
| 22 | 97.48 | 93 | 102 | 1.001 | 0.13326653 | 0.153 | 0.87801743 |
| 23 | 97.48 | 93 | 102 | 1.001 | 0.13326653 | 0.153 | 0.87801743 |
| 24 | 100.35 | 96 | 105 | 1 | 0.12928302 | 0.139 | 0.88976693 |
| 25 | 68.66 | 66 | 72 | 1 | 0.12553088 | 0.149 | 0.88183704 |
| 26 | 68.66 | 66 | 72 | 1 | 0.12553088 | 0.149 | 0.88183704 |
| 27 | 68.66 | 66 | 72 | 1 | 0.12553088 | 0.149 | 0.88183704 |
| 28 | 68.66 | 66 | 72 | 1 | 0.12553088 | 0.149 | 0.88183704 |
| 29 | 68.66 | 66 | 72 | 1 | 0.12553088 | 0.149 | 0.88183704 |
| 30 | 68.66 | 66 | 72 | 1 | 0.12553088 | 0.149 | 0.88183704 |
| 31 | 68.66 | 66 | 72 | 1 | 0.12553088 | 0.149 | 0.88183704 |
| 32 | 68.66 | 66 | 72 | 1 | 0.12553088 | 0.149 | 0.88183704 |
| 33 | 68.66 | 66 | 72 | 1 | 0.12553088 | 0.149 | 0.88183704 |
| 34 | 68.66 | 66 | 72 | 1 | 0.12553088 | 0.149 | 0.88183704 |
| 35 | 68.66 | 66 | 72 | 1 | 0.12553088 | 0.149 | 0.88183704 |
| 36 | 68.66 | 66 | 72 | 1 | 0.12553088 | 0.149 | 0.88183704 |
| 37 | 68.66 | 66 | 72 | 1 | 0.12553088 | 0.149 | 0.88183704 |
| 38 | 68.66 | 66 | 72 | 1 | 0.12553088 | 0.149 | 0.88183704 |
| 39 | 187.03 | 179 | 195 | 1 | 0.12351454 | 0.09 | 0.92816155 |
| 40 | 187.03 | 179 | 195 | 1 | 0.12351454 | 0.09 | 0.92816155 |
| 41 | 187.03 | 179 | 195 | 1 | 0.12351454 | 0.09 | 0.92816155 |
| 42 | 187.03 | 179 | 195 | 1 | 0.12351454 | 0.09 | 0.92816155 |
| 43 | 187.03 | 179 | 195 | 1 | 0.12351454 | 0.09 | 0.92816155 |
| 44 | 187.03 | 179 | 195 | 1 | 0.12351454 | 0.09 | 0.92816155 |
| 45 | 187.03 | 179 | 195 | 1 | 0.12351454 | 0.09 | 0.92816155 |
| 46 | 187.03 | 179 | 195 | 1 | 0.12351454 | 0.09 | 0.92816155 |
| 47 | 187.03 | 179 | 195 | 1 | 0.12351454 | 0.09 | 0.92816155 |
| 48 | 187.03 | 179 | 195 | 1 | 0.12351454 | 0.09 | 0.92816155 |
| 49 | 187.03 | 179 | 195 | 1 | 0.12351454 | 0.09 | 0.92816155 |
| 50 | 187.03 | 179 | 195 | 1 | 0.12351454 | 0.09 | 0.92816155 |
| 51 | 187.03 | 179 | 195 | 1 | 0.12351454 | 0.09 | 0.92816155 |
| 52 | 187.03 | 179 | 195 | 1 | 0.12351454 | 0.09 | 0.92816155 |
| 53 | 187.03 | 179 | 195 | 1 | 0.12351454 | 0.09 | 0.92816155 |
| 54 | 187.03 | 179 | 195 | 1 | 0.12351454 | 0.09 | 0.92816155 |
| 55 | 187.03 | 179 | 195 | 1 | 0.12351454 | 0.09 | 0.92816155 |
| 56 | 90.86 | 88 | 94 | 1 | 0.09515723 | 0.079 | 0.93668218 |
| 57 | 106.51 | 103 | 110 | 1 | 0.09485919 | 0.097 | 0.92234618 |
| 58 | 106.51 | 103 | 110 | 1 | 0.09485919 | 0.097 | 0.92234618 |
| 59 | 106.51 | 103 | 110 | 1 | 0.09485919 | 0.097 | 0.92234618 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|---------|---------|---|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 4 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 5 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 6 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 7 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 8 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 9 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 10 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 11 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 12 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 13 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 14 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 15 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 16 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 17 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 18 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 19 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 20 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 21 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 22 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 23 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 24 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 25 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 26 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 27 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 28 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 29 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 30 | 119.17 | 116 | 123 | 1 | 0.08453351 | 0.101 | 0.91988506 |
| 31 | 121.76 | 118 | 125 | 1 | 0.08314124 | 0.103 | 0.91798369 |
| 32 | 110.33 | 107 | 113 | 1 | 0.07871198 | 0.095 | 0.92413182 |
| 33 | 110.33 | 107 | 113 | 1 | 0.07871198 | 0.095 | 0.92413182 |
| 34 | 110.33 | 107 | 113 | 1 | 0.07871198 | 0.095 | 0.92413182 |
| 35 | 256.62 | 250 | 264 | 1 | 0.07860983 | 0.082 | 0.93443419 |
| 36 | 291.88 | 285 | 299 | 1 | 0.06918357 | 0.092 | 0.92658997 |
| 37 | 56.08 | 55 | 57 | 1 | 0.0515303 | 0.046 | 0.96318627 |
| 38 | 461.71 | 454 | 470 | 1 | 0.04996846 | 0.062 | 0.95081656 |
| 39 | 461.71 | 454 | 470 | 1 | 0.04996846 | 0.062 | 0.95081656 |
| 40 | 461.71 | 454 | 470 | 1 | 0.04996846 | 0.062 | 0.95081656 |
| 41 | 461.71 | 454 | 470 | 1 | 0.04996846 | 0.062 | 0.95081656 |
| 42 | 461.71 | 454 | 470 | 1 | 0.04996846 | 0.062 | 0.95081656 |
| 43 | 461.71 | 454 | 470 | 1 | 0.04996846 | 0.062 | 0.95081656 |
| 44 | 63.99 | 63 | 65 | 1 | 0.04508789 | 0.025 | 0.97972935 |
| 45 | 63.99 | 63 | 65 | 1 | 0.04508789 | 0.025 | 0.97972935 |
| 46 | 63.99 | 63 | 65 | 1 | 0.04508789 | 0.025 | 0.97972935 |
| 47 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 48 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 49 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 50 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 51 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 52 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 53 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 54 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 55 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 56 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 57 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 58 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 59 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|---------|---------|---|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 4 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 5 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 6 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 7 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 8 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 9 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 10 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 11 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 12 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 13 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 14 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 15 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 16 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 17 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 18 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 19 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 20 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 21 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 22 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 23 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 24 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 25 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 26 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 27 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 28 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 29 | 1123962.24 | 1108777 | 1139147 | 1 | 0.03898469 | 0.037 | 0.97055362 |
| 30 | 19474.19 | 19244 | 19705 | 1 | 0.03415304 | 0.038 | 0.96979777 |
| 31 | 55.75 | 55 | 56 | 1 | 0.02599521 | 0.045 | 0.96400203 |
| 32 | 55.75 | 55 | 56 | 1 | 0.02599521 | 0.045 | 0.96400203 |
| 33 | 55.75 | 55 | 56 | 1 | 0.02599521 | 0.045 | 0.96400203 |
| 34 | 55.75 | 55 | 56 | 1 | 0.02599521 | 0.045 | 0.96400203 |
| 35 | 55.75 | 55 | 56 | 1 | 0.02599521 | 0.045 | 0.96400203 |
| 36 | 55.75 | 55 | 56 | 1 | 0.02599521 | 0.045 | 0.96400203 |
| 37 | 55.75 | 55 | 56 | 1 | 0.02599521 | 0.045 | 0.96400203 |
| 38 | 55.75 | 55 | 56 | 1 | 0.02599521 | 0.045 | 0.96400203 |
| 39 | 55.75 | 55 | 56 | 1 | 0.02599521 | 0.045 | 0.96400203 |
| 40 | 55.75 | 55 | 56 | 1 | 0.02599521 | 0.045 | 0.96400203 |
| 41 | | | | | | | |
| 42 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 43 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 44 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 45 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 46 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 47 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 48 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 49 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 50 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 51 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 52 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 53 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 54 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 55 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 56 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 57 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 58 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 59 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|---|------------|-------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 4 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 5 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 6 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 7 | 37566.59 | 37315 | 37818 | 1 | 0.01931738 | 0.02 | 0.98421645 |
| 8 | | | | | | | |
| 9 | 6460.62 | 6419 | 6502 | 1 | 0.018535 | 0.021 | 0.98285815 |
| 10 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 11 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 12 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 13 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 14 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 15 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 16 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 17 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 18 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 19 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 20 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 21 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 22 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 23 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 24 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 25 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 26 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 27 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 28 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 29 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 30 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 31 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 32 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 33 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 34 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 35 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 36 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 37 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 38 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 39 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 40 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 41 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 42 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 43 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 44 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 45 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 46 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 47 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 48 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 49 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 50 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 51 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 52 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 53 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 54 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 55 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 56 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 57 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 58 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 59 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|---|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 4 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 5 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 6 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 7 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 8 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 9 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 10 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 11 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 12 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 13 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 14 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 15 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 16 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 17 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 18 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 19 | 6433.82 | 6394 | 6473 | 1 | 0.01771576 | 0.021 | 0.98357156 |
| 20 | 6442.49 | 6403 | 6482 | 1 | 0.01769101 | 0.021 | 0.98339667 |
| 21 | 6442.49 | 6403 | 6482 | 1 | 0.01769101 | 0.021 | 0.98339667 |
| 22 | 6442.49 | 6403 | 6482 | 1 | 0.01769101 | 0.021 | 0.98339667 |
| 23 | 6442.49 | 6403 | 6482 | 1 | 0.01769101 | 0.021 | 0.98339667 |
| 24 | 37699.49 | 37477 | 37922 | 1 | 0.01702958 | 0.017 | 0.98611562 |
| 25 | 43484.42 | 43461 | 43508 | 1 | 0.00155933 | 0.002 | 0.99873247 |
| 26 | 43484.42 | 43461 | 43508 | 1 | 0.00155933 | 0.002 | 0.99873247 |
| 27 | 43484.42 | 43461 | 43508 | 1 | 0.00155933 | 0.002 | 0.99873247 |
| 28 | 43484.42 | 43461 | 43508 | 1 | 0.00155933 | 0.002 | 0.99873247 |
| 29 | 43484.42 | 43461 | 43508 | 1 | 0.00155933 | 0.002 | 0.99873247 |
| 30 | 43484.42 | 43461 | 43508 | 1 | 0.00155933 | 0.002 | 0.99873247 |
| 31 | 43484.42 | 43461 | 43508 | 1 | 0.00155933 | 0.002 | 0.99873247 |
| 32 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 33 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 34 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 35 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 36 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 37 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 38 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 39 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 40 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 41 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 42 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 43 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 44 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 45 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 46 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 47 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 48 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 49 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 50 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 51 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 52 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 53 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 54 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 55 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 56 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 57 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 58 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 59 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|---|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 4 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 5 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 6 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 7 | 363.7 | 364 | 364 | 1 | 0 | -0.003 | 0.9972818 |
| 8 | | | | | | | |
| 9 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 10 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 11 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 12 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 13 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 14 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 15 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 16 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 17 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 18 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 19 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 20 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 21 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 22 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 23 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 24 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 25 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 26 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 27 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 28 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 29 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 30 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 31 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 32 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 33 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 34 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 35 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 36 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 37 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 38 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 39 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 40 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 41 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 42 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 43 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 44 | 335.09 | 335 | 335 | 1 | 0 | 0 | 0.9996958 |
| 45 | | | | | | | |
| 46 | 247.64 | 249 | 247 | 1 | -0.0116347 | -0.012 | 0.99038722 |
| 47 | 23635.07 | 23795 | 23475 | 1 | -0.0195333 | -0.021 | 0.98299019 |
| 48 | 23635.07 | 23795 | 23475 | 1 | -0.0195333 | -0.021 | 0.98299019 |
| 49 | 23635.07 | 23795 | 23475 | 1 | -0.0195333 | -0.021 | 0.98299019 |
| 50 | 23635.07 | 23795 | 23475 | 1 | -0.0195333 | -0.021 | 0.98299019 |
| 51 | 23635.07 | 23795 | 23475 | 1 | -0.0195333 | -0.021 | 0.98299019 |
| 52 | 23635.07 | 23795 | 23475 | 1 | -0.0195333 | -0.021 | 0.98299019 |
| 53 | 23635.07 | 23795 | 23475 | 1 | -0.0195333 | -0.021 | 0.98299019 |
| 54 | 23635.07 | 23795 | 23475 | 1 | -0.0195333 | -0.021 | 0.98299019 |
| 55 | 23635.07 | 23795 | 23475 | 1 | -0.0195333 | -0.021 | 0.98299019 |
| 56 | 23635.07 | 23795 | 23475 | 1 | -0.0195333 | -0.021 | 0.98299019 |
| 57 | 23635.07 | 23795 | 23475 | 1 | -0.0195333 | -0.021 | 0.98299019 |
| 58 | 23635.07 | 23795 | 23475 | 1 | -0.0195333 | -0.021 | 0.98299019 |
| 59 | 23635.07 | 23795 | 23475 | 1 | -0.0195333 | -0.021 | 0.98299019 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|---|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 5299.88 | 5384 | 5216 | 1 | -0.0457345 | -0.05 | 0.96011256 |
| 4 | 11348.02 | 11600 | 11096 | 1 | -0.0640851 | -0.079 | 0.93736682 |
| 5 | 11348.02 | 11600 | 11096 | 1 | -0.0640851 | -0.079 | 0.93736682 |
| 6 | 516.35 | 530 | 502 | 1 | -0.078305 | -0.088 | 0.93002306 |
| 7 | 516.35 | 530 | 502 | 1 | -0.078305 | -0.088 | 0.93002306 |
| 8 | 516.35 | 530 | 502 | 1 | -0.078305 | -0.088 | 0.93002306 |
| 9 | 516.35 | 530 | 502 | 1 | -0.078305 | -0.088 | 0.93002306 |
| 10 | 516.35 | 530 | 502 | 1 | -0.078305 | -0.088 | 0.93002306 |
| 11 | 516.35 | 530 | 502 | 1 | -0.078305 | -0.088 | 0.93002306 |
| 12 | 516.35 | 530 | 502 | 1 | -0.078305 | -0.088 | 0.93002306 |
| 13 | 516.35 | 530 | 502 | 1 | -0.078305 | -0.088 | 0.93002306 |
| 14 | 516.35 | 530 | 502 | 1 | -0.078305 | -0.088 | 0.93002306 |
| 15 | 516.35 | 530 | 502 | 1 | -0.078305 | -0.088 | 0.93002306 |
| 16 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 17 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 18 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 19 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 20 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 21 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 22 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 23 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 24 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 25 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 26 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 27 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 28 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 29 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 30 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 31 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 32 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 33 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 34 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 35 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 36 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 37 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 38 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 39 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 40 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 41 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 42 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 43 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 44 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 45 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 46 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 47 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 48 | 388.68 | 400 | 378 | 1 | -0.0816138 | -0.094 | 0.92502052 |
| 49 | 66.12 | 68 | 64 | 1 | -0.0874628 | -0.066 | 0.94756194 |
| 50 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 |
| 51 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 |
| 52 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 |
| 53 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 |
| 54 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 |
| 55 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 |
| 56 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 |
| 57 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 |
| 58 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 |
| 59 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 |
| 60 | | | | | | | |

| | | | | | | | | |
|----|-----------|--------|--------|---|------------|--------|------------|--|
| 1 | | | | | | | | |
| 2 | | | | | | | | |
| 3 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 | |
| 4 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 | |
| 5 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 | |
| 6 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 | |
| 7 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 | |
| 8 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 | |
| 9 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 | |
| 10 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 | |
| 11 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 | |
| 12 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 | |
| 13 | 65.25 | 67 | 63 | 1 | -0.0888093 | -0.094 | 0.92513432 | |
| 14 | 385.05 | 397 | 373 | 1 | -0.0899634 | -0.081 | 0.935329 | |
| 15 | 385.05 | 397 | 373 | 1 | -0.0899634 | -0.081 | 0.935329 | |
| 16 | 385.05 | 397 | 373 | 1 | -0.0899634 | -0.081 | 0.935329 | |
| 17 | 385.05 | 397 | 373 | 1 | -0.0899634 | -0.081 | 0.935329 | |
| 18 | 385.05 | 397 | 373 | 1 | -0.0899634 | -0.081 | 0.935329 | |
| 19 | 385.05 | 397 | 373 | 1 | -0.0899634 | -0.081 | 0.935329 | |
| 20 | 176.23 | 183 | 170 | 1 | -0.1063089 | -0.126 | 0.89950882 | |
| 21 | 176.23 | 183 | 170 | 1 | -0.1063089 | -0.126 | 0.89950882 | |
| 22 | 176.23 | 183 | 170 | 1 | -0.1063089 | -0.126 | 0.89950882 | |
| 23 | 176.23 | 183 | 170 | 1 | -0.1063089 | -0.126 | 0.89950882 | |
| 24 | 176.23 | 183 | 170 | 1 | -0.1063089 | -0.126 | 0.89950882 | |
| 25 | 176.23 | 183 | 170 | 1 | -0.1063089 | -0.126 | 0.89950882 | |
| 26 | 176.23 | 183 | 170 | 1 | -0.1063089 | -0.126 | 0.89950882 | |
| 27 | 176.23 | 183 | 170 | 1 | -0.1063089 | -0.126 | 0.89950882 | |
| 28 | 176.23 | 183 | 170 | 1 | -0.1063089 | -0.126 | 0.89950882 | |
| 29 | 176.23 | 183 | 170 | 1 | -0.1063089 | -0.126 | 0.89950882 | |
| 30 | 176.23 | 183 | 170 | 1 | -0.1063089 | -0.126 | 0.89950882 | |
| 31 | 176.23 | 183 | 170 | 1 | -0.1063089 | -0.126 | 0.89950882 | |
| 32 | 176.23 | 183 | 170 | 1 | -0.1063089 | -0.126 | 0.89950882 | |
| 33 | 176.23 | 183 | 170 | 1 | -0.1063089 | -0.126 | 0.89950882 | |
| 34 | 176.23 | 183 | 170 | 1 | -0.1063089 | -0.126 | 0.89950882 | |
| 35 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 36 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 37 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 38 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 39 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 40 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 41 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 42 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 43 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 44 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 45 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 46 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 47 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 48 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 49 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 50 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 51 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 52 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 53 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 54 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 55 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 56 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 57 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 58 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 59 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 | |
| 60 | | | | | | | | |

| | | | | | | | |
|----|-----------|--------|--------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 |
| 4 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 |
| 5 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 |
| 6 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 |
| 7 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 |
| 8 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 |
| 9 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 |
| 10 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 |
| 11 | 154653.38 | 160722 | 148585 | 1 | -0.1132789 | -0.099 | 0.92105354 |
| 12 | 16649.39 | 17335 | 15964 | 1 | -0.1188657 | -0.101 | 0.91935059 |
| 13 | 16649.39 | 17335 | 15964 | 1 | -0.1188657 | -0.101 | 0.91935059 |
| 14 | 16649.39 | 17335 | 15964 | 1 | -0.1188657 | -0.101 | 0.91935059 |
| 15 | 16649.39 | 17335 | 15964 | 1 | -0.1188657 | -0.101 | 0.91935059 |
| 16 | 325.4 | 340 | 311 | 0.999 | -0.1286202 | -0.149 | 0.88130482 |
| 17 | 325.4 | 340 | 311 | 0.999 | -0.1286202 | -0.149 | 0.88130482 |
| 18 | 325.4 | 340 | 311 | 0.999 | -0.1286202 | -0.149 | 0.88130482 |
| 19 | 325.4 | 340 | 311 | 0.999 | -0.1286202 | -0.149 | 0.88130482 |
| 20 | 367.54 | 384 | 351 | 0.999 | -0.1296353 | -0.147 | 0.88282692 |
| 21 | 2350.02 | 2457 | 2243 | 1 | -0.1314682 | -0.13 | 0.89684263 |
| 22 | 2350.02 | 2457 | 2243 | 1 | -0.1314682 | -0.13 | 0.89684263 |
| 23 | 2379.37 | 2489 | 2269 | 1 | -0.1335096 | -0.132 | 0.89478386 |
| 24 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 25 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 26 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 27 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 28 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 29 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 30 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 31 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 32 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 33 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 34 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 35 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 36 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 37 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 38 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 39 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 40 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 41 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 42 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 43 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 44 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 45 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 46 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 47 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 48 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 49 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 50 | 322.21 | 339 | 306 | 0.999 | -0.1477536 | -0.172 | 0.86369006 |
| 51 | 705.37 | 743 | 668 | 0.999 | -0.1535141 | -0.192 | 0.84795306 |
| 52 | 705.37 | 743 | 668 | 0.999 | -0.1535141 | -0.192 | 0.84795306 |
| 53 | 826.88 | 871 | 783 | 0.999 | -0.1536604 | -0.168 | 0.86627939 |
| 54 | 826.88 | 871 | 783 | 0.999 | -0.1536604 | -0.168 | 0.86627939 |
| 55 | 826.88 | 871 | 783 | 0.999 | -0.1536604 | -0.168 | 0.86627939 |
| 56 | 826.88 | 871 | 783 | 0.999 | -0.1536604 | -0.168 | 0.86627939 |
| 57 | 826.88 | 871 | 783 | 0.999 | -0.1536604 | -0.168 | 0.86627939 |
| 58 | 826.88 | 871 | 783 | 0.999 | -0.1536604 | -0.168 | 0.86627939 |
| 59 | 826.88 | 871 | 783 | 0.999 | -0.1536604 | -0.168 | 0.86627939 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 4 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 5 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 6 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 7 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 8 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 9 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 10 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 11 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 12 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 13 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 14 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 15 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 16 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 17 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 18 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 19 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 20 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 21 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 22 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 23 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 24 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 25 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 26 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 27 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 28 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 29 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 30 | 687.88 | 725 | 651 | 0.999 | -0.1553235 | -0.196 | 0.84428396 |
| 31 | 40876.58 | 43295 | 38458 | 1 | -0.1709167 | -0.16 | 0.87261571 |
| 32 | 40876.58 | 43295 | 38458 | 1 | -0.1709167 | -0.16 | 0.87261571 |
| 33 | 40423.86 | 42817 | 38031 | 1 | -0.1710078 | -0.16 | 0.87313129 |
| 34 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 35 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 36 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 37 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 38 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 39 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 40 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 41 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 42 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 43 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 44 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 45 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 46 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 47 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 48 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 49 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 50 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 51 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 52 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 53 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 54 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 55 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 56 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 57 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 58 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 59 | 159.75 | 169 | 150 | 1 | -0.1720607 | -0.164 | 0.86979297 |
| 60 | | | | | | | |

| | | | | | | | | |
|----|---------|------|------|-------|------------|--------|------------|--|
| 1 | | | | | | | | |
| 2 | | | | | | | | |
| 3 | 93.97 | 100 | 88 | 1 | -0.1844246 | -0.174 | 0.86208683 | |
| 4 | 93.97 | 100 | 88 | 1 | -0.1844246 | -0.174 | 0.86208683 | |
| 5 | 93.97 | 100 | 88 | 1 | -0.1844246 | -0.174 | 0.86208683 | |
| 6 | 93.97 | 100 | 88 | 1 | -0.1844246 | -0.174 | 0.86208683 | |
| 7 | 93.97 | 100 | 88 | 1 | -0.1844246 | -0.174 | 0.86208683 | |
| 8 | 93.97 | 100 | 88 | 1 | -0.1844246 | -0.174 | 0.86208683 | |
| 9 | 93.97 | 100 | 88 | 1 | -0.1844246 | -0.174 | 0.86208683 | |
| 10 | 93.97 | 100 | 88 | 1 | -0.1844246 | -0.174 | 0.86208683 | |
| 11 | 93.97 | 100 | 88 | 1 | -0.1844246 | -0.174 | 0.86208683 | |
| 12 | 93.97 | 100 | 88 | 1 | -0.1844246 | -0.174 | 0.86208683 | |
| 13 | 93.97 | 100 | 88 | 1 | -0.1844246 | -0.174 | 0.86208683 | |
| 14 | 93.97 | 100 | 88 | 1 | -0.1844246 | -0.174 | 0.86208683 | |
| 15 | 93.97 | 100 | 88 | 1 | -0.1844246 | -0.174 | 0.86208683 | |
| 16 | 93.97 | 100 | 88 | 1 | -0.1844246 | -0.174 | 0.86208683 | |
| 17 | 93.97 | 100 | 88 | 1 | -0.1844246 | -0.174 | 0.86208683 | |
| 18 | 92.94 | 99 | 86 | 0.999 | -0.2030919 | -0.23 | 0.81805809 | |
| 19 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 20 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 21 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 22 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 23 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 24 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 25 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 26 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 27 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 28 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 29 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 30 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 31 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 32 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 33 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 34 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 35 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 36 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 37 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 38 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 39 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 40 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 41 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 42 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 43 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 44 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 45 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 46 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 47 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 48 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 49 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 50 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 51 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 52 | 7356.39 | 7885 | 6827 | 0.999 | -0.207859 | -0.281 | 0.77896211 | |
| 53 | 7406.14 | 7945 | 6867 | 0.999 | -0.2103673 | -0.284 | 0.7763552 | |
| 54 | 7406.14 | 7945 | 6867 | 0.999 | -0.2103673 | -0.284 | 0.7763552 | |
| 55 | 7406.14 | 7945 | 6867 | 0.999 | -0.2103673 | -0.284 | 0.7763552 | |
| 56 | 7548.95 | 8113 | 6985 | 0.999 | -0.2159754 | -0.291 | 0.77092824 | |
| 57 | 7548.95 | 8113 | 6985 | 0.999 | -0.2159754 | -0.291 | 0.77092824 | |
| 58 | 7548.95 | 8113 | 6985 | 0.999 | -0.2159754 | -0.291 | 0.77092824 | |
| 59 | 7548.95 | 8113 | 6985 | 0.999 | -0.2159754 | -0.291 | 0.77092824 | |
| 60 | | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 7548.95 | 8113 | 6985 | 0.999 | -0.2159754 | -0.291 | 0.77092824 |
| 4 | 45.44 | 49 | 42 | 0.999 | -0.2223924 | -0.202 | 0.8397141 |
| 5 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 6 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 7 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 8 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 9 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 10 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 11 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 12 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 13 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 14 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 15 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 16 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 17 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 18 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 19 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 20 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 21 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 22 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 23 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 24 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 25 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 26 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 27 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 28 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 29 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 30 | 70.76 | 76 | 65 | 1 | -0.2255597 | -0.058 | NA |
| 31 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 32 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 33 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 34 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 35 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 36 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 37 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 38 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 39 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 40 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 41 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 42 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 43 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 44 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 45 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 46 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 47 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 48 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 49 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 50 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 51 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 52 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 53 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 54 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 55 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 56 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 57 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 58 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 59 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|-------|------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 4 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 5 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 6 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 7 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 8 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 9 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 10 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 11 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 12 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 13 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 14 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 15 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 16 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 17 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 18 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 19 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 20 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 21 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 22 | 4502.45 | 4868 | 4137 | 0.999 | -0.2347442 | -0.238 | 0.81163701 |
| 23 | 3947.77 | 4270 | 3625 | 0.999 | -0.2362551 | -0.216 | 0.82914349 |
| 24 | 3947.77 | 4270 | 3625 | 0.999 | -0.2362551 | -0.216 | 0.82914349 |
| 25 | | | | | | | |
| 26 | 3816 | 4149 | 3483 | 0.999 | -0.2524332 | -0.238 | 0.81214347 |
| 27 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 28 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 29 | | | | | | | |
| 30 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 31 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 32 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 33 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 34 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 35 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 36 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 37 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 38 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 39 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 40 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 41 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 42 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 43 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 44 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 45 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 46 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 47 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 48 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 49 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 50 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 51 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 52 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 53 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 54 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 55 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 56 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 57 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 58 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 59 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 4 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 5 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 6 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 7 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 8 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 9 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 10 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 11 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 12 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 13 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 14 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 15 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 16 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 17 | 10245.5 | 11164 | 9327 | 0.999 | -0.259369 | -0.345 | 0.73025313 |
| 18 | 3751.73 | 4090 | 3414 | 0.999 | -0.2606378 | -0.243 | 0.80805202 |
| 19 | 3751.73 | 4090 | 3414 | 0.999 | -0.2606378 | -0.243 | 0.80805202 |
| 20 | 3751.73 | 4090 | 3414 | 0.999 | -0.2606378 | -0.243 | 0.80805202 |
| 21 | 3751.73 | 4090 | 3414 | 0.999 | -0.2606378 | -0.243 | 0.80805202 |
| 22 | 3751.73 | 4090 | 3414 | 0.999 | -0.2606378 | -0.243 | 0.80805202 |
| 23 | 3751.73 | 4090 | 3414 | 0.999 | -0.2606378 | -0.243 | 0.80805202 |
| 24 | 88 | 96 | 80 | 0.999 | -0.2630344 | -0.296 | 0.76754171 |
| 25 | 88 | 96 | 80 | 0.999 | -0.2630344 | -0.296 | 0.76754171 |
| 26 | 88 | 96 | 80 | 0.999 | -0.2630344 | -0.296 | 0.76754171 |
| 27 | 959.94 | 1050 | 869 | 0.999 | -0.2729612 | -0.348 | 0.72787069 |
| 28 | 57.82 | 63 | 52 | 0.999 | -0.2768402 | -0.285 | 0.77580654 |
| 29 | 57.82 | 63 | 52 | 0.999 | -0.2768402 | -0.285 | 0.77580654 |
| 30 | 57.82 | 63 | 52 | 0.999 | -0.2768402 | -0.285 | 0.77580654 |
| 31 | 57.82 | 63 | 52 | 0.999 | -0.2768402 | -0.285 | 0.77580654 |
| 32 | 57.82 | 63 | 52 | 0.999 | -0.2768402 | -0.285 | 0.77580654 |
| 33 | 57.82 | 63 | 52 | 0.999 | -0.2768402 | -0.285 | 0.77580654 |
| 34 | 57.82 | 63 | 52 | 0.999 | -0.2768402 | -0.285 | 0.77580654 |
| 35 | 57.82 | 63 | 52 | 0.999 | -0.2768402 | -0.285 | 0.77580654 |
| 36 | 20998.43 | 23080 | 18916 | 0.999 | -0.2870362 | -0.276 | 0.78260435 |
| 37 | 20998.28 | 23080 | 18916 | 0.999 | -0.2870362 | -0.276 | 0.78261844 |
| 38 | 20998.28 | 23080 | 18916 | 0.999 | -0.2870362 | -0.276 | 0.78261844 |
| 39 | 20998.28 | 23080 | 18916 | 0.999 | -0.2870362 | -0.276 | 0.78261844 |
| 40 | 20998.28 | 23080 | 18916 | 0.999 | -0.2870362 | -0.276 | 0.78261844 |
| 41 | 20998.28 | 23080 | 18916 | 0.999 | -0.2870362 | -0.276 | 0.78261844 |
| 42 | 20998.28 | 23080 | 18916 | 0.999 | -0.2870362 | -0.276 | 0.78261844 |
| 43 | 20998.28 | 23080 | 18916 | 0.999 | -0.2870362 | -0.276 | 0.78261844 |
| 44 | 20998.28 | 23080 | 18916 | 0.999 | -0.2870362 | -0.276 | 0.78261844 |
| 45 | 20998.28 | 23080 | 18916 | 0.999 | -0.2870362 | -0.276 | 0.78261844 |
| 46 | 20998.28 | 23080 | 18916 | 0.999 | -0.2870362 | -0.276 | 0.78261844 |
| 47 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 48 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 49 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 50 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 51 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 52 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 53 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 54 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 55 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 56 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 57 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 58 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 59 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 4 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 5 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 6 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 7 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 8 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 9 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 10 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 11 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 12 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 13 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 14 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 15 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 16 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 17 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 18 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 19 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 20 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 21 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 22 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 23 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 24 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 25 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 26 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 27 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 28 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 29 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 30 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 31 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 32 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 33 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 34 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 35 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 36 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 37 | 20636.53 | 22694 | 18579 | 0.999 | -0.2886381 | -0.277 | 0.78173469 |
| 38 | 20647.31 | 22708 | 18586 | 0.999 | -0.2889843 | -0.277 | 0.78149503 |
| 39 | 3701.86 | 4072 | 3332 | 0.999 | -0.2893492 | -0.263 | 0.79265493 |
| 40 | 20737.94 | 22813 | 18663 | 0.999 | -0.2896753 | -0.278 | 0.78100729 |
| 41 | 20737.94 | 22813 | 18663 | 0.999 | -0.2896753 | -0.278 | 0.78100729 |
| 42 | 20737.94 | 22813 | 18663 | 0.999 | -0.2896753 | -0.278 | 0.78100729 |
| 43 | 3772.21 | 4151 | 3393 | 0.999 | -0.2908975 | -0.266 | 0.79056893 |
| 44 | 3772.21 | 4151 | 3393 | 0.999 | -0.2908975 | -0.266 | 0.79056893 |
| 45 | 3772.21 | 4151 | 3393 | 0.999 | -0.2908975 | -0.266 | 0.79056893 |
| 46 | 3772.21 | 4151 | 3393 | 0.999 | -0.2908975 | -0.266 | 0.79056893 |
| 47 | 3772.21 | 4151 | 3393 | 0.999 | -0.2908975 | -0.266 | 0.79056893 |
| 48 | 3772.21 | 4151 | 3393 | 0.999 | -0.2908975 | -0.266 | 0.79056893 |
| 49 | 3772.21 | 4151 | 3393 | 0.999 | -0.2908975 | -0.266 | 0.79056893 |
| 50 | 3772.21 | 4151 | 3393 | 0.999 | -0.2908975 | -0.266 | 0.79056893 |
| 51 | 3772.21 | 4151 | 3393 | 0.999 | -0.2908975 | -0.266 | 0.79056893 |
| 52 | 3772.21 | 4151 | 3393 | 0.999 | -0.2908975 | -0.266 | 0.79056893 |
| 53 | 3772.21 | 4151 | 3393 | 0.999 | -0.2908975 | -0.266 | 0.79056893 |
| 54 | 20761.15 | 22849 | 18673 | 0.999 | -0.2911773 | -0.279 | 0.77993646 |
| 55 | 20761.15 | 22849 | 18673 | 0.999 | -0.2911773 | -0.279 | 0.77993646 |
| 56 | 20761.15 | 22849 | 18673 | 0.999 | -0.2911773 | -0.279 | 0.77993646 |
| 57 | 20761.15 | 22849 | 18673 | 0.999 | -0.2911773 | -0.279 | 0.77993646 |
| 58 | 20761.15 | 22849 | 18673 | 0.999 | -0.2911773 | -0.279 | 0.77993646 |
| 59 | 20761.15 | 22849 | 18673 | 0.999 | -0.2911773 | -0.279 | 0.77993646 |
| 60 | | | | | | | |

| | | | | | | | |
|----|-----------|--------|--------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 20761.15 | 22849 | 18673 | 0.999 | -0.2911773 | -0.279 | 0.77993646 |
| 4 | 20761.15 | 22849 | 18673 | 0.999 | -0.2911773 | -0.279 | 0.77993646 |
| 5 | 20761.15 | 22849 | 18673 | 0.999 | -0.2911773 | -0.279 | 0.77993646 |
| 6 | 20761.15 | 22849 | 18673 | 0.999 | -0.2911773 | -0.279 | 0.77993646 |
| 7 | 20761.15 | 22849 | 18673 | 0.999 | -0.2911773 | -0.279 | 0.77993646 |
| 8 | 20761.15 | 22849 | 18673 | 0.999 | -0.2911773 | -0.279 | 0.77993646 |
| 9 | 20761.15 | 22849 | 18673 | 0.999 | -0.2911773 | -0.279 | 0.77993646 |
| 10 | 338667.77 | 372959 | 304377 | 0.999 | -0.2931577 | -0.343 | 0.73122556 |
| 11 | 338667.77 | 372959 | 304377 | 0.999 | -0.2931577 | -0.343 | 0.73122556 |
| 12 | 338667.77 | 372959 | 304377 | 0.999 | -0.2931577 | -0.343 | 0.73122556 |
| 13 | 338667.77 | 372959 | 304377 | 0.999 | -0.2931577 | -0.343 | 0.73122556 |
| 14 | 1090.26 | 1203 | 978 | 0.999 | -0.2987303 | -0.381 | 0.70345402 |
| 15 | 169.68 | 187 | 152 | 0.999 | -0.2989669 | -0.352 | 0.7251722 |
| 16 | 169.68 | 187 | 152 | 0.999 | -0.2989669 | -0.352 | 0.7251722 |
| 17 | 169.68 | 187 | 152 | 0.999 | -0.2989669 | -0.352 | 0.7251722 |
| 18 | 169.68 | 187 | 152 | 0.999 | -0.2989669 | -0.352 | 0.7251722 |
| 19 | 169.68 | 187 | 152 | 0.999 | -0.2989669 | -0.352 | 0.7251722 |
| 20 | 169.68 | 187 | 152 | 0.999 | -0.2989669 | -0.352 | 0.7251722 |
| 21 | 169.68 | 187 | 152 | 0.999 | -0.2989669 | -0.352 | 0.7251722 |
| 22 | 169.68 | 187 | 152 | 0.999 | -0.2989669 | -0.352 | 0.7251722 |
| 23 | 3856.89 | 4256 | 3458 | 0.999 | -0.2995603 | -0.271 | 0.78650537 |
| 24 | 3856.89 | 4256 | 3458 | 0.999 | -0.2995603 | -0.271 | 0.78650537 |
| 25 | 3856.89 | 4256 | 3458 | 0.999 | -0.2995603 | -0.271 | 0.78650537 |
| 26 | 3856.89 | 4256 | 3458 | 0.999 | -0.2995603 | -0.271 | 0.78650537 |
| 27 | 3856.89 | 4256 | 3458 | 0.999 | -0.2995603 | -0.271 | 0.78650537 |
| 28 | 171.89 | 190 | 154 | 0.999 | -0.3030691 | -0.355 | 0.72240338 |
| 29 | 171.89 | 190 | 154 | 0.999 | -0.3030691 | -0.355 | 0.72240338 |
| 30 | 171.89 | 190 | 154 | 0.999 | -0.3030691 | -0.355 | 0.72240338 |
| 31 | 171.89 | 190 | 154 | 0.999 | -0.3030691 | -0.355 | 0.72240338 |
| 32 | 171.89 | 190 | 154 | 0.999 | -0.3030691 | -0.355 | 0.72240338 |
| 33 | 171.89 | 190 | 154 | 0.999 | -0.3030691 | -0.355 | 0.72240338 |
| 34 | 171.89 | 190 | 154 | 0.999 | -0.3030691 | -0.355 | 0.72240338 |
| 35 | 171.89 | 190 | 154 | 0.999 | -0.3030691 | -0.355 | 0.72240338 |
| 36 | 171.89 | 190 | 154 | 0.999 | -0.3030691 | -0.355 | 0.72240338 |
| 37 | 171.89 | 190 | 154 | 0.999 | -0.3030691 | -0.355 | 0.72240338 |
| 38 | 171.89 | 190 | 154 | 0.999 | -0.3030691 | -0.355 | 0.72240338 |
| 39 | 171.89 | 190 | 154 | 0.999 | -0.3030691 | -0.355 | 0.72240338 |
| 40 | 5152.37 | 5710 | 4595 | 0.999 | -0.3134259 | -0.373 | 0.70920272 |
| 41 | 5152.37 | 5710 | 4595 | 0.999 | -0.3134259 | -0.373 | 0.70920272 |
| 42 | 5152.37 | 5710 | 4595 | 0.999 | -0.3134259 | -0.373 | 0.70920272 |
| 43 | 105.37 | 117 | 94 | 0.998 | -0.3157759 | -0.406 | 0.6848422 |
| 44 | 144.39 | 160 | 128 | 0.999 | -0.3219281 | -0.34 | 0.73378703 |
| 45 | 12048.53 | 13437 | 10660 | 0.999 | -0.3340036 | -0.357 | 0.72120175 |
| 46 | 12048.53 | 13437 | 10660 | 0.999 | -0.3340036 | -0.357 | 0.72120175 |
| 47 | 12048.53 | 13437 | 10660 | 0.999 | -0.3340036 | -0.357 | 0.72120175 |
| 48 | 13227.51 | 14790 | 11665 | 0.998 | -0.3424357 | -0.429 | 0.66819434 |
| 49 | 13227.51 | 14790 | 11665 | 0.998 | -0.3424357 | -0.429 | 0.66819434 |
| 50 | 13227.51 | 14790 | 11665 | 0.998 | -0.3424357 | -0.429 | 0.66819434 |
| 51 | 13227.51 | 14790 | 11665 | 0.998 | -0.3424357 | -0.429 | 0.66819434 |
| 52 | 13227.51 | 14790 | 11665 | 0.998 | -0.3424357 | -0.429 | 0.66819434 |
| 53 | 13227.51 | 14790 | 11665 | 0.998 | -0.3424357 | -0.429 | 0.66819434 |
| 54 | 13227.51 | 14790 | 11665 | 0.998 | -0.3424357 | -0.429 | 0.66819434 |
| 55 | 13227.51 | 14790 | 11665 | 0.998 | -0.3424357 | -0.429 | 0.66819434 |
| 56 | 13227.51 | 14790 | 11665 | 0.998 | -0.3424357 | -0.429 | 0.66819434 |
| 57 | 13227.51 | 14790 | 11665 | 0.998 | -0.3424357 | -0.429 | 0.66819434 |
| 58 | 13227.51 | 14790 | 11665 | 0.998 | -0.3424357 | -0.429 | 0.66819434 |
| 59 | 13227.51 | 14790 | 11665 | 0.998 | -0.3424357 | -0.429 | 0.66819434 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 12257.71 | 13722 | 10793 | 0.999 | -0.3463948 | -0.413 | 0.67983967 |
| 4 | 12257.71 | 13722 | 10793 | 0.999 | -0.3463948 | -0.413 | 0.67983967 |
| 5 | 12271.67 | 13740 | 10804 | 0.999 | -0.3468165 | -0.413 | 0.67943045 |
| 6 | 12271.67 | 13740 | 10804 | 0.999 | -0.3468165 | -0.413 | 0.67943045 |
| 7 | 12271.67 | 13740 | 10804 | 0.999 | -0.3468165 | -0.413 | 0.67943045 |
| 8 | 12271.67 | 13740 | 10804 | 0.999 | -0.3468165 | -0.413 | 0.67943045 |
| 9 | 12988.06 | 14551 | 11425 | 0.998 | -0.3489241 | -0.456 | 0.64857196 |
| 10 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 11 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 12 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 13 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 14 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 15 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 16 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 17 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 18 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 19 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 20 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 21 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 22 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 23 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 24 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 25 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 26 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 27 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 28 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 29 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 30 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 31 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 32 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 33 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 34 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 35 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 36 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 37 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 38 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 39 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 40 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 41 | 55.15 | 62 | 48 | 0.999 | -0.3692338 | -0.321 | 0.74800089 |
| 42 | 140.2 | 158 | 122 | 0.999 | -0.3730434 | -0.362 | 0.71728644 |
| 43 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 44 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 45 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 46 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 47 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 48 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 49 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 50 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 51 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 52 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 53 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 54 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 55 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 56 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 57 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 58 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 59 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 60 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |

| | | | | | | | |
|----|---------|------|-----|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 4 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 5 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 6 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 7 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 8 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 9 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 10 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 11 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 12 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 13 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 14 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 15 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 16 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 17 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 18 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 19 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 20 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 21 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 22 | 70.17 | 79 | 61 | 0.999 | -0.3730434 | -0.293 | 0.76937977 |
| 23 | 286.36 | 324 | 249 | 0.999 | -0.3798481 | -0.424 | 0.67151471 |
| 24 | 286.36 | 324 | 249 | 0.999 | -0.3798481 | -0.424 | 0.67151471 |
| 25 | 273.16 | 309 | 237 | 0.999 | -0.3827198 | -0.425 | 0.6706357 |
| 26 | 273.16 | 309 | 237 | 0.999 | -0.3827198 | -0.425 | 0.6706357 |
| 27 | 273.16 | 309 | 237 | 0.999 | -0.3827198 | -0.425 | 0.6706357 |
| 28 | 273.16 | 309 | 237 | 0.999 | -0.3827198 | -0.425 | 0.6706357 |
| 29 | 273.16 | 309 | 237 | 0.999 | -0.3827198 | -0.425 | 0.6706357 |
| 30 | 273.16 | 309 | 237 | 0.999 | -0.3827198 | -0.425 | 0.6706357 |
| 31 | 273.16 | 309 | 237 | 0.999 | -0.3827198 | -0.425 | 0.6706357 |
| 32 | 273.16 | 309 | 237 | 0.999 | -0.3827198 | -0.425 | 0.6706357 |
| 33 | 273.16 | 309 | 237 | 0.999 | -0.3827198 | -0.425 | 0.6706357 |
| 34 | 273.16 | 309 | 237 | 0.999 | -0.3827198 | -0.425 | 0.6706357 |
| 35 | 273.16 | 309 | 237 | 0.999 | -0.3827198 | -0.425 | 0.6706357 |
| 36 | 273.16 | 309 | 237 | 0.999 | -0.3827198 | -0.425 | 0.6706357 |
| 37 | 273.16 | 309 | 237 | 0.999 | -0.3827198 | -0.425 | 0.6706357 |
| 38 | 273.16 | 309 | 237 | 0.999 | -0.3827198 | -0.425 | 0.6706357 |
| 39 | 222.36 | 252 | 192 | 0.999 | -0.3923174 | -0.367 | 0.71389273 |
| 40 | 289.54 | 329 | 250 | 0.998 | -0.3961595 | -0.483 | 0.62931211 |
| 41 | 289.54 | 329 | 250 | 0.998 | -0.3961595 | -0.483 | 0.62931211 |
| 42 | 289.54 | 329 | 250 | 0.998 | -0.3961595 | -0.483 | 0.62931211 |
| 43 | 289.54 | 329 | 250 | 0.998 | -0.3961595 | -0.483 | 0.62931211 |
| 44 | 289.54 | 329 | 250 | 0.998 | -0.3961595 | -0.483 | 0.62931211 |
| 45 | 289.54 | 329 | 250 | 0.998 | -0.3961595 | -0.483 | 0.62931211 |
| 46 | 289.54 | 329 | 250 | 0.998 | -0.3961595 | -0.483 | 0.62931211 |
| 47 | 289.54 | 329 | 250 | 0.998 | -0.3961595 | -0.483 | 0.62931211 |
| 48 | 289.54 | 329 | 250 | 0.998 | -0.3961595 | -0.483 | 0.62931211 |
| 49 | 289.54 | 329 | 250 | 0.998 | -0.3961595 | -0.483 | 0.62931211 |
| 50 | 289.54 | 329 | 250 | 0.998 | -0.3961595 | -0.483 | 0.62931211 |
| 51 | 289.54 | 329 | 250 | 0.998 | -0.3961595 | -0.483 | 0.62931211 |
| 52 | 289.54 | 329 | 250 | 0.998 | -0.3961595 | -0.483 | 0.62931211 |
| 53 | 289.54 | 329 | 250 | 0.998 | -0.3961595 | -0.483 | 0.62931211 |
| 54 | 289.54 | 329 | 250 | 0.998 | -0.3961595 | -0.483 | 0.62931211 |
| 55 | 1157.14 | 1317 | 998 | 0.998 | -0.4001436 | -0.469 | 0.63925448 |
| 56 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 57 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 58 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 59 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 4 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 5 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 6 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 7 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 8 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 9 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 10 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 11 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 12 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 13 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 14 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 15 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 16 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 17 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 18 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 19 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 20 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 21 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 22 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 23 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 24 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 25 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 26 | 216.86 | 247 | 186 | 0.999 | -0.4092084 | -0.383 | 0.70181793 |
| 27 | 1301.41 | 1486 | 1117 | 0.998 | -0.4118049 | -0.468 | 0.63987864 |
| 28 | 1362.69 | 1556 | 1169 | 0.998 | -0.4125671 | -0.467 | 0.64070153 |
| 29 | 1362.69 | 1556 | 1169 | 0.998 | -0.4125671 | -0.467 | 0.64070153 |
| 30 | 1362.69 | 1556 | 1169 | 0.998 | -0.4125671 | -0.467 | 0.64070153 |
| 31 | 1362.69 | 1556 | 1169 | 0.998 | -0.4125671 | -0.467 | 0.64070153 |
| 32 | 1362.69 | 1556 | 1169 | 0.998 | -0.4125671 | -0.467 | 0.64070153 |
| 33 | 1362.69 | 1556 | 1169 | 0.998 | -0.4125671 | -0.467 | 0.64070153 |
| 34 | 1362.69 | 1556 | 1169 | 0.998 | -0.4125671 | -0.467 | 0.64070153 |
| 35 | 1362.69 | 1556 | 1169 | 0.998 | -0.4125671 | -0.467 | 0.64070153 |
| 36 | 1362.69 | 1556 | 1169 | 0.998 | -0.4125671 | -0.467 | 0.64070153 |
| 37 | 1362.69 | 1556 | 1169 | 0.998 | -0.4125671 | -0.467 | 0.64070153 |
| 38 | 291.81 | 333 | 250 | 0.998 | -0.4135941 | -0.497 | 0.61944521 |
| 39 | 291.81 | 333 | 250 | 0.998 | -0.4135941 | -0.497 | 0.61944521 |
| 40 | 291.81 | 333 | 250 | 0.998 | -0.4135941 | -0.497 | 0.61944521 |
| 41 | 291.81 | 333 | 250 | 0.998 | -0.4135941 | -0.497 | 0.61944521 |
| 42 | 291.81 | 333 | 250 | 0.998 | -0.4135941 | -0.497 | 0.61944521 |
| 43 | 44193.5 | 50500 | 37887 | 0.998 | -0.4145805 | -0.548 | 0.58337314 |
| 44 | 44193.5 | 50500 | 37887 | 0.998 | -0.4145805 | -0.548 | 0.58337314 |
| 45 | 44193.5 | 50500 | 37887 | 0.998 | -0.4145805 | -0.548 | 0.58337314 |
| 46 | 44193.5 | 50500 | 37887 | 0.998 | -0.4145805 | -0.548 | 0.58337314 |
| 47 | 44193.5 | 50500 | 37887 | 0.998 | -0.4145805 | -0.548 | 0.58337314 |
| 48 | 44193.5 | 50500 | 37887 | 0.998 | -0.4145805 | -0.548 | 0.58337314 |
| 49 | 44193.5 | 50500 | 37887 | 0.998 | -0.4145805 | -0.548 | 0.58337314 |
| 50 | 44193.5 | 50500 | 37887 | 0.998 | -0.4145805 | -0.548 | 0.58337314 |
| 51 | 44193.5 | 50500 | 37887 | 0.998 | -0.4145805 | -0.548 | 0.58337314 |
| 52 | 44193.5 | 50500 | 37887 | 0.998 | -0.4145805 | -0.548 | 0.58337314 |
| 53 | 44193.5 | 50500 | 37887 | 0.998 | -0.4145805 | -0.548 | 0.58337314 |
| 54 | 44193.5 | 50500 | 37887 | 0.998 | -0.4145805 | -0.548 | 0.58337314 |
| 55 | 71.58 | 82 | 61 | 0.999 | -0.4268147 | -0.333 | 0.73912638 |
| 56 | 73.48 | 85 | 63 | 0.999 | -0.432111 | -0.424 | 0.67140481 |
| 57 | 10911.11 | 12551 | 9272 | 0.998 | -0.4368498 | -0.482 | 0.63009799 |
| 58 | 10911.11 | 12551 | 9272 | 0.998 | -0.4368498 | -0.482 | 0.63009799 |
| 59 | 10911.11 | 12551 | 9272 | 0.998 | -0.4368498 | -0.482 | 0.63009799 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 10911.11 | 12551 | 9272 | 0.998 | -0.4368498 | -0.482 | 0.63009799 |
| 4 | 10911.11 | 12551 | 9272 | 0.998 | -0.4368498 | -0.482 | 0.63009799 |
| 5 | 10911.11 | 12551 | 9272 | 0.998 | -0.4368498 | -0.482 | 0.63009799 |
| 6 | 10911.11 | 12551 | 9272 | 0.998 | -0.4368498 | -0.482 | 0.63009799 |
| 7 | 10911.11 | 12551 | 9272 | 0.998 | -0.4368498 | -0.482 | 0.63009799 |
| 8 | 10911.11 | 12551 | 9272 | 0.998 | -0.4368498 | -0.482 | 0.63009799 |
| 9 | 10911.11 | 12551 | 9272 | 0.998 | -0.4368498 | -0.482 | 0.63009799 |
| 10 | 10911.11 | 12551 | 9272 | 0.998 | -0.4368498 | -0.482 | 0.63009799 |
| 11 | 10911.11 | 12551 | 9272 | 0.998 | -0.4368498 | -0.482 | 0.63009799 |
| 12 | 10911.11 | 12551 | 9272 | 0.998 | -0.4368498 | -0.482 | 0.63009799 |
| 13 | 10911.11 | 12551 | 9272 | 0.998 | -0.4368498 | -0.482 | 0.63009799 |
| 14 | 10911.11 | 12551 | 9272 | 0.998 | -0.4368498 | -0.482 | 0.63009799 |
| 15 | 3700.6 | 4285 | 3116 | 0.998 | -0.4596 | -0.502 | 0.61583562 |
| 16 | 3700.6 | 4285 | 3116 | 0.998 | -0.4596 | -0.502 | 0.61583562 |
| 17 | 1617.32 | 1873 | 1362 | 0.998 | -0.4596242 | -0.567 | 0.57042232 |
| 18 | 405.15 | 472 | 338 | 0.998 | -0.4817636 | -0.486 | 0.62687205 |
| 19 | 83.92 | 98 | 70 | 0.998 | -0.4854268 | -0.542 | 0.58771849 |
| 20 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 21 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 22 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 23 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 24 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 25 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 26 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 27 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 28 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 29 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 30 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 31 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 32 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 33 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 34 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 35 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 36 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 37 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 38 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 39 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 40 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 41 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 42 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 43 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 44 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 45 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 46 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 47 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 48 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 49 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 50 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 51 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 52 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 53 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 54 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 55 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 56 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 57 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 58 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 59 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|-------|------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 4 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 5 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 6 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 7 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 8 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 9 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 10 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 11 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 12 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 13 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 14 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 15 | 59.94 | 70 | 50 | 0.998 | -0.4854268 | -0.502 | 0.61600239 |
| 16 | 181.54 | 212 | 151 | 0.998 | -0.4895157 | -0.553 | 0.57998893 |
| 17 | 181.31 | 212 | 151 | 0.998 | -0.4895157 | -0.552 | 0.58089997 |
| 18 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 19 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 20 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 21 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 22 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 23 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 24 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 25 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 26 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 27 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 28 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 29 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 30 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 31 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 32 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 33 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 34 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 35 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 36 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 37 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 38 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 39 | 180.53 | 211 | 150 | 0.998 | -0.4922805 | -0.547 | 0.58469687 |
| 40 | 60.49 | 71 | 50 | 0.998 | -0.5058909 | -0.507 | 0.61247395 |
| 41 | 60.49 | 71 | 50 | 0.998 | -0.5058909 | -0.507 | 0.61247395 |
| 42 | 60.49 | 71 | 50 | 0.998 | -0.5058909 | -0.507 | 0.61247395 |
| 43 | 9637.02 | 11376 | 7899 | 0.998 | -0.5262514 | -0.541 | 0.58840402 |
| 44 | 9567.8 | 11300 | 7836 | 0.998 | -0.5281335 | -0.543 | 0.58683539 |
| 45 | 9567.8 | 11300 | 7836 | 0.998 | -0.5281335 | -0.543 | 0.58683539 |
| 46 | 9567.8 | 11300 | 7836 | 0.998 | -0.5281335 | -0.543 | 0.58683539 |
| 47 | 9567.8 | 11300 | 7836 | 0.998 | -0.5281335 | -0.543 | 0.58683539 |
| 48 | 9567.8 | 11300 | 7836 | 0.998 | -0.5281335 | -0.543 | 0.58683539 |
| 49 | 9567.8 | 11300 | 7836 | 0.998 | -0.5281335 | -0.543 | 0.58683539 |
| 50 | 9567.8 | 11300 | 7836 | 0.998 | -0.5281335 | -0.543 | 0.58683539 |
| 51 | 9567.8 | 11300 | 7836 | 0.998 | -0.5281335 | -0.543 | 0.58683539 |
| 52 | 9567.8 | 11300 | 7836 | 0.998 | -0.5281335 | -0.543 | 0.58683539 |
| 53 | 9567.8 | 11300 | 7836 | 0.998 | -0.5281335 | -0.543 | 0.58683539 |
| 54 | 295.68 | 349 | 242 | 0.997 | -0.52822 | -0.69 | 0.49031927 |
| 55 | 295.68 | 349 | 242 | 0.997 | -0.52822 | -0.69 | 0.49031927 |
| 56 | 295.68 | 349 | 242 | 0.997 | -0.52822 | -0.69 | 0.49031927 |
| 57 | 295.68 | 349 | 242 | 0.997 | -0.52822 | -0.69 | 0.49031927 |
| 58 | 295.68 | 349 | 242 | 0.997 | -0.52822 | -0.69 | 0.49031927 |
| 59 | 295.68 | 349 | 242 | 0.997 | -0.52822 | -0.69 | 0.49031927 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 429.97 | 508 | 352 | 0.998 | -0.5292531 | -0.536 | 0.5918884 |
| 4 | 429.97 | 508 | 352 | 0.998 | -0.5292531 | -0.536 | 0.5918884 |
| 5 | 429.97 | 508 | 352 | 0.998 | -0.5292531 | -0.536 | 0.5918884 |
| 6 | 429.97 | 508 | 352 | 0.998 | -0.5292531 | -0.536 | 0.5918884 |
| 7 | 429.97 | 508 | 352 | 0.998 | -0.5292531 | -0.536 | 0.5918884 |
| 8 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 9 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 10 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 11 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 12 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 13 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 14 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 15 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 16 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 17 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 18 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 19 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 20 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 21 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 22 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 23 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 24 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 25 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 26 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 27 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 28 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 29 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 30 | 121.28 | 145 | 98 | 0.998 | -0.5651992 | -0.639 | 0.52275261 |
| 31 | 52566.48 | 63130 | 42003 | 0.998 | -0.5878334 | -0.7 | 0.48368857 |
| 32 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 33 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 34 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 35 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 36 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 37 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 38 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 39 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 40 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 41 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 42 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 43 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 44 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 45 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 46 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 47 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 48 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 49 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 50 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 51 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 52 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 53 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 54 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 55 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 56 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 57 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 58 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 59 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 4 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 5 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 6 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 7 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 8 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 9 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 10 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 11 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 12 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 13 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 14 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 15 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 16 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 17 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 18 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 19 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 20 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 21 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 22 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 23 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 24 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 25 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 26 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 27 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 28 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 29 | 50865.29 | 61209 | 40521 | 0.997 | -0.595074 | -0.706 | 0.48017854 |
| 30 | 50881.71 | 61230 | 40533 | 0.997 | -0.5951417 | -0.706 | 0.48015451 |
| 31 | 50881.71 | 61230 | 40533 | 0.997 | -0.5951417 | -0.706 | 0.48015451 |
| 32 | 50881.71 | 61230 | 40533 | 0.997 | -0.5951417 | -0.706 | 0.48015451 |
| 33 | 50881.71 | 61230 | 40533 | 0.997 | -0.5951417 | -0.706 | 0.48015451 |
| 34 | 50881.71 | 61230 | 40533 | 0.997 | -0.5951417 | -0.706 | 0.48015451 |
| 35 | 50881.71 | 61230 | 40533 | 0.997 | -0.5951417 | -0.706 | 0.48015451 |
| 36 | 51080.12 | 61513 | 40647 | 0.997 | -0.5977425 | -0.709 | 0.47855111 |
| 37 | 51080.12 | 61513 | 40647 | 0.997 | -0.5977425 | -0.709 | 0.47855111 |
| 38 | 51080.12 | 61513 | 40647 | 0.997 | -0.5977425 | -0.709 | 0.47855111 |
| 39 | 51080.12 | 61513 | 40647 | 0.997 | -0.5977425 | -0.709 | 0.47855111 |
| 40 | 74050.66 | 90004 | 58097 | 0.998 | -0.6315255 | -0.648 | 0.51692531 |
| 41 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 42 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 43 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 44 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 45 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 46 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 47 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 48 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 49 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 50 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 51 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 52 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 53 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 54 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 55 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 56 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 57 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 58 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 59 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 4 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 5 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 6 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 7 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 8 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 9 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 10 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 11 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 12 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 13 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 14 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 15 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 16 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 17 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 18 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 19 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 20 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 21 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 22 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 23 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 24 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 25 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 26 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 27 | 73901.6 | 89841 | 57963 | 0.998 | -0.6322417 | -0.649 | 0.51644109 |
| 28 | 34996.84 | 42660 | 27334 | 0.997 | -0.6421874 | -0.763 | 0.44520616 |
| 29 | 34996.84 | 42660 | 27334 | 0.997 | -0.6421874 | -0.763 | 0.44520616 |
| 30 | 34996.84 | 42660 | 27334 | 0.997 | -0.6421874 | -0.763 | 0.44520616 |
| 31 | 34996.84 | 42660 | 27334 | 0.997 | -0.6421874 | -0.763 | 0.44520616 |
| 32 | 34996.84 | 42660 | 27334 | 0.997 | -0.6421874 | -0.763 | 0.44520616 |
| 33 | 34996.84 | 42660 | 27334 | 0.997 | -0.6421874 | -0.763 | 0.44520616 |
| 34 | 34996.84 | 42660 | 27334 | 0.997 | -0.6421874 | -0.763 | 0.44520616 |
| 35 | 34996.84 | 42660 | 27334 | 0.997 | -0.6421874 | -0.763 | 0.44520616 |
| 36 | 34996.84 | 42660 | 27334 | 0.997 | -0.6421874 | -0.763 | 0.44520616 |
| 37 | 34996.84 | 42660 | 27334 | 0.997 | -0.6421874 | -0.763 | 0.44520616 |
| 38 | 34996.84 | 42660 | 27334 | 0.997 | -0.6421874 | -0.763 | 0.44520616 |
| 39 | 34996.84 | 42660 | 27334 | 0.997 | -0.6421874 | -0.763 | 0.44520616 |
| 40 | 34996.84 | 42660 | 27334 | 0.997 | -0.6421874 | -0.763 | 0.44520616 |
| 41 | 34996.84 | 42660 | 27334 | 0.997 | -0.6421874 | -0.763 | 0.44520616 |
| 42 | 34996.84 | 42660 | 27334 | 0.997 | -0.6421874 | -0.763 | 0.44520616 |
| 43 | 34996.84 | 42660 | 27334 | 0.997 | -0.6421874 | -0.763 | 0.44520616 |
| 44 | 11945.94 | 14613 | 9279 | 0.998 | -0.6552111 | -0.598 | 0.55017117 |
| 45 | 11945.94 | 14613 | 9279 | 0.998 | -0.6552111 | -0.598 | 0.55017117 |
| 46 | 1535.81 | 1893 | 1179 | 0.997 | -0.6831107 | -0.808 | 0.41892083 |
| 47 | 1535.81 | 1893 | 1179 | 0.997 | -0.6831107 | -0.808 | 0.41892083 |
| 48 | 1535.81 | 1893 | 1179 | 0.997 | -0.6831107 | -0.808 | 0.41892083 |
| 49 | 1535.81 | 1893 | 1179 | 0.997 | -0.6831107 | -0.808 | 0.41892083 |
| 50 | 1535.81 | 1893 | 1179 | 0.997 | -0.6831107 | -0.808 | 0.41892083 |
| 51 | 1535.81 | 1893 | 1179 | 0.997 | -0.6831107 | -0.808 | 0.41892083 |
| 52 | 1535.81 | 1893 | 1179 | 0.997 | -0.6831107 | -0.808 | 0.41892083 |
| 53 | 1535.81 | 1893 | 1179 | 0.997 | -0.6831107 | -0.808 | 0.41892083 |
| 54 | 1535.81 | 1893 | 1179 | 0.997 | -0.6831107 | -0.808 | 0.41892083 |
| 55 | 1535.81 | 1893 | 1179 | 0.997 | -0.6831107 | -0.808 | 0.41892083 |
| 56 | 1535.81 | 1893 | 1179 | 0.997 | -0.6831107 | -0.808 | 0.41892083 |
| 57 | 1535.81 | 1893 | 1179 | 0.997 | -0.6831107 | -0.808 | 0.41892083 |
| 58 | 1535.81 | 1893 | 1179 | 0.997 | -0.6831107 | -0.808 | 0.41892083 |
| 59 | 1535.81 | 1893 | 1179 | 0.997 | -0.6831107 | -0.808 | 0.41892083 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 402.47 | 498 | 307 | 0.997 | -0.6979071 | -0.802 | 0.42252068 |
| 4 | 59.11 | 73 | 45 | 0.998 | -0.6979715 | -0.744 | 0.45708247 |
| 5 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 6 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 7 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 8 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 9 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 10 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 11 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 12 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 13 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 14 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 15 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 16 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 17 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 18 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 19 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 20 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 21 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 22 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 23 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 24 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 25 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 26 | 9837.47 | 12174 | 7501 | 0.998 | -0.6986484 | -0.58 | 0.56200568 |
| 27 | 92.56 | 115 | 70 | 0.997 | -0.716207 | -0.808 | 0.41890161 |
| 28 | 14160.18 | 17640 | 10681 | 0.997 | -0.7238038 | -0.863 | 0.38813449 |
| 29 | 14160.18 | 17640 | 10681 | 0.997 | -0.7238038 | -0.863 | 0.38813449 |
| 30 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 31 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 32 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 33 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 34 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 35 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 36 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 37 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 38 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 39 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 40 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 41 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 42 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 43 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 44 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 45 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 46 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 47 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 48 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 49 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 50 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 51 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 52 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 53 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 54 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 55 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 56 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 57 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 58 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 59 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 4 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 5 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 6 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 7 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 8 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 9 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 10 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 11 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 12 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 13 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 14 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 15 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 16 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 17 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 18 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 19 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 20 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 21 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 22 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 23 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 24 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 25 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 26 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 27 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 28 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 29 | 650.99 | 812 | 489 | 0.997 | -0.7316453 | -0.851 | 0.3945691 |
| 30 | 651.18 | 815 | 487 | 0.997 | -0.7428783 | -0.867 | 0.38611964 |
| 31 | 75236.85 | 94452 | 56022 | 0.997 | -0.7535879 | -0.918 | 0.35871936 |
| 32 | 75236.85 | 94452 | 56022 | 0.997 | -0.7535879 | -0.918 | 0.35871936 |
| 33 | 75236.85 | 94452 | 56022 | 0.997 | -0.7535879 | -0.918 | 0.35871936 |
| 34 | 75236.85 | 94452 | 56022 | 0.997 | -0.7535879 | -0.918 | 0.35871936 |
| 35 | 75236.85 | 94452 | 56022 | 0.997 | -0.7535879 | -0.918 | 0.35871936 |
| 36 | 131.91 | 167 | 97 | 0.998 | -0.7837915 | -0.753 | 0.45150374 |
| 37 | 8917.48 | 11316 | 6518 | 0.997 | -0.7958628 | -0.948 | 0.34324251 |
| 38 | 8917.48 | 11316 | 6518 | 0.997 | -0.7958628 | -0.948 | 0.34324251 |
| 39 | 8917.48 | 11316 | 6518 | 0.997 | -0.7958628 | -0.948 | 0.34324251 |
| 40 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 41 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 42 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 43 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 44 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 45 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 46 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 47 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 48 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 49 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 50 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 51 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 52 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 53 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 54 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 55 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 56 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 57 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 58 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 59 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 4 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 5 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 6 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 7 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 8 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 9 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 10 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 11 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 12 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 13 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 14 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 15 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 16 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 17 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 18 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 19 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 20 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 21 | 8910.85 | 11309 | 6513 | 0.997 | -0.7960772 | -0.948 | 0.34313428 |
| 22 | 116.13 | 148 | 85 | 0.998 | -0.8000624 | -0.622 | NA |
| 23 | 116.13 | 148 | 85 | 0.998 | -0.8000624 | -0.622 | NA |
| 24 | 129.88 | 165 | 94 | 0.998 | -0.8117334 | -0.772 | 0.43997844 |
| 25 | 1905.75 | 2429 | 1383 | 0.998 | -0.8125613 | -0.787 | 0.43113665 |
| 26 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 27 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 28 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 29 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 30 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 31 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 32 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 33 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 34 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 35 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 36 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 37 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 38 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 39 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 40 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 41 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 42 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 43 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 44 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 45 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 46 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 47 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 48 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 49 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 50 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 51 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 52 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 53 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 54 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 55 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 56 | 10865.99 | 13857 | 7875 | 0.997 | -0.8152631 | -0.916 | 0.35956605 |
| 57 | 610.96 | 781 | 441 | 0.997 | -0.8245439 | -0.878 | 0.38004258 |
| 58 | 567.3 | 727 | 408 | 0.996 | -0.8333862 | -0.981 | 0.32673794 |
| 59 | | | | | | | |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|-------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 348.86 | 447 | 250 | 0.997 | -0.8383467 | -0.962 | 0.33603045 |
| 4 | 348.86 | 447 | 250 | 0.997 | -0.8383467 | -0.962 | 0.33603045 |
| 5 | 348.86 | 447 | 250 | 0.997 | -0.8383467 | -0.962 | 0.33603045 |
| 6 | 348.86 | 447 | 250 | 0.997 | -0.8383467 | -0.962 | 0.33603045 |
| 7 | 348.86 | 447 | 250 | 0.997 | -0.8383467 | -0.962 | 0.33603045 |
| 8 | 348.86 | 447 | 250 | 0.997 | -0.8383467 | -0.962 | 0.33603045 |
| 9 | 348.86 | 447 | 250 | 0.997 | -0.8383467 | -0.962 | 0.33603045 |
| 10 | 348.86 | 447 | 250 | 0.997 | -0.8383467 | -0.962 | 0.33603045 |
| 11 | 348.86 | 447 | 250 | 0.997 | -0.8383467 | -0.962 | 0.33603045 |
| 12 | 348.86 | 447 | 250 | 0.997 | -0.8383467 | -0.962 | 0.33603045 |
| 13 | 348.86 | 447 | 250 | 0.997 | -0.8383467 | -0.962 | 0.33603045 |
| 14 | 348.86 | 447 | 250 | 0.997 | -0.8383467 | -0.962 | 0.33603045 |
| 15 | 348.86 | 447 | 250 | 0.997 | -0.8383467 | -0.962 | 0.33603045 |
| 16 | 348.86 | 447 | 250 | 0.997 | -0.8383467 | -0.962 | 0.33603045 |
| 17 | 348.86 | 447 | 250 | 0.997 | -0.8383467 | -0.962 | 0.33603045 |
| 18 | 348.86 | 447 | 250 | 0.997 | -0.8383467 | -0.962 | 0.33603045 |
| 19 | 348.86 | 447 | 250 | 0.997 | -0.8383467 | -0.962 | 0.33603045 |
| 20 | 348.86 | 447 | 250 | 0.997 | -0.8383467 | -0.962 | 0.33603045 |
| 21 | 348.86 | 447 | 250 | 0.997 | -0.8383467 | -0.962 | 0.33603045 |
| 22 | 14920.99 | 19181 | 10661 | 0.996 | -0.8473352 | -1.001 | 0.31680124 |
| 23 | 50.52 | 65 | 36 | 0.997 | -0.8524428 | -0.867 | 0.38608549 |
| 24 | 2607.45 | 3361 | 1854 | 0.996 | -0.8582493 | -1.026 | 0.30488752 |
| 25 | 2518.33 | 3258 | 1779 | 0.996 | -0.8729201 | -1.037 | 0.2999259 |
| 26 | 2518.33 | 3258 | 1779 | 0.996 | -0.8729201 | -1.037 | 0.2999259 |
| 27 | 2467.82 | 3201 | 1735 | 0.996 | -0.883587 | -1.047 | 0.2952488 |
| 28 | 2467.82 | 3201 | 1735 | 0.996 | -0.883587 | -1.047 | 0.2952488 |
| 29 | 2467.82 | 3201 | 1735 | 0.996 | -0.883587 | -1.047 | 0.2952488 |
| 30 | 2467.82 | 3201 | 1735 | 0.996 | -0.883587 | -1.047 | 0.2952488 |
| 31 | 2467.82 | 3201 | 1735 | 0.996 | -0.883587 | -1.047 | 0.2952488 |
| 32 | 2467.82 | 3201 | 1735 | 0.996 | -0.883587 | -1.047 | 0.2952488 |
| 33 | 2467.82 | 3201 | 1735 | 0.996 | -0.883587 | -1.047 | 0.2952488 |
| 34 | 2467.82 | 3201 | 1735 | 0.996 | -0.883587 | -1.047 | 0.2952488 |
| 35 | 2467.82 | 3201 | 1735 | 0.996 | -0.883587 | -1.047 | 0.2952488 |
| 36 | 2467.82 | 3201 | 1735 | 0.996 | -0.883587 | -1.047 | 0.2952488 |
| 37 | 2467.82 | 3201 | 1735 | 0.996 | -0.883587 | -1.047 | 0.2952488 |
| 38 | 2467.82 | 3201 | 1735 | 0.996 | -0.883587 | -1.047 | 0.2952488 |
| 39 | 2467.82 | 3201 | 1735 | 0.996 | -0.883587 | -1.047 | 0.2952488 |
| 40 | 76.6 | 100 | 54 | 0.997 | -0.8889687 | -1.001 | 0.31673814 |
| 41 | 76.6 | 100 | 54 | 0.997 | -0.8889687 | -1.001 | 0.31673814 |
| 42 | 76.6 | 100 | 54 | 0.997 | -0.8889687 | -1.001 | 0.31673814 |
| 43 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 44 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 45 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 46 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 47 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 48 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 49 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 50 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 51 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 52 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 53 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 54 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 55 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 56 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 57 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 58 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 59 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|-------|------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 4 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 5 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 6 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 7 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 8 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 9 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 10 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 11 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 12 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 13 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 14 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 15 | 436.58 | 567 | 306 | 0.996 | -0.8898171 | -1.007 | 0.31406573 |
| 16 | 523.23 | 681 | 366 | 0.996 | -0.8958111 | -1.051 | 0.29343267 |
| 17 | 2465.19 | 3209 | 1721 | 0.996 | -0.8988767 | -1.088 | 0.27662661 |
| 18 | 404.24 | 527 | 281 | 0.996 | -0.9072328 | -1.055 | 0.29121466 |
| 19 | 403.74 | 527 | 280 | 0.996 | -0.9123761 | -1.058 | 0.28988532 |
| 20 | 403.74 | 527 | 280 | 0.996 | -0.9123761 | -1.058 | 0.28988532 |
| 21 | 68.18 | 89 | 47 | 0.997 | -0.9211446 | -0.9 | 0.36830718 |
| 22 | 68.18 | 89 | 47 | 0.997 | -0.9211446 | -0.9 | 0.36830718 |
| 23 | 68.18 | 89 | 47 | 0.997 | -0.9211446 | -0.9 | 0.36830718 |
| 24 | 68.18 | 89 | 47 | 0.997 | -0.9211446 | -0.9 | 0.36830718 |
| 25 | 68.18 | 89 | 47 | 0.997 | -0.9211446 | -0.9 | 0.36830718 |
| 26 | 68.18 | 89 | 47 | 0.997 | -0.9211446 | -0.9 | 0.36830718 |
| 27 | 68.18 | 89 | 47 | 0.997 | -0.9211446 | -0.9 | 0.36830718 |
| 28 | 68.18 | 89 | 47 | 0.997 | -0.9211446 | -0.9 | 0.36830718 |
| 29 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 30 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 31 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 32 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 33 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 34 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 35 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 36 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 37 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 38 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 39 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 40 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 41 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 42 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 43 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 44 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 45 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 46 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 47 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 48 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 49 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 50 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 51 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 52 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 53 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 54 | 6857.55 | 8998 | 4716 | 0.996 | -0.9320406 | -1.081 | 0.27968845 |
| 55 | 3396.98 | 4459 | 2335 | 0.997 | -0.9332976 | -1.014 | 0.31065541 |
| 56 | 3396.98 | 4459 | 2335 | 0.997 | -0.9332976 | -1.014 | 0.31065541 |
| 57 | 11221.4 | 14731 | 7712 | 0.996 | -0.9336784 | -1.083 | 0.27870223 |
| 58 | 3400.45 | 4464 | 2337 | 0.997 | -0.9336793 | -1.014 | 0.31054327 |
| 59 | | | | | | | |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 3400.45 | 4464 | 2337 | 0.997 | -0.9336793 | -1.014 | 0.31054327 |
| 4 | 5327.5 | 6997 | 3658 | 0.996 | -0.9356814 | -1.03 | 0.30308961 |
| 5 | 5327.5 | 6997 | 3658 | 0.996 | -0.9356814 | -1.03 | 0.30308961 |
| 6 | 5327.5 | 6997 | 3658 | 0.996 | -0.9356814 | -1.03 | 0.30308961 |
| 7 | 5327.5 | 6997 | 3658 | 0.996 | -0.9356814 | -1.03 | 0.30308961 |
| 8 | 5649.44 | 7426 | 3873 | 0.996 | -0.9391338 | -1.035 | 0.30044327 |
| 9 | 5649.44 | 7426 | 3873 | 0.996 | -0.9391338 | -1.035 | 0.30044327 |
| 10 | 5649.44 | 7426 | 3873 | 0.996 | -0.9391338 | -1.035 | 0.30044327 |
| 11 | 5649.44 | 7426 | 3873 | 0.996 | -0.9391338 | -1.035 | 0.30044327 |
| 12 | 5649.44 | 7426 | 3873 | 0.996 | -0.9391338 | -1.035 | 0.30044327 |
| 13 | 5649.44 | 7426 | 3873 | 0.996 | -0.9391338 | -1.035 | 0.30044327 |
| 14 | 5649.44 | 7426 | 3873 | 0.996 | -0.9391338 | -1.035 | 0.30044327 |
| 15 | 5649.44 | 7426 | 3873 | 0.996 | -0.9391338 | -1.035 | 0.30044327 |
| 16 | 5649.44 | 7426 | 3873 | 0.996 | -0.9391338 | -1.035 | 0.30044327 |
| 17 | 5649.44 | 7426 | 3873 | 0.996 | -0.9391338 | -1.035 | 0.30044327 |
| 18 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 19 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 20 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 21 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 22 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 23 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 24 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 25 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 26 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 27 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 28 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 29 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 30 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 31 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 32 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 33 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 34 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 35 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 36 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 37 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 38 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 39 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 40 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 41 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 42 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 43 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 44 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 45 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 46 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 47 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 48 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 49 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 50 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 51 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 52 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 53 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 54 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 55 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 56 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 57 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 58 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 59 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----------|-------|------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 4 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 5 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 6 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 7 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 8 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 9 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 10 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 11 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 12 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 13 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 14 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 15 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 16 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 17 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 18 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 19 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 20 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 21 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 22 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 23 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 24 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 25 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 26 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 27 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 28 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 29 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 30 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 31 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 32 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 33 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 34 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 35 | 11060.49 | 14543 | 7578 | 0.996 | -0.9404359 | -1.087 | 0.27690788 |
| 36 | 11095.07 | 14590 | 7599 | 0.996 | -0.9410984 | -1.088 | 0.27659444 |
| 37 | | | | | | | |
| 38 | 729.95 | 960 | 500 | 0.997 | -0.9411063 | -1.021 | 0.30744734 |
| 39 | 729.95 | 960 | 500 | 0.997 | -0.9411063 | -1.021 | 0.30744734 |
| 40 | 729.95 | 960 | 500 | 0.997 | -0.9411063 | -1.021 | 0.30744734 |
| 41 | | | | | | | |
| 42 | 731.98 | 963 | 501 | 0.997 | -0.9427252 | -1.022 | 0.30683827 |
| 43 | 6287.05 | 8288 | 4286 | 0.996 | -0.9513922 | -1.089 | 0.27611283 |
| 44 | 6287.05 | 8288 | 4286 | 0.996 | -0.9513922 | -1.089 | 0.27611283 |
| 45 | | | | | | | |
| 46 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 47 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 48 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 49 | | | | | | | |
| 50 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 51 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 52 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 53 | | | | | | | |
| 54 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 55 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 56 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 57 | | | | | | | |
| 58 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 59 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 4 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 5 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 6 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 7 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 8 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 9 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 10 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 11 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 12 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 13 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 14 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 15 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 16 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 17 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 18 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 19 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 20 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 21 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 22 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 23 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 24 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 25 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 26 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 27 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 28 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 29 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 30 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 31 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 32 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 33 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 34 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 35 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 36 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 37 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 38 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 39 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 40 | 6243.96 | 8246 | 4242 | 0.996 | -0.9589498 | -1.095 | 0.2735755 |
| 41 | 445.57 | 590 | 302 | 0.998 | -0.9661664 | -0.79 | 0.42980971 |
| 42 | 445.57 | 590 | 302 | 0.998 | -0.9661664 | -0.79 | 0.42980971 |
| 43 | 445.57 | 590 | 302 | 0.998 | -0.9661664 | -0.79 | 0.42980971 |
| 44 | 445.57 | 590 | 302 | 0.998 | -0.9661664 | -0.79 | 0.42980971 |
| 45 | 445.57 | 590 | 302 | 0.998 | -0.9661664 | -0.79 | 0.42980971 |
| 46 | 445.57 | 590 | 302 | 0.998 | -0.9661664 | -0.79 | 0.42980971 |
| 47 | 445.57 | 590 | 302 | 0.998 | -0.9661664 | -0.79 | 0.42980971 |
| 48 | 445.57 | 590 | 302 | 0.998 | -0.9661664 | -0.79 | 0.42980971 |
| 49 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 50 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 51 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 52 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 53 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 54 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 55 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 56 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 57 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 58 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 59 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 60 | | | | | | | |

| | | | | | | | |
|----|---------|------|------|-------|------------|--------|------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 4 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 5 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 6 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 7 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 8 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 9 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 10 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 11 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 12 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 13 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 14 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 15 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 16 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 17 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 18 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 19 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 20 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 21 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 22 | 2022.28 | 2683 | 1362 | 0.996 | -0.9781204 | -1.181 | 0.23775145 |
| 23 | 109.18 | 146 | 72 | 0.998 | -1.0198996 | -0.795 | NA |
| 24 | 396.88 | 540 | 254 | 0.998 | -1.0881309 | -0.783 | NA |
| 25 | 52.74 | 74 | 32 | 0.998 | -1.2094534 | -0.898 | 0.3693508 |
| 26 | 366.47 | 520 | 213 | 0.998 | -1.2876582 | -0.905 | NA |
| 27 | 266.39 | 378 | 154 | 0.997 | -1.2954559 | -1.081 | 0.27972876 |
| 28 | 266.39 | 378 | 154 | 0.997 | -1.2954559 | -1.081 | 0.27972876 |
| 29 | 266.39 | 378 | 154 | 0.997 | -1.2954559 | -1.081 | 0.27972876 |
| 30 | 266.39 | 378 | 154 | 0.997 | -1.2954559 | -1.081 | 0.27972876 |
| 31 | 1560.39 | 2223 | 897 | 0.997 | -1.3093281 | -1.141 | 0.25404287 |
| 32 | 1560.39 | 2223 | 897 | 0.997 | -1.3093281 | -1.141 | 0.25404287 |
| 33 | 1560.39 | 2223 | 897 | 0.997 | -1.3093281 | -1.141 | 0.25404287 |
| 34 | 1560.39 | 2223 | 897 | 0.997 | -1.3093281 | -1.141 | 0.25404287 |
| 35 | 1560.39 | 2223 | 897 | 0.997 | -1.3093281 | -1.141 | 0.25404287 |
| 36 | 1560.39 | 2223 | 897 | 0.997 | -1.3093281 | -1.141 | 0.25404287 |
| 37 | 1560.39 | 2223 | 897 | 0.997 | -1.3093281 | -1.141 | 0.25404287 |
| 38 | 1560.39 | 2223 | 897 | 0.997 | -1.3093281 | -1.141 | 0.25404287 |
| 39 | 1560.39 | 2223 | 897 | 0.997 | -1.3093281 | -1.141 | 0.25404287 |
| 40 | 1560.39 | 2223 | 897 | 0.997 | -1.3093281 | -1.141 | 0.25404287 |
| 41 | 1560.39 | 2223 | 897 | 0.997 | -1.3093281 | -1.141 | 0.25404287 |
| 42 | 1560.39 | 2223 | 897 | 0.997 | -1.3093281 | -1.141 | 0.25404287 |
| 43 | 1560.39 | 2223 | 897 | 0.997 | -1.3093281 | -1.141 | 0.25404287 |
| 44 | 1560.39 | 2223 | 897 | 0.997 | -1.3093281 | -1.141 | 0.25404287 |
| 45 | 1560.39 | 2223 | 897 | 0.997 | -1.3093281 | -1.141 | 0.25404287 |
| 46 | 1560.39 | 2223 | 897 | 0.997 | -1.3093281 | -1.141 | 0.25404287 |
| 47 | 1566.79 | 2234 | 900 | 0.997 | -1.3116323 | -1.143 | 0.25303822 |
| 48 | 404.88 | 609 | 201 | 0.998 | -1.5992467 | -0.858 | NA |
| 49 | 404.88 | 609 | 201 | 0.998 | -1.5992467 | -0.858 | NA |
| 50 | 404.88 | 609 | 201 | 0.998 | -1.5992467 | -0.858 | NA |
| 51 | 404.88 | 609 | 201 | 0.998 | -1.5992467 | -0.858 | NA |
| 52 | 404.88 | 609 | 201 | 0.998 | -1.5992467 | -0.858 | NA |
| 53 | 404.88 | 609 | 201 | 0.998 | -1.5992467 | -0.858 | NA |
| 54 | 404.88 | 609 | 201 | 0.998 | -1.5992467 | -0.858 | NA |
| 55 | 404.88 | 609 | 201 | 0.998 | -1.5992467 | -0.858 | NA |
| 56 | 215.73 | 372 | 60 | 0.991 | -2.6322682 | -1.854 | 0.06379377 |
| 57 | 100.29 | 178 | 23 | 0.996 | -2.9521715 | -0.79 | NA |
| 58 | 100.29 | 178 | 23 | 0.996 | -2.9521715 | -0.79 | NA |
| 59 | | | | | | | |
| 60 | | | | | | | |

| | | | | | | |
|----|--------|-----|----|-------|------------|-----------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | 100.29 | 178 | 23 | 0.996 | -2.9521715 | -0.79 NA |
| 4 | 100.29 | 178 | 23 | 0.996 | -2.9521715 | -0.79 NA |
| 5 | 100.29 | 178 | 23 | 0.996 | -2.9521715 | -0.79 NA |
| 6 | 100.29 | 178 | 23 | 0.996 | -2.9521715 | -0.79 NA |
| 7 | 100.29 | 178 | 23 | 0.996 | -2.9521715 | -0.79 NA |
| 8 | 100.29 | 178 | 23 | 0.996 | -2.9521715 | -0.79 NA |
| 9 | 100.29 | 178 | 23 | 0.996 | -2.9521715 | -0.79 NA |
| 10 | 100.29 | 178 | 23 | 0.996 | -2.9521715 | -0.79 NA |
| 11 | 100.29 | 178 | 23 | 0.996 | -2.9521715 | -0.79 NA |
| 12 | 100.29 | 178 | 23 | 0.996 | -2.9521715 | -0.79 NA |
| 13 | 100.29 | 178 | 23 | 0.996 | -2.9521715 | -0.79 NA |
| 14 | 100.29 | 178 | 23 | 0.996 | -2.9521715 | -0.79 NA |
| 15 | 100.29 | 178 | 23 | 0.996 | -2.9521715 | -0.79 NA |
| 16 | 100.29 | 178 | 23 | 0.996 | -2.9521715 | -0.79 NA |
| 17 | 100.29 | 178 | 23 | 0.996 | -2.9521715 | -0.79 NA |
| 18 | 102.05 | 181 | 23 | 0.996 | -2.9762839 | -0.795 NA |
| 19 | 102.05 | 181 | 23 | 0.996 | -2.9762839 | -0.795 NA |
| 20 | 102.05 | 181 | 23 | 0.996 | -2.9762839 | -0.795 NA |
| 21 | 102.05 | 181 | 23 | 0.996 | -2.9762839 | -0.795 NA |
| 22 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 23 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 24 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 25 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 26 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 27 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 28 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 29 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 30 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 31 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 32 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 33 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 34 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 35 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 36 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 37 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 38 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 39 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 40 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 41 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 42 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 43 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 44 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 45 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 46 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 47 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 48 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 49 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 50 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 51 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 52 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 53 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 54 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 55 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 56 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 57 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 58 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 59 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 60 | | | | | | |

| | | | | | | |
|----|--------|-----|---|-------|------------|-----------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 4 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 5 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 6 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 7 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 8 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 9 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 10 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 11 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 12 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 13 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 14 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 15 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 16 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 17 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 18 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 19 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 20 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 21 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 22 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 23 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 24 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 25 | 79.35 | 156 | 3 | 0.873 | -5.7004397 | -2.812 NA |
| 26 | 149.72 | 298 | 1 | 0.945 | -8.2191685 | -2.105 NA |
| 27 | | | | | | |
| 28 | | | | | | |
| 29 | | | | | | |
| 30 | | | | | | |
| 31 | | | | | | |
| 32 | | | | | | |
| 33 | | | | | | |
| 34 | | | | | | |
| 35 | | | | | | |
| 36 | | | | | | |
| 37 | | | | | | |
| 38 | | | | | | |
| 39 | | | | | | |
| 40 | | | | | | |
| 41 | | | | | | |
| 42 | | | | | | |
| 43 | | | | | | |
| 44 | | | | | | |
| 45 | | | | | | |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.3739 | 0.9256 | 0.6296 | 0.6296 | TRUE | 0.1389 |
| 4 | 0.99848065 | 0.3739 | 0.9256 | 0.6296 | 0.6296 | TRUE | 0.1389 |
| 5 | 0.99848065 | 0.3739 | 0.9256 | 0.6296 | 0.6296 | TRUE | 0.1389 |
| 6 | 0.99848065 | 0.3739 | 0.9256 | 0.6296 | 0.6296 | TRUE | 0.1389 |
| 7 | 0.99848065 | 0.3739 | 0.9256 | 0.6296 | 0.6296 | TRUE | 0.1389 |
| 8 | 0.99848065 | 0.3739 | 0.9256 | 0.6296 | 0.6296 | TRUE | 0.1389 |
| 9 | 0.99848065 | 0.3739 | 0.9256 | 0.6296 | 0.6296 | TRUE | 0.1389 |
| 10 | 0.99848065 | 0.3698 | 0.9254 | 0.6273 | 0.6273 | TRUE | 0.135 |
| 11 | 0.99848065 | 1.4366 | 0.902 | 1.1906 | 1.1906 | TRUE | 3.4109 |
| 12 | 0.99848065 | 1.4366 | 0.902 | 1.1906 | 1.1906 | TRUE | 3.4109 |
| 13 | 0.99848065 | 1.4366 | 0.902 | 1.1906 | 1.1906 | TRUE | 3.4109 |
| 14 | 0.99848065 | 1.4366 | 0.902 | 1.1906 | 1.1906 | TRUE | 3.4109 |
| 15 | 0.99848065 | 1.4366 | 0.902 | 1.1906 | 1.1906 | TRUE | 3.4109 |
| 16 | 0.99848065 | 1.4366 | 0.902 | 1.1906 | 1.1906 | TRUE | 3.4109 |
| 17 | 0.99848065 | 1.4366 | 0.902 | 1.1906 | 1.1906 | TRUE | 3.4109 |
| 18 | 0.99848065 | 1.4366 | 0.902 | 1.1906 | 1.1906 | TRUE | 3.4109 |
| 19 | 0.99848065 | 1.4366 | 0.902 | 1.1906 | 1.1906 | TRUE | 3.4109 |
| 20 | 0.99848065 | 1.4366 | 0.902 | 1.1906 | 1.1906 | TRUE | 3.4109 |
| 21 | 0.99848065 | 1.4366 | 0.902 | 1.1906 | 1.1906 | TRUE | 3.4109 |
| 22 | 0.99848065 | 1.4366 | 0.902 | 1.1906 | 1.1906 | TRUE | 3.4109 |
| 23 | 0.99848065 | 1.8349 | 0.912 | 1.3772 | 1.3772 | TRUE | 0.8975 |
| 24 | 0.99848065 | 1.8349 | 0.912 | 1.3772 | 1.3772 | TRUE | 0.8975 |
| 25 | 0.99848065 | 1.8349 | 0.912 | 1.3772 | 1.3772 | TRUE | 0.8975 |
| 26 | 0.99848065 | 1.8349 | 0.912 | 1.3772 | 1.3772 | TRUE | 0.8975 |
| 27 | 0.99848065 | 1.8349 | 0.912 | 1.3772 | 1.3772 | TRUE | 0.8975 |
| 28 | 0.99848065 | 1.8349 | 0.912 | 1.3772 | 1.3772 | TRUE | 0.8975 |
| 29 | 0.99848065 | 1.8349 | 0.912 | 1.3772 | 1.3772 | TRUE | 0.8975 |
| 30 | 0.99848065 | 1.8349 | 0.912 | 1.3772 | 1.3772 | TRUE | 0.8975 |
| 31 | 0.99848065 | 1.8349 | 0.912 | 1.3772 | 1.3772 | TRUE | 0.8975 |
| 32 | 0.99848065 | 1.8349 | 0.912 | 1.3772 | 1.3772 | TRUE | 0.8975 |
| 33 | 0.99848065 | 1.8349 | 0.912 | 1.3772 | 1.3772 | TRUE | 0.8975 |
| 34 | 0.99848065 | 1.8349 | 0.912 | 1.3772 | 1.3772 | TRUE | 0.8975 |
| 35 | 0.99848065 | 1.8349 | 0.912 | 1.3772 | 1.3772 | TRUE | 0.8975 |
| 36 | 0.99848065 | 1.8349 | 0.912 | 1.3772 | 1.3772 | TRUE | 0.8975 |
| 37 | 0.99848065 | 1.8349 | 0.912 | 1.3772 | 1.3772 | TRUE | 0.8975 |
| 38 | 0.99848065 | 1.8349 | 0.912 | 1.3772 | 1.3772 | TRUE | 0.8975 |
| 39 | NA | 10 | 0.9131 | 3.778 | 10 | TRUE | 38.4286 |
| 40 | NA | 10 | 0.9153 | 3.7555 | 10 | TRUE | 38.4242 |
| 41 | NA | 10 | 0.9547 | 3.5328 | 10 | TRUE | 38.1432 |
| 42 | NA | 10 | 0.9691 | 3.9333 | 10 | TRUE | 38.054 |
| 43 | NA | 10 | 0.9796 | 3.908 | 10 | TRUE | 37.8974 |
| 44 | NA | 10 | 0.9801 | 3.907 | 10 | TRUE | 37.889 |
| 45 | NA | 10 | 1.0014 | 3.4243 | 10 | TRUE | 37.6283 |
| 46 | NA | 10 | 1.0217 | 3.844 | 10 | TRUE | 37.3926 |
| 47 | NA | 10 | 1.2632 | 3.8574 | 10 | TRUE | 34.3386 |
| 48 | NA | 10 | 1.266 | 3.8576 | 10 | TRUE | 34.3033 |
| 49 | NA | 10 | 1.3274 | 3.3816 | 3.3816 | TRUE | 38.6105 |
| 50 | NA | 10 | 1.3672 | 3.3995 | 3.3995 | TRUE | 38.1316 |
| 51 | NA | 10 | 0.9016 | 4.0394 | 10 | TRUE | 38.4149 |
| 52 | NA | 10 | 0.8954 | 4.428 | 10 | TRUE | 38.3422 |
| 53 | NA | 10 | 0.8918 | 4.7954 | 10 | TRUE | 38.2585 |
| 54 | NA | 10 | 0.9095 | 3.9194 | 10 | TRUE | 38.4327 |
| 55 | | | | | | | |
| 56 | | | | | | | |
| 57 | | | | | | | |
| 58 | | | | | | | |
| 59 | | | | | | | |
| 60 | | | | | | | |

| | | | | | | | |
|----|----|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | NA | 10 | 0.9185 | 3.8272 | 10 | TRUE | 38.4125 |
| 4 | NA | 10 | 0.929 | 3.7519 | 10 | TRUE | 38.3528 |
| 5 | NA | 10 | 0.9998 | 3.6394 | 10 | TRUE | 37.6422 |
| 6 | NA | 2.6879 | 0.9662 | 1.8089 | 1.8089 | TRUE | 34.9219 |
| 7 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 8 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 9 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 10 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 11 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 12 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 13 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 14 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 15 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 16 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 17 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 18 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 19 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 20 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 21 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 22 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 23 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 24 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 25 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 26 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 27 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 28 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 29 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 30 | NA | 3.25 | 1.2234 | 2.0631 | 2.0631 | TRUE | 30.087 |
| 31 | NA | 2.0885 | 1.1116 | 1.6022 | 1.6022 | TRUE | 30.9412 |
| 32 | NA | 2.075 | 1.1727 | 1.6265 | 1.6265 | TRUE | 29.8463 |
| 33 | NA | 2.812 | 0.9715 | 1.8717 | 1.8717 | TRUE | 33.7721 |
| 34 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 35 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 36 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 37 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 38 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 39 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 40 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 41 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 42 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 43 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 44 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 45 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 46 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 47 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 48 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 49 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 50 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 51 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 52 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 53 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 54 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 55 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 56 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 57 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 58 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 59 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 4 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 5 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 6 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 7 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 8 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 9 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 10 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 11 | NA | 2.8116 | 0.9715 | 1.8716 | 1.8716 | TRUE | 33.77 |
| 12 | NA | 2.8246 | 0.9711 | 1.8778 | 1.8778 | TRUE | 33.7829 |
| 13 | NA | 2.1309 | 0.9632 | 1.5483 | 1.5483 | TRUE | 33.549 |
| 14 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 15 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 16 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 17 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 18 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 19 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 20 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 21 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 22 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 23 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 24 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 25 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 26 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 27 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 28 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 29 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 30 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 31 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 32 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 33 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 34 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 35 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 36 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 37 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 38 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 39 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 40 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 41 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 42 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 43 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 44 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 45 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 46 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 47 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 48 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 49 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 50 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 51 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 52 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 53 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 54 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 55 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 56 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 57 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 58 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 59 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 4 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 5 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 6 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 7 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 8 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 9 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 10 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 11 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 12 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 13 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 14 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 15 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 16 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 17 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 18 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 19 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 20 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 21 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 22 | NA | 2.1306 | 0.9632 | 1.5482 | 1.5482 | TRUE | 33.5469 |
| 23 | NA | 2.1613 | 1.1674 | 1.6593 | 1.6593 | TRUE | 27.2604 |
| 24 | NA | 2.1613 | 1.1674 | 1.6593 | 1.6593 | TRUE | 27.2604 |
| 25 | NA | 2.1613 | 1.1674 | 1.6593 | 1.6593 | TRUE | 27.2604 |
| 26 | NA | 2.1613 | 1.1674 | 1.6593 | 1.6593 | TRUE | 27.2604 |
| 27 | NA | 2.1613 | 1.1674 | 1.6593 | 1.6593 | TRUE | 27.2604 |
| 28 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 29 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 30 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 31 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 32 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 33 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 34 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 35 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 36 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 37 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 38 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 39 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 40 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 41 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 42 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 43 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 44 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 45 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 46 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 47 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 48 | NA | 2.0897 | 1.2904 | 1.686 | 1.686 | TRUE | 25.687 |
| 49 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 50 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 51 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 52 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 53 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 54 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 55 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 56 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 57 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 58 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 59 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 4 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 5 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 6 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 7 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 8 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 9 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 10 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 11 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 12 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 13 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 14 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 15 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 16 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 17 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 18 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 19 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 20 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 21 | NA | 1.5663 | 1.1896 | 1.384 | 1.384 | TRUE | 26.1921 |
| 22 | NA | 1.6213 | 1.1709 | 1.4027 | 1.4027 | TRUE | 26.8095 |
| 23 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 24 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 25 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 26 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 27 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 28 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 29 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 30 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 31 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 32 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 33 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 34 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 35 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 36 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 37 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 38 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 39 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 40 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 41 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 42 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 43 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 44 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 45 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 46 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 47 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 48 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 49 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 50 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 51 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 52 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 53 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 54 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 55 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 56 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 57 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 58 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 59 | NA | 1.5392 | 0.912 | 1.229 | 1.229 | TRUE | 28.6108 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 4 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 5 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 6 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 7 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 8 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 9 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 10 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 11 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 12 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 13 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 14 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 15 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 16 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 17 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 18 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 19 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 20 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 21 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 22 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 23 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 24 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 25 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 26 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 27 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 28 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 29 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 30 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 31 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 32 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 33 | NA | 1.0098 | 0.9011 | 0.9533 | 0.9533 | TRUE | 24.9272 |
| 34 | NA | 1.0067 | 0.9009 | 0.951 | 0.951 | TRUE | 24.865 |
| 35 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 36 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 37 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 38 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 39 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 40 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 41 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 42 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 43 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 44 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 45 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 46 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 47 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 48 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 49 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 50 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 51 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 52 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 53 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 54 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 55 | 0.99848065 | 1.0335 | 1.1627 | 1.0966 | 1.0966 | TRUE | 1.0169 |
| 56 | 0.99848065 | 1.2907 | 0.9496 | 1.1325 | 1.1325 | TRUE | 7.36 |
| 57 | 0.99848065 | 1.2889 | 0.9498 | 1.1313 | 1.1313 | TRUE | 7.2958 |
| 58 | 0.99848065 | 1.2889 | 0.9498 | 1.1313 | 1.1313 | TRUE | 7.2958 |
| 59 | 0.99848065 | 1.2889 | 0.9498 | 1.1313 | 1.1313 | TRUE | 7.2958 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 1.2889 | 0.9498 | 1.1313 | 1.1313 | TRUE | 7.2958 |
| 4 | 0.99848065 | 1.2889 | 0.9498 | 1.1313 | 1.1313 | TRUE | 7.2958 |
| 5 | 0.99848065 | 1.2889 | 0.9498 | 1.1313 | 1.1313 | TRUE | 7.2958 |
| 6 | 0.99848065 | 1.2889 | 0.9498 | 1.1313 | 1.1313 | TRUE | 7.2958 |
| 7 | 0.99848065 | 1.2889 | 0.9498 | 1.1313 | 1.1313 | TRUE | 7.2958 |
| 8 | 0.99848065 | 1.2889 | 0.9498 | 1.1313 | 1.1313 | TRUE | 7.2958 |
| 9 | 0.99848065 | 1.2889 | 0.9498 | 1.1313 | 1.1313 | TRUE | 7.2958 |
| 10 | 0.99848065 | 0.9874 | 1.1188 | 1.0516 | 1.0516 | TRUE | 1.6529 |
| 11 | 0.99848065 | 0.9874 | 1.1188 | 1.0516 | 1.0516 | TRUE | 1.6529 |
| 12 | 0.99848065 | 0.9874 | 1.1188 | 1.0516 | 1.0516 | TRUE | 1.6529 |
| 13 | 0.99848065 | 0.9874 | 1.1188 | 1.0516 | 1.0516 | TRUE | 1.6529 |
| 14 | 0.99848065 | 0.9874 | 1.1188 | 1.0516 | 1.0516 | TRUE | 1.6529 |
| 15 | 0.99848065 | 0.9874 | 1.1188 | 1.0516 | 1.0516 | TRUE | 1.6529 |
| 16 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 17 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 18 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 19 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 20 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 21 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 22 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 23 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 24 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 25 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 26 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 27 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 28 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 29 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 30 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 31 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 32 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 33 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 34 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 35 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 36 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 37 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 38 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 39 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 40 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 41 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 42 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 43 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 44 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 45 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 46 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 47 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 48 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 49 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 50 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 51 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 52 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 53 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 54 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 55 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 56 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 57 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 58 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 59 | NA | 0.9482 | 0.9047 | 0.912 | 0.912 | TRUE | 23.4869 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 1.2644 | 0.9673 | 1.1198 | 1.1198 | TRUE | 6.3628 |
| 4 | NA | 0.9152 | 1.0323 | 0.969 | 0.969 | TRUE | 21.098 |
| 5 | NA | 0.9152 | 1.0323 | 0.969 | 0.969 | TRUE | 21.098 |
| 6 | NA | 0.9152 | 1.0323 | 0.969 | 0.969 | TRUE | 21.098 |
| 7 | NA | 0.9152 | 1.0323 | 0.969 | 0.969 | TRUE | 21.098 |
| 8 | NA | 0.9152 | 1.0323 | 0.969 | 0.969 | TRUE | 21.098 |
| 9 | NA | 0.9152 | 1.0323 | 0.969 | 0.969 | TRUE | 21.098 |
| 10 | NA | 0.9152 | 1.0323 | 0.969 | 0.969 | TRUE | 21.098 |
| 11 | NA | 0.9152 | 1.0323 | 0.969 | 0.969 | TRUE | 21.098 |
| 12 | 0.99848065 | 2.7906 | 1.0726 | 1.7796 | 1.7796 | TRUE | 8.7809 |
| 13 | 0.99848065 | 2.7906 | 1.0726 | 1.7796 | 1.7796 | TRUE | 8.7809 |
| 14 | 0.99848065 | 2.7906 | 1.0726 | 1.7796 | 1.7796 | TRUE | 8.7809 |
| 15 | 0.99848065 | 2.7906 | 1.0726 | 1.7796 | 1.7796 | TRUE | 8.7809 |
| 16 | 0.99848065 | 2.7906 | 1.0726 | 1.7796 | 1.7796 | TRUE | 8.7809 |
| 17 | 0.99848065 | 2.7906 | 1.0726 | 1.7796 | 1.7796 | TRUE | 8.7809 |
| 18 | 0.99848065 | 2.7906 | 1.0726 | 1.7796 | 1.7796 | TRUE | 8.7809 |
| 19 | 0.99848065 | 2.7906 | 1.0726 | 1.7796 | 1.7796 | TRUE | 8.7809 |
| 20 | 0.99848065 | 2.7906 | 1.0726 | 1.7796 | 1.7796 | TRUE | 8.7809 |
| 21 | 0.99848065 | 2.7906 | 1.0726 | 1.7796 | 1.7796 | TRUE | 8.7809 |
| 22 | 0.99848065 | 2.7906 | 1.0726 | 1.7796 | 1.7796 | TRUE | 8.7809 |
| 23 | 0.99848065 | 2.7906 | 1.0726 | 1.7796 | 1.7796 | TRUE | 8.7809 |
| 24 | 0.99848065 | 2.7906 | 1.0726 | 1.7796 | 1.7796 | TRUE | 8.7809 |
| 25 | 0.99848065 | 2.7906 | 1.0726 | 1.7796 | 1.7796 | TRUE | 8.7809 |
| 26 | NA | 0.8102 | 0.9535 | 0.8783 | 0.8783 | TRUE | 20.3384 |
| 27 | NA | 0.8102 | 0.9535 | 0.8783 | 0.8783 | TRUE | 20.3384 |
| 28 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 29 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 30 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 31 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 32 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 33 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 34 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 35 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 36 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 37 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 38 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 39 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 40 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 41 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 42 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 43 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 44 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 45 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 46 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 47 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 48 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 49 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 50 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 51 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 52 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 53 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 54 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 55 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 56 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 57 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 58 | NA | 0.8134 | 0.9538 | 0.8802 | 0.8802 | TRUE | 20.4049 |
| 59 | 0.99848065 | 0.8814 | 0.9216 | 0.9019 | 0.9019 | TRUE | 9.129 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 4 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 5 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 6 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 7 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 8 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 9 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 10 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 11 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 12 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 13 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 14 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 15 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 16 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 17 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 18 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 19 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 20 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 21 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 22 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 23 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 24 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 25 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 26 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 27 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 28 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 29 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 30 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 31 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 32 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 33 | 0.99848065 | 0.4939 | 0.9137 | 0.6898 | 0.6898 | TRUE | 12.6189 |
| 34 | 0.99848065 | 0.4932 | 0.9136 | 0.6894 | 0.6894 | TRUE | 11.9383 |
| 35 | NA | 2.5286 | 0.9295 | 1.7188 | 1.7188 | TRUE | 21.0823 |
| 36 | NA | 2.5286 | 0.9295 | 1.7188 | 1.7188 | TRUE | 21.0823 |
| 37 | NA | 2.6557 | 0.9353 | 1.7794 | 1.7794 | TRUE | 23.6516 |
| 38 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 39 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 40 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 41 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 42 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 43 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 44 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 45 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 46 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 47 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 48 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 49 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 50 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 51 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 52 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 53 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 54 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 55 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 56 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 57 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 58 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 59 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 4 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 5 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 6 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 7 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 8 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 9 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 10 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 11 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 12 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 13 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 14 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 15 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 16 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 17 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 18 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 19 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 20 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 21 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 22 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 23 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 24 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 25 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 26 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 27 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 28 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 29 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 30 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 31 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 32 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 33 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 34 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 35 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 36 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 37 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 38 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 39 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 40 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 41 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 42 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 43 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 44 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 45 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 46 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 47 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 48 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 49 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 50 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 51 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 52 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 53 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 54 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 55 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 56 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 57 | NA | 2.6627 | 0.9354 | 1.7832 | 1.7832 | TRUE | 23.6343 |
| 58 | NA | 2.6668 | 0.9352 | 1.7851 | 1.7851 | TRUE | 23.7809 |
| 59 | 0.99848065 | 0.3573 | 1.0494 | 0.6766 | 0.6766 | TRUE | 7.4465 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.3573 | 1.0494 | 0.6766 | 0.6766 | TRUE | 7.4465 |
| 4 | 0.99848065 | 0.3573 | 1.0494 | 0.6766 | 0.6766 | TRUE | 7.4465 |
| 5 | 0.99848065 | 0.748 | 0.9221 | 0.8317 | 0.8317 | TRUE | 2.4767 |
| 6 | 0.99848065 | 0.748 | 0.9221 | 0.8317 | 0.8317 | TRUE | 2.4767 |
| 7 | 0.99848065 | 0.7516 | 0.9239 | 0.8345 | 0.8345 | TRUE | 2.2837 |
| 8 | 0.99848065 | 0.7516 | 0.9239 | 0.8345 | 0.8345 | TRUE | 2.2837 |
| 9 | 0.99848065 | 0.7516 | 0.9239 | 0.8345 | 0.8345 | TRUE | 2.2837 |
| 10 | 0.99848065 | 0.7516 | 0.9239 | 0.8345 | 0.8345 | TRUE | 2.2837 |
| 11 | 0.99848065 | 0.7516 | 0.9239 | 0.8345 | 0.8345 | TRUE | 2.2837 |
| 12 | 0.99848065 | 0.7516 | 0.9239 | 0.8345 | 0.8345 | TRUE | 2.2837 |
| 13 | 0.99848065 | 0.7754 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8077 |
| 14 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 15 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 16 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 17 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 18 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 19 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 20 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 21 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 22 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 23 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 24 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 25 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 26 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 27 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 28 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 29 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 30 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 31 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 32 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 33 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 34 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 35 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 36 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 37 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 38 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 39 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 40 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 41 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 42 | 0.99848065 | 0.7753 | 0.9289 | 0.8495 | 0.8495 | TRUE | 1.8067 |
| 43 | 0.99848065 | 0.787 | 0.9313 | 0.8567 | 0.8567 | TRUE | 1.6487 |
| 44 | 0.99848065 | 0.787 | 0.9313 | 0.8567 | 0.8567 | TRUE | 1.6487 |
| 45 | 0.99848065 | 0.787 | 0.9313 | 0.8567 | 0.8567 | TRUE | 1.6487 |
| 46 | 0.99848065 | 0.787 | 0.9313 | 0.8567 | 0.8567 | TRUE | 1.6487 |
| 47 | 0.99848065 | 0.787 | 0.9313 | 0.8567 | 0.8567 | TRUE | 1.6487 |
| 48 | 0.99848065 | 0.787 | 0.9313 | 0.8567 | 0.8567 | TRUE | 1.6487 |
| 49 | 0.99848065 | 0.787 | 0.9313 | 0.8567 | 0.8567 | TRUE | 1.6487 |
| 50 | 0.99848065 | 0.787 | 0.9313 | 0.8567 | 0.8567 | TRUE | 1.6487 |
| 51 | 0.99848065 | 0.787 | 0.9313 | 0.8567 | 0.8567 | TRUE | 1.6487 |
| 52 | 0.99848065 | 0.787 | 0.9313 | 0.8567 | 0.8567 | TRUE | 1.6487 |
| 53 | 0.99848065 | 0.787 | 0.9313 | 0.8567 | 0.8567 | TRUE | 1.6487 |
| 54 | 0.99848065 | 0.787 | 0.9313 | 0.8567 | 0.8567 | TRUE | 1.6487 |
| 55 | 0.99848065 | 0.787 | 0.9313 | 0.8567 | 0.8567 | TRUE | 1.6487 |
| 56 | 0.99848065 | 0.787 | 0.9313 | 0.8567 | 0.8567 | TRUE | 1.6487 |
| 57 | 0.99848065 | 0.787 | 0.9313 | 0.8567 | 0.8567 | TRUE | 1.6487 |
| 58 | 0.99848065 | 0.787 | 0.9313 | 0.8567 | 0.8567 | TRUE | 1.6487 |
| 59 | 0.99848065 | 0.787 | 0.9313 | 0.8567 | 0.8567 | TRUE | 1.6487 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 4 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 5 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 6 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 7 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 8 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 9 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 10 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 11 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 12 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 13 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 14 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 15 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 16 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 17 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 18 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 19 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 20 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 21 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 22 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 23 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 24 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 25 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 26 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 27 | 0.99848065 | 1.0325 | 1.0306 | 1.0317 | 1.0317 | TRUE | 14.9934 |
| 28 | 0.99848065 | 0.6597 | 0.9976 | 0.8185 | 0.8185 | TRUE | 16.2617 |
| 29 | 0.99848065 | 0.6597 | 0.9976 | 0.8185 | 0.8185 | TRUE | 16.2617 |
| 30 | 0.99848065 | 0.6597 | 0.9976 | 0.8185 | 0.8185 | TRUE | 16.2617 |
| 31 | 0.99848065 | 0.6597 | 0.9976 | 0.8185 | 0.8185 | TRUE | 16.2617 |
| 32 | 0.99848065 | 0.6597 | 0.9976 | 0.8185 | 0.8185 | TRUE | 16.2617 |
| 33 | 0.99848065 | 0.6597 | 0.9976 | 0.8185 | 0.8185 | TRUE | 16.2617 |
| 34 | 0.99848065 | 0.6597 | 0.9976 | 0.8185 | 0.8185 | TRUE | 16.2617 |
| 35 | 0.99848065 | 0.7804 | 1.1955 | 0.9855 | 0.9855 | TRUE | 1.4791 |
| 36 | 0.99848065 | 0.7804 | 1.1955 | 0.9855 | 0.9855 | TRUE | 1.4791 |
| 37 | 0.99848065 | 0.7804 | 1.1955 | 0.9855 | 0.9855 | TRUE | 1.4791 |
| 38 | 0.99848065 | 0.7804 | 1.1955 | 0.9855 | 0.9855 | TRUE | 1.4791 |
| 39 | 0.99848065 | 0.7804 | 1.1955 | 0.9855 | 0.9855 | TRUE | 1.4791 |
| 40 | 0.99848065 | 0.7804 | 1.1955 | 0.9855 | 0.9855 | TRUE | 1.4791 |
| 41 | 0.99848065 | 0.7804 | 1.1955 | 0.9855 | 0.9855 | TRUE | 1.4791 |
| 42 | 0.99848065 | 0.7804 | 1.1955 | 0.9855 | 0.9855 | TRUE | 1.4791 |
| 43 | 0.99848065 | 0.7804 | 1.1955 | 0.9855 | 0.9855 | TRUE | 1.4791 |
| 44 | 0.99848065 | 0.7804 | 1.1955 | 0.9855 | 0.9855 | TRUE | 1.4791 |
| 45 | 0.99848065 | 0.7804 | 1.1955 | 0.9855 | 0.9855 | TRUE | 1.4791 |
| 46 | 0.99848065 | 0.7804 | 1.1955 | 0.9855 | 0.9855 | TRUE | 1.4791 |
| 47 | 0.99848065 | 0.7804 | 1.1955 | 0.9855 | 0.9855 | TRUE | 1.4791 |
| 48 | 0.99848065 | 1.6677 | 1.0678 | 1.363 | 1.363 | TRUE | 1.2491 |
| 49 | 0.99848065 | 1.6666 | 1.068 | 1.3625 | 1.3625 | TRUE | 1.2444 |
| 50 | 0.99848065 | 1.6666 | 1.068 | 1.3625 | 1.3625 | TRUE | 1.2444 |
| 51 | 0.99848065 | 1.6666 | 1.068 | 1.3625 | 1.3625 | TRUE | 1.2444 |
| 52 | 0.99848065 | 1.6666 | 1.068 | 1.3625 | 1.3625 | TRUE | 1.2444 |
| 53 | 0.99848065 | 1.6666 | 1.068 | 1.3625 | 1.3625 | TRUE | 1.2444 |
| 54 | 0.99848065 | 1.6666 | 1.068 | 1.3625 | 1.3625 | TRUE | 1.2444 |
| 55 | 0.99848065 | 1.6666 | 1.068 | 1.3625 | 1.3625 | TRUE | 1.2444 |
| 56 | 0.99848065 | 1.6666 | 1.068 | 1.3625 | 1.3625 | TRUE | 1.2444 |
| 57 | 0.99848065 | 1.6666 | 1.068 | 1.3625 | 1.3625 | TRUE | 1.2444 |
| 58 | 0.99848065 | 1.6666 | 1.068 | 1.3625 | 1.3625 | TRUE | 1.2444 |
| 59 | 0.99848065 | 1.6666 | 1.068 | 1.3625 | 1.3625 | TRUE | 1.2444 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.5793 | 0.9088 | 0.7349 | 0.7349 | TRUE | 1.1796 |
| 4 | 0.99848065 | 0.5793 | 0.9088 | 0.7349 | 0.7349 | TRUE | 1.1796 |
| 5 | 0.99848065 | 0.5793 | 0.9088 | 0.7349 | 0.7349 | TRUE | 1.1796 |
| 6 | 0.99848065 | 0.5793 | 0.9088 | 0.7349 | 0.7349 | TRUE | 1.1796 |
| 7 | 0.99848065 | 0.5793 | 0.9088 | 0.7349 | 0.7349 | TRUE | 1.1796 |
| 8 | 0.99848065 | 0.5793 | 0.9088 | 0.7349 | 0.7349 | TRUE | 1.1796 |
| 9 | 0.99848065 | 0.5793 | 0.9088 | 0.7349 | 0.7349 | TRUE | 1.1796 |
| 10 | 0.99848065 | 0.5793 | 0.9088 | 0.7349 | 0.7349 | TRUE | 1.1796 |
| 11 | 0.99848065 | 0.5793 | 0.9088 | 0.7349 | 0.7349 | TRUE | 1.1796 |
| 12 | 0.99848065 | 0.5793 | 0.9088 | 0.7349 | 0.7349 | TRUE | 1.1796 |
| 13 | 0.99848065 | 0.5793 | 0.9088 | 0.7349 | 0.7349 | TRUE | 1.1796 |
| 14 | 0.99848065 | 0.5793 | 0.9088 | 0.7349 | 0.7349 | TRUE | 1.1796 |
| 15 | 0.99848065 | 0.5793 | 0.9088 | 0.7349 | 0.7349 | TRUE | 1.1796 |
| 16 | 0.99848065 | 0.5793 | 0.9088 | 0.7349 | 0.7349 | TRUE | 1.1796 |
| 17 | 0.99848065 | 0.5793 | 0.9088 | 0.7349 | 0.7349 | TRUE | 1.1796 |
| 18 | 0.99848065 | 0.5793 | 0.9088 | 0.7349 | 0.7349 | TRUE | 1.1796 |
| 19 | 0.99848065 | 0.5793 | 0.9088 | 0.7349 | 0.7349 | TRUE | 1.1796 |
| 20 | 0.99848065 | 0.5793 | 0.9088 | 0.7349 | 0.7349 | TRUE | 1.1796 |
| 21 | 0.99848065 | 0.5787 | 0.9087 | 0.7345 | 0.7345 | TRUE | 1.2044 |
| 22 | 0.99848065 | 0.5787 | 0.9087 | 0.7345 | 0.7345 | TRUE | 1.2044 |
| 23 | 0.99848065 | 0.5787 | 0.9087 | 0.7345 | 0.7345 | TRUE | 1.2044 |
| 24 | 0.99848065 | 0.4117 | 0.8895 | 0.6332 | 0.6332 | TRUE | 11.6504 |
| 25 | 0.99848065 | 0.4117 | 0.8895 | 0.6332 | 0.6332 | TRUE | 11.6504 |
| 26 | 0.99848065 | 0.4117 | 0.8895 | 0.6332 | 0.6332 | TRUE | 11.6504 |
| 27 | 0.99848065 | 0.4117 | 0.8895 | 0.6332 | 0.6332 | TRUE | 11.6504 |
| 28 | 0.99848065 | 0.4117 | 0.8895 | 0.6332 | 0.6332 | TRUE | 11.6504 |
| 29 | 0.99848065 | 0.4117 | 0.8895 | 0.6332 | 0.6332 | TRUE | 11.6504 |
| 30 | 0.99848065 | 0.4117 | 0.8895 | 0.6332 | 0.6332 | TRUE | 11.6504 |
| 31 | 0.99848065 | 0.4124 | 0.8896 | 0.6336 | 0.6336 | TRUE | 11.6664 |
| 32 | 0.99848065 | 0.4124 | 0.8896 | 0.6336 | 0.6336 | TRUE | 11.6664 |
| 33 | 0.99848065 | 0.4124 | 0.8896 | 0.6336 | 0.6336 | TRUE | 11.6664 |
| 34 | 0.99848065 | 0.4124 | 0.8896 | 0.6336 | 0.6336 | TRUE | 11.6664 |
| 35 | 0.99848065 | 0.4124 | 0.8896 | 0.6336 | 0.6336 | TRUE | 11.6664 |
| 36 | 0.99848065 | 0.4124 | 0.8896 | 0.6336 | 0.6336 | TRUE | 11.6664 |
| 37 | 0.99848065 | 0.4124 | 0.8896 | 0.6336 | 0.6336 | TRUE | 11.6664 |
| 38 | 0.99848065 | 0.4124 | 0.8896 | 0.6336 | 0.6336 | TRUE | 11.6664 |
| 39 | 0.99848065 | 0.4124 | 0.8896 | 0.6336 | 0.6336 | TRUE | 11.6664 |
| 40 | 0.99848065 | 0.4124 | 0.8896 | 0.6336 | 0.6336 | TRUE | 11.6664 |
| 41 | 0.99848065 | 0.4124 | 0.8896 | 0.6336 | 0.6336 | TRUE | 11.6664 |
| 42 | 0.99848065 | 0.4124 | 0.8896 | 0.6336 | 0.6336 | TRUE | 11.6664 |
| 43 | 0.99848065 | 0.4124 | 0.8896 | 0.6336 | 0.6336 | TRUE | 11.6664 |
| 44 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 45 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 46 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 47 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 48 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 49 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 50 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 51 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 52 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 53 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 54 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 55 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 56 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 57 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 58 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 59 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 4 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 5 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 6 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 7 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 8 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 9 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 10 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 11 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 12 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 13 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 14 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 15 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 16 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 17 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 18 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 19 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 20 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 21 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 22 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 23 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 24 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 25 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 26 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 27 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 28 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 29 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 30 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 31 | 0.99848065 | 0.652 | 0.9177 | 0.7786 | 0.7786 | TRUE | 0.5942 |
| 32 | 0.99848065 | 0.9952 | 0.8884 | 0.9436 | 0.9436 | TRUE | 0.5118 |
| 33 | 0.99848065 | 0.9952 | 0.8884 | 0.9436 | 0.9436 | TRUE | 0.5118 |
| 34 | 0.99848065 | 0.9952 | 0.8884 | 0.9436 | 0.9436 | TRUE | 0.5118 |
| 35 | 0.99848065 | 0.9952 | 0.8884 | 0.9436 | 0.9436 | TRUE | 0.5118 |
| 36 | 0.99848065 | 0.9952 | 0.8884 | 0.9436 | 0.9436 | TRUE | 0.5118 |
| 37 | 0.99848065 | 0.639 | 0.9153 | 0.7704 | 0.7704 | TRUE | 0.4762 |
| 38 | 0.99848065 | 0.639 | 0.9153 | 0.7704 | 0.7704 | TRUE | 0.4762 |
| 39 | 0.99848065 | 0.639 | 0.9153 | 0.7704 | 0.7704 | TRUE | 0.4762 |
| 40 | 0.99848065 | 0.639 | 0.9153 | 0.7704 | 0.7704 | TRUE | 0.4762 |
| 41 | 0.99848065 | 0.639 | 0.9153 | 0.7704 | 0.7704 | TRUE | 0.4762 |
| 42 | 0.99848065 | 0.639 | 0.9153 | 0.7704 | 0.7704 | TRUE | 0.4762 |
| 43 | 0.99848065 | 0.639 | 0.9153 | 0.7704 | 0.7704 | TRUE | 0.4762 |
| 44 | 0.99848065 | 0.639 | 0.9153 | 0.7704 | 0.7704 | TRUE | 0.4762 |
| 45 | 0.99848065 | 0.639 | 0.9153 | 0.7704 | 0.7704 | TRUE | 0.4762 |
| 46 | 0.99848065 | 0.639 | 0.9153 | 0.7704 | 0.7704 | TRUE | 0.4762 |
| 47 | 0.99848065 | 0.639 | 0.9153 | 0.7704 | 0.7704 | TRUE | 0.4762 |
| 48 | 0.99848065 | 0.639 | 0.9153 | 0.7704 | 0.7704 | TRUE | 0.4762 |
| 49 | 0.99848065 | 0.2791 | 1.0998 | 0.6545 | 0.6545 | TRUE | 1.9597 |
| 50 | 0.99848065 | 0.2791 | 1.0998 | 0.6545 | 0.6545 | TRUE | 1.9597 |
| 51 | 0.99848065 | 0.2791 | 1.0998 | 0.6545 | 0.6545 | TRUE | 1.9597 |
| 52 | 0.99848065 | 0.2791 | 1.0998 | 0.6545 | 0.6545 | TRUE | 1.9597 |
| 53 | 0.99848065 | 0.2791 | 1.0998 | 0.6545 | 0.6545 | TRUE | 1.9597 |
| 54 | 0.99848065 | 0.2791 | 1.0998 | 0.6545 | 0.6545 | TRUE | 1.9597 |
| 55 | 0.99848065 | 0.2791 | 1.0998 | 0.6545 | 0.6545 | TRUE | 1.9597 |
| 56 | 0.99848065 | 0.2791 | 1.0998 | 0.6545 | 0.6545 | TRUE | 1.9597 |
| 57 | 0.99848065 | 0.2791 | 1.0998 | 0.6545 | 0.6545 | TRUE | 1.9597 |
| 58 | 0.99848065 | 0.2791 | 1.0998 | 0.6545 | 0.6545 | TRUE | 1.9597 |
| 59 | 0.99848065 | 0.2791 | 1.0998 | 0.6545 | 0.6545 | TRUE | 1.9597 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.2172 | 0.9057 | 0.5285 | 0.5285 | TRUE | 1.2392 |
| 4 | 0.99848065 | 0.2172 | 0.9057 | 0.5285 | 0.5285 | TRUE | 1.2392 |
| 5 | 0.99848065 | 0.2172 | 0.9057 | 0.5285 | 0.5285 | TRUE | 1.2392 |
| 6 | 0.99848065 | 0.2172 | 0.9057 | 0.5285 | 0.5285 | TRUE | 1.2392 |
| 7 | 0.99848065 | 0.2172 | 0.9057 | 0.5285 | 0.5285 | TRUE | 1.2392 |
| 8 | 0.99848065 | 0.2172 | 0.9057 | 0.5285 | 0.5285 | TRUE | 1.2392 |
| 9 | 0.99848065 | 0.2172 | 0.9057 | 0.5285 | 0.5285 | TRUE | 1.2392 |
| 10 | 0.99848065 | 0.2172 | 0.9057 | 0.5285 | 0.5285 | TRUE | 1.2392 |
| 11 | 0.99848065 | 0.2172 | 0.9057 | 0.5285 | 0.5285 | TRUE | 1.2392 |
| 12 | 0.99848065 | 0.2172 | 0.9057 | 0.5285 | 0.5285 | TRUE | 1.2392 |
| 13 | 0.99848065 | 0.2172 | 0.9057 | 0.5285 | 0.5285 | TRUE | 1.2392 |
| 14 | 0.99848065 | 0.2172 | 0.9057 | 0.5285 | 0.5285 | TRUE | 1.2392 |
| 15 | 0.99848065 | 0.2172 | 0.9057 | 0.5285 | 0.5285 | TRUE | 1.2392 |
| 16 | 0.99848065 | 0.2172 | 0.9057 | 0.5285 | 0.5285 | TRUE | 1.2392 |
| 17 | 0.99848065 | 0.2172 | 0.9057 | 0.5285 | 0.5285 | TRUE | 1.2392 |
| 18 | 0.99848065 | 0.2172 | 0.9057 | 0.5285 | 0.5285 | TRUE | 1.2392 |
| 19 | 0.99848065 | 0.1506 | 1.1166 | 0.5953 | 0.5953 | TRUE | 1.22 |
| 20 | 0.99848065 | 0.1506 | 1.1166 | 0.5953 | 0.5953 | TRUE | 1.22 |
| 21 | 0.99848065 | 0.1506 | 1.1166 | 0.5953 | 0.5953 | TRUE | 1.22 |
| 22 | 0.99848065 | 0.1506 | 1.1166 | 0.5953 | 0.5953 | TRUE | 1.22 |
| 23 | 0.99848065 | 0.1506 | 1.1166 | 0.5953 | 0.5953 | TRUE | 1.22 |
| 24 | 0.99848065 | 0.1506 | 1.1166 | 0.5953 | 0.5953 | TRUE | 1.22 |
| 25 | 0.99848065 | 0.1506 | 1.1166 | 0.5953 | 0.5953 | TRUE | 1.22 |
| 26 | 0.99848065 | 0.1506 | 1.1166 | 0.5953 | 0.5953 | TRUE | 1.22 |
| 27 | 0.99848065 | 0.1506 | 1.1166 | 0.5953 | 0.5953 | TRUE | 1.22 |
| 28 | 0.99848065 | 0.1506 | 1.1166 | 0.5953 | 0.5953 | TRUE | 1.22 |
| 29 | 0.99848065 | 0.1506 | 1.1166 | 0.5953 | 0.5953 | TRUE | 1.22 |
| 30 | 0.99848065 | 0.1506 | 1.1166 | 0.5953 | 0.5953 | TRUE | 1.22 |
| 31 | 0.99848065 | 0.1506 | 1.1166 | 0.5953 | 0.5953 | TRUE | 1.22 |
| 32 | 0.99848065 | 0.7787 | 0.9315 | 0.8514 | 0.8514 | TRUE | 0.4832 |
| 33 | 0.99848065 | 0.3817 | 1.0142 | 0.6778 | 0.6778 | TRUE | 5.3986 |
| 34 | 0.99848065 | 0.3922 | 1.0156 | 0.6842 | 0.6842 | TRUE | 6.2365 |
| 35 | 0.99848065 | 0.3922 | 1.0156 | 0.6842 | 0.6842 | TRUE | 6.2365 |
| 36 | 0.99848065 | 0.3922 | 1.0156 | 0.6842 | 0.6842 | TRUE | 6.2365 |
| 37 | 0.99848065 | 0.3922 | 1.0156 | 0.6842 | 0.6842 | TRUE | 6.2365 |
| 38 | 0.99848065 | 0.3922 | 1.0156 | 0.6842 | 0.6842 | TRUE | 6.2365 |
| 39 | NA | 1.6013 | 1.1293 | 1.3727 | 1.3727 | TRUE | 22.8793 |
| 40 | NA | 1.6013 | 1.1293 | 1.3727 | 1.3727 | TRUE | 22.8793 |
| 41 | 0.99848065 | 0.4492 | 1.1118 | 0.7557 | 0.7557 | TRUE | 8.3175 |
| 42 | 0.99848065 | 0.4492 | 1.1118 | 0.7557 | 0.7557 | TRUE | 8.3175 |
| 43 | 0.99848065 | 0.4492 | 1.1118 | 0.7557 | 0.7557 | TRUE | 8.3175 |
| 44 | 0.99848065 | 0.4492 | 1.1118 | 0.7557 | 0.7557 | TRUE | 8.3175 |
| 45 | 0.99848065 | 0.4492 | 1.1118 | 0.7557 | 0.7557 | TRUE | 8.3175 |
| 46 | 0.99848065 | 0.4492 | 1.1118 | 0.7557 | 0.7557 | TRUE | 8.3175 |
| 47 | 0.99848065 | 0.4492 | 1.1118 | 0.7557 | 0.7557 | TRUE | 8.3175 |
| 48 | 0.99848065 | 0.3783 | 1.015 | 0.6759 | 0.6759 | TRUE | 7.2141 |
| 49 | 0.99848065 | 0.3895 | 1.0147 | 0.6823 | 0.6823 | TRUE | 5.4956 |
| 50 | 0.99848065 | 0.4784 | 0.958 | 0.7017 | 0.7017 | TRUE | 11.7551 |
| 51 | 0.99848065 | 0.4784 | 0.958 | 0.7017 | 0.7017 | TRUE | 11.7551 |
| 52 | 0.99848065 | 0.4784 | 0.958 | 0.7017 | 0.7017 | TRUE | 11.7551 |
| 53 | 0.99848065 | 0.4784 | 0.958 | 0.7017 | 0.7017 | TRUE | 11.7551 |
| 54 | 0.99848065 | 0.4784 | 0.958 | 0.7017 | 0.7017 | TRUE | 11.7551 |
| 55 | 0.99848065 | 0.4784 | 0.958 | 0.7017 | 0.7017 | TRUE | 11.7551 |
| 56 | 0.99848065 | 0.4784 | 0.958 | 0.7017 | 0.7017 | TRUE | 11.7551 |
| 57 | 0.99848065 | 0.4784 | 0.958 | 0.7017 | 0.7017 | TRUE | 11.7551 |
| 58 | 0.99848065 | 0.4784 | 0.958 | 0.7017 | 0.7017 | TRUE | 11.7551 |
| 59 | 0.99848065 | 0.4784 | 0.958 | 0.7017 | 0.7017 | TRUE | 11.7551 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 4 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 5 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 6 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 7 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 8 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 9 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 10 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 11 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 12 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 13 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 14 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 15 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 16 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 17 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 18 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 19 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 20 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 21 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 22 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 23 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 24 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 25 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 26 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 27 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 28 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 29 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 30 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 31 | 0.99848065 | 0.1459 | 0.9269 | 0.4931 | 0.4931 | TRUE | 3.7483 |
| 32 | NA | 1.2555 | 1.1099 | 1.1857 | 1.1857 | TRUE | 20.02 |
| 33 | | | | | | | |
| 34 | 0.99848065 | 0.1579 | 1.1111 | 0.5903 | 0.5903 | TRUE | 2.1772 |
| 35 | 0.99848065 | 0.1579 | 1.1111 | 0.5903 | 0.5903 | TRUE | 2.1772 |
| 36 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 37 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 38 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 39 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 40 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 41 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 42 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 43 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 44 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 45 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 46 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 47 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 48 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 49 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 50 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 51 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 52 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 53 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 54 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 55 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 56 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 57 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 58 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 59 | 0.99848065 | 0.1057 | 1.0392 | 0.5276 | 0.5276 | TRUE | 0.4663 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.1099 | 1.0484 | 0.5297 | 0.5297 | TRUE | 1.4828 |
| 4 | 0.99848065 | 0.1099 | 1.0484 | 0.5297 | 0.5297 | TRUE | 1.4828 |
| 5 | 0.99848065 | 0.1099 | 1.0484 | 0.5297 | 0.5297 | TRUE | 1.4828 |
| 6 | 0.99848065 | 0.1099 | 1.0484 | 0.5297 | 0.5297 | TRUE | 1.4828 |
| 7 | 0.99848065 | 0.1099 | 1.0484 | 0.5297 | 0.5297 | TRUE | 1.4828 |
| 8 | 0.99848065 | 0.1099 | 1.0484 | 0.5297 | 0.5297 | TRUE | 1.4828 |
| 9 | 0.99848065 | 0.1099 | 1.0484 | 0.5297 | 0.5297 | TRUE | 1.4828 |
| 10 | 0.99848065 | 0.1099 | 1.0484 | 0.5297 | 0.5297 | TRUE | 1.4828 |
| 11 | 0.99848065 | 0.1099 | 1.0484 | 0.5297 | 0.5297 | TRUE | 1.4828 |
| 12 | 0.99848065 | 0.1099 | 1.0484 | 0.5297 | 0.5297 | TRUE | 1.4828 |
| 13 | 0.99848065 | 0.1099 | 1.0484 | 0.5297 | 0.5297 | TRUE | 1.4828 |
| 14 | 0.99848065 | 0.1099 | 1.0484 | 0.5297 | 0.5297 | TRUE | 1.4828 |
| 15 | 0.99848065 | 0.1099 | 1.0484 | 0.5297 | 0.5297 | TRUE | 1.4828 |
| 16 | 0.99848065 | 0.1099 | 1.0484 | 0.5297 | 0.5297 | TRUE | 1.4828 |
| 17 | 0.99848065 | 0.1099 | 1.0484 | 0.5297 | 0.5297 | TRUE | 1.4828 |
| 18 | 0.99848065 | 0.1099 | 1.0484 | 0.5297 | 0.5297 | TRUE | 1.4828 |
| 19 | 0.99848065 | 0.5449 | 1.0491 | 0.7845 | 0.7845 | TRUE | 2.2755 |
| 20 | 0.99848065 | 0.5449 | 1.0491 | 0.7845 | 0.7845 | TRUE | 2.2755 |
| 21 | 0.99848065 | 0.5449 | 1.0491 | 0.7845 | 0.7845 | TRUE | 2.2755 |
| 22 | 0.99848065 | 0.5449 | 1.0491 | 0.7845 | 0.7845 | TRUE | 2.2755 |
| 23 | 0.99848065 | 0.5449 | 1.0491 | 0.7845 | 0.7845 | TRUE | 2.2755 |
| 24 | 0.99848065 | 0.5449 | 1.0491 | 0.7845 | 0.7845 | TRUE | 2.2755 |
| 25 | 0.99848065 | 0.5449 | 1.0491 | 0.7845 | 0.7845 | TRUE | 2.2755 |
| 26 | 0.99848065 | 0.5449 | 1.0491 | 0.7845 | 0.7845 | TRUE | 2.2755 |
| 27 | 0.99848065 | 0.5449 | 1.0491 | 0.7845 | 0.7845 | TRUE | 2.2755 |
| 28 | 0.99848065 | 0.151 | 0.9114 | 0.4916 | 0.4916 | TRUE | 1.7065 |
| 29 | 0.99848065 | 0.151 | 0.9114 | 0.4916 | 0.4916 | TRUE | 1.7065 |
| 30 | 0.99848065 | 0.3373 | 0.9738 | 0.6332 | 0.6332 | TRUE | 0.5599 |
| 31 | 0.99848065 | 0.3373 | 0.9738 | 0.6332 | 0.6332 | TRUE | 0.5599 |
| 32 | 0.99848065 | 0.1105 | 1.0473 | 0.5294 | 0.5294 | TRUE | 1.443 |
| 33 | 0.99848065 | 0.6522 | 0.8977 | 0.7685 | 0.7685 | TRUE | 0.3985 |
| 34 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 35 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 36 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 37 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 38 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 39 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 40 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 41 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 42 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 43 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 44 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 45 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 46 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 47 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 48 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 49 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 50 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 51 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 52 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 53 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 54 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 55 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 56 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 57 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 58 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 59 | 0.99848065 | 0.6555 | 0.8977 | 0.7703 | 0.7703 | TRUE | 0.3993 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 1.4605 | 1.0596 | 1.265 | 1.265 | TRUE | 5.7218 |
| 4 | 0.99848065 | 1.4605 | 1.0596 | 1.265 | 1.265 | TRUE | 5.7218 |
| 5 | 0.99848065 | 1.4605 | 1.0596 | 1.265 | 1.265 | TRUE | 5.7218 |
| 6 | 0.99848065 | 1.4311 | 1.057 | 1.2486 | 1.2486 | TRUE | 5.0296 |
| 7 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 8 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 9 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 10 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 11 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 12 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 13 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 14 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 15 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 16 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 17 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 18 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 19 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 20 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 21 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 22 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 23 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 24 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 25 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 26 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 27 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 28 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 29 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 30 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 31 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 32 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 33 | 0.99848065 | 0.3328 | 0.9802 | 0.6336 | 0.6336 | TRUE | 0.564 |
| 34 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 35 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 36 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 37 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 38 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 39 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 40 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 41 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 42 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 43 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 44 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 45 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 46 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 47 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 48 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 49 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 50 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 51 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 52 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 53 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 54 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 55 | 0.99848065 | 0.1487 | 1.1017 | 0.5747 | 0.5747 | TRUE | 2.184 |
| 56 | 0.99848065 | 0.057 | 0.9095 | 0.4289 | 0.4289 | TRUE | 0.3274 |
| 57 | 0.99848065 | 0.057 | 0.9095 | 0.4289 | 0.4289 | TRUE | 0.3274 |
| 58 | 0.99848065 | 0.057 | 0.9095 | 0.4289 | 0.4289 | TRUE | 0.3274 |
| 59 | 0.99848065 | 0.057 | 0.9095 | 0.4289 | 0.4289 | TRUE | 0.3274 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.2934 | 0.9343 | 0.5826 | 0.5826 | TRUE | 3.5417 |
| 4 | 0.99848065 | 0.3142 | 1.0042 | 0.6308 | 0.6308 | TRUE | 4.182 |
| 5 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 6 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 7 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 8 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 9 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 10 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 11 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 12 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 13 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 14 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 15 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 16 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 17 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 18 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 19 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 20 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 21 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 22 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 23 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 24 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 25 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 26 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 27 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 28 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 29 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 30 | 0.99848065 | 0.3598 | 1.015 | 0.6622 | 0.6622 | TRUE | 3.0186 |
| 31 | 0.99848065 | 0.6941 | 0.8883 | 0.7717 | 0.7717 | TRUE | 1.0172 |
| 32 | 0.99848065 | 0.9043 | 0.889 | 0.8974 | 0.8974 | TRUE | 0.5704 |
| 33 | 0.99848065 | 0.186 | 0.9651 | 0.5415 | 0.5415 | TRUE | 0.8406 |
| 34 | 0.99848065 | 0.186 | 0.9651 | 0.5415 | 0.5415 | TRUE | 0.8406 |
| 35 | 0.99848065 | 0.186 | 0.9651 | 0.5415 | 0.5415 | TRUE | 0.8406 |
| 36 | 0.99848065 | 0.186 | 0.9651 | 0.5415 | 0.5415 | TRUE | 0.8406 |
| 37 | 0.99848065 | 0.186 | 0.9651 | 0.5415 | 0.5415 | TRUE | 0.8406 |
| 38 | 0.99848065 | 0.186 | 0.9651 | 0.5415 | 0.5415 | TRUE | 0.8406 |
| 39 | 0.99848065 | 0.186 | 0.9651 | 0.5415 | 0.5415 | TRUE | 0.8406 |
| 40 | 0.99848065 | 0.186 | 0.9651 | 0.5415 | 0.5415 | TRUE | 0.8406 |
| 41 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 42 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 43 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 44 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 45 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 46 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 47 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 48 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 49 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 50 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 51 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 52 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 53 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 54 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 55 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 56 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 57 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 58 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 59 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 4 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 5 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 6 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 7 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 8 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 9 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 10 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 11 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 12 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 13 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 14 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 15 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 16 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 17 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 18 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 19 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 20 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 21 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 22 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 23 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 24 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 25 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 26 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 27 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 28 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 29 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 30 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 31 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 32 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 33 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 34 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 35 | 0.99848065 | 0.1941 | 0.9774 | 0.553 | 0.553 | TRUE | 2.7677 |
| 36 | 0.99848065 | 0.1783 | 0.9642 | 0.5363 | 0.5363 | TRUE | 0.7762 |
| 37 | 0.99848065 | 0.5592 | 1.0835 | 0.8027 | 0.8027 | TRUE | 5.2847 |
| 38 | 0.99848065 | 0.5592 | 1.0835 | 0.8027 | 0.8027 | TRUE | 5.2847 |
| 39 | 0.99848065 | 0.0755 | 0.9442 | 0.4607 | 0.4607 | TRUE | 0.299 |
| 40 | 0.99848065 | 0.0755 | 0.9442 | 0.4607 | 0.4607 | TRUE | 0.299 |
| 41 | 0.99848065 | 0.1305 | 0.9171 | 0.4815 | 0.4815 | TRUE | 1.1233 |
| 42 | 0.99848065 | 0.1305 | 0.9171 | 0.4815 | 0.4815 | TRUE | 1.1233 |
| 43 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 44 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 45 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 46 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 47 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 48 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 49 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 50 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 51 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 52 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 53 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 54 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 55 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 56 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 57 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 58 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 59 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 4 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 5 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 6 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 7 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 8 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 9 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 10 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 11 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 12 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 13 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 14 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 15 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 16 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 17 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 18 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 19 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 20 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 21 | 0.99848065 | 0.1315 | 0.9172 | 0.4822 | 0.4822 | TRUE | 1.1353 |
| 22 | 0.99848065 | 1.6087 | 0.9672 | 1.2919 | 1.2919 | TRUE | 3.7481 |
| 23 | 0.99848065 | 1.5678 | 0.9653 | 1.2711 | 1.2711 | TRUE | 5.9406 |
| 24 | 0.99848065 | 0.0552 | 0.8896 | 0.4186 | 0.4186 | TRUE | 0.8472 |
| 25 | 0.99848065 | 0.0552 | 0.8896 | 0.4186 | 0.4186 | TRUE | 0.8472 |
| 26 | 0.99848065 | 0.0552 | 0.8896 | 0.4186 | 0.4186 | TRUE | 0.8472 |
| 27 | 0.99848065 | 0.0552 | 0.8896 | 0.4186 | 0.4186 | TRUE | 0.8472 |
| 28 | 0.99848065 | 0.0552 | 0.8896 | 0.4186 | 0.4186 | TRUE | 0.8472 |
| 29 | 0.99848065 | 0.0552 | 0.8896 | 0.4186 | 0.4186 | TRUE | 0.8472 |
| 30 | 0.99848065 | 0.0552 | 0.8896 | 0.4186 | 0.4186 | TRUE | 0.8472 |
| 31 | 0.99848065 | 0.0552 | 0.8896 | 0.4186 | 0.4186 | TRUE | 0.8472 |
| 32 | 0.99848065 | 0.0552 | 0.8896 | 0.4186 | 0.4186 | TRUE | 0.8472 |
| 33 | 0.99848065 | 0.0552 | 0.8896 | 0.4186 | 0.4186 | TRUE | 0.8472 |
| 34 | 0.99848065 | 0.0552 | 0.8896 | 0.4186 | 0.4186 | TRUE | 0.8472 |
| 35 | 0.99848065 | 0.0552 | 0.8896 | 0.4186 | 0.4186 | TRUE | 0.8472 |
| 36 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 37 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 38 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 39 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 40 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 41 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 42 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 43 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 44 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 45 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 46 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 47 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 48 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 49 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 50 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 51 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 52 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 53 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 54 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 55 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 56 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 57 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 58 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 59 | 0.99848065 | 0.3303 | 0.9283 | 0.6052 | 0.6052 | TRUE | 0.3087 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 4 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 5 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 6 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 7 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 8 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 9 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 10 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 11 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 12 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 13 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 14 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 15 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 16 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 17 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 18 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 19 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 20 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 21 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 22 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 23 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 24 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 25 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 26 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 27 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 28 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 29 | 0.99848065 | 1.7065 | 0.9547 | 1.3331 | 1.3331 | TRUE | 1.1716 |
| 30 | 0.99848065 | 1.7106 | 0.9544 | 1.335 | 1.335 | TRUE | 1.1853 |
| 31 | 0.99848065 | 0.0633 | 0.9457 | 0.4545 | 0.4545 | TRUE | 1.2571 |
| 32 | 0.99848065 | 0.0633 | 0.9457 | 0.4545 | 0.4545 | TRUE | 1.2571 |
| 33 | 0.99848065 | 0.0694 | 0.9491 | 0.4603 | 0.4603 | TRUE | 1.3204 |
| 34 | 0.99848065 | 0.0694 | 0.9491 | 0.4603 | 0.4603 | TRUE | 1.3204 |
| 35 | 0.99848065 | 0.0694 | 0.9491 | 0.4603 | 0.4603 | TRUE | 1.3204 |
| 36 | 0.99848065 | 0.0694 | 0.9491 | 0.4603 | 0.4603 | TRUE | 1.3204 |
| 37 | 0.99848065 | 0.0694 | 0.9491 | 0.4603 | 0.4603 | TRUE | 1.3204 |
| 38 | 0.99848065 | 0.0694 | 0.9491 | 0.4603 | 0.4603 | TRUE | 1.3204 |
| 39 | 0.99848065 | 0.0694 | 0.9491 | 0.4603 | 0.4603 | TRUE | 1.3204 |
| 40 | 0.99848065 | 0.0694 | 0.9491 | 0.4603 | 0.4603 | TRUE | 1.3204 |
| 41 | 0.99848065 | 0.0694 | 0.9491 | 0.4603 | 0.4603 | TRUE | 1.3204 |
| 42 | 0.99848065 | 0.0694 | 0.9491 | 0.4603 | 0.4603 | TRUE | 1.3204 |
| 43 | 0.99848065 | 0.0694 | 0.9491 | 0.4603 | 0.4603 | TRUE | 1.3204 |
| 44 | 0.99848065 | 1.2568 | 0.9222 | 1.093 | 1.093 | TRUE | 0.3286 |
| 45 | 0.99848065 | 1.2821 | 0.9232 | 1.1061 | 1.1061 | TRUE | 0.3134 |
| 46 | 0.99848065 | 0.2652 | 0.9083 | 0.5569 | 0.5569 | TRUE | 1.9845 |
| 47 | 0.99848065 | 0.2652 | 0.9083 | 0.5569 | 0.5569 | TRUE | 1.9845 |
| 48 | 0.99848065 | 0.2652 | 0.9083 | 0.5569 | 0.5569 | TRUE | 1.9845 |
| 49 | 0.99848065 | 1.2599 | 0.9247 | 1.0957 | 1.0957 | TRUE | 0.3569 |
| 50 | 0.99848065 | 1.2599 | 0.9247 | 1.0957 | 1.0957 | TRUE | 0.3569 |
| 51 | 0.99848065 | 1.2599 | 0.9247 | 1.0957 | 1.0957 | TRUE | 0.3569 |
| 52 | 0.99848065 | 1.2599 | 0.9247 | 1.0957 | 1.0957 | TRUE | 0.3569 |
| 53 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 54 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 55 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 56 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 57 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 58 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 59 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 4 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 5 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 6 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 7 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 8 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 9 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 10 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 11 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 12 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 13 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 14 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 15 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 16 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 17 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 18 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 19 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 20 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 21 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 22 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 23 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 24 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 25 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 26 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 27 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 28 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 29 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 30 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 31 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 32 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 33 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 34 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 35 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 36 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 37 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 38 | 0.99848065 | 1.2591 | 0.9248 | 1.0953 | 1.0953 | TRUE | 0.3559 |
| 39 | 0.99848065 | 0.5081 | 0.9881 | 0.7317 | 0.7317 | TRUE | 3.3237 |
| 40 | 0.99848065 | 0.5081 | 0.9881 | 0.7317 | 0.7317 | TRUE | 3.3237 |
| 41 | 0.99848065 | 0.0803 | 0.9428 | 0.464 | 0.464 | TRUE | 1.2933 |
| 42 | 0.99848065 | 0.0803 | 0.9428 | 0.464 | 0.464 | TRUE | 1.2933 |
| 43 | 0.99848065 | 0.0803 | 0.9428 | 0.464 | 0.464 | TRUE | 1.2933 |
| 44 | 0.99848065 | 0.0803 | 0.9428 | 0.464 | 0.464 | TRUE | 1.2933 |
| 45 | 0.99848065 | 0.0803 | 0.9428 | 0.464 | 0.464 | TRUE | 1.2933 |
| 46 | 0.99848065 | 0.0803 | 0.9428 | 0.464 | 0.464 | TRUE | 1.2933 |
| 47 | 0.99848065 | 0.0803 | 0.9428 | 0.464 | 0.464 | TRUE | 1.2933 |
| 48 | 0.99848065 | 0.0803 | 0.9428 | 0.464 | 0.464 | TRUE | 1.2933 |
| 49 | 0.99848065 | 0.0803 | 0.9428 | 0.464 | 0.464 | TRUE | 1.2933 |
| 50 | 0.99848065 | 0.0803 | 0.9428 | 0.464 | 0.464 | TRUE | 1.2933 |
| 51 | 0.99848065 | 1.5661 | 0.9503 | 1.2624 | 1.2624 | TRUE | 1.1491 |
| 52 | 0.99848065 | 1.5661 | 0.9503 | 1.2624 | 1.2624 | TRUE | 1.1491 |
| 53 | 0.99848065 | 1.5661 | 0.9503 | 1.2624 | 1.2624 | TRUE | 1.1491 |
| 54 | 0.99848065 | 1.5661 | 0.9503 | 1.2624 | 1.2624 | TRUE | 1.1491 |
| 55 | 0.99848065 | 1.5661 | 0.9503 | 1.2624 | 1.2624 | TRUE | 1.1491 |
| 56 | 0.99848065 | 1.5661 | 0.9503 | 1.2624 | 1.2624 | TRUE | 1.1491 |
| 57 | 0.99848065 | 1.5661 | 0.9503 | 1.2624 | 1.2624 | TRUE | 1.1491 |
| 58 | 0.99848065 | 1.5661 | 0.9503 | 1.2624 | 1.2624 | TRUE | 1.1491 |
| 59 | 0.99848065 | 1.5661 | 0.9503 | 1.2624 | 1.2624 | TRUE | 1.1491 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 1.5661 | 0.9503 | 1.2624 | 1.2624 | TRUE | 1.1491 |
| 4 | 0.99848065 | 0.3017 | 0.9519 | 0.5997 | 0.5997 | TRUE | 2.6316 |
| 5 | 0.99848065 | 0.3017 | 0.9519 | 0.5997 | 0.5997 | TRUE | 2.6316 |
| 6 | 0.99848065 | 0.3017 | 0.9519 | 0.5997 | 0.5997 | TRUE | 2.6316 |
| 7 | 0.99848065 | 0.3017 | 0.9519 | 0.5997 | 0.5997 | TRUE | 2.6316 |
| 8 | 0.99848065 | 0.3017 | 0.9519 | 0.5997 | 0.5997 | TRUE | 2.6316 |
| 9 | 0.99848065 | 0.3017 | 0.9519 | 0.5997 | 0.5997 | TRUE | 2.6316 |
| 10 | 0.99848065 | 0.3017 | 0.9519 | 0.5997 | 0.5997 | TRUE | 2.6316 |
| 11 | 0.99848065 | 0.3017 | 0.9519 | 0.5997 | 0.5997 | TRUE | 2.6316 |
| 12 | 0.99848065 | 0.3017 | 0.9519 | 0.5997 | 0.5997 | TRUE | 2.6316 |
| 13 | 0.99848065 | 0.3017 | 0.9519 | 0.5997 | 0.5997 | TRUE | 2.6316 |
| 14 | 0.99848065 | 0.3017 | 0.9519 | 0.5997 | 0.5997 | TRUE | 2.6316 |
| 15 | 0.99848065 | 0.7832 | 1.0093 | 0.8927 | 0.8927 | TRUE | 1.5532 |
| 16 | 0.99848065 | 0.7832 | 1.0093 | 0.8927 | 0.8927 | TRUE | 1.5532 |
| 17 | 0.99848065 | 0.7832 | 1.0093 | 0.8927 | 0.8927 | TRUE | 1.5532 |
| 18 | 0.99848065 | 0.7832 | 1.0093 | 0.8927 | 0.8927 | TRUE | 1.5532 |
| 19 | 0.99848065 | 0.7832 | 1.0093 | 0.8927 | 0.8927 | TRUE | 1.5532 |
| 20 | 0.99848065 | 0.7832 | 1.0093 | 0.8927 | 0.8927 | TRUE | 1.5532 |
| 21 | 0.99848065 | 0.7832 | 1.0093 | 0.8927 | 0.8927 | TRUE | 1.5532 |
| 22 | 0.99848065 | 0.1091 | 1.0067 | 0.5141 | 0.5141 | TRUE | 0.23 |
| 23 | 0.99848065 | 0.1091 | 1.0067 | 0.5141 | 0.5141 | TRUE | 0.23 |
| 24 | 0.99848065 | 0.1036 | 1.0032 | 0.5088 | 0.5088 | TRUE | 0.237 |
| 25 | 0.99848065 | 0.2465 | 1.0572 | 0.6187 | 0.6187 | TRUE | 0.4444 |
| 26 | 0.99848065 | 0.2465 | 1.0572 | 0.6187 | 0.6187 | TRUE | 0.4444 |
| 27 | 0.99848065 | 0.2465 | 1.0572 | 0.6187 | 0.6187 | TRUE | 0.4444 |
| 28 | 0.99848065 | 0.2465 | 1.0572 | 0.6187 | 0.6187 | TRUE | 0.4444 |
| 29 | 0.99848065 | 0.2465 | 1.0572 | 0.6187 | 0.6187 | TRUE | 0.4444 |
| 30 | 0.99848065 | 0.2465 | 1.0572 | 0.6187 | 0.6187 | TRUE | 0.4444 |
| 31 | 0.99848065 | 0.2465 | 1.0572 | 0.6187 | 0.6187 | TRUE | 0.4444 |
| 32 | 0.99848065 | 0.2465 | 1.0572 | 0.6187 | 0.6187 | TRUE | 0.4444 |
| 33 | 0.99848065 | 0.2465 | 1.0572 | 0.6187 | 0.6187 | TRUE | 0.4444 |
| 34 | 0.99848065 | 0.2465 | 1.0572 | 0.6187 | 0.6187 | TRUE | 0.4444 |
| 35 | 0.99848065 | 0.2465 | 1.0572 | 0.6187 | 0.6187 | TRUE | 0.4444 |
| 36 | 0.99848065 | 0.2465 | 1.0572 | 0.6187 | 0.6187 | TRUE | 0.4444 |
| 37 | 0.99848065 | 0.2465 | 1.0572 | 0.6187 | 0.6187 | TRUE | 0.4444 |
| 38 | 0.99848065 | 0.2465 | 1.0572 | 0.6187 | 0.6187 | TRUE | 0.4444 |
| 39 | 0.99848065 | 1.7755 | 0.949 | 1.3488 | 1.3488 | TRUE | 0.409 |
| 40 | 0.99848065 | 1.7755 | 0.949 | 1.3488 | 1.3488 | TRUE | 0.409 |
| 41 | 0.99848065 | 1.7755 | 0.949 | 1.3488 | 1.3488 | TRUE | 0.409 |
| 42 | 0.99848065 | 1.7755 | 0.949 | 1.3488 | 1.3488 | TRUE | 0.409 |
| 43 | 0.99848065 | 1.7755 | 0.949 | 1.3488 | 1.3488 | TRUE | 0.409 |
| 44 | 0.99848065 | 1.7755 | 0.949 | 1.3488 | 1.3488 | TRUE | 0.409 |
| 45 | 0.99848065 | 1.7755 | 0.949 | 1.3488 | 1.3488 | TRUE | 0.409 |
| 46 | 0.99848065 | 1.7755 | 0.949 | 1.3488 | 1.3488 | TRUE | 0.409 |
| 47 | 0.99848065 | 1.7755 | 0.949 | 1.3488 | 1.3488 | TRUE | 0.409 |
| 48 | 0.99848065 | 1.7755 | 0.949 | 1.3488 | 1.3488 | TRUE | 0.409 |
| 49 | 0.99848065 | 1.7755 | 0.949 | 1.3488 | 1.3488 | TRUE | 0.409 |
| 50 | 0.99848065 | 1.7755 | 0.949 | 1.3488 | 1.3488 | TRUE | 0.409 |
| 51 | 0.99848065 | 1.7755 | 0.949 | 1.3488 | 1.3488 | TRUE | 0.409 |
| 52 | 0.99848065 | 1.7755 | 0.949 | 1.3488 | 1.3488 | TRUE | 0.409 |
| 53 | 0.99848065 | 1.7755 | 0.949 | 1.3488 | 1.3488 | TRUE | 0.409 |
| 54 | 0.99848065 | 1.7755 | 0.949 | 1.3488 | 1.3488 | TRUE | 0.409 |
| 55 | 0.99848065 | 1.7755 | 0.949 | 1.3488 | 1.3488 | TRUE | 0.409 |
| 56 | 0.99848065 | 0.792 | 1.0154 | 0.8978 | 0.8978 | TRUE | 0.3103 |
| 57 | 0.99848065 | 0.1605 | 0.9965 | 0.5385 | 0.5385 | TRUE | 0.2503 |
| 58 | 0.99848065 | 0.1605 | 0.9965 | 0.5385 | 0.5385 | TRUE | 0.2503 |
| 59 | 0.99848065 | 0.1605 | 0.9965 | 0.5385 | 0.5385 | TRUE | 0.2503 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 4 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 5 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 6 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 7 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 8 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 9 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 10 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 11 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 12 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 13 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 14 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 15 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 16 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 17 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 18 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 19 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 20 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 21 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 22 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 23 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 24 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 25 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 26 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 27 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 28 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 29 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 30 | 0.99848065 | 0.1586 | 0.9848 | 0.5324 | 0.5324 | TRUE | 0.4223 |
| 31 | 0.99848065 | 0.1459 | 0.9827 | 0.5237 | 0.5237 | TRUE | 0.4203 |
| 32 | 0.99848065 | 0.1594 | 0.9926 | 0.536 | 0.536 | TRUE | 0.2103 |
| 33 | 0.99848065 | 0.1594 | 0.9926 | 0.536 | 0.536 | TRUE | 0.2103 |
| 34 | 0.99848065 | 0.1594 | 0.9926 | 0.536 | 0.536 | TRUE | 0.2103 |
| 35 | 0.99848065 | 0.3389 | 0.932 | 0.6116 | 0.6116 | TRUE | 0.3884 |
| 36 | 0.99848065 | 0.0147 | 0.9265 | 0.41 | 0.41 | TRUE | 0.2902 |
| 37 | 0.99848065 | 0.3436 | 1.0955 | 0.6931 | 0.6931 | TRUE | 0.8144 |
| 38 | 0.99848065 | 0.1347 | 0.9117 | 0.4814 | 0.4814 | TRUE | 1.5426 |
| 39 | 0.99848065 | 0.1347 | 0.9117 | 0.4814 | 0.4814 | TRUE | 1.5426 |
| 40 | 0.99848065 | 0.1347 | 0.9117 | 0.4814 | 0.4814 | TRUE | 1.5426 |
| 41 | 0.99848065 | 0.1347 | 0.9117 | 0.4814 | 0.4814 | TRUE | 1.5426 |
| 42 | 0.99848065 | 0.1347 | 0.9117 | 0.4814 | 0.4814 | TRUE | 1.5426 |
| 43 | 0.99848065 | 0.1347 | 0.9117 | 0.4814 | 0.4814 | TRUE | 1.5426 |
| 44 | 0.99848065 | 0.8108 | 1.0697 | 0.9368 | 0.9368 | TRUE | 1.3683 |
| 45 | 0.99848065 | 0.8108 | 1.0697 | 0.9368 | 0.9368 | TRUE | 1.3683 |
| 46 | 0.99848065 | 0.3769 | 0.8863 | 0.8042 | 0.8042 | TRUE | 0.6651 |
| 47 | 0.99848065 | 0.3769 | 0.8863 | 0.8042 | 0.8042 | TRUE | 0.6651 |
| 48 | 0.99848065 | 0.3769 | 0.8863 | 0.8042 | 0.8042 | TRUE | 0.6651 |
| 49 | 0.99848065 | 0.3769 | 0.8863 | 0.8042 | 0.8042 | TRUE | 0.6651 |
| 50 | 0.99848065 | 0.3769 | 0.8863 | 0.8042 | 0.8042 | TRUE | 0.6651 |
| 51 | 0.99848065 | 0.3769 | 0.8863 | 0.8042 | 0.8042 | TRUE | 0.6651 |
| 52 | 0.99848065 | 0.3769 | 0.8863 | 0.8042 | 0.8042 | TRUE | 0.6651 |
| 53 | 0.99848065 | 0.3769 | 0.8863 | 0.8042 | 0.8042 | TRUE | 0.6651 |
| 54 | 0.99848065 | 0.3769 | 0.8863 | 0.8042 | 0.8042 | TRUE | 0.6651 |
| 55 | 0.99848065 | 0.3769 | 0.8863 | 0.8042 | 0.8042 | TRUE | 0.6651 |
| 56 | 0.99848065 | 0.3769 | 0.8863 | 0.8042 | 0.8042 | TRUE | 0.6651 |
| 57 | 0.99848065 | 0.3769 | 0.8863 | 0.8042 | 0.8042 | TRUE | 0.6651 |
| 58 | 0.99848065 | 0.3769 | 0.8863 | 0.8042 | 0.8042 | TRUE | 0.6651 |
| 59 | 0.99848065 | 0.3769 | 0.8863 | 0.8042 | 0.8042 | TRUE | 0.6651 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.2084 | 0.8881 | 0.5231 | 0.5231 | TRUE | 5.7214 |
| 4 | 0.99848065 | 0.2084 | 0.8881 | 0.5231 | 0.5231 | TRUE | 5.7214 |
| 5 | 0.99848065 | 0.2084 | 0.8881 | 0.5231 | 0.5231 | TRUE | 5.7214 |
| 6 | 0.99848065 | 0.2084 | 0.8881 | 0.5231 | 0.5231 | TRUE | 5.7214 |
| 7 | 0.99848065 | 0.2084 | 0.8881 | 0.5231 | 0.5231 | TRUE | 5.7214 |
| 8 | 0.99848065 | 0.2084 | 0.8881 | 0.5231 | 0.5231 | TRUE | 5.7214 |
| 9 | 0.99848065 | 0.2084 | 0.8881 | 0.5231 | 0.5231 | TRUE | 5.7214 |
| 10 | 0.99848065 | 0.2084 | 0.8881 | 0.5231 | 0.5231 | TRUE | 5.7214 |
| 11 | 0.99848065 | 0.2084 | 0.8881 | 0.5231 | 0.5231 | TRUE | 5.7214 |
| 12 | 0.99848065 | 0.2084 | 0.8881 | 0.5231 | 0.5231 | TRUE | 5.7214 |
| 13 | 0.99848065 | 0.2084 | 0.8881 | 0.5231 | 0.5231 | TRUE | 5.7214 |
| 14 | 0.99848065 | 0.2084 | 0.8881 | 0.5231 | 0.5231 | TRUE | 5.7214 |
| 15 | 0.99848065 | 0.2084 | 0.8881 | 0.5231 | 0.5231 | TRUE | 5.7214 |
| 16 | 0.99848065 | 0.2084 | 0.8881 | 0.5231 | 0.5231 | TRUE | 5.7214 |
| 17 | 0.99848065 | 0.2084 | 0.8881 | 0.5231 | 0.5231 | TRUE | 5.7214 |
| 18 | 0.99848065 | 0.2084 | 0.8881 | 0.5231 | 0.5231 | TRUE | 5.7214 |
| 19 | 0.99848065 | 0.2084 | 0.8881 | 0.5231 | 0.5231 | TRUE | 5.7214 |
| 20 | 0.99848065 | 0.2086 | 0.8881 | 0.5232 | 0.5232 | TRUE | 5.7287 |
| 21 | 0.99848065 | 0.2086 | 0.8881 | 0.5232 | 0.5232 | TRUE | 5.7287 |
| 22 | 0.99848065 | 0.2086 | 0.8881 | 0.5232 | 0.5232 | TRUE | 5.7287 |
| 23 | 0.99848065 | 0.2086 | 0.8881 | 0.5232 | 0.5232 | TRUE | 5.7287 |
| 24 | 0.99848065 | 0.5149 | 0.8866 | 0.6889 | 0.6889 | TRUE | 0.4773 |
| 25 | 0.9996958 | 0.5517 | 0.8866 | 0.7089 | 0.7089 | TRUE | 0.5047 |
| 26 | 0.9996958 | 0.5517 | 0.8866 | 0.7089 | 0.7089 | TRUE | 0.5047 |
| 27 | 0.9996958 | 0.5517 | 0.8866 | 0.7089 | 0.7089 | TRUE | 0.5047 |
| 28 | 0.9996958 | 0.5517 | 0.8866 | 0.7089 | 0.7089 | TRUE | 0.5047 |
| 29 | 0.9996958 | 0.5517 | 0.8866 | 0.7089 | 0.7089 | TRUE | 0.5047 |
| 30 | 0.9996958 | 0.5517 | 0.8866 | 0.7089 | 0.7089 | TRUE | 0.5047 |
| 31 | 0.9996958 | 0.5517 | 0.8866 | 0.7089 | 0.7089 | TRUE | 0.5047 |
| 32 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 33 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 34 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 35 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 36 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 37 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 38 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 39 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 40 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 41 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 42 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 43 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 44 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 45 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 46 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 47 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 48 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 49 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 50 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 51 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 52 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 53 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 54 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 55 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 56 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 57 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 58 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 59 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 4 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 5 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 6 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 7 | 0.9996958 | 0.0299 | 0.9186 | 0.4168 | 0.4168 | TRUE | 0.6303 |
| 8 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 9 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 10 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 11 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 12 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 13 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 14 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 15 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 16 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 17 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 18 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 19 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 20 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 21 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 22 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 23 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 24 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 25 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 26 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 27 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 28 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 29 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 30 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 31 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 32 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 33 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 34 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 35 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 36 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 37 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 38 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 39 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 40 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 41 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 42 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 43 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 44 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 45 | 0.9996958 | 0.1213 | 0.9213 | 0.4778 | 0.4778 | TRUE | 0.8586 |
| 46 | 0.99848065 | 0.2221 | 0.9337 | 0.5449 | 0.5449 | TRUE | 0.2481 |
| 47 | 0.99848065 | 0.3683 | 0.8868 | 0.6076 | 0.6076 | TRUE | 0.3303 |
| 48 | 0.99848065 | 0.3683 | 0.8868 | 0.6076 | 0.6076 | TRUE | 0.3303 |
| 49 | 0.99848065 | 0.3683 | 0.8868 | 0.6076 | 0.6076 | TRUE | 0.3303 |
| 50 | 0.99848065 | 0.3683 | 0.8868 | 0.6076 | 0.6076 | TRUE | 0.3303 |
| 51 | 0.99848065 | 0.3683 | 0.8868 | 0.6076 | 0.6076 | TRUE | 0.3303 |
| 52 | 0.99848065 | 0.3683 | 0.8868 | 0.6076 | 0.6076 | TRUE | 0.3303 |
| 53 | 0.99848065 | 0.3683 | 0.8868 | 0.6076 | 0.6076 | TRUE | 0.3303 |
| 54 | 0.99848065 | 0.3683 | 0.8868 | 0.6076 | 0.6076 | TRUE | 0.3303 |
| 55 | 0.99848065 | 0.3683 | 0.8868 | 0.6076 | 0.6076 | TRUE | 0.3303 |
| 56 | 0.99848065 | 0.3683 | 0.8868 | 0.6076 | 0.6076 | TRUE | 0.3303 |
| 57 | 0.99848065 | 0.3683 | 0.8868 | 0.6076 | 0.6076 | TRUE | 0.3303 |
| 58 | 0.99848065 | 0.3683 | 0.8868 | 0.6076 | 0.6076 | TRUE | 0.3303 |
| 59 | 0.99848065 | 0.3683 | 0.8868 | 0.6076 | 0.6076 | TRUE | 0.3303 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.3593 | 0.8885 | 0.6035 | 0.6035 | TRUE | 0.2656 |
| 4 | 0.99848065 | 0.1494 | 0.8873 | 0.4786 | 0.4786 | TRUE | 2.258 |
| 5 | 0.99848065 | 0.1494 | 0.8873 | 0.4786 | 0.4786 | TRUE | 2.258 |
| 6 | 0.99848065 | 0.3297 | 0.909 | 0.5959 | 0.5959 | TRUE | 0.5677 |
| 7 | 0.99848065 | 0.3297 | 0.909 | 0.5959 | 0.5959 | TRUE | 0.5677 |
| 8 | 0.99848065 | 0.3297 | 0.909 | 0.5959 | 0.5959 | TRUE | 0.5677 |
| 9 | 0.99848065 | 0.3297 | 0.909 | 0.5959 | 0.5959 | TRUE | 0.5677 |
| 10 | 0.99848065 | 0.3297 | 0.909 | 0.5959 | 0.5959 | TRUE | 0.5677 |
| 11 | 0.99848065 | 0.3297 | 0.909 | 0.5959 | 0.5959 | TRUE | 0.5677 |
| 12 | 0.99848065 | 0.3297 | 0.909 | 0.5959 | 0.5959 | TRUE | 0.5677 |
| 13 | 0.99848065 | 0.3297 | 0.909 | 0.5959 | 0.5959 | TRUE | 0.5677 |
| 14 | 0.99848065 | 0.3297 | 0.909 | 0.5959 | 0.5959 | TRUE | 0.5677 |
| 15 | 0.99848065 | 0.3297 | 0.909 | 0.5959 | 0.5959 | TRUE | 0.5677 |
| 16 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 17 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 18 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 19 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 20 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 21 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 22 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 23 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 24 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 25 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 26 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 27 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 28 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 29 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 30 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 31 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 32 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 33 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 34 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 35 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 36 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 37 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 38 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 39 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 40 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 41 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 42 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 43 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 44 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 45 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 46 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 47 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 48 | 0.99848065 | 0.2796 | 0.9165 | 0.5702 | 0.5702 | TRUE | 0.4627 |
| 49 | 0.99848065 | 0.8624 | 1.0637 | 0.9577 | 0.9577 | TRUE | 1.3669 |
| 50 | 0.99848065 | 0.076 | 1.0661 | 0.5231 | 0.5231 | TRUE | 0.1833 |
| 51 | 0.99848065 | 0.076 | 1.0661 | 0.5231 | 0.5231 | TRUE | 0.1833 |
| 52 | 0.99848065 | 0.076 | 1.0661 | 0.5231 | 0.5231 | TRUE | 0.1833 |
| 53 | 0.99848065 | 0.076 | 1.0661 | 0.5231 | 0.5231 | TRUE | 0.1833 |
| 54 | 0.99848065 | 0.076 | 1.0661 | 0.5231 | 0.5231 | TRUE | 0.1833 |
| 55 | 0.99848065 | 0.076 | 1.0661 | 0.5231 | 0.5231 | TRUE | 0.1833 |
| 56 | 0.99848065 | 0.076 | 1.0661 | 0.5231 | 0.5231 | TRUE | 0.1833 |
| 57 | 0.99848065 | 0.076 | 1.0661 | 0.5231 | 0.5231 | TRUE | 0.1833 |
| 58 | 0.99848065 | 0.076 | 1.0661 | 0.5231 | 0.5231 | TRUE | 0.1833 |
| 59 | 0.99848065 | 0.076 | 1.0661 | 0.5231 | 0.5231 | TRUE | 0.1833 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.5792 | 0.8864 | 0.9414 | 0.9414 | TRUE | 0.4243 |
| 4 | 0.99848065 | 0.5792 | 0.8864 | 0.9414 | 0.9414 | TRUE | 0.4243 |
| 5 | 0.99848065 | 0.5792 | 0.8864 | 0.9414 | 0.9414 | TRUE | 0.4243 |
| 6 | 0.99848065 | 0.5792 | 0.8864 | 0.9414 | 0.9414 | TRUE | 0.4243 |
| 7 | 0.99848065 | 0.5792 | 0.8864 | 0.9414 | 0.9414 | TRUE | 0.4243 |
| 8 | 0.99848065 | 0.5792 | 0.8864 | 0.9414 | 0.9414 | TRUE | 0.4243 |
| 9 | 0.99848065 | 0.5792 | 0.8864 | 0.9414 | 0.9414 | TRUE | 0.4243 |
| 10 | 0.99848065 | 0.5792 | 0.8864 | 0.9414 | 0.9414 | TRUE | 0.4243 |
| 11 | 0.99848065 | 0.5792 | 0.8864 | 0.9414 | 0.9414 | TRUE | 0.4243 |
| 12 | 0.99848065 | 1.0949 | 0.887 | 0.9941 | 0.9941 | TRUE | 0.4982 |
| 13 | 0.99848065 | 1.0949 | 0.887 | 0.9941 | 0.9941 | TRUE | 0.4982 |
| 14 | 0.99848065 | 1.0949 | 0.887 | 0.9941 | 0.9941 | TRUE | 0.4982 |
| 15 | 0.99848065 | 0.2376 | 0.9224 | 0.5483 | 0.5483 | TRUE | 0.4362 |
| 16 | 0.99848065 | 0.2376 | 0.9224 | 0.5483 | 0.5483 | TRUE | 0.4362 |
| 17 | 0.99848065 | 0.2376 | 0.9224 | 0.5483 | 0.5483 | TRUE | 0.4362 |
| 18 | 0.99848065 | 0.2233 | 0.9182 | 0.538 | 0.538 | TRUE | 0.3609 |
| 19 | 0.99848065 | 0.6111 | 0.8913 | 0.7432 | 0.7432 | TRUE | 0.3525 |
| 20 | 0.99848065 | 0.6111 | 0.8913 | 0.7432 | 0.7432 | TRUE | 0.3525 |
| 21 | 0.99848065 | 0.5965 | 0.8912 | 0.7353 | 0.7353 | TRUE | 0.342 |
| 22 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 23 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 24 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 25 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 26 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 27 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 28 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 29 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 30 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 31 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 32 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 33 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 34 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 35 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 36 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 37 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 38 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 39 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 40 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 41 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 42 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 43 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 44 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 45 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 46 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 47 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 48 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 49 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 50 | 0.99848065 | 0.2507 | 0.9227 | 0.5561 | 0.5561 | TRUE | 0.4734 |
| 51 | 0.99848065 | 0.0977 | 0.9029 | 0.4535 | 0.4535 | TRUE | 0.6743 |
| 52 | 0.99848065 | 0.0977 | 0.9029 | 0.4535 | 0.4535 | TRUE | 0.6743 |
| 53 | 0.99848065 | 0.3342 | 0.9005 | 0.5947 | 0.5947 | TRUE | 0.5843 |
| 54 | 0.99848065 | 0.3342 | 0.9005 | 0.5947 | 0.5947 | TRUE | 0.5843 |
| 55 | 0.99848065 | 0.3342 | 0.9005 | 0.5947 | 0.5947 | TRUE | 0.5843 |
| 56 | 0.99848065 | 0.3342 | 0.9005 | 0.5947 | 0.5947 | TRUE | 0.5843 |
| 57 | 0.99848065 | 0.3342 | 0.9005 | 0.5947 | 0.5947 | TRUE | 0.5843 |
| 58 | 0.99848065 | 0.3342 | 0.9005 | 0.5947 | 0.5947 | TRUE | 0.5843 |
| 59 | 0.99848065 | 0.3342 | 0.9005 | 0.5947 | 0.5947 | TRUE | 0.5843 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.7116 | 1.0112 | 0.8528 | 0.8528 | TRUE | 0.6114 |
| 4 | 0.99848065 | 0.7116 | 1.0112 | 0.8528 | 0.8528 | TRUE | 0.6114 |
| 5 | 0.99848065 | 0.7116 | 1.0112 | 0.8528 | 0.8528 | TRUE | 0.6114 |
| 6 | 0.99848065 | 0.7116 | 1.0112 | 0.8528 | 0.8528 | TRUE | 0.6114 |
| 7 | 0.99848065 | 0.7116 | 1.0112 | 0.8528 | 0.8528 | TRUE | 0.6114 |
| 8 | 0.99848065 | 0.7116 | 1.0112 | 0.8528 | 0.8528 | TRUE | 0.6114 |
| 9 | 0.99848065 | 0.7116 | 1.0112 | 0.8528 | 0.8528 | TRUE | 0.6114 |
| 10 | 0.99848065 | 0.7116 | 1.0112 | 0.8528 | 0.8528 | TRUE | 0.6114 |
| 11 | 0.99848065 | 0.7116 | 1.0112 | 0.8528 | 0.8528 | TRUE | 0.6114 |
| 12 | 0.99848065 | 0.7116 | 1.0112 | 0.8528 | 0.8528 | TRUE | 0.6114 |
| 13 | 0.99848065 | 0.7116 | 1.0112 | 0.8528 | 0.8528 | TRUE | 0.6114 |
| 14 | 0.99848065 | 0.7116 | 1.0112 | 0.8528 | 0.8528 | TRUE | 0.6114 |
| 15 | 0.99848065 | 0.7116 | 1.0112 | 0.8528 | 0.8528 | TRUE | 0.6114 |
| 16 | 0.99848065 | 0.7116 | 1.0112 | 0.8528 | 0.8528 | TRUE | 0.6114 |
| 17 | 0.99848065 | 0.7116 | 1.0112 | 0.8528 | 0.8528 | TRUE | 0.6114 |
| 18 | 0.99848065 | 0.197 | 1.0126 | 0.567 | 0.567 | TRUE | 2.0055 |
| 19 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 20 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 21 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 22 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 23 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 24 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 25 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 26 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 27 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 28 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 29 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 30 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 31 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 32 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 33 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 34 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 35 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 36 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 37 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 38 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 39 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 40 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 41 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 42 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 43 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 44 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 45 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 46 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 47 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 48 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 49 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 50 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 51 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 52 | 0.99848065 | 0.0227 | 0.8879 | 0.3951 | 0.3951 | TRUE | 0.3956 |
| 53 | 0.99848065 | 0.0232 | 0.8879 | 0.3955 | 0.3955 | TRUE | 0.4118 |
| 54 | 0.99848065 | 0.0232 | 0.8879 | 0.3955 | 0.3955 | TRUE | 0.4118 |
| 55 | 0.99848065 | 0.0241 | 0.8879 | 0.396 | 0.396 | TRUE | 0.3012 |
| 56 | 0.99848065 | 0.0241 | 0.8879 | 0.396 | 0.396 | TRUE | 0.3012 |
| 57 | 0.99848065 | 0.0241 | 0.8879 | 0.396 | 0.396 | TRUE | 0.3012 |
| 58 | 0.99848065 | 0.0241 | 0.8879 | 0.396 | 0.396 | TRUE | 0.3012 |
| 59 | 0.99848065 | 0.0241 | 0.8879 | 0.396 | 0.396 | TRUE | 0.3012 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.0241 | 0.8879 | 0.396 | 0.396 | TRUE | 0.3012 |
| 4 | 0.99848065 | 0.6705 | 1.1445 | 0.8923 | 0.8923 | TRUE | 1.1361 |
| 5 | 0.99848065 | 0.6705 | 1.1445 | 0.8923 | 0.8923 | TRUE | 1.1361 |
| 6 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 7 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 8 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 9 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 10 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 11 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 12 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 13 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 14 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 15 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 16 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 17 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 18 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 19 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 20 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 21 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 22 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 23 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 24 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 25 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 26 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 27 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 28 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 29 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 30 | NA | 10 | 1.0521 | 3.9213 | 10 | TRUE | 34.5483 |
| 31 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 32 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 33 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 34 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 35 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 36 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 37 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 38 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 39 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 40 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 41 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 42 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 43 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 44 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 45 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 46 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 47 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 48 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 49 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 50 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 51 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 52 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 53 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 54 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 55 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 56 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 57 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 58 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 59 | 0.99848065 | 0.5447 | 0.8889 | 0.6992 | 0.6992 | TRUE | 9.2955 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.042 | 0.8874 | 0.4079 | 0.4079 | TRUE | 0.4585 |
| 4 | 0.99848065 | 0.042 | 0.8874 | 0.4079 | 0.4079 | TRUE | 0.4585 |
| 5 | 0.99848065 | 0.042 | 0.8874 | 0.4079 | 0.4079 | TRUE | 0.4585 |
| 6 | 0.99848065 | 0.042 | 0.8874 | 0.4079 | 0.4079 | TRUE | 0.4585 |
| 7 | 0.99848065 | 0.042 | 0.8874 | 0.4079 | 0.4079 | TRUE | 0.4585 |
| 8 | 0.99848065 | 0.042 | 0.8874 | 0.4079 | 0.4079 | TRUE | 0.4585 |
| 9 | 0.99848065 | 0.042 | 0.8874 | 0.4079 | 0.4079 | TRUE | 0.4585 |
| 10 | 0.99848065 | 0.042 | 0.8874 | 0.4079 | 0.4079 | TRUE | 0.4585 |
| 11 | 0.99848065 | 0.042 | 0.8874 | 0.4079 | 0.4079 | TRUE | 0.4585 |
| 12 | 0.99848065 | 0.042 | 0.8874 | 0.4079 | 0.4079 | TRUE | 0.4585 |
| 13 | 0.99848065 | 0.042 | 0.8874 | 0.4079 | 0.4079 | TRUE | 0.4585 |
| 14 | 0.99848065 | 0.042 | 0.8874 | 0.4079 | 0.4079 | TRUE | 0.4585 |
| 15 | 0.99848065 | 0.042 | 0.8874 | 0.4079 | 0.4079 | TRUE | 0.4585 |
| 16 | 0.99848065 | 0.042 | 0.8874 | 0.4079 | 0.4079 | TRUE | 0.4585 |
| 17 | 0.99848065 | 0.042 | 0.8874 | 0.4079 | 0.4079 | TRUE | 0.4585 |
| 18 | 0.99848065 | 0.7749 | 0.8894 | 0.8294 | 0.8294 | TRUE | 0.4725 |
| 19 | 0.99848065 | 0.7749 | 0.8894 | 0.8294 | 0.8294 | TRUE | 0.4725 |
| 20 | 0.99848065 | 0.7749 | 0.8894 | 0.8294 | 0.8294 | TRUE | 0.4725 |
| 21 | 0.99848065 | 0.7749 | 0.8894 | 0.8294 | 0.8294 | TRUE | 0.4725 |
| 22 | 0.99848065 | 0.7749 | 0.8894 | 0.8294 | 0.8294 | TRUE | 0.4725 |
| 23 | 0.99848065 | 0.7749 | 0.8894 | 0.8294 | 0.8294 | TRUE | 0.4725 |
| 24 | 0.99848065 | 0.1947 | 1.0196 | 0.5692 | 0.5692 | TRUE | 2.0003 |
| 25 | 0.99848065 | 0.1947 | 1.0196 | 0.5692 | 0.5692 | TRUE | 2.0003 |
| 26 | 0.99848065 | 0.1947 | 1.0196 | 0.5692 | 0.5692 | TRUE | 2.0003 |
| 27 | 0.99848065 | 0.0874 | 0.8985 | 0.4443 | 0.4443 | TRUE | 0.5052 |
| 28 | 0.99848065 | 0.2408 | 1.0892 | 0.6336 | 0.6336 | TRUE | 0.2183 |
| 29 | 0.99848065 | 0.2408 | 1.0892 | 0.6336 | 0.6336 | TRUE | 0.2183 |
| 30 | 0.99848065 | 0.2408 | 1.0892 | 0.6336 | 0.6336 | TRUE | 0.2183 |
| 31 | 0.99848065 | 0.2408 | 1.0892 | 0.6336 | 0.6336 | TRUE | 0.2183 |
| 32 | 0.99848065 | 0.2408 | 1.0892 | 0.6336 | 0.6336 | TRUE | 0.2183 |
| 33 | 0.99848065 | 0.2408 | 1.0892 | 0.6336 | 0.6336 | TRUE | 0.2183 |
| 34 | 0.99848065 | 0.2408 | 1.0892 | 0.6336 | 0.6336 | TRUE | 0.2183 |
| 35 | 0.99848065 | 0.2408 | 1.0892 | 0.6336 | 0.6336 | TRUE | 0.2183 |
| 36 | 0.99848065 | 0.6833 | 0.8869 | 0.7798 | 0.7798 | TRUE | 0.3573 |
| 37 | 0.99848065 | 0.6833 | 0.8869 | 0.7798 | 0.7798 | TRUE | 0.3574 |
| 38 | 0.99848065 | 0.6833 | 0.8869 | 0.7798 | 0.7798 | TRUE | 0.3574 |
| 39 | 0.99848065 | 0.6833 | 0.8869 | 0.7798 | 0.7798 | TRUE | 0.3574 |
| 40 | 0.99848065 | 0.6833 | 0.8869 | 0.7798 | 0.7798 | TRUE | 0.3574 |
| 41 | 0.99848065 | 0.6833 | 0.8869 | 0.7798 | 0.7798 | TRUE | 0.3574 |
| 42 | 0.99848065 | 0.6833 | 0.8869 | 0.7798 | 0.7798 | TRUE | 0.3574 |
| 43 | 0.99848065 | 0.6833 | 0.8869 | 0.7798 | 0.7798 | TRUE | 0.3574 |
| 44 | 0.99848065 | 0.6833 | 0.8869 | 0.7798 | 0.7798 | TRUE | 0.3574 |
| 45 | 0.99848065 | 0.6833 | 0.8869 | 0.7798 | 0.7798 | TRUE | 0.3574 |
| 46 | 0.99848065 | 0.6833 | 0.8869 | 0.7798 | 0.7798 | TRUE | 0.3574 |
| 47 | 0.99848065 | 0.6875 | 0.8869 | 0.7821 | 0.7821 | TRUE | 0.3605 |
| 48 | 0.99848065 | 0.6875 | 0.8869 | 0.7821 | 0.7821 | TRUE | 0.3605 |
| 49 | 0.99848065 | 0.6875 | 0.8869 | 0.7821 | 0.7821 | TRUE | 0.3605 |
| 50 | 0.99848065 | 0.6875 | 0.8869 | 0.7821 | 0.7821 | TRUE | 0.3605 |
| 51 | 0.99848065 | 0.6875 | 0.8869 | 0.7821 | 0.7821 | TRUE | 0.3605 |
| 52 | 0.99848065 | 0.6875 | 0.8869 | 0.7821 | 0.7821 | TRUE | 0.3605 |
| 53 | 0.99848065 | 0.6875 | 0.8869 | 0.7821 | 0.7821 | TRUE | 0.3605 |
| 54 | 0.99848065 | 0.6875 | 0.8869 | 0.7821 | 0.7821 | TRUE | 0.3605 |
| 55 | 0.99848065 | 0.6875 | 0.8869 | 0.7821 | 0.7821 | TRUE | 0.3605 |
| 56 | 0.99848065 | 0.6875 | 0.8869 | 0.7821 | 0.7821 | TRUE | 0.3605 |
| 57 | 0.99848065 | 0.6875 | 0.8869 | 0.7821 | 0.7821 | TRUE | 0.3605 |
| 58 | 0.99848065 | 0.6875 | 0.8869 | 0.7821 | 0.7821 | TRUE | 0.3605 |
| 59 | 0.99848065 | 0.6875 | 0.8869 | 0.7821 | 0.7821 | TRUE | 0.3605 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.6887 | 0.8869 | 0.7827 | 0.7827 | TRUE | 0.3611 |
| 4 | 0.99848065 | 0.6887 | 0.8869 | 0.7827 | 0.7827 | TRUE | 0.3611 |
| 5 | 0.99848065 | 0.6887 | 0.8869 | 0.7827 | 0.7827 | TRUE | 0.3611 |
| 6 | 0.99848065 | 0.6887 | 0.8869 | 0.7827 | 0.7827 | TRUE | 0.3611 |
| 7 | 0.99848065 | 0.6887 | 0.8869 | 0.7827 | 0.7827 | TRUE | 0.3611 |
| 8 | 0.99848065 | 0.6887 | 0.8869 | 0.7827 | 0.7827 | TRUE | 0.3611 |
| 9 | 0.99848065 | 0.6887 | 0.8869 | 0.7827 | 0.7827 | TRUE | 0.3611 |
| 10 | 0.99848065 | 0.2234 | 0.8863 | 0.5249 | 0.5249 | TRUE | 0.7719 |
| 11 | 0.99848065 | 0.2234 | 0.8863 | 0.5249 | 0.5249 | TRUE | 0.7719 |
| 12 | 0.99848065 | 0.2234 | 0.8863 | 0.5249 | 0.5249 | TRUE | 0.7719 |
| 13 | 0.99848065 | 0.2234 | 0.8863 | 0.5249 | 0.5249 | TRUE | 0.7719 |
| 14 | 0.99848065 | 0.0828 | 0.8971 | 0.4406 | 0.4406 | TRUE | 0.283 |
| 15 | 0.99848065 | 0.1528 | 0.9555 | 0.5129 | 0.5129 | TRUE | 0.4177 |
| 16 | 0.99848065 | 0.1528 | 0.9555 | 0.5129 | 0.5129 | TRUE | 0.4177 |
| 17 | 0.99848065 | 0.1528 | 0.9555 | 0.5129 | 0.5129 | TRUE | 0.4177 |
| 18 | 0.99848065 | 0.1528 | 0.9555 | 0.5129 | 0.5129 | TRUE | 0.4177 |
| 19 | 0.99848065 | 0.1528 | 0.9555 | 0.5129 | 0.5129 | TRUE | 0.4177 |
| 20 | 0.99848065 | 0.1528 | 0.9555 | 0.5129 | 0.5129 | TRUE | 0.4177 |
| 21 | 0.99848065 | 0.1528 | 0.9555 | 0.5129 | 0.5129 | TRUE | 0.4177 |
| 22 | 0.99848065 | 0.1528 | 0.9555 | 0.5129 | 0.5129 | TRUE | 0.4177 |
| 23 | 0.99848065 | 0.8752 | 0.8893 | 0.8814 | 0.8814 | TRUE | 0.5692 |
| 24 | 0.99848065 | 0.8752 | 0.8893 | 0.8814 | 0.8814 | TRUE | 0.5692 |
| 25 | 0.99848065 | 0.8752 | 0.8893 | 0.8814 | 0.8814 | TRUE | 0.5692 |
| 26 | 0.99848065 | 0.8752 | 0.8893 | 0.8814 | 0.8814 | TRUE | 0.5692 |
| 27 | 0.99848065 | 0.8752 | 0.8893 | 0.8814 | 0.8814 | TRUE | 0.5692 |
| 28 | 0.99848065 | 0.1463 | 0.9546 | 0.5085 | 0.5085 | TRUE | 0.3534 |
| 29 | 0.99848065 | 0.1463 | 0.9546 | 0.5085 | 0.5085 | TRUE | 0.3534 |
| 30 | 0.99848065 | 0.1463 | 0.9546 | 0.5085 | 0.5085 | TRUE | 0.3534 |
| 31 | 0.99848065 | 0.1463 | 0.9546 | 0.5085 | 0.5085 | TRUE | 0.3534 |
| 32 | 0.99848065 | 0.1463 | 0.9546 | 0.5085 | 0.5085 | TRUE | 0.3534 |
| 33 | 0.99848065 | 0.1463 | 0.9546 | 0.5085 | 0.5085 | TRUE | 0.3534 |
| 34 | 0.99848065 | 0.1463 | 0.9546 | 0.5085 | 0.5085 | TRUE | 0.3534 |
| 35 | 0.99848065 | 0.1463 | 0.9546 | 0.5085 | 0.5085 | TRUE | 0.3534 |
| 36 | 0.99848065 | 0.1463 | 0.9546 | 0.5085 | 0.5085 | TRUE | 0.3534 |
| 37 | 0.99848065 | 0.1463 | 0.9546 | 0.5085 | 0.5085 | TRUE | 0.3534 |
| 38 | 0.99848065 | 0.1463 | 0.9546 | 0.5085 | 0.5085 | TRUE | 0.3534 |
| 39 | 0.99848065 | 0.1463 | 0.9546 | 0.5085 | 0.5085 | TRUE | 0.3534 |
| 40 | 0.99848065 | 0.1776 | 0.8886 | 0.5085 | 0.5085 | TRUE | 0.1556 |
| 41 | 0.99848065 | 0.1776 | 0.8886 | 0.5085 | 0.5085 | TRUE | 0.1556 |
| 42 | 0.99848065 | 0.1776 | 0.8886 | 0.5085 | 0.5085 | TRUE | 0.1556 |
| 43 | 0.99848065 | 0.0109 | 0.9976 | 0.4432 | 0.4432 | TRUE | 0.2926 |
| 44 | 0.99848065 | 0.3774 | 0.9676 | 0.6502 | 0.6502 | TRUE | 9.0847 |
| 45 | 0.99848065 | 0.3655 | 0.8873 | 0.6313 | 0.6313 | TRUE | 0.6019 |
| 46 | 0.99848065 | 0.3655 | 0.8873 | 0.6313 | 0.6313 | TRUE | 0.6019 |
| 47 | 0.99848065 | 0.3655 | 0.8873 | 0.6313 | 0.6313 | TRUE | 0.6019 |
| 48 | 0.99848065 | 0.1133 | 0.8872 | 0.4602 | 0.4602 | TRUE | 0.2339 |
| 49 | 0.99848065 | 0.1133 | 0.8872 | 0.4602 | 0.4602 | TRUE | 0.2339 |
| 50 | 0.99848065 | 0.1133 | 0.8872 | 0.4602 | 0.4602 | TRUE | 0.2339 |
| 51 | 0.99848065 | 0.1133 | 0.8872 | 0.4602 | 0.4602 | TRUE | 0.2339 |
| 52 | 0.99848065 | 0.1133 | 0.8872 | 0.4602 | 0.4602 | TRUE | 0.2339 |
| 53 | 0.99848065 | 0.1133 | 0.8872 | 0.4602 | 0.4602 | TRUE | 0.2339 |
| 54 | 0.99848065 | 0.1133 | 0.8872 | 0.4602 | 0.4602 | TRUE | 0.2339 |
| 55 | 0.99848065 | 0.1133 | 0.8872 | 0.4602 | 0.4602 | TRUE | 0.2339 |
| 56 | 0.99848065 | 0.1133 | 0.8872 | 0.4602 | 0.4602 | TRUE | 0.2339 |
| 57 | 0.99848065 | 0.1133 | 0.8872 | 0.4602 | 0.4602 | TRUE | 0.2339 |
| 58 | 0.99848065 | 0.1133 | 0.8872 | 0.4602 | 0.4602 | TRUE | 0.2339 |
| 59 | 0.99848065 | 0.1133 | 0.8872 | 0.4602 | 0.4602 | TRUE | 0.2339 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.1729 | 0.8873 | 0.5077 | 0.5077 | TRUE | 0.2551 |
| 4 | 0.99848065 | 0.1729 | 0.8873 | 0.5077 | 0.5077 | TRUE | 0.2551 |
| 5 | 0.99848065 | 0.1729 | 0.8873 | 0.5077 | 0.5077 | TRUE | 0.2551 |
| 6 | 0.99848065 | 0.1728 | 0.8873 | 0.5075 | 0.5075 | TRUE | 0.2563 |
| 7 | 0.99848065 | 0.1728 | 0.8873 | 0.5075 | 0.5075 | TRUE | 0.2563 |
| 8 | 0.99848065 | 0.0627 | 0.8872 | 0.4222 | 0.4222 | TRUE | 0.8517 |
| 9 | 0.99848065 | 0.0627 | 0.8872 | 0.4222 | 0.4222 | TRUE | 0.8517 |
| 10 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 11 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 12 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 13 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 14 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 15 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 16 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 17 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 18 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 19 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 20 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 21 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 22 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 23 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 24 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 25 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 26 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 27 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 28 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 29 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 30 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 31 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 32 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 33 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 34 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 35 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 36 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 37 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 38 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 39 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 40 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 41 | 0.99848065 | 0.8088 | 1.099 | 0.9466 | 0.9466 | TRUE | 14.8254 |
| 42 | 0.99848065 | 0.4707 | 0.97 | 0.7029 | 0.7029 | TRUE | 0.8753 |
| 43 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 44 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 45 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 46 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 47 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 48 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 49 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 50 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 51 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 52 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 53 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 54 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 55 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 56 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 57 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 58 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 59 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 4 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 5 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 6 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 7 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 8 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 9 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 10 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 11 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 12 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 13 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 14 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 15 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 16 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 17 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 18 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 19 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 20 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 21 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 22 | 0.99848065 | 1.1702 | 1.0535 | 1.1139 | 1.1139 | TRUE | 3.1657 |
| 23 | 0.99848065 | 0.2943 | 0.9273 | 0.5838 | 0.5838 | TRUE | 0.8903 |
| 24 | 0.99848065 | 0.2943 | 0.9273 | 0.5838 | 0.5838 | TRUE | 0.8903 |
| 25 | 0.99848065 | 0.3127 | 0.9293 | 0.5955 | 0.5955 | TRUE | 1.2671 |
| 26 | 0.99848065 | 0.3127 | 0.9293 | 0.5955 | 0.5955 | TRUE | 1.2671 |
| 27 | 0.99848065 | 0.3127 | 0.9293 | 0.5955 | 0.5955 | TRUE | 1.2671 |
| 28 | 0.99848065 | 0.3127 | 0.9293 | 0.5955 | 0.5955 | TRUE | 1.2671 |
| 29 | 0.99848065 | 0.3127 | 0.9293 | 0.5955 | 0.5955 | TRUE | 1.2671 |
| 30 | 0.99848065 | 0.3127 | 0.9293 | 0.5955 | 0.5955 | TRUE | 1.2671 |
| 31 | 0.99848065 | 0.3127 | 0.9293 | 0.5955 | 0.5955 | TRUE | 1.2671 |
| 32 | 0.99848065 | 0.3127 | 0.9293 | 0.5955 | 0.5955 | TRUE | 1.2671 |
| 33 | 0.99848065 | 0.3127 | 0.9293 | 0.5955 | 0.5955 | TRUE | 1.2671 |
| 34 | 0.99848065 | 0.3127 | 0.9293 | 0.5955 | 0.5955 | TRUE | 1.2671 |
| 35 | 0.99848065 | 0.3127 | 0.9293 | 0.5955 | 0.5955 | TRUE | 1.2671 |
| 36 | 0.99848065 | 0.3127 | 0.9293 | 0.5955 | 0.5955 | TRUE | 1.2671 |
| 37 | 0.99848065 | 0.3127 | 0.9293 | 0.5955 | 0.5955 | TRUE | 1.2671 |
| 38 | 0.99848065 | 0.3127 | 0.9293 | 0.5955 | 0.5955 | TRUE | 1.2671 |
| 39 | 0.99848065 | 0.6933 | 0.9391 | 0.8195 | 0.8195 | TRUE | 1.0902 |
| 40 | 0.99848065 | 0.1532 | 0.9268 | 0.4997 | 0.4997 | TRUE | 0.4204 |
| 41 | 0.99848065 | 0.1532 | 0.9268 | 0.4997 | 0.4997 | TRUE | 0.4204 |
| 42 | 0.99848065 | 0.1532 | 0.9268 | 0.4997 | 0.4997 | TRUE | 0.4204 |
| 43 | 0.99848065 | 0.1532 | 0.9268 | 0.4997 | 0.4997 | TRUE | 0.4204 |
| 44 | 0.99848065 | 0.1532 | 0.9268 | 0.4997 | 0.4997 | TRUE | 0.4204 |
| 45 | 0.99848065 | 0.1532 | 0.9268 | 0.4997 | 0.4997 | TRUE | 0.4204 |
| 46 | 0.99848065 | 0.1532 | 0.9268 | 0.4997 | 0.4997 | TRUE | 0.4204 |
| 47 | 0.99848065 | 0.1532 | 0.9268 | 0.4997 | 0.4997 | TRUE | 0.4204 |
| 48 | 0.99848065 | 0.1532 | 0.9268 | 0.4997 | 0.4997 | TRUE | 0.4204 |
| 49 | 0.99848065 | 0.1532 | 0.9268 | 0.4997 | 0.4997 | TRUE | 0.4204 |
| 50 | 0.99848065 | 0.1532 | 0.9268 | 0.4997 | 0.4997 | TRUE | 0.4204 |
| 51 | 0.99848065 | 0.1532 | 0.9268 | 0.4997 | 0.4997 | TRUE | 0.4204 |
| 52 | 0.99848065 | 0.1532 | 0.9268 | 0.4997 | 0.4997 | TRUE | 0.4204 |
| 53 | 0.99848065 | 0.1532 | 0.9268 | 0.4997 | 0.4997 | TRUE | 0.4204 |
| 54 | 0.99848065 | 0.1532 | 0.9268 | 0.4997 | 0.4997 | TRUE | 0.4204 |
| 55 | 0.99848065 | 0.2203 | 0.8964 | 0.5261 | 0.5261 | TRUE | 1.181 |
| 56 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 57 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 58 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 59 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 4 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 5 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 6 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 7 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 8 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 9 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 10 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 11 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 12 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 13 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 14 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 15 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 16 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 17 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 18 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 19 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 20 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 21 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 22 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 23 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 24 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 25 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 26 | 0.99848065 | 0.7046 | 0.9404 | 0.8173 | 0.8173 | TRUE | 1.214 |
| 27 | 0.99848065 | 0.2909 | 0.8953 | 0.5586 | 0.5586 | TRUE | 5.1055 |
| 28 | 0.99848065 | 0.2972 | 0.8949 | 0.5636 | 0.5636 | TRUE | 5.1739 |
| 29 | 0.99848065 | 0.2972 | 0.8949 | 0.5636 | 0.5636 | TRUE | 5.1739 |
| 30 | 0.99848065 | 0.2972 | 0.8949 | 0.5636 | 0.5636 | TRUE | 5.1739 |
| 31 | 0.99848065 | 0.2972 | 0.8949 | 0.5636 | 0.5636 | TRUE | 5.1739 |
| 32 | 0.99848065 | 0.2972 | 0.8949 | 0.5636 | 0.5636 | TRUE | 5.1739 |
| 33 | 0.99848065 | 0.2972 | 0.8949 | 0.5636 | 0.5636 | TRUE | 5.1739 |
| 34 | 0.99848065 | 0.2972 | 0.8949 | 0.5636 | 0.5636 | TRUE | 5.1739 |
| 35 | 0.99848065 | 0.2972 | 0.8949 | 0.5636 | 0.5636 | TRUE | 5.1739 |
| 36 | 0.99848065 | 0.2972 | 0.8949 | 0.5636 | 0.5636 | TRUE | 5.1739 |
| 37 | 0.99848065 | 0.2972 | 0.8949 | 0.5636 | 0.5636 | TRUE | 5.1739 |
| 38 | 0.99848065 | 0.1526 | 0.9265 | 0.4991 | 0.4991 | TRUE | 0.4218 |
| 39 | 0.99848065 | 0.1526 | 0.9265 | 0.4991 | 0.4991 | TRUE | 0.4218 |
| 40 | 0.99848065 | 0.1526 | 0.9265 | 0.4991 | 0.4991 | TRUE | 0.4218 |
| 41 | 0.99848065 | 0.1526 | 0.9265 | 0.4991 | 0.4991 | TRUE | 0.4218 |
| 42 | 0.99848065 | 0.1526 | 0.9265 | 0.4991 | 0.4991 | TRUE | 0.4218 |
| 43 | 0.99848065 | 0.0446 | 0.8866 | 0.4118 | 0.4118 | TRUE | 0.7664 |
| 44 | 0.99848065 | 0.0446 | 0.8866 | 0.4118 | 0.4118 | TRUE | 0.7664 |
| 45 | 0.99848065 | 0.0446 | 0.8866 | 0.4118 | 0.4118 | TRUE | 0.7664 |
| 46 | 0.99848065 | 0.0446 | 0.8866 | 0.4118 | 0.4118 | TRUE | 0.7664 |
| 47 | 0.99848065 | 0.0446 | 0.8866 | 0.4118 | 0.4118 | TRUE | 0.7664 |
| 48 | 0.99848065 | 0.0446 | 0.8866 | 0.4118 | 0.4118 | TRUE | 0.7664 |
| 49 | 0.99848065 | 0.0446 | 0.8866 | 0.4118 | 0.4118 | TRUE | 0.7664 |
| 50 | 0.99848065 | 0.0446 | 0.8866 | 0.4118 | 0.4118 | TRUE | 0.7664 |
| 51 | 0.99848065 | 0.0446 | 0.8866 | 0.4118 | 0.4118 | TRUE | 0.7664 |
| 52 | 0.99848065 | 0.0446 | 0.8866 | 0.4118 | 0.4118 | TRUE | 0.7664 |
| 53 | 0.99848065 | 0.0446 | 0.8866 | 0.4118 | 0.4118 | TRUE | 0.7664 |
| 54 | 0.99848065 | 0.0446 | 0.8866 | 0.4118 | 0.4118 | TRUE | 0.7664 |
| 55 | 0.99848065 | 1.1796 | 1.0502 | 1.1171 | 1.1171 | TRUE | 6.9224 |
| 56 | 0.99848065 | 0.5311 | 1.046 | 0.771 | 0.771 | TRUE | 0.4632 |
| 57 | 0.99848065 | 0.276 | 0.8874 | 0.593 | 0.593 | TRUE | 0.2606 |
| 58 | 0.99848065 | 0.276 | 0.8874 | 0.593 | 0.593 | TRUE | 0.2606 |
| 59 | 0.99848065 | 0.276 | 0.8874 | 0.593 | 0.593 | TRUE | 0.2606 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.276 | 0.8874 | 0.593 | 0.593 | TRUE | 0.2606 |
| 4 | 0.99848065 | 0.276 | 0.8874 | 0.593 | 0.593 | TRUE | 0.2606 |
| 5 | 0.99848065 | 0.276 | 0.8874 | 0.593 | 0.593 | TRUE | 0.2606 |
| 6 | 0.99848065 | 0.276 | 0.8874 | 0.593 | 0.593 | TRUE | 0.2606 |
| 7 | 0.99848065 | 0.276 | 0.8874 | 0.593 | 0.593 | TRUE | 0.2606 |
| 8 | 0.99848065 | 0.276 | 0.8874 | 0.593 | 0.593 | TRUE | 0.2606 |
| 9 | 0.99848065 | 0.276 | 0.8874 | 0.593 | 0.593 | TRUE | 0.2606 |
| 10 | 0.99848065 | 0.276 | 0.8874 | 0.593 | 0.593 | TRUE | 0.2606 |
| 11 | 0.99848065 | 0.276 | 0.8874 | 0.593 | 0.593 | TRUE | 0.2606 |
| 12 | 0.99848065 | 0.276 | 0.8874 | 0.593 | 0.593 | TRUE | 0.2606 |
| 13 | 0.99848065 | 0.276 | 0.8874 | 0.593 | 0.593 | TRUE | 0.2606 |
| 14 | 0.99848065 | 0.276 | 0.8874 | 0.593 | 0.593 | TRUE | 0.2606 |
| 15 | 0.99848065 | 0.4067 | 0.8895 | 0.6039 | 0.6039 | TRUE | 3.4941 |
| 16 | 0.99848065 | 0.4067 | 0.8895 | 0.6039 | 0.6039 | TRUE | 3.4941 |
| 17 | 0.99848065 | 0.1377 | 0.8936 | 0.4743 | 0.4743 | TRUE | 2.3521 |
| 18 | 0.99848065 | 0.5386 | 0.9153 | 0.7151 | 0.7151 | TRUE | 0.7391 |
| 19 | 0.99848065 | 0.1594 | 1.0261 | 0.5525 | 0.5525 | TRUE | 0.1968 |
| 20 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 21 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 22 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 23 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 24 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 25 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 26 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 27 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 28 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 29 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 30 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 31 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 32 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 33 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 34 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 35 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 36 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 37 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 38 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 39 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 40 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 41 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 42 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 43 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 44 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 45 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 46 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 47 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 48 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 49 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 50 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 51 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 52 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 53 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 54 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 55 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 56 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 57 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 58 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 59 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 4 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 5 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 6 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 7 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 8 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 9 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 10 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 11 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 12 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 13 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 14 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 15 | 0.99848065 | 0.3443 | 1.082 | 0.6828 | 0.6828 | TRUE | 1.7848 |
| 16 | 0.99848065 | 0.2604 | 0.9509 | 0.5746 | 0.5746 | TRUE | 0.6009 |
| 17 | 0.99848065 | 0.263 | 0.951 | 0.5761 | 0.5761 | TRUE | 0.6047 |
| 18 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 19 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 20 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 21 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 22 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 23 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 24 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 25 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 26 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 27 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 28 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 29 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 30 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 31 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 32 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 33 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 34 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 35 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 36 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 37 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 38 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 39 | 0.99848065 | 0.2634 | 0.9513 | 0.5765 | 0.5765 | TRUE | 0.6187 |
| 40 | 0.99848065 | 0.346 | 1.0803 | 0.683 | 0.683 | TRUE | 1.847 |
| 41 | 0.99848065 | 0.346 | 1.0803 | 0.683 | 0.683 | TRUE | 1.847 |
| 42 | 0.99848065 | 0.5005 | 0.8875 | 0.6815 | 0.6815 | TRUE | 0.1437 |
| 43 | 0.99848065 | 0.4993 | 0.8875 | 0.6808 | 0.6808 | TRUE | 0.1442 |
| 44 | 0.99848065 | 0.4993 | 0.8875 | 0.6808 | 0.6808 | TRUE | 0.1442 |
| 45 | 0.99848065 | 0.4993 | 0.8875 | 0.6808 | 0.6808 | TRUE | 0.1442 |
| 46 | 0.99848065 | 0.4993 | 0.8875 | 0.6808 | 0.6808 | TRUE | 0.1442 |
| 47 | 0.99848065 | 0.4993 | 0.8875 | 0.6808 | 0.6808 | TRUE | 0.1442 |
| 48 | 0.99848065 | 0.4993 | 0.8875 | 0.6808 | 0.6808 | TRUE | 0.1442 |
| 49 | 0.99848065 | 0.4993 | 0.8875 | 0.6808 | 0.6808 | TRUE | 0.1442 |
| 50 | 0.99848065 | 0.4993 | 0.8875 | 0.6808 | 0.6808 | TRUE | 0.1442 |
| 51 | 0.99848065 | 0.4993 | 0.8875 | 0.6808 | 0.6808 | TRUE | 0.1442 |
| 52 | 0.99848065 | 0.4993 | 0.8875 | 0.6808 | 0.6808 | TRUE | 0.1442 |
| 53 | 0.99848065 | 0.0346 | 0.926 | 0.4234 | 0.4234 | TRUE | 0.4668 |
| 54 | 0.99848065 | 0.0346 | 0.926 | 0.4234 | 0.4234 | TRUE | 0.4668 |
| 55 | 0.99848065 | 0.0346 | 0.926 | 0.4234 | 0.4234 | TRUE | 0.4668 |
| 56 | 0.99848065 | 0.0346 | 0.926 | 0.4234 | 0.4234 | TRUE | 0.4668 |
| 57 | 0.99848065 | 0.0346 | 0.926 | 0.4234 | 0.4234 | TRUE | 0.4668 |
| 58 | 0.99848065 | 0.0346 | 0.926 | 0.4234 | 0.4234 | TRUE | 0.4668 |
| 59 | 0.99848065 | 0.0346 | 0.926 | 0.4234 | 0.4234 | TRUE | 0.4668 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.2421 | 0.9155 | 0.5477 | 0.5477 | TRUE | 0.3769 |
| 4 | 0.99848065 | 0.2431 | 1.0848 | 0.6267 | 0.6267 | TRUE | 0.2227 |
| 5 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 6 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 7 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 8 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 9 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 10 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 11 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 12 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 13 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 14 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 15 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 16 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 17 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 18 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 19 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 20 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 21 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 22 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 23 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 24 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 25 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 26 | 0.99848065 | 1.1971 | 0.8875 | 1.0466 | 1.0466 | TRUE | 0.4986 |
| 27 | 0.99848065 | 0.1383 | 1.0131 | 0.5302 | 0.5302 | TRUE | 2.9615 |
| 28 | 0.99848065 | 0.1809 | 0.8871 | 0.5069 | 0.5069 | TRUE | 0.7899 |
| 29 | 0.99848065 | 0.1809 | 0.8871 | 0.5069 | 0.5069 | TRUE | 0.7899 |
| 30 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 31 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 32 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 33 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 34 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 35 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 36 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 37 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 38 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 39 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 40 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 41 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 42 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 43 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 44 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 45 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 46 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 47 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 48 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 49 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 50 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 51 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 52 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 53 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 54 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 55 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 56 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 57 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 58 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 59 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 4 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 5 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 6 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 7 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 8 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 9 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 10 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 11 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 12 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 13 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 14 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 15 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 16 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 17 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 18 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 19 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 20 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 21 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 22 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 23 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 24 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 25 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 26 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 27 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 28 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 29 | 0.99848065 | 0.2265 | 0.9043 | 0.5307 | 0.5307 | TRUE | 0.4462 |
| 30 | 0.99848065 | 0.2206 | 0.9043 | 0.5279 | 0.5279 | TRUE | 0.3113 |
| 31 | 0.99848065 | 0.1717 | 0.8865 | 0.4858 | 0.4858 | TRUE | 2.5645 |
| 32 | 0.99848065 | 0.1717 | 0.8865 | 0.4858 | 0.4858 | TRUE | 2.5645 |
| 33 | 0.99848065 | 0.1717 | 0.8865 | 0.4858 | 0.4858 | TRUE | 2.5645 |
| 34 | 0.99848065 | 0.1717 | 0.8865 | 0.4858 | 0.4858 | TRUE | 2.5645 |
| 35 | 0.99848065 | 0.1717 | 0.8865 | 0.4858 | 0.4858 | TRUE | 2.5645 |
| 36 | 0.99848065 | 0.5817 | 0.9753 | 0.766 | 0.766 | TRUE | 5.8724 |
| 37 | 0.99848065 | 0.1759 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1534 |
| 38 | 0.99848065 | 0.1759 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1534 |
| 39 | 0.99848065 | 0.1759 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1534 |
| 40 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 41 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 42 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 43 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 44 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 45 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 46 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 47 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 48 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 49 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 50 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 51 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 52 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 53 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 54 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 55 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 56 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 57 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 58 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 59 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 4 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 5 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 6 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 7 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 8 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 9 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 10 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 11 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 12 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 13 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 14 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 15 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 16 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 17 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 18 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 19 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 20 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 21 | 0.99848065 | 0.176 | 0.8876 | 0.508 | 0.508 | TRUE | 0.1529 |
| 22 | NA | 1.3338 | 0.9873 | 1.1659 | 1.1659 | TRUE | 19.7433 |
| 23 | NA | 1.3338 | 0.9873 | 1.1659 | 1.1659 | TRUE | 19.7433 |
| 24 | 0.99848065 | 0.5797 | 0.9766 | 0.7656 | 0.7656 | TRUE | 6.8216 |
| 25 | 0.99848065 | 0.6576 | 0.8925 | 0.7687 | 0.7687 | TRUE | 0.9719 |
| 26 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 27 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 28 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 29 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 30 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 31 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 32 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 33 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 34 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 35 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 36 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 37 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 38 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 39 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 40 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 41 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 42 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 43 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 44 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 45 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 46 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 47 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 48 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 49 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 50 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 51 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 52 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 53 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 54 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 55 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 56 | 0.99848065 | 0.3169 | 0.8874 | 0.5707 | 0.5707 | TRUE | 0.527 |
| 57 | 0.99848065 | 0.4035 | 0.9055 | 0.6362 | 0.6362 | TRUE | 5.1643 |
| 58 | 0.99848065 | 0.201 | 0.907 | 0.5221 | 0.5221 | TRUE | 0.2014 |
| 59 | 0.99848065 | 0.201 | 0.907 | 0.5221 | 0.5221 | TRUE | 0.2014 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.2276 | 0.9199 | 0.5414 | 0.5414 | TRUE | 0.908 |
| 4 | 0.99848065 | 0.2276 | 0.9199 | 0.5414 | 0.5414 | TRUE | 0.908 |
| 5 | 0.99848065 | 0.2276 | 0.9199 | 0.5414 | 0.5414 | TRUE | 0.908 |
| 6 | 0.99848065 | 0.2276 | 0.9199 | 0.5414 | 0.5414 | TRUE | 0.908 |
| 7 | 0.99848065 | 0.2276 | 0.9199 | 0.5414 | 0.5414 | TRUE | 0.908 |
| 8 | 0.99848065 | 0.2276 | 0.9199 | 0.5414 | 0.5414 | TRUE | 0.908 |
| 9 | 0.99848065 | 0.2276 | 0.9199 | 0.5414 | 0.5414 | TRUE | 0.908 |
| 10 | 0.99848065 | 0.2276 | 0.9199 | 0.5414 | 0.5414 | TRUE | 0.908 |
| 11 | 0.99848065 | 0.2276 | 0.9199 | 0.5414 | 0.5414 | TRUE | 0.908 |
| 12 | 0.99848065 | 0.2276 | 0.9199 | 0.5414 | 0.5414 | TRUE | 0.908 |
| 13 | 0.99848065 | 0.2276 | 0.9199 | 0.5414 | 0.5414 | TRUE | 0.908 |
| 14 | 0.99848065 | 0.2276 | 0.9199 | 0.5414 | 0.5414 | TRUE | 0.908 |
| 15 | 0.99848065 | 0.2276 | 0.9199 | 0.5414 | 0.5414 | TRUE | 0.908 |
| 16 | 0.99848065 | 0.2276 | 0.9199 | 0.5414 | 0.5414 | TRUE | 0.908 |
| 17 | 0.99848065 | 0.2276 | 0.9199 | 0.5414 | 0.5414 | TRUE | 0.908 |
| 18 | 0.99848065 | 0.2276 | 0.9199 | 0.5414 | 0.5414 | TRUE | 0.908 |
| 19 | 0.99848065 | 0.2276 | 0.9199 | 0.5414 | 0.5414 | TRUE | 0.908 |
| 20 | 0.99848065 | 0.2276 | 0.9199 | 0.5414 | 0.5414 | TRUE | 0.908 |
| 21 | 0.99848065 | 0.2276 | 0.9199 | 0.5414 | 0.5414 | TRUE | 0.908 |
| 22 | 0.99848065 | 0.2307 | 0.8871 | 0.5163 | 0.5163 | TRUE | 3.7539 |
| 23 | 0.99848065 | 0.3279 | 1.1185 | 0.6909 | 0.6909 | TRUE | 0.1222 |
| 24 | 0.99848065 | 0.1886 | 0.8908 | 0.5043 | 0.5043 | TRUE | 0.4283 |
| 25 | 0.99848065 | 0.199 | 0.891 | 0.5107 | 0.5107 | TRUE | 0.314 |
| 26 | 0.99848065 | 0.199 | 0.891 | 0.5107 | 0.5107 | TRUE | 0.314 |
| 27 | 0.99848065 | 0.2032 | 0.8911 | 0.5132 | 0.5132 | TRUE | 0.3126 |
| 28 | 0.99848065 | 0.2032 | 0.8911 | 0.5132 | 0.5132 | TRUE | 0.3126 |
| 29 | 0.99848065 | 0.2032 | 0.8911 | 0.5132 | 0.5132 | TRUE | 0.3126 |
| 30 | 0.99848065 | 0.2032 | 0.8911 | 0.5132 | 0.5132 | TRUE | 0.3126 |
| 31 | 0.99848065 | 0.2032 | 0.8911 | 0.5132 | 0.5132 | TRUE | 0.3126 |
| 32 | 0.99848065 | 0.2032 | 0.8911 | 0.5132 | 0.5132 | TRUE | 0.3126 |
| 33 | 0.99848065 | 0.2032 | 0.8911 | 0.5132 | 0.5132 | TRUE | 0.3126 |
| 34 | 0.99848065 | 0.2032 | 0.8911 | 0.5132 | 0.5132 | TRUE | 0.3126 |
| 35 | 0.99848065 | 0.2032 | 0.8911 | 0.5132 | 0.5132 | TRUE | 0.3126 |
| 36 | 0.99848065 | 0.2032 | 0.8911 | 0.5132 | 0.5132 | TRUE | 0.3126 |
| 37 | 0.99848065 | 0.2032 | 0.8911 | 0.5132 | 0.5132 | TRUE | 0.3126 |
| 38 | 0.99848065 | 0.2032 | 0.8911 | 0.5132 | 0.5132 | TRUE | 0.3126 |
| 39 | 0.99848065 | 0.2032 | 0.8911 | 0.5132 | 0.5132 | TRUE | 0.3126 |
| 40 | 0.99848065 | 0.187 | 1.0395 | 0.5773 | 0.5773 | TRUE | 0.2223 |
| 41 | 0.99848065 | 0.187 | 1.0395 | 0.5773 | 0.5773 | TRUE | 0.2223 |
| 42 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 43 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 44 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 45 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 46 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 47 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 48 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 49 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 50 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 51 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 52 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 53 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 54 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 55 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 56 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 57 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 58 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 59 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 4 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 5 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 6 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 7 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 8 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 9 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 10 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 11 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 12 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 13 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 14 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 15 | 0.99848065 | 0.2699 | 0.9132 | 0.5629 | 0.5629 | TRUE | 4.1642 |
| 16 | 0.99848065 | 0.2055 | 0.9087 | 0.523 | 0.523 | TRUE | 0.9043 |
| 17 | 0.99848065 | 0.1794 | 0.8911 | 0.4919 | 0.4919 | TRUE | 0.2225 |
| 18 | 0.99848065 | 0.2111 | 0.9153 | 0.5293 | 0.5293 | TRUE | 0.1463 |
| 19 | 0.99848065 | 0.2105 | 0.9154 | 0.5289 | 0.5289 | TRUE | 0.1455 |
| 20 | 0.99848065 | 0.2105 | 0.9154 | 0.5289 | 0.5289 | TRUE | 0.1455 |
| 21 | 0.99848065 | 0.2105 | 0.9154 | 0.5289 | 0.5289 | TRUE | 0.1455 |
| 22 | 0.99848065 | 0.4572 | 1.0584 | 0.7364 | 0.7364 | TRUE | 1.84 |
| 23 | 0.99848065 | 0.4572 | 1.0584 | 0.7364 | 0.7364 | TRUE | 1.84 |
| 24 | 0.99848065 | 0.4572 | 1.0584 | 0.7364 | 0.7364 | TRUE | 1.84 |
| 25 | 0.99848065 | 0.4572 | 1.0584 | 0.7364 | 0.7364 | TRUE | 1.84 |
| 26 | 0.99848065 | 0.4572 | 1.0584 | 0.7364 | 0.7364 | TRUE | 1.84 |
| 27 | 0.99848065 | 0.4572 | 1.0584 | 0.7364 | 0.7364 | TRUE | 1.84 |
| 28 | 0.99848065 | 0.4572 | 1.0584 | 0.7364 | 0.7364 | TRUE | 1.84 |
| 29 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 30 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 31 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 32 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 33 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 34 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 35 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 36 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 37 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 38 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 39 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 40 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 41 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 42 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 43 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 44 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 45 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 46 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 47 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 48 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 49 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 50 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 51 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 52 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 53 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 54 | 0.99848065 | 0.2251 | 0.888 | 0.5355 | 0.5355 | TRUE | 0.1592 |
| 55 | 0.99848065 | 0.3703 | 0.8898 | 0.6103 | 0.6103 | TRUE | 9.5306 |
| 56 | 0.99848065 | 0.3703 | 0.8898 | 0.6103 | 0.6103 | TRUE | 9.5306 |
| 57 | 0.99848065 | 0.2728 | 0.8873 | 0.5354 | 0.5354 | TRUE | 2.5672 |
| 58 | 0.99848065 | 0.3706 | 0.8898 | 0.6104 | 0.6104 | TRUE | 9.536 |
| 59 | 0.99848065 | 0.3706 | 0.8898 | 0.6104 | 0.6104 | TRUE | 9.536 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|--------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 4 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 5 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 6 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 7 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 8 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 9 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 10 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 11 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 12 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 13 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 14 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 15 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 16 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 17 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 18 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 19 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 20 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 21 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 22 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 23 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 24 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 25 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 26 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 27 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 28 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 29 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 30 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 31 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 32 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 33 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 34 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 35 | 0.99848065 | 0.2806 | 0.8874 | 0.5389 | 0.5389 | TRUE | 2.8617 |
| 36 | 0.99848065 | 0.2808 | 0.8874 | 0.539 | 0.539 | TRUE | 2.8694 |
| 37 | 0.99848065 | 0.3633 | 0.9024 | 0.6122 | 0.6122 | TRUE | 3.1789 |
| 38 | 0.99848065 | 0.3633 | 0.9024 | 0.6122 | 0.6122 | TRUE | 3.1789 |
| 39 | 0.99848065 | 0.3633 | 0.9024 | 0.6122 | 0.6122 | TRUE | 3.1789 |
| 40 | 0.99848065 | 0.3633 | 0.9024 | 0.6122 | 0.6122 | TRUE | 3.1789 |
| 41 | 0.99848065 | 0.3628 | 0.9023 | 0.6119 | 0.6119 | TRUE | 2.9924 |
| 42 | 0.99848065 | 0.25 | 0.8882 | 0.5496 | 0.5496 | TRUE | 0.2022 |
| 43 | 0.99848065 | 0.25 | 0.8882 | 0.5496 | 0.5496 | TRUE | 0.2022 |
| 44 | 0.99848065 | 0.2539 | 0.8882 | 0.5526 | 0.5526 | TRUE | 0.2003 |
| 45 | 0.99848065 | 0.2539 | 0.8882 | 0.5526 | 0.5526 | TRUE | 0.2003 |
| 46 | 0.99848065 | 0.2539 | 0.8882 | 0.5526 | 0.5526 | TRUE | 0.2003 |
| 47 | 0.99848065 | 0.2539 | 0.8882 | 0.5526 | 0.5526 | TRUE | 0.2003 |
| 48 | 0.99848065 | 0.2539 | 0.8882 | 0.5526 | 0.5526 | TRUE | 0.2003 |
| 49 | 0.99848065 | 0.2539 | 0.8882 | 0.5526 | 0.5526 | TRUE | 0.2003 |
| 50 | 0.99848065 | 0.2539 | 0.8882 | 0.5526 | 0.5526 | TRUE | 0.2003 |
| 51 | 0.99848065 | 0.2539 | 0.8882 | 0.5526 | 0.5526 | TRUE | 0.2003 |
| 52 | 0.99848065 | 0.2539 | 0.8882 | 0.5526 | 0.5526 | TRUE | 0.2003 |
| 53 | 0.99848065 | 0.2539 | 0.8882 | 0.5526 | 0.5526 | TRUE | 0.2003 |
| 54 | 0.99848065 | 0.2539 | 0.8882 | 0.5526 | 0.5526 | TRUE | 0.2003 |
| 55 | 0.99848065 | 0.2539 | 0.8882 | 0.5526 | 0.5526 | TRUE | 0.2003 |
| 56 | 0.99848065 | 0.2539 | 0.8882 | 0.5526 | 0.5526 | TRUE | 0.2003 |
| 57 | 0.99848065 | 0.2539 | 0.8882 | 0.5526 | 0.5526 | TRUE | 0.2003 |
| 58 | 0.99848065 | 0.2539 | 0.8882 | 0.5526 | 0.5526 | TRUE | 0.2003 |
| 59 | 0.99848065 | 0.2539 | 0.8882 | 0.5526 | 0.5526 | TRUE | 0.2003 |
| 60 | | | | | | | |

| | | | | | | | |
|----|------------|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 4 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 5 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 6 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 7 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 8 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 9 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 10 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 11 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 12 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 13 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 14 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 15 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 16 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 17 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 18 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 19 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 20 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 21 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 22 | 0.99848065 | 0.1596 | 0.8921 | 0.494 | 0.494 | TRUE | 0.1337 |
| 23 | NA | 1.3182 | 0.9938 | 1.1611 | 1.1611 | TRUE | 19.3212 |
| 24 | NA | 1.8446 | 0.9159 | 1.3852 | 1.3852 | TRUE | 27.308 |
| 25 | 0.99848065 | 1.4413 | 1.1088 | 1.2777 | 1.2777 | TRUE | 3.8058 |
| 26 | NA | 1.9927 | 0.9183 | 1.4593 | 1.4593 | TRUE | 28.4691 |
| 27 | 0.99848065 | 1.1259 | 0.9303 | 1.0314 | 1.0314 | TRUE | 1.4759 |
| 28 | 0.99848065 | 1.1259 | 0.9303 | 1.0314 | 1.0314 | TRUE | 1.4759 |
| 29 | 0.99848065 | 1.1259 | 0.9303 | 1.0314 | 1.0314 | TRUE | 1.4759 |
| 30 | 0.99848065 | 1.1259 | 0.9303 | 1.0314 | 1.0314 | TRUE | 1.4759 |
| 31 | 0.99848065 | 1.1259 | 0.9303 | 1.0314 | 1.0314 | TRUE | 1.4759 |
| 32 | 0.99848065 | 1.0306 | 0.8938 | 0.9485 | 0.9485 | TRUE | 16.7866 |
| 33 | 0.99848065 | 1.0306 | 0.8938 | 0.9485 | 0.9485 | TRUE | 16.7866 |
| 34 | 0.99848065 | 1.0306 | 0.8938 | 0.9485 | 0.9485 | TRUE | 16.7866 |
| 35 | 0.99848065 | 1.0306 | 0.8938 | 0.9485 | 0.9485 | TRUE | 16.7866 |
| 36 | 0.99848065 | 1.0306 | 0.8938 | 0.9485 | 0.9485 | TRUE | 16.7866 |
| 37 | 0.99848065 | 1.0306 | 0.8938 | 0.9485 | 0.9485 | TRUE | 16.7866 |
| 38 | 0.99848065 | 1.0306 | 0.8938 | 0.9485 | 0.9485 | TRUE | 16.7866 |
| 39 | 0.99848065 | 1.0306 | 0.8938 | 0.9485 | 0.9485 | TRUE | 16.7866 |
| 40 | 0.99848065 | 1.0306 | 0.8938 | 0.9485 | 0.9485 | TRUE | 16.7866 |
| 41 | 0.99848065 | 1.0306 | 0.8938 | 0.9485 | 0.9485 | TRUE | 16.7866 |
| 42 | 0.99848065 | 1.0306 | 0.8938 | 0.9485 | 0.9485 | TRUE | 16.7866 |
| 43 | 0.99848065 | 1.0306 | 0.8938 | 0.9485 | 0.9485 | TRUE | 16.7866 |
| 44 | 0.99848065 | 1.0306 | 0.8938 | 0.9485 | 0.9485 | TRUE | 16.7866 |
| 45 | 0.99848065 | 1.0306 | 0.8938 | 0.9485 | 0.9485 | TRUE | 16.7866 |
| 46 | 0.99848065 | 1.0306 | 0.8938 | 0.9485 | 0.9485 | TRUE | 16.7866 |
| 47 | 0.99848065 | 1.0296 | 0.8938 | 0.9479 | 0.9479 | TRUE | 16.4382 |
| 48 | NA | 4.2054 | 0.9153 | 2.49 | 2.49 | TRUE | 35.125 |
| 49 | NA | 4.2054 | 0.9153 | 2.49 | 2.49 | TRUE | 35.125 |
| 50 | NA | 4.2054 | 0.9153 | 2.49 | 2.49 | TRUE | 35.125 |
| 51 | NA | 4.2054 | 0.9153 | 2.49 | 2.49 | TRUE | 35.125 |
| 52 | NA | 4.2054 | 0.9153 | 2.49 | 2.49 | TRUE | 35.125 |
| 53 | NA | 4.2054 | 0.9153 | 2.49 | 2.49 | TRUE | 35.125 |
| 54 | NA | 4.2054 | 0.9153 | 2.49 | 2.49 | TRUE | 35.125 |
| 55 | NA | 4.2054 | 0.9153 | 2.49 | 2.49 | TRUE | 35.125 |
| 56 | 0.99848065 | 1.9474 | 0.9407 | 1.4455 | 1.4455 | TRUE | 0.3724 |
| 57 | NA | 10 | 1.0033 | 4.5623 | 10 | TRUE | 32.3951 |
| 58 | NA | 10 | 1.0033 | 4.5623 | 10 | TRUE | 32.3951 |
| 59 | NA | 10 | 1.0033 | 4.5623 | 10 | TRUE | 32.3951 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | NA | 10 | 1.0033 | 4.5623 | 10 | TRUE | 32.3951 |
| 4 | NA | 10 | 1.0033 | 4.5623 | 10 | TRUE | 32.3951 |
| 5 | NA | 10 | 1.0033 | 4.5623 | 10 | TRUE | 32.3951 |
| 6 | NA | 10 | 1.0033 | 4.5623 | 10 | TRUE | 32.3951 |
| 7 | NA | 10 | 1.0033 | 4.5623 | 10 | TRUE | 32.3951 |
| 8 | NA | 10 | 1.0033 | 4.5623 | 10 | TRUE | 32.3951 |
| 9 | NA | 10 | 1.0033 | 4.5623 | 10 | TRUE | 32.3951 |
| 10 | NA | 10 | 1.0033 | 4.5623 | 10 | TRUE | 32.3951 |
| 11 | NA | 10 | 1.0033 | 4.5623 | 10 | TRUE | 32.3951 |
| 12 | NA | 10 | 1.0033 | 4.5623 | 10 | TRUE | 32.3951 |
| 13 | NA | 10 | 1.0033 | 4.5623 | 10 | TRUE | 32.3951 |
| 14 | NA | 10 | 1.0033 | 4.5623 | 10 | TRUE | 32.3951 |
| 15 | NA | 10 | 1.0033 | 4.5623 | 10 | TRUE | 32.3951 |
| 16 | NA | 10 | 1.0033 | 4.5623 | 10 | TRUE | 32.3951 |
| 17 | NA | 10 | 1.0033 | 4.5623 | 10 | TRUE | 32.3951 |
| 18 | NA | 10 | 1.0013 | 4.5666 | 10 | TRUE | 32.4775 |
| 19 | NA | 10 | 1.0013 | 4.5666 | 10 | TRUE | 32.4775 |
| 20 | NA | 10 | 1.0013 | 4.5666 | 10 | TRUE | 32.4775 |
| 21 | NA | 10 | 1.0013 | 4.5666 | 10 | TRUE | 32.4775 |
| 22 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 23 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 24 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 25 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 26 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 27 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 28 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 29 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 30 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 31 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 32 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 33 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 34 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 35 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 36 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 37 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 38 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 39 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 40 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 41 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 42 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 43 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 44 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 45 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 46 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 47 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 48 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 49 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 50 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 51 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 52 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 53 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 54 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 55 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 56 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 57 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 58 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 59 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 60 | | | | | | | |

| | | | | | | | |
|----|----|--------|--------|--------|--------|------|---------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 4 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 5 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 6 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 7 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 8 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 9 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 10 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 11 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 12 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 13 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 14 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 15 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 16 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 17 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 18 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 19 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 20 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 21 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 22 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 23 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 24 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 25 | NA | 6.8182 | 1.0342 | 2.8523 | 2.8523 | TRUE | 29.6685 |
| 26 | NA | 10 | 0.9647 | 3.0817 | 10 | TRUE | 33.2758 |
| 27 | | | | | | | |
| 28 | | | | | | | |
| 29 | | | | | | | |
| 30 | | | | | | | |
| 31 | | | | | | | |
| 32 | | | | | | | |
| 33 | | | | | | | |
| 34 | | | | | | | |
| 35 | | | | | | | |
| 36 | | | | | | | |
| 37 | | | | | | | |
| 38 | | | | | | | |
| 39 | | | | | | | |
| 40 | | | | | | | |
| 41 | | | | | | | |
| 42 | | | | | | | |
| 43 | | | | | | | |
| 44 | | | | | | | |
| 45 | | | | | | | |
| 46 | | | | | | | |
| 47 | | | | | | | |
| 48 | | | | | | | |
| 49 | | | | | | | |
| 50 | | | | | | | |
| 51 | | | | | | | |
| 52 | | | | | | | |
| 53 | | | | | | | |
| 54 | | | | | | | |
| 55 | | | | | | | |
| 56 | | | | | | | |
| 57 | | | | | | | |
| 58 | | | | | | | |
| 59 | | | | | | | |
| 60 | | | | | | | |

| | mean | 5% | 1% |
|----|-------------|----|----|
| 1 | | | |
| 2 | | | |
| 3 | | | |
| 4 | | | |
| 5 | 59.1666667 | 1 | 0 |
| 6 | 59.1666667 | 1 | 0 |
| 7 | 59.1666667 | 1 | 0 |
| 8 | | | |
| 9 | 59.1666667 | 1 | 0 |
| 10 | 295.8333333 | 1 | 0 |
| 11 | 295.8333333 | 1 | 0 |
| 12 | | | |
| 13 | 295.8333333 | 1 | 0 |
| 14 | 295.8333333 | 1 | 0 |
| 15 | 295.8333333 | 1 | 0 |
| 16 | | | |
| 17 | 295.8333333 | 1 | 0 |
| 18 | 295.8333333 | 1 | 0 |
| 19 | 295.8333333 | 1 | 0 |
| 20 | | | |
| 21 | 295.8333333 | 1 | 0 |
| 22 | 295.8333333 | 1 | 0 |
| 23 | 295.8333333 | 1 | 0 |
| 24 | | | |
| 25 | 295.8333333 | 1 | 0 |
| 26 | 295.8333333 | 1 | 0 |
| 27 | 295.8333333 | 1 | 0 |
| 28 | | | |
| 29 | 295.8333333 | 1 | 0 |
| 30 | 295.8333333 | 1 | 0 |
| 31 | 295.8333333 | 1 | 0 |
| 32 | 295.8333333 | 1 | 0 |
| 33 | | | |
| 34 | 295.8333333 | 1 | 0 |
| 35 | 295.8333333 | 1 | 0 |
| 36 | | | |
| 37 | 295.8333333 | 1 | 0 |
| 38 | 295.8333333 | 1 | 0 |
| 39 | 295.8333333 | 1 | 0 |
| 40 | | | |
| 41 | 295.8333333 | 1 | 0 |
| 42 | 295.8333333 | 1 | 0 |
| 43 | 295.8333333 | 1 | 0 |
| 44 | | | |
| 45 | 295.8333333 | 1 | 0 |
| 46 | 295.8333333 | 1 | 0 |
| 47 | 295.8333333 | 1 | 0 |
| 48 | | | |
| 49 | 295.8333333 | 1 | 0 |
| 50 | 295.8333333 | 1 | 0 |
| 51 | 295.8333333 | 1 | 0 |
| 52 | | | |
| 53 | 295.8333333 | 1 | 0 |
| 54 | 295.8333333 | 1 | 0 |
| 55 | 295.8333333 | 1 | 0 |
| 56 | | | |
| 57 | 295.8333333 | 1 | 0 |
| 58 | 295.8333333 | 1 | 0 |
| 59 | 295.8333333 | 1 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 295.833333 | 1 | 0 |
| 4 | 295.833333 | 1 | 0 |
| 5 | 295.833333 | 1 | 0 |
| 6 | 295.833333 | 1 | 0 |
| 7 | 295.833333 | 1 | 0 |
| 8 | 295.833333 | 1 | 0 |
| 9 | 295.833333 | 1 | 0 |
| 10 | 295.833333 | 1 | 0 |
| 11 | 295.833333 | 1 | 0 |
| 12 | 295.833333 | 1 | 0 |
| 13 | 295.833333 | 1 | 0 |
| 14 | 295.833333 | 1 | 0 |
| 15 | 295.833333 | 1 | 0 |
| 16 | 295.833333 | 1 | 0 |
| 17 | 295.833333 | 1 | 0 |
| 18 | 295.833333 | 1 | 0 |
| 19 | 295.833333 | 1 | 0 |
| 20 | 295.833333 | 1 | 0 |
| 21 | 295.833333 | 1 | 0 |
| 22 | 295.833333 | 1 | 0 |
| 23 | 295.833333 | 1 | 0 |
| 24 | 295.833333 | 1 | 0 |
| 25 | 295.833333 | 1 | 0 |
| 26 | 295.833333 | 1 | 0 |
| 27 | 295.833333 | 1 | 0 |
| 28 | 295.833333 | 1 | 0 |
| 29 | 295.833333 | 1 | 0 |
| 30 | 295.833333 | 1 | 0 |
| 31 | 295.833333 | 1 | 0 |
| 32 | 295.833333 | 1 | 0 |
| 33 | 295.833333 | 1 | 0 |
| 34 | 295.833333 | 1 | 0 |
| 35 | 295.833333 | 1 | 0 |
| 36 | 295.833333 | 1 | 0 |
| 37 | 295.833333 | 1 | 0 |
| 38 | 295.833333 | 1 | 0 |
| 39 | 295.833333 | 1 | 0 |
| 40 | 295.833333 | 1 | 0 |
| 41 | 295.833333 | 1 | 0 |
| 42 | 295.833333 | 1 | 0 |
| 43 | 295.833333 | 1 | 0 |
| 44 | 295.833333 | 1 | 0 |
| 45 | 295.833333 | 1 | 0 |
| 46 | 295.833333 | 1 | 0 |
| 47 | 295.833333 | 1 | 0 |
| 48 | 295.833333 | 1 | 0 |
| 49 | 295.833333 | 1 | 0 |
| 50 | 295.833333 | 1 | 0 |
| 51 | 295.833333 | 1 | 0 |
| 52 | 295.833333 | 1 | 0 |
| 53 | 295.833333 | 1 | 0 |
| 54 | 295.833333 | 1 | 0 |
| 55 | 295.833333 | 1 | 0 |
| 56 | 295.833333 | 1 | 0 |
| 57 | 295.833333 | 1 | 0 |
| 58 | 295.833333 | 1 | 0 |
| 59 | 295.833333 | 1 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 295.833333 | 1 | 0 |
| 4 | 295.833333 | 1 | 0 |
| 5 | 295.833333 | 1 | 0 |
| 6 | 295.833333 | 1 | 0 |
| 7 | 295.833333 | 1 | 0 |
| 8 | 295.833333 | 1 | 0 |
| 9 | 295.833333 | 1 | 0 |
| 10 | 297.333333 | 1 | 0 |
| 11 | 734.666667 | 1 | 0 |
| 12 | 734.666667 | 1 | 0 |
| 13 | 734.666667 | 1 | 0 |
| 14 | 734.666667 | 1 | 0 |
| 15 | 734.666667 | 1 | 0 |
| 16 | 734.666667 | 1 | 0 |
| 17 | 734.666667 | 1 | 0 |
| 18 | 734.666667 | 1 | 0 |
| 19 | 734.666667 | 1 | 0 |
| 20 | 734.666667 | 1 | 0 |
| 21 | 734.666667 | 1 | 0 |
| 22 | 734.666667 | 1 | 0 |
| 23 | 455.666667 | 1 | 0 |
| 24 | 455.666667 | 1 | 0 |
| 25 | 455.666667 | 1 | 0 |
| 26 | 455.666667 | 1 | 0 |
| 27 | 455.666667 | 1 | 0 |
| 28 | 455.666667 | 1 | 0 |
| 29 | 455.666667 | 1 | 0 |
| 30 | 455.666667 | 1 | 0 |
| 31 | 455.666667 | 1 | 0 |
| 32 | 455.666667 | 1 | 0 |
| 33 | 455.666667 | 1 | 0 |
| 34 | 455.666667 | 1 | 0 |
| 35 | 455.666667 | 1 | 0 |
| 36 | 455.666667 | 1 | 0 |
| 37 | 455.666667 | 1 | 0 |
| 38 | 455.666667 | 1 | 0 |
| 39 | 928.166667 | 0 | 0 |
| 40 | 856.166667 | 0 | 0 |
| 41 | 363.666667 | 0 | 0 |
| 42 | 363.666667 | 0 | 0 |
| 43 | 300.5 | 0 | 0 |
| 44 | 266.5 | 0 | 0 |
| 45 | 265.166667 | 0 | 0 |
| 46 | 265.166667 | 0 | 0 |
| 47 | 215.833333 | 0 | 0 |
| 48 | 183.666667 | 0 | 0 |
| 49 | 183.666667 | 0 | 0 |
| 50 | 66 | 0 | 0 |
| 51 | 65.5 | 0 | 0 |
| 52 | 56.166667 | 0 | 0 |
| 53 | 56.166667 | 0 | 0 |
| 54 | 51.5 | 0 | 0 |
| 55 | 1628.66667 | 0 | 0 |
| 56 | 2717.66667 | 0 | 0 |
| 57 | 2717.66667 | 0 | 0 |
| 58 | 4487.16667 | 0 | 0 |
| 59 | 1073.33333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 771.833333 | 0 | 0 |
| 4 | | | |
| 5 | 581.5 | 0 | 0 |
| 6 | 218.5 | 0 | 0 |
| 7 | 305.5 | 0 | 0 |
| 8 | | | |
| 9 | 71.666667 | 0 | 0 |
| 10 | 71.666667 | 0 | 0 |
| 11 | 71.666667 | 0 | 0 |
| 12 | | | |
| 13 | 71.666667 | 0 | 0 |
| 14 | 71.666667 | 0 | 0 |
| 15 | 71.666667 | 0 | 0 |
| 16 | | | |
| 17 | 71.666667 | 0 | 0 |
| 18 | 71.666667 | 0 | 0 |
| 19 | 71.666667 | 0 | 0 |
| 20 | | | |
| 21 | 71.666667 | 0 | 0 |
| 22 | 71.666667 | 0 | 0 |
| 23 | 71.666667 | 0 | 0 |
| 24 | | | |
| 25 | 71.666667 | 0 | 0 |
| 26 | 71.666667 | 0 | 0 |
| 27 | 71.666667 | 0 | 0 |
| 28 | | | |
| 29 | 71.666667 | 0 | 0 |
| 30 | 71.666667 | 0 | 0 |
| 31 | 105.666667 | 0 | 0 |
| 32 | | | |
| 33 | 83 | 0 | 0 |
| 34 | 278.333333 | 0 | 0 |
| 35 | 278.166667 | 0 | 0 |
| 36 | 278.166667 | 0 | 0 |
| 37 | | | |
| 38 | 278.166667 | 0 | 0 |
| 39 | 278.166667 | 0 | 0 |
| 40 | | | |
| 41 | 278.166667 | 0 | 0 |
| 42 | 278.166667 | 0 | 0 |
| 43 | 278.166667 | 0 | 0 |
| 44 | | | |
| 45 | 278.166667 | 0 | 0 |
| 46 | 278.166667 | 0 | 0 |
| 47 | 278.166667 | 0 | 0 |
| 48 | | | |
| 49 | 278.166667 | 0 | 0 |
| 50 | 278.166667 | 0 | 0 |
| 51 | 278.166667 | 0 | 0 |
| 52 | | | |
| 53 | 278.166667 | 0 | 0 |
| 54 | 278.166667 | 0 | 0 |
| 55 | 278.166667 | 0 | 0 |
| 56 | | | |
| 57 | 278.166667 | 0 | 0 |
| 58 | 278.166667 | 0 | 0 |
| 59 | 278.166667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 278.166667 | 0 | 0 |
| 4 | 278.166667 | 0 | 0 |
| 5 | 278.166667 | 0 | 0 |
| 6 | 278.166667 | 0 | 0 |
| 7 | 278.166667 | 0 | 0 |
| 8 | 278.166667 | 0 | 0 |
| 9 | 278.166667 | 0 | 0 |
| 10 | 278.166667 | 0 | 0 |
| 11 | 278.166667 | 0 | 0 |
| 12 | 279.333333 | 0 | 0 |
| 13 | 279.333333 | 0 | 0 |
| 14 | 305.166667 | 0 | 0 |
| 15 | 305 | 0 | 0 |
| 16 | 305 | 0 | 0 |
| 17 | 305 | 0 | 0 |
| 18 | 305 | 0 | 0 |
| 19 | 305 | 0 | 0 |
| 20 | 305 | 0 | 0 |
| 21 | 305 | 0 | 0 |
| 22 | 305 | 0 | 0 |
| 23 | 305 | 0 | 0 |
| 24 | 305 | 0 | 0 |
| 25 | 305 | 0 | 0 |
| 26 | 305 | 0 | 0 |
| 27 | 305 | 0 | 0 |
| 28 | 305 | 0 | 0 |
| 29 | 305 | 0 | 0 |
| 30 | 305 | 0 | 0 |
| 31 | 305 | 0 | 0 |
| 32 | 305 | 0 | 0 |
| 33 | 305 | 0 | 0 |
| 34 | 305 | 0 | 0 |
| 35 | 305 | 0 | 0 |
| 36 | 305 | 0 | 0 |
| 37 | 305 | 0 | 0 |
| 38 | 305 | 0 | 0 |
| 39 | 305 | 0 | 0 |
| 40 | 305 | 0 | 0 |
| 41 | 305 | 0 | 0 |
| 42 | 305 | 0 | 0 |
| 43 | 305 | 0 | 0 |
| 44 | 305 | 0 | 0 |
| 45 | 305 | 0 | 0 |
| 46 | 305 | 0 | 0 |
| 47 | 305 | 0 | 0 |
| 48 | 305 | 0 | 0 |
| 49 | 305 | 0 | 0 |
| 50 | 305 | 0 | 0 |
| 51 | 305 | 0 | 0 |
| 52 | 305 | 0 | 0 |
| 53 | 305 | 0 | 0 |
| 54 | 305 | 0 | 0 |
| 55 | 305 | 0 | 0 |
| 56 | 305 | 0 | 0 |
| 57 | 305 | 0 | 0 |
| 58 | 305 | 0 | 0 |
| 59 | 305 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 305 | 0 | 0 |
| 4 | 305 | 0 | 0 |
| 5 | 305 | 0 | 0 |
| 6 | 305 | 0 | 0 |
| 7 | 305 | 0 | 0 |
| 8 | 305 | 0 | 0 |
| 9 | 305 | 0 | 0 |
| 10 | 305 | 0 | 0 |
| 11 | 305 | 0 | 0 |
| 12 | 305 | 0 | 0 |
| 13 | 305 | 0 | 0 |
| 14 | 305 | 0 | 0 |
| 15 | 305 | 0 | 0 |
| 16 | 305 | 0 | 0 |
| 17 | 305 | 0 | 0 |
| 18 | 305 | 0 | 0 |
| 19 | 305 | 0 | 0 |
| 20 | 305 | 0 | 0 |
| 21 | 305 | 0 | 0 |
| 22 | 305 | 0 | 0 |
| 23 | 80 | 0 | 0 |
| 24 | 80 | 0 | 0 |
| 25 | 80 | 0 | 0 |
| 26 | 80 | 0 | 0 |
| 27 | 80 | 0 | 0 |
| 28 | 55.5 | 0 | 0 |
| 29 | 55.5 | 0 | 0 |
| 30 | 55.5 | 0 | 0 |
| 31 | 55.5 | 0 | 0 |
| 32 | 55.5 | 0 | 0 |
| 33 | 55.5 | 0 | 0 |
| 34 | 55.5 | 0 | 0 |
| 35 | 55.5 | 0 | 0 |
| 36 | 55.5 | 0 | 0 |
| 37 | 55.5 | 0 | 0 |
| 38 | 55.5 | 0 | 0 |
| 39 | 55.5 | 0 | 0 |
| 40 | 55.5 | 0 | 0 |
| 41 | 55.5 | 0 | 0 |
| 42 | 55.5 | 0 | 0 |
| 43 | 55.5 | 0 | 0 |
| 44 | 55.5 | 0 | 0 |
| 45 | 55.5 | 0 | 0 |
| 46 | 55.5 | 0 | 0 |
| 47 | 55.5 | 0 | 0 |
| 48 | 55.5 | 0 | 0 |
| 49 | 73 | 0 | 0 |
| 50 | 73 | 0 | 0 |
| 51 | 73 | 0 | 0 |
| 52 | 73 | 0 | 0 |
| 53 | 73 | 0 | 0 |
| 54 | 73 | 0 | 0 |
| 55 | 73 | 0 | 0 |
| 56 | 73 | 0 | 0 |
| 57 | 73 | 0 | 0 |
| 58 | 73 | 0 | 0 |
| 59 | 73 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 73 | 0 | 0 |
| 4 | 73 | 0 | 0 |
| 5 | 73 | 0 | 0 |
| 6 | 73 | 0 | 0 |
| 7 | 73 | 0 | 0 |
| 8 | 73 | 0 | 0 |
| 9 | 73 | 0 | 0 |
| 10 | 73 | 0 | 0 |
| 11 | 73 | 0 | 0 |
| 12 | 73 | 0 | 0 |
| 13 | 73 | 0 | 0 |
| 14 | 73 | 0 | 0 |
| 15 | 73 | 0 | 0 |
| 16 | 73 | 0 | 0 |
| 17 | 73 | 0 | 0 |
| 18 | 73 | 0 | 0 |
| 19 | 73 | 0 | 0 |
| 20 | 73 | 0 | 0 |
| 21 | 73 | 0 | 0 |
| 22 | 78.1666667 | 0 | 0 |
| 23 | 846.666667 | 0 | 0 |
| 24 | 846.666667 | 0 | 0 |
| 25 | 846.666667 | 0 | 0 |
| 26 | 846.666667 | 0 | 0 |
| 27 | 846.666667 | 0 | 0 |
| 28 | 846.666667 | 0 | 0 |
| 29 | 846.666667 | 0 | 0 |
| 30 | 846.666667 | 0 | 0 |
| 31 | 846.666667 | 0 | 0 |
| 32 | 846.666667 | 0 | 0 |
| 33 | 846.666667 | 0 | 0 |
| 34 | 846.666667 | 0 | 0 |
| 35 | 846.666667 | 0 | 0 |
| 36 | 846.666667 | 0 | 0 |
| 37 | 846.666667 | 0 | 0 |
| 38 | 846.666667 | 0 | 0 |
| 39 | 846.666667 | 0 | 0 |
| 40 | 846.666667 | 0 | 0 |
| 41 | 846.666667 | 0 | 0 |
| 42 | 846.666667 | 0 | 0 |
| 43 | 846.666667 | 0 | 0 |
| 44 | 846.666667 | 0 | 0 |
| 45 | 846.666667 | 0 | 0 |
| 46 | 846.666667 | 0 | 0 |
| 47 | 846.666667 | 0 | 0 |
| 48 | 846.666667 | 0 | 0 |
| 49 | 846.666667 | 0 | 0 |
| 50 | 846.666667 | 0 | 0 |
| 51 | 846.666667 | 0 | 0 |
| 52 | 846.666667 | 0 | 0 |
| 53 | 846.666667 | 0 | 0 |
| 54 | 846.666667 | 0 | 0 |
| 55 | 846.666667 | 0 | 0 |
| 56 | 846.666667 | 0 | 0 |
| 57 | 846.666667 | 0 | 0 |
| 58 | 846.666667 | 0 | 0 |
| 59 | 846.666667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 846.66667 | 0 | 0 |
| 4 | 1416.16667 | 0 | 0 |
| 5 | 1416.16667 | 0 | 0 |
| 6 | 1416.16667 | 0 | 0 |
| 7 | 1416.16667 | 0 | 0 |
| 8 | 1416.16667 | 0 | 0 |
| 9 | 1416.16667 | 0 | 0 |
| 10 | 1416.16667 | 0 | 0 |
| 11 | 1416.16667 | 0 | 0 |
| 12 | 1416.16667 | 0 | 0 |
| 13 | 1416.16667 | 0 | 0 |
| 14 | 1416.16667 | 0 | 0 |
| 15 | 1416.16667 | 0 | 0 |
| 16 | 1416.16667 | 0 | 0 |
| 17 | 1416.16667 | 0 | 0 |
| 18 | 1416.16667 | 0 | 0 |
| 19 | 1416.16667 | 0 | 0 |
| 20 | 1416.16667 | 0 | 0 |
| 21 | 1416.16667 | 0 | 0 |
| 22 | 1416.16667 | 0 | 0 |
| 23 | 1416.16667 | 0 | 0 |
| 24 | 1416.16667 | 0 | 0 |
| 25 | 1416.16667 | 0 | 0 |
| 26 | 1416.16667 | 0 | 0 |
| 27 | 1416.16667 | 0 | 0 |
| 28 | 1416.16667 | 0 | 0 |
| 29 | 1416.16667 | 0 | 0 |
| 30 | 1416.16667 | 0 | 0 |
| 31 | 1416.16667 | 0 | 0 |
| 32 | 1416.16667 | 0 | 0 |
| 33 | 1416.16667 | 0 | 0 |
| 34 | 1416.16667 | 0 | 0 |
| 35 | 1416.16667 | 0 | 0 |
| 36 | 1416.16667 | 0 | 0 |
| 37 | 1416.16667 | 0 | 0 |
| 38 | 1416.16667 | 0 | 0 |
| 39 | 1416.16667 | 0 | 0 |
| 40 | 1416.16667 | 0 | 0 |
| 41 | 1416.16667 | 0 | 0 |
| 42 | 1416.16667 | 0 | 0 |
| 43 | 1416.16667 | 0 | 0 |
| 44 | 1416.16667 | 0 | 0 |
| 45 | 1416.16667 | 0 | 0 |
| 46 | 1416.16667 | 0 | 0 |
| 47 | 1416.16667 | 0 | 0 |
| 48 | 1416.16667 | 0 | 0 |
| 49 | 1416.16667 | 0 | 0 |
| 50 | 1416.16667 | 0 | 0 |
| 51 | 1416.16667 | 0 | 0 |
| 52 | 1416.16667 | 0 | 0 |
| 53 | 1416.16667 | 0 | 0 |
| 54 | 1416.16667 | 0 | 0 |
| 55 | 1416.16667 | 0 | 0 |
| 56 | 1416.16667 | 0 | 0 |
| 57 | 1416.16667 | 0 | 0 |
| 58 | 1416.16667 | 0 | 0 |
| 59 | 1416.16667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 1416.16667 | 0 | 0 |
| 4 | 1416.16667 | 0 | 0 |
| 5 | 1416.16667 | 0 | 0 |
| 6 | 1416.16667 | 0 | 0 |
| 7 | 1416.16667 | 0 | 0 |
| 8 | 1416.16667 | 0 | 0 |
| 9 | 1416.16667 | 0 | 0 |
| 10 | 1416.16667 | 0 | 0 |
| 11 | 1416.16667 | 0 | 0 |
| 12 | 1416.16667 | 0 | 0 |
| 13 | 1416.16667 | 0 | 0 |
| 14 | 1416.16667 | 0 | 0 |
| 15 | 1416.16667 | 0 | 0 |
| 16 | 1416.16667 | 0 | 0 |
| 17 | 1416.16667 | 0 | 0 |
| 18 | 1416.16667 | 0 | 0 |
| 19 | 1416.16667 | 0 | 0 |
| 20 | 1416.16667 | 0 | 0 |
| 21 | 1416.16667 | 0 | 0 |
| 22 | 1416.16667 | 0 | 0 |
| 23 | 1416.16667 | 0 | 0 |
| 24 | 1416.16667 | 0 | 0 |
| 25 | 1416.16667 | 0 | 0 |
| 26 | 1416.16667 | 0 | 0 |
| 27 | 1416.16667 | 0 | 0 |
| 28 | 1416.16667 | 0 | 0 |
| 29 | 1416.16667 | 0 | 0 |
| 30 | 1416.16667 | 0 | 0 |
| 31 | 1416.16667 | 0 | 0 |
| 32 | 1416.16667 | 0 | 0 |
| 33 | 1416.16667 | 0 | 0 |
| 34 | 1440.16667 | 0 | 0 |
| 35 | 67.5 | 0 | 0 |
| 36 | 67.5 | 0 | 0 |
| 37 | 67.5 | 0 | 0 |
| 38 | 67.5 | 0 | 0 |
| 39 | 67.5 | 0 | 0 |
| 40 | 67.5 | 0 | 0 |
| 41 | 67.5 | 0 | 0 |
| 42 | 67.5 | 0 | 0 |
| 43 | 67.5 | 0 | 0 |
| 44 | 67.5 | 0 | 0 |
| 45 | 67.5 | 0 | 0 |
| 46 | 67.5 | 0 | 0 |
| 47 | 67.5 | 0 | 0 |
| 48 | 67.5 | 0 | 0 |
| 49 | 67.5 | 0 | 0 |
| 50 | 67.5 | 0 | 0 |
| 51 | 67.5 | 0 | 0 |
| 52 | 67.5 | 0 | 0 |
| 53 | 67.5 | 0 | 0 |
| 54 | 67.5 | 0 | 0 |
| 55 | 67.5 | 0 | 0 |
| 56 | 331.666667 | 0 | 0 |
| 57 | 330.333333 | 0 | 0 |
| 58 | 330.333333 | 0 | 0 |
| 59 | 330.333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 330.333333 | 0 | 0 |
| 4 | 330.333333 | 0 | 0 |
| 5 | 330.333333 | 0 | 0 |
| 6 | 330.333333 | 0 | 0 |
| 7 | 330.333333 | 0 | 0 |
| 8 | 330.333333 | 0 | 0 |
| 9 | 330.333333 | 0 | 0 |
| 10 | 80 | 0 | 0 |
| 11 | 80 | 0 | 0 |
| 12 | 80 | 0 | 0 |
| 13 | 80 | 0 | 0 |
| 14 | 80 | 0 | 0 |
| 15 | 80 | 0 | 0 |
| 16 | 1120.66667 | 0 | 0 |
| 17 | 1120.66667 | 0 | 0 |
| 18 | 1120.66667 | 0 | 0 |
| 19 | 1120.66667 | 0 | 0 |
| 20 | 1120.66667 | 0 | 0 |
| 21 | 1120.66667 | 0 | 0 |
| 22 | 1120.66667 | 0 | 0 |
| 23 | 1120.66667 | 0 | 0 |
| 24 | 1120.66667 | 0 | 0 |
| 25 | 1120.66667 | 0 | 0 |
| 26 | 1120.66667 | 0 | 0 |
| 27 | 1120.66667 | 0 | 0 |
| 28 | 1120.66667 | 0 | 0 |
| 29 | 1120.66667 | 0 | 0 |
| 30 | 1120.66667 | 0 | 0 |
| 31 | 1120.66667 | 0 | 0 |
| 32 | 1120.66667 | 0 | 0 |
| 33 | 1120.66667 | 0 | 0 |
| 34 | 1120.66667 | 0 | 0 |
| 35 | 1120.66667 | 0 | 0 |
| 36 | 1120.66667 | 0 | 0 |
| 37 | 1120.66667 | 0 | 0 |
| 38 | 1120.66667 | 0 | 0 |
| 39 | 1120.66667 | 0 | 0 |
| 40 | 1120.66667 | 0 | 0 |
| 41 | 1120.66667 | 0 | 0 |
| 42 | 1120.66667 | 0 | 0 |
| 43 | 1120.66667 | 0 | 0 |
| 44 | 1120.66667 | 0 | 0 |
| 45 | 1120.66667 | 0 | 0 |
| 46 | 1120.66667 | 0 | 0 |
| 47 | 1120.66667 | 0 | 0 |
| 48 | 1120.66667 | 0 | 0 |
| 49 | 1120.66667 | 0 | 0 |
| 50 | 1120.66667 | 0 | 0 |
| 51 | 1120.66667 | 0 | 0 |
| 52 | 1120.66667 | 0 | 0 |
| 53 | 1120.66667 | 0 | 0 |
| 54 | 1120.66667 | 0 | 0 |
| 55 | 1120.66667 | 0 | 0 |
| 56 | 1120.66667 | 0 | 0 |
| 57 | 1120.66667 | 0 | 0 |
| 58 | 1120.66667 | 0 | 0 |
| 59 | 1120.66667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 1120.66667 | 0 | 0 |
| 4 | 1120.66667 | 0 | 0 |
| 5 | 1120.66667 | 0 | 0 |
| 6 | 1120.66667 | 0 | 0 |
| 7 | 1120.66667 | 0 | 0 |
| 8 | 1120.66667 | 0 | 0 |
| 9 | 1120.66667 | 0 | 0 |
| 10 | 1120.66667 | 0 | 0 |
| 11 | 255.66667 | 0 | 0 |
| 12 | 255.66667 | 0 | 0 |
| 13 | 255.66667 | 0 | 0 |
| 14 | 255.66667 | 0 | 0 |
| 15 | 255.66667 | 0 | 0 |
| 16 | 255.66667 | 0 | 0 |
| 17 | 255.66667 | 0 | 0 |
| 18 | 255.66667 | 0 | 0 |
| 19 | 255.66667 | 0 | 0 |
| 20 | 255.66667 | 0 | 0 |
| 21 | 255.66667 | 0 | 0 |
| 22 | 255.66667 | 0 | 0 |
| 23 | 255.66667 | 0 | 0 |
| 24 | 255.66667 | 0 | 0 |
| 25 | 255.66667 | 0 | 0 |
| 26 | 255.66667 | 0 | 0 |
| 27 | 255.66667 | 0 | 0 |
| 28 | 255.66667 | 0 | 0 |
| 29 | 255.66667 | 0 | 0 |
| 30 | 255.66667 | 0 | 0 |
| 31 | 255.66667 | 0 | 0 |
| 32 | 255.66667 | 0 | 0 |
| 33 | 255.66667 | 0 | 0 |
| 34 | 255.66667 | 0 | 0 |
| 35 | 255.66667 | 0 | 0 |
| 36 | 255.66667 | 0 | 0 |
| 37 | 255.66667 | 0 | 0 |
| 38 | 255.66667 | 0 | 0 |
| 39 | 255.66667 | 0 | 0 |
| 40 | 255.66667 | 0 | 0 |
| 41 | 255.66667 | 0 | 0 |
| 42 | 255.66667 | 0 | 0 |
| 43 | 255.66667 | 0 | 0 |
| 44 | 255.66667 | 0 | 0 |
| 45 | 255.66667 | 0 | 0 |
| 46 | 255.66667 | 0 | 0 |
| 47 | 255.66667 | 0 | 0 |
| 48 | 255.66667 | 0 | 0 |
| 49 | 255.66667 | 0 | 0 |
| 50 | 255.66667 | 0 | 0 |
| 51 | 255.66667 | 0 | 0 |
| 52 | 255.66667 | 0 | 0 |
| 53 | 255.66667 | 0 | 0 |
| 54 | 255.66667 | 0 | 0 |
| 55 | 255.66667 | 0 | 0 |
| 56 | 255.66667 | 0 | 0 |
| 57 | 255.66667 | 0 | 0 |
| 58 | 255.66667 | 0 | 0 |
| 59 | 255.66667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 255.666667 | 0 | 0 |
| 4 | 140.166667 | 0 | 0 |
| 5 | 140.166667 | 0 | 0 |
| 6 | 140.166667 | 0 | 0 |
| 7 | 140.166667 | 0 | 0 |
| 8 | 140.166667 | 0 | 0 |
| 9 | 140.166667 | 0 | 0 |
| 10 | 140.166667 | 0 | 0 |
| 11 | 140.166667 | 0 | 0 |
| 12 | 114.333333 | 0 | 0 |
| 13 | 114.333333 | 0 | 0 |
| 14 | 114.333333 | 0 | 0 |
| 15 | 114.333333 | 0 | 0 |
| 16 | 114.333333 | 0 | 0 |
| 17 | 114.333333 | 0 | 0 |
| 18 | 114.333333 | 0 | 0 |
| 19 | 114.333333 | 0 | 0 |
| 20 | 114.333333 | 0 | 0 |
| 21 | 114.333333 | 0 | 0 |
| 22 | 114.333333 | 0 | 0 |
| 23 | 114.333333 | 0 | 0 |
| 24 | 114.333333 | 0 | 0 |
| 25 | 114.333333 | 0 | 0 |
| 26 | 296.666667 | 0 | 0 |
| 27 | 296.666667 | 0 | 0 |
| 28 | 295.166667 | 0 | 0 |
| 29 | 295.166667 | 0 | 0 |
| 30 | 295.166667 | 0 | 0 |
| 31 | 295.166667 | 0 | 0 |
| 32 | 295.166667 | 0 | 0 |
| 33 | 295.166667 | 0 | 0 |
| 34 | 295.166667 | 0 | 0 |
| 35 | 295.166667 | 0 | 0 |
| 36 | 295.166667 | 0 | 0 |
| 37 | 295.166667 | 0 | 0 |
| 38 | 295.166667 | 0 | 0 |
| 39 | 295.166667 | 0 | 0 |
| 40 | 295.166667 | 0 | 0 |
| 41 | 295.166667 | 0 | 0 |
| 42 | 295.166667 | 0 | 0 |
| 43 | 295.166667 | 0 | 0 |
| 44 | 295.166667 | 0 | 0 |
| 45 | 295.166667 | 0 | 0 |
| 46 | 295.166667 | 0 | 0 |
| 47 | 295.166667 | 0 | 0 |
| 48 | 295.166667 | 0 | 0 |
| 49 | 295.166667 | 0 | 0 |
| 50 | 295.166667 | 0 | 0 |
| 51 | 295.166667 | 0 | 0 |
| 52 | 295.166667 | 0 | 0 |
| 53 | 295.166667 | 0 | 0 |
| 54 | 295.166667 | 0 | 0 |
| 55 | 295.166667 | 0 | 0 |
| 56 | 295.166667 | 0 | 0 |
| 57 | 295.166667 | 0 | 0 |
| 58 | 295.166667 | 0 | 0 |
| 59 | 559.333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 559.333333 | 0 | 0 |
| 4 | 559.333333 | 0 | 0 |
| 5 | 559.333333 | 0 | 0 |
| 6 | 559.333333 | 0 | 0 |
| 7 | 559.333333 | 0 | 0 |
| 8 | 559.333333 | 0 | 0 |
| 9 | 559.333333 | 0 | 0 |
| 10 | 559.333333 | 0 | 0 |
| 11 | 559.333333 | 0 | 0 |
| 12 | 559.333333 | 0 | 0 |
| 13 | 559.333333 | 0 | 0 |
| 14 | 559.333333 | 0 | 0 |
| 15 | 559.333333 | 0 | 0 |
| 16 | 559.333333 | 0 | 0 |
| 17 | 559.333333 | 0 | 0 |
| 18 | 559.333333 | 0 | 0 |
| 19 | 559.333333 | 0 | 0 |
| 20 | 559.333333 | 0 | 0 |
| 21 | 559.333333 | 0 | 0 |
| 22 | 559.333333 | 0 | 0 |
| 23 | 559.333333 | 0 | 0 |
| 24 | 559.333333 | 0 | 0 |
| 25 | 559.333333 | 0 | 0 |
| 26 | 559.333333 | 0 | 0 |
| 27 | 559.333333 | 0 | 0 |
| 28 | 559.333333 | 0 | 0 |
| 29 | 559.333333 | 0 | 0 |
| 30 | 559.333333 | 0 | 0 |
| 31 | 559.333333 | 0 | 0 |
| 32 | 559.333333 | 0 | 0 |
| 33 | 559.333333 | 0 | 0 |
| 34 | 559.333333 | 0 | 0 |
| 35 | 559.333333 | 0 | 0 |
| 36 | 559.333333 | 0 | 0 |
| 37 | 559.333333 | 0 | 0 |
| 38 | 559.333333 | 0 | 0 |
| 39 | 559.333333 | 0 | 0 |
| 40 | 559.333333 | 0 | 0 |
| 41 | 559.333333 | 0 | 0 |
| 42 | 507.833333 | 0 | 0 |
| 43 | 504 | 0 | 0 |
| 44 | 504 | 0 | 0 |
| 45 | 504 | 0 | 0 |
| 46 | 504 | 0 | 0 |
| 47 | 504 | 0 | 0 |
| 48 | 504 | 0 | 0 |
| 49 | 504 | 0 | 0 |
| 50 | 504 | 0 | 0 |
| 51 | 504 | 0 | 0 |
| 52 | 504 | 0 | 0 |
| 53 | 504 | 0 | 0 |
| 54 | 504 | 0 | 0 |
| 55 | 504 | 0 | 0 |
| 56 | 504 | 0 | 0 |
| 57 | 504 | 0 | 0 |
| 58 | 504 | 0 | 0 |
| 59 | 504 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 504 | 0 | 0 |
| 4 | 504 | 0 | 0 |
| 5 | 504 | 0 | 0 |
| 6 | 504 | 0 | 0 |
| 7 | 504 | 0 | 0 |
| 8 | 504 | 0 | 0 |
| 9 | 504 | 0 | 0 |
| 10 | 504 | 0 | 0 |
| 11 | 504 | 0 | 0 |
| 12 | 504 | 0 | 0 |
| 13 | 504 | 0 | 0 |
| 14 | 504 | 0 | 0 |
| 15 | 504 | 0 | 0 |
| 16 | 504 | 0 | 0 |
| 17 | 504 | 0 | 0 |
| 18 | 504 | 0 | 0 |
| 19 | 504 | 0 | 0 |
| 20 | 504 | 0 | 0 |
| 21 | 504 | 0 | 0 |
| 22 | 504 | 0 | 0 |
| 23 | 504 | 0 | 0 |
| 24 | 504 | 0 | 0 |
| 25 | 504 | 0 | 0 |
| 26 | 504 | 0 | 0 |
| 27 | 504 | 0 | 0 |
| 28 | 504 | 0 | 0 |
| 29 | 504 | 0 | 0 |
| 30 | 504 | 0 | 0 |
| 31 | 504 | 0 | 0 |
| 32 | 504 | 0 | 0 |
| 33 | 504 | 0 | 0 |
| 34 | 504 | 0 | 0 |
| 35 | 504 | 0 | 0 |
| 36 | 504 | 0 | 0 |
| 37 | 504 | 0 | 0 |
| 38 | 504 | 0 | 0 |
| 39 | 476.5 | 0 | 0 |
| 40 | 476.5 | 0 | 0 |
| 41 | 476.5 | 0 | 0 |
| 42 | 476.5 | 0 | 0 |
| 43 | 476.5 | 0 | 0 |
| 44 | 663.833333 | 0 | 0 |
| 45 | 663.833333 | 0 | 0 |
| 46 | 663.833333 | 0 | 0 |
| 47 | 663.833333 | 0 | 0 |
| 48 | 663.833333 | 0 | 0 |
| 49 | 663.833333 | 0 | 0 |
| 50 | 663.833333 | 0 | 0 |
| 51 | 663.833333 | 0 | 0 |
| 52 | 663.833333 | 0 | 0 |
| 53 | 663.833333 | 0 | 0 |
| 54 | 663.833333 | 0 | 0 |
| 55 | 663.833333 | 0 | 0 |
| 56 | 663.833333 | 0 | 0 |
| 57 | 663.833333 | 0 | 0 |
| 58 | 663.833333 | 0 | 0 |
| 59 | 663.833333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 663.833333 | 0 | 0 |
| 4 | 663.833333 | 0 | 0 |
| 5 | 663.833333 | 0 | 0 |
| 6 | 663.833333 | 0 | 0 |
| 7 | 663.833333 | 0 | 0 |
| 8 | 663.833333 | 0 | 0 |
| 9 | 663.833333 | 0 | 0 |
| 10 | 663.833333 | 0 | 0 |
| 11 | 663.833333 | 0 | 0 |
| 12 | 663.833333 | 0 | 0 |
| 13 | 663.833333 | 0 | 0 |
| 14 | 663.833333 | 0 | 0 |
| 15 | 663.833333 | 0 | 0 |
| 16 | 663.833333 | 0 | 0 |
| 17 | 663.833333 | 0 | 0 |
| 18 | 663.833333 | 0 | 0 |
| 19 | 663.833333 | 0 | 0 |
| 20 | 663.833333 | 0 | 0 |
| 21 | 663.833333 | 0 | 0 |
| 22 | 663.833333 | 0 | 0 |
| 23 | 663.833333 | 0 | 0 |
| 24 | 663.833333 | 0 | 0 |
| 25 | 663.833333 | 0 | 0 |
| 26 | 663.833333 | 0 | 0 |
| 27 | 663.833333 | 0 | 0 |
| 28 | 663.833333 | 0 | 0 |
| 29 | 663.833333 | 0 | 0 |
| 30 | 663.833333 | 0 | 0 |
| 31 | 663.833333 | 0 | 0 |
| 32 | 663.833333 | 0 | 0 |
| 33 | 663.833333 | 0 | 0 |
| 34 | 666.833333 | 0 | 0 |
| 35 | 480 | 0 | 0 |
| 36 | 480 | 0 | 0 |
| 37 | | | |
| 38 | 421.166667 | 0 | 0 |
| 39 | 420.5 | 0 | 0 |
| 40 | 420.5 | 0 | 0 |
| 41 | 420.5 | 0 | 0 |
| 42 | 420.5 | 0 | 0 |
| 43 | 420.5 | 0 | 0 |
| 44 | 420.5 | 0 | 0 |
| 45 | 420.5 | 0 | 0 |
| 46 | 420.5 | 0 | 0 |
| 47 | 420.5 | 0 | 0 |
| 48 | 420.5 | 0 | 0 |
| 49 | 420.5 | 0 | 0 |
| 50 | 420.5 | 0 | 0 |
| 51 | 420.5 | 0 | 0 |
| 52 | 420.5 | 0 | 0 |
| 53 | 420.5 | 0 | 0 |
| 54 | 420.5 | 0 | 0 |
| 55 | 420.5 | 0 | 0 |
| 56 | 420.5 | 0 | 0 |
| 57 | 420.5 | 0 | 0 |
| 58 | 420.5 | 0 | 0 |
| 59 | 420.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 420.5 | 0 | 0 |
| 4 | 420.5 | 0 | 0 |
| 5 | 420.5 | 0 | 0 |
| 6 | 420.5 | 0 | 0 |
| 7 | 420.5 | 0 | 0 |
| 8 | 420.5 | 0 | 0 |
| 9 | 420.5 | 0 | 0 |
| 10 | 420.5 | 0 | 0 |
| 11 | 420.5 | 0 | 0 |
| 12 | 420.5 | 0 | 0 |
| 13 | 420.5 | 0 | 0 |
| 14 | 420.5 | 0 | 0 |
| 15 | 420.5 | 0 | 0 |
| 16 | 420.5 | 0 | 0 |
| 17 | 420.5 | 0 | 0 |
| 18 | 420.5 | 0 | 0 |
| 19 | 420.5 | 0 | 0 |
| 20 | 420.5 | 0 | 0 |
| 21 | 420.5 | 0 | 0 |
| 22 | 420.5 | 0 | 0 |
| 23 | 420.5 | 0 | 0 |
| 24 | 420.5 | 0 | 0 |
| 25 | 420.5 | 0 | 0 |
| 26 | 420.5 | 0 | 0 |
| 27 | 420.5 | 0 | 0 |
| 28 | 420.5 | 0 | 0 |
| 29 | 420.5 | 0 | 0 |
| 30 | 420.5 | 0 | 0 |
| 31 | 420.5 | 0 | 0 |
| 32 | 420.5 | 0 | 0 |
| 33 | 420.5 | 0 | 0 |
| 34 | 420.5 | 0 | 0 |
| 35 | 420.5 | 0 | 0 |
| 36 | 420.5 | 0 | 0 |
| 37 | 420.5 | 0 | 0 |
| 38 | 420.5 | 0 | 0 |
| 39 | 420.5 | 0 | 0 |
| 40 | 420.5 | 0 | 0 |
| 41 | 420.5 | 0 | 0 |
| 42 | 420.5 | 0 | 0 |
| 43 | 420.5 | 0 | 0 |
| 44 | 420.5 | 0 | 0 |
| 45 | 420.5 | 0 | 0 |
| 46 | 420.5 | 0 | 0 |
| 47 | 420.5 | 0 | 0 |
| 48 | 420.5 | 0 | 0 |
| 49 | 420.5 | 0 | 0 |
| 50 | 420.5 | 0 | 0 |
| 51 | 420.5 | 0 | 0 |
| 52 | 420.5 | 0 | 0 |
| 53 | 420.5 | 0 | 0 |
| 54 | 420.5 | 0 | 0 |
| 55 | 420.5 | 0 | 0 |
| 56 | 420.5 | 0 | 0 |
| 57 | 421.5 | 0 | 0 |
| 58 | 421.5 | 0 | 0 |
| 59 | 105.333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 105.333333 | 0 | 0 |
| 4 | 105.333333 | 0 | 0 |
| 5 | 105.333333 | 0 | 0 |
| 6 | 412.833333 | 0 | 0 |
| 7 | 412.833333 | 0 | 0 |
| 8 | 396.333333 | 0 | 0 |
| 9 | 396.333333 | 0 | 0 |
| 10 | 396.333333 | 0 | 0 |
| 11 | 396.333333 | 0 | 0 |
| 12 | 396.333333 | 0 | 0 |
| 13 | 396.333333 | 0 | 0 |
| 14 | 348.5 | 0 | 0 |
| 15 | 348.333333 | 0 | 0 |
| 16 | 348.333333 | 0 | 0 |
| 17 | 348.333333 | 0 | 0 |
| 18 | 348.333333 | 0 | 0 |
| 19 | 348.333333 | 0 | 0 |
| 20 | 348.333333 | 0 | 0 |
| 21 | 348.333333 | 0 | 0 |
| 22 | 348.333333 | 0 | 0 |
| 23 | 348.333333 | 0 | 0 |
| 24 | 348.333333 | 0 | 0 |
| 25 | 348.333333 | 0 | 0 |
| 26 | 348.333333 | 0 | 0 |
| 27 | 348.333333 | 0 | 0 |
| 28 | 348.333333 | 0 | 0 |
| 29 | 348.333333 | 0 | 0 |
| 30 | 348.333333 | 0 | 0 |
| 31 | 348.333333 | 0 | 0 |
| 32 | 348.333333 | 0 | 0 |
| 33 | 348.333333 | 0 | 0 |
| 34 | 348.333333 | 0 | 0 |
| 35 | 348.333333 | 0 | 0 |
| 36 | 348.333333 | 0 | 0 |
| 37 | 348.333333 | 0 | 0 |
| 38 | 348.333333 | 0 | 0 |
| 39 | 348.333333 | 0 | 0 |
| 40 | 348.333333 | 0 | 0 |
| 41 | 348.333333 | 0 | 0 |
| 42 | 348.333333 | 0 | 0 |
| 43 | 332.666667 | 0 | 0 |
| 44 | 332.666667 | 0 | 0 |
| 45 | 332.666667 | 0 | 0 |
| 46 | 332.666667 | 0 | 0 |
| 47 | 332.666667 | 0 | 0 |
| 48 | 332.666667 | 0 | 0 |
| 49 | 332.666667 | 0 | 0 |
| 50 | 332.666667 | 0 | 0 |
| 51 | 332.666667 | 0 | 0 |
| 52 | 332.666667 | 0 | 0 |
| 53 | 332.666667 | 0 | 0 |
| 54 | 332.666667 | 0 | 0 |
| 55 | 332.666667 | 0 | 0 |
| 56 | 332.666667 | 0 | 0 |
| 57 | 332.666667 | 0 | 0 |
| 58 | 332.666667 | 0 | 0 |
| 59 | 332.666667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 332.666667 | 0 | 0 |
| 4 | 332.666667 | 0 | 0 |
| 5 | 332.666667 | 0 | 0 |
| 6 | 332.666667 | 0 | 0 |
| 7 | 332.666667 | 0 | 0 |
| 8 | 332.666667 | 0 | 0 |
| 9 | 332.666667 | 0 | 0 |
| 10 | 332.666667 | 0 | 0 |
| 11 | 332.666667 | 0 | 0 |
| 12 | 332.666667 | 0 | 0 |
| 13 | 332.666667 | 0 | 0 |
| 14 | 332.666667 | 0 | 0 |
| 15 | 332.666667 | 0 | 0 |
| 16 | 332.666667 | 0 | 0 |
| 17 | 332.666667 | 0 | 0 |
| 18 | 332.666667 | 0 | 0 |
| 19 | 332.666667 | 0 | 0 |
| 20 | 332.666667 | 0 | 0 |
| 21 | 332.666667 | 0 | 0 |
| 22 | 332.666667 | 0 | 0 |
| 23 | 332.666667 | 0 | 0 |
| 24 | 332.666667 | 0 | 0 |
| 25 | 332.666667 | 0 | 0 |
| 26 | 332.666667 | 0 | 0 |
| 27 | 332.666667 | 0 | 0 |
| 28 | 128.333333 | 0 | 0 |
| 29 | 128.333333 | 0 | 0 |
| 30 | 128.333333 | 0 | 0 |
| 31 | 128.333333 | 0 | 0 |
| 32 | 128.333333 | 0 | 0 |
| 33 | 128.333333 | 0 | 0 |
| 34 | 128.333333 | 0 | 0 |
| 35 | 128.333333 | 0 | 0 |
| 36 | 128.333333 | 0 | 0 |
| 37 | 128.333333 | 0 | 0 |
| 38 | 128.333333 | 0 | 0 |
| 39 | 128.333333 | 0 | 0 |
| 40 | 128.333333 | 0 | 0 |
| 41 | 128.333333 | 0 | 0 |
| 42 | 128.333333 | 0 | 0 |
| 43 | 128.333333 | 0 | 0 |
| 44 | 128.333333 | 0 | 0 |
| 45 | 128.333333 | 0 | 0 |
| 46 | 128.333333 | 0 | 0 |
| 47 | 128.333333 | 0 | 0 |
| 48 | 128.333333 | 0 | 0 |
| 49 | 128.333333 | 0 | 0 |
| 50 | 128.333333 | 0 | 0 |
| 51 | 128.333333 | 0 | 0 |
| 52 | 128.333333 | 0 | 0 |
| 53 | 128.333333 | 0 | 0 |
| 54 | 128.333333 | 0 | 0 |
| 55 | 128.333333 | 0 | 0 |
| 56 | 128.333333 | 0 | 0 |
| 57 | 128.333333 | 0 | 0 |
| 58 | 128.333333 | 0 | 0 |
| 59 | 128.333333 | 0 | 0 |
| 60 | | | |

1
2
3 128.333333 0 0
4 128.333333 0 0
5 128.333333 0 0
6 128.333333 0 0
7 128.333333 0 0
8 128.333333 0 0
9 128.333333 0 0
10 128.333333 0 0
11 128.333333 0 0
12 128.333333 0 0
13 128.333333 0 0
14 128.333333 0 0
15 128.333333 0 0
16 128.333333 0 0
17 128.333333 0 0
18 128.333333 0 0
19 128.333333 0 0
20 128.333333 0 0
21 128.333333 0 0
22 128.333333 0 0
23 128.333333 0 0
24 128.333333 0 0
25 128.333333 0 0
26 128.333333 0 0
27 128.333333 0 0
28 128.333333 0 0
29 128.333333 0 0
30 128.333333 0 0
31 128.333333 0 0
32 128.333333 0 0
33 128.333333 0 0
34 128.333333 0 0
35 128.333333 0 0
36 128.333333 0 0
37 128.333333 0 0
38 128.333333 0 0
39 128.333333 0 0
40 128.333333 0 0
41 128.333333 0 0
42 128.333333 0 0
43 128.333333 0 0
44 128.333333 0 0
45 128.333333 0 0
46 128.333333 0 0
47 128.333333 0 0
48 128.333333 0 0
49 128.333333 0 0
50 128.333333 0 0
51 128.333333 0 0
52 128.333333 0 0
53 128.333333 0 0
54 128.333333 0 0
55 128.333333 0 0
56 128.333333 0 0
57 128.333333 0 0
58 128.333333 0 0
59 128.333333 0 0
60

Do not distribute

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 128.333333 | 0 | 0 |
| 4 | 128.333333 | 0 | 0 |
| 5 | 128.333333 | 0 | 0 |
| 6 | 128.333333 | 0 | 0 |
| 7 | 128.333333 | 0 | 0 |
| 8 | 128.333333 | 0 | 0 |
| 9 | 128.333333 | 0 | 0 |
| 10 | 128.333333 | 0 | 0 |
| 11 | 128.333333 | 0 | 0 |
| 12 | 128.333333 | 0 | 0 |
| 13 | 128.333333 | 0 | 0 |
| 14 | 128.333333 | 0 | 0 |
| 15 | 128.333333 | 0 | 0 |
| 16 | 128.333333 | 0 | 0 |
| 17 | 128.333333 | 0 | 0 |
| 18 | 128.333333 | 0 | 0 |
| 19 | 128.333333 | 0 | 0 |
| 20 | 128.333333 | 0 | 0 |
| 21 | 128.333333 | 0 | 0 |
| 22 | 128.333333 | 0 | 0 |
| 23 | 128.333333 | 0 | 0 |
| 24 | 128.333333 | 0 | 0 |
| 25 | 128.333333 | 0 | 0 |
| 26 | 128.333333 | 0 | 0 |
| 27 | 128.333333 | 0 | 0 |
| 28 | 165 | 0 | 0 |
| 29 | 165 | 0 | 0 |
| 30 | 165 | 0 | 0 |
| 31 | 165 | 0 | 0 |
| 32 | 165 | 0 | 0 |
| 33 | 165 | 0 | 0 |
| 34 | 165 | 0 | 0 |
| 35 | 55.3333333 | 0 | 0 |
| 36 | 55.3333333 | 0 | 0 |
| 37 | 55.3333333 | 0 | 0 |
| 38 | 55.3333333 | 0 | 0 |
| 39 | 55.3333333 | 0 | 0 |
| 40 | 55.3333333 | 0 | 0 |
| 41 | 55.3333333 | 0 | 0 |
| 42 | 55.3333333 | 0 | 0 |
| 43 | 55.3333333 | 0 | 0 |
| 44 | 55.3333333 | 0 | 0 |
| 45 | 55.3333333 | 0 | 0 |
| 46 | 55.3333333 | 0 | 0 |
| 47 | 55.3333333 | 0 | 0 |
| 48 | 102.166667 | 0 | 0 |
| 49 | 102 | 0 | 0 |
| 50 | 102 | 0 | 0 |
| 51 | 102 | 0 | 0 |
| 52 | 102 | 0 | 0 |
| 53 | 102 | 0 | 0 |
| 54 | 102 | 0 | 0 |
| 55 | 102 | 0 | 0 |
| 56 | 102 | 0 | 0 |
| 57 | 102 | 0 | 0 |
| 58 | 102 | 0 | 0 |
| 59 | 102 | 0 | 0 |
| 60 | | | |

| | | | |
|----|-------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 102 | 0 | 0 |
| 4 | 102 | 0 | 0 |
| 5 | 102 | 0 | 0 |
| 6 | 102 | 0 | 0 |
| 7 | 102 | 0 | 0 |
| 8 | 102 | 0 | 0 |
| 9 | 102 | 0 | 0 |
| 10 | 102 | 0 | 0 |
| 11 | 715.5 | 0 | 0 |
| 12 | 715.5 | 0 | 0 |
| 13 | 715.5 | 0 | 0 |
| 14 | 715.5 | 0 | 0 |
| 15 | 715.5 | 0 | 0 |
| 16 | 715.5 | 0 | 0 |
| 17 | 715.5 | 0 | 0 |
| 18 | 715.5 | 0 | 0 |
| 19 | 715.5 | 0 | 0 |
| 20 | 715.5 | 0 | 0 |
| 21 | 715.5 | 0 | 0 |
| 22 | 715.5 | 0 | 0 |
| 23 | 715.5 | 0 | 0 |
| 24 | 715.5 | 0 | 0 |
| 25 | 715.5 | 0 | 0 |
| 26 | 715.5 | 0 | 0 |
| 27 | 715.5 | 0 | 0 |
| 28 | 715.5 | 0 | 0 |
| 29 | 715.5 | 0 | 0 |
| 30 | 715.5 | 0 | 0 |
| 31 | 715.5 | 0 | 0 |
| 32 | 715.5 | 0 | 0 |
| 33 | 715.5 | 0 | 0 |
| 34 | 715.5 | 0 | 0 |
| 35 | 715.5 | 0 | 0 |
| 36 | 715.5 | 0 | 0 |
| 37 | 715.5 | 0 | 0 |
| 38 | 715.5 | 0 | 0 |
| 39 | 715.5 | 0 | 0 |
| 40 | 715.5 | 0 | 0 |
| 41 | 715.5 | 0 | 0 |
| 42 | 715.5 | 0 | 0 |
| 43 | 715.5 | 0 | 0 |
| 44 | 715.5 | 0 | 0 |
| 45 | 715.5 | 0 | 0 |
| 46 | 715.5 | 0 | 0 |
| 47 | 715.5 | 0 | 0 |
| 48 | 715.5 | 0 | 0 |
| 49 | 715.5 | 0 | 0 |
| 50 | 715.5 | 0 | 0 |
| 51 | 715.5 | 0 | 0 |
| 52 | 715.5 | 0 | 0 |
| 53 | 715.5 | 0 | 0 |
| 54 | 715.5 | 0 | 0 |
| 55 | 715.5 | 0 | 0 |
| 56 | 715.5 | 0 | 0 |
| 57 | 715.5 | 0 | 0 |
| 58 | 715.5 | 0 | 0 |
| 59 | 715.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 715.5 | 0 | 0 |
| 4 | 715.5 | 0 | 0 |
| 5 | 715.5 | 0 | 0 |
| 6 | 715.5 | 0 | 0 |
| 7 | 715.5 | 0 | 0 |
| 8 | 715.5 | 0 | 0 |
| 9 | 715.5 | 0 | 0 |
| 10 | 715.5 | 0 | 0 |
| 11 | 715.5 | 0 | 0 |
| 12 | 715.5 | 0 | 0 |
| 13 | 715.5 | 0 | 0 |
| 14 | 715.5 | 0 | 0 |
| 15 | 715.5 | 0 | 0 |
| 16 | 715.5 | 0 | 0 |
| 17 | 715.5 | 0 | 0 |
| 18 | 715.5 | 0 | 0 |
| 19 | 715.5 | 0 | 0 |
| 20 | 715.5 | 0 | 0 |
| 21 | 715.5 | 0 | 0 |
| 22 | 718.16667 | 0 | 0 |
| 23 | 718.16667 | 0 | 0 |
| 24 | 5297.16667 | 0 | 0 |
| 25 | 5297.16667 | 0 | 0 |
| 26 | 5297.16667 | 0 | 0 |
| 27 | 5297.16667 | 0 | 0 |
| 28 | 5297.16667 | 0 | 0 |
| 29 | 5297.16667 | 0 | 0 |
| 30 | 5297.16667 | 0 | 0 |
| 31 | 5255 | 0 | 0 |
| 32 | 5255 | 0 | 0 |
| 33 | 5255 | 0 | 0 |
| 34 | 5255 | 0 | 0 |
| 35 | 5255 | 0 | 0 |
| 36 | 5255 | 0 | 0 |
| 37 | 5255 | 0 | 0 |
| 38 | 5255 | 0 | 0 |
| 39 | 5255 | 0 | 0 |
| 40 | 5255 | 0 | 0 |
| 41 | 5255 | 0 | 0 |
| 42 | 5255 | 0 | 0 |
| 43 | 5255 | 0 | 0 |
| 44 | 469 | 0 | 0 |
| 45 | 469 | 0 | 0 |
| 46 | 469 | 0 | 0 |
| 47 | 469 | 0 | 0 |
| 48 | 469 | 0 | 0 |
| 49 | 469 | 0 | 0 |
| 50 | 469 | 0 | 0 |
| 51 | 469 | 0 | 0 |
| 52 | 469 | 0 | 0 |
| 53 | 469 | 0 | 0 |
| 54 | 469 | 0 | 0 |
| 55 | 469 | 0 | 0 |
| 56 | 469 | 0 | 0 |
| 57 | 469 | 0 | 0 |
| 58 | 469 | 0 | 0 |
| 59 | 469 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 469 | 0 | 0 |
| 4 | 469 | 0 | 0 |
| 5 | 469 | 0 | 0 |
| 6 | 469 | 0 | 0 |
| 7 | 469 | 0 | 0 |
| 8 | 469 | 0 | 0 |
| 9 | 469 | 0 | 0 |
| 10 | 469 | 0 | 0 |
| 11 | 469 | 0 | 0 |
| 12 | 469 | 0 | 0 |
| 13 | 469 | 0 | 0 |
| 14 | 469 | 0 | 0 |
| 15 | 469 | 0 | 0 |
| 16 | 469 | 0 | 0 |
| 17 | 469 | 0 | 0 |
| 18 | 469 | 0 | 0 |
| 19 | 469 | 0 | 0 |
| 20 | 469 | 0 | 0 |
| 21 | 469 | 0 | 0 |
| 22 | 469 | 0 | 0 |
| 23 | 469 | 0 | 0 |
| 24 | 469 | 0 | 0 |
| 25 | 469 | 0 | 0 |
| 26 | 469 | 0 | 0 |
| 27 | 469 | 0 | 0 |
| 28 | 469 | 0 | 0 |
| 29 | 469 | 0 | 0 |
| 30 | 469 | 0 | 0 |
| 31 | 469 | 0 | 0 |
| 32 | 4498.66667 | 0 | 0 |
| 33 | 4498.66667 | 0 | 0 |
| 34 | 4498.66667 | 0 | 0 |
| 35 | 4498.66667 | 0 | 0 |
| 36 | 4498.66667 | 0 | 0 |
| 37 | 507 | 0 | 0 |
| 38 | 507 | 0 | 0 |
| 39 | 507 | 0 | 0 |
| 40 | 507 | 0 | 0 |
| 41 | 507 | 0 | 0 |
| 42 | 507 | 0 | 0 |
| 43 | 507 | 0 | 0 |
| 44 | 507 | 0 | 0 |
| 45 | 507 | 0 | 0 |
| 46 | 507 | 0 | 0 |
| 47 | 507 | 0 | 0 |
| 48 | 507 | 0 | 0 |
| 49 | 75.3333333 | 0 | 0 |
| 50 | 75.3333333 | 0 | 0 |
| 51 | 75.3333333 | 0 | 0 |
| 52 | 75.3333333 | 0 | 0 |
| 53 | 75.3333333 | 0 | 0 |
| 54 | 75.3333333 | 0 | 0 |
| 55 | 75.3333333 | 0 | 0 |
| 56 | 75.3333333 | 0 | 0 |
| 57 | 75.3333333 | 0 | 0 |
| 58 | 75.3333333 | 0 | 0 |
| 59 | 75.3333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 85.6666667 | 0 | 0 |
| 4 | 85.6666667 | 0 | 0 |
| 5 | 85.6666667 | 0 | 0 |
| 6 | 85.6666667 | 0 | 0 |
| 7 | 85.6666667 | 0 | 0 |
| 8 | 85.6666667 | 0 | 0 |
| 9 | 85.6666667 | 0 | 0 |
| 10 | 85.6666667 | 0 | 0 |
| 11 | 85.6666667 | 0 | 0 |
| 12 | 85.6666667 | 0 | 0 |
| 13 | 85.6666667 | 0 | 0 |
| 14 | 85.6666667 | 0 | 0 |
| 15 | 85.6666667 | 0 | 0 |
| 16 | 85.6666667 | 0 | 0 |
| 17 | 85.6666667 | 0 | 0 |
| 18 | 85.6666667 | 0 | 0 |
| 19 | 85.6666667 | 0 | 0 |
| 20 | 85.6666667 | 0 | 0 |
| 21 | 85.6666667 | 0 | 0 |
| 22 | 85.6666667 | 0 | 0 |
| 23 | 87.6666667 | 0 | 0 |
| 24 | 826 | 0 | 0 |
| 25 | 826 | 0 | 0 |
| 26 | 826 | 0 | 0 |
| 27 | 826 | 0 | 0 |
| 28 | 826 | 0 | 0 |
| 29 | 826 | 0 | 0 |
| 30 | 826 | 0 | 0 |
| 31 | 822.5 | 0 | 0 |
| 32 | 822.5 | 0 | 0 |
| 33 | 822.5 | 0 | 0 |
| 34 | 822.5 | 0 | 0 |
| 35 | 822.5 | 0 | 0 |
| 36 | 822.5 | 0 | 0 |
| 37 | 822.5 | 0 | 0 |
| 38 | 822.5 | 0 | 0 |
| 39 | 822.5 | 0 | 0 |
| 40 | 822.5 | 0 | 0 |
| 41 | 822.5 | 0 | 0 |
| 42 | 822.5 | 0 | 0 |
| 43 | 822.5 | 0 | 0 |
| 44 | 822.5 | 0 | 0 |
| 45 | 822.5 | 0 | 0 |
| 46 | 822.5 | 0 | 0 |
| 47 | 822.5 | 0 | 0 |
| 48 | 822.5 | 0 | 0 |
| 49 | 822.5 | 0 | 0 |
| 50 | 822.5 | 0 | 0 |
| 51 | 822.5 | 0 | 0 |
| 52 | 822.5 | 0 | 0 |
| 53 | 822.5 | 0 | 0 |
| 54 | 822.5 | 0 | 0 |
| 55 | 822.5 | 0 | 0 |
| 56 | 822.5 | 0 | 0 |
| 57 | 822.5 | 0 | 0 |
| 58 | 822.5 | 0 | 0 |
| 59 | 822.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 822.5 | 0 | 0 |
| 4 | 822.5 | 0 | 0 |
| 5 | 822.5 | 0 | 0 |
| 6 | 822.5 | 0 | 0 |
| 7 | 822.5 | 0 | 0 |
| 8 | 822.5 | 0 | 0 |
| 9 | 822.5 | 0 | 0 |
| 10 | 822.5 | 0 | 0 |
| 11 | 822.5 | 0 | 0 |
| 12 | 822.5 | 0 | 0 |
| 13 | 822.5 | 0 | 0 |
| 14 | 822.5 | 0 | 0 |
| 15 | 822.5 | 0 | 0 |
| 16 | 822.5 | 0 | 0 |
| 17 | 822.5 | 0 | 0 |
| 18 | 822.5 | 0 | 0 |
| 19 | 60.3333333 | 0 | 0 |
| 20 | 60.3333333 | 0 | 0 |
| 21 | 60.3333333 | 0 | 0 |
| 22 | 60.3333333 | 0 | 0 |
| 23 | 60.3333333 | 0 | 0 |
| 24 | 60.3333333 | 0 | 0 |
| 25 | 60.3333333 | 0 | 0 |
| 26 | 60.3333333 | 0 | 0 |
| 27 | 60.3333333 | 0 | 0 |
| 28 | 60.3333333 | 0 | 0 |
| 29 | 60.3333333 | 0 | 0 |
| 30 | 60.3333333 | 0 | 0 |
| 31 | 60.3333333 | 0 | 0 |
| 32 | 228.166667 | 0 | 0 |
| 33 | 107.166667 | 0 | 0 |
| 34 | 105.166667 | 0 | 0 |
| 35 | 105.166667 | 0 | 0 |
| 36 | 105.166667 | 0 | 0 |
| 37 | 105.166667 | 0 | 0 |
| 38 | 105.166667 | 0 | 0 |
| 39 | 76.6666667 | 0 | 0 |
| 40 | 76.6666667 | 0 | 0 |
| 41 | 73 | 0 | 0 |
| 42 | 73 | 0 | 0 |
| 43 | 73 | 0 | 0 |
| 44 | 73 | 0 | 0 |
| 45 | 73 | 0 | 0 |
| 46 | 73 | 0 | 0 |
| 47 | 73 | 0 | 0 |
| 48 | 106 | 0 | 0 |
| 49 | 105.666667 | 0 | 0 |
| 50 | 234.666667 | 0 | 0 |
| 51 | 234.666667 | 0 | 0 |
| 52 | 234.666667 | 0 | 0 |
| 53 | 234.666667 | 0 | 0 |
| 54 | 234.666667 | 0 | 0 |
| 55 | 234.666667 | 0 | 0 |
| 56 | 234.666667 | 0 | 0 |
| 57 | 234.666667 | 0 | 0 |
| 58 | 234.666667 | 0 | 0 |
| 59 | 234.666667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 234.666667 | 0 | 0 |
| 4 | 234.666667 | 0 | 0 |
| 5 | 234.666667 | 0 | 0 |
| 6 | 234.666667 | 0 | 0 |
| 7 | 234.666667 | 0 | 0 |
| 8 | 234.666667 | 0 | 0 |
| 9 | 234.666667 | 0 | 0 |
| 10 | 234.666667 | 0 | 0 |
| 11 | 234.666667 | 0 | 0 |
| 12 | 234.666667 | 0 | 0 |
| 13 | 234.666667 | 0 | 0 |
| 14 | 234.666667 | 0 | 0 |
| 15 | 234.666667 | 0 | 0 |
| 16 | 234.666667 | 0 | 0 |
| 17 | 234.666667 | 0 | 0 |
| 18 | 234.666667 | 0 | 0 |
| 19 | 234.666667 | 0 | 0 |
| 20 | 234.666667 | 0 | 0 |
| 21 | 234.666667 | 0 | 0 |
| 22 | 234.666667 | 0 | 0 |
| 23 | 234.666667 | 0 | 0 |
| 24 | 234.666667 | 0 | 0 |
| 25 | 234.666667 | 0 | 0 |
| 26 | 234.666667 | 0 | 0 |
| 27 | 234.666667 | 0 | 0 |
| 28 | 234.666667 | 0 | 0 |
| 29 | 234.666667 | 0 | 0 |
| 30 | 234.666667 | 0 | 0 |
| 31 | 234.666667 | 0 | 0 |
| 32 | 234.666667 | 0 | 0 |
| 33 | 234.666667 | 0 | 0 |
| 34 | 234.666667 | 0 | 0 |
| 35 | 234.666667 | 0 | 0 |
| 36 | 103.166667 | 0 | 0 |
| 37 | 103.166667 | 0 | 0 |
| 38 | 103.166667 | 0 | 0 |
| 39 | 103.166667 | 0 | 0 |
| 40 | 103.166667 | 0 | 0 |
| 41 | 103.166667 | 0 | 0 |
| 42 | 103.166667 | 0 | 0 |
| 43 | 103.166667 | 0 | 0 |
| 44 | 103.166667 | 0 | 0 |
| 45 | 103.166667 | 0 | 0 |
| 46 | 103.166667 | 0 | 0 |
| 47 | 103.166667 | 0 | 0 |
| 48 | 103.166667 | 0 | 0 |
| 49 | 103.166667 | 0 | 0 |
| 50 | 103.166667 | 0 | 0 |
| 51 | 103.166667 | 0 | 0 |
| 52 | 103.166667 | 0 | 0 |
| 53 | 103.166667 | 0 | 0 |
| 54 | 103.166667 | 0 | 0 |
| 55 | 333 | 0 | 0 |
| 56 | 333 | 0 | 0 |
| 57 | 333 | 0 | 0 |
| 58 | 333 | 0 | 0 |
| 59 | 333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 333 | 0 | 0 |
| 4 | 333 | 0 | 0 |
| 5 | 333 | 0 | 0 |
| 6 | 333 | 0 | 0 |
| 7 | 333 | 0 | 0 |
| 8 | 333 | 0 | 0 |
| 9 | 333 | 0 | 0 |
| 10 | 333 | 0 | 0 |
| 11 | 333 | 0 | 0 |
| 12 | 333 | 0 | 0 |
| 13 | 333 | 0 | 0 |
| 14 | 333 | 0 | 0 |
| 15 | 333 | 0 | 0 |
| 16 | 333 | 0 | 0 |
| 17 | 333 | 0 | 0 |
| 18 | 333 | 0 | 0 |
| 19 | 333 | 0 | 0 |
| 20 | 333 | 0 | 0 |
| 21 | 333 | 0 | 0 |
| 22 | 333 | 0 | 0 |
| 23 | 333 | 0 | 0 |
| 24 | 333 | 0 | 0 |
| 25 | 333 | 0 | 0 |
| 26 | 333 | 0 | 0 |
| 27 | 333 | 0 | 0 |
| 28 | 333 | 0 | 0 |
| 29 | 333 | 0 | 0 |
| 30 | 333 | 0 | 0 |
| 31 | 333 | 0 | 0 |
| 32 | 81 | 0 | 0 |
| 33 | | | |
| 34 | 64.8333333 | 0 | 0 |
| 35 | 64.8333333 | 0 | 0 |
| 36 | 91 | 0 | 0 |
| 37 | 91 | 0 | 0 |
| 38 | 91 | 0 | 0 |
| 39 | 91 | 0 | 0 |
| 40 | 91 | 0 | 0 |
| 41 | 91 | 0 | 0 |
| 42 | 91 | 0 | 0 |
| 43 | 91 | 0 | 0 |
| 44 | 91 | 0 | 0 |
| 45 | 91 | 0 | 0 |
| 46 | 91 | 0 | 0 |
| 47 | 91 | 0 | 0 |
| 48 | 91 | 0 | 0 |
| 49 | 91 | 0 | 0 |
| 50 | 91 | 0 | 0 |
| 51 | 91 | 0 | 0 |
| 52 | 91 | 0 | 0 |
| 53 | 91 | 0 | 0 |
| 54 | 91 | 0 | 0 |
| 55 | 91 | 0 | 0 |
| 56 | 91 | 0 | 0 |
| 57 | 91 | 0 | 0 |
| 58 | 91 | 0 | 0 |
| 59 | 91 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 91 | 0 | 0 |
| 4 | 91 | 0 | 0 |
| 5 | 91 | 0 | 0 |
| 6 | 63 | 0 | 0 |
| 7 | 63 | 0 | 0 |
| 8 | 63 | 0 | 0 |
| 9 | 63 | 0 | 0 |
| 10 | 63 | 0 | 0 |
| 11 | 63 | 0 | 0 |
| 12 | 63 | 0 | 0 |
| 13 | 63 | 0 | 0 |
| 14 | 63 | 0 | 0 |
| 15 | 63 | 0 | 0 |
| 16 | 63 | 0 | 0 |
| 17 | 63 | 0 | 0 |
| 18 | 63 | 0 | 0 |
| 19 | 63 | 0 | 0 |
| 20 | 63 | 0 | 0 |
| 21 | 63 | 0 | 0 |
| 22 | 63 | 0 | 0 |
| 23 | 63 | 0 | 0 |
| 24 | 63 | 0 | 0 |
| 25 | 63 | 0 | 0 |
| 26 | 63 | 0 | 0 |
| 27 | 63 | 0 | 0 |
| 28 | 63 | 0 | 0 |
| 29 | 63 | 0 | 0 |
| 30 | 63 | 0 | 0 |
| 31 | 63 | 0 | 0 |
| 32 | 63 | 0 | 0 |
| 33 | 63 | 0 | 0 |
| 34 | 63 | 0 | 0 |
| 35 | 63 | 0 | 0 |
| 36 | 63 | 0 | 0 |
| 37 | 63 | 0 | 0 |
| 38 | 63 | 0 | 0 |
| 39 | 63 | 0 | 0 |
| 40 | 63 | 0 | 0 |
| 41 | 63 | 0 | 0 |
| 42 | 63 | 0 | 0 |
| 43 | 63 | 0 | 0 |
| 44 | 63 | 0 | 0 |
| 45 | 63 | 0 | 0 |
| 46 | 63 | 0 | 0 |
| 47 | 63 | 0 | 0 |
| 48 | 63 | 0 | 0 |
| 49 | 63 | 0 | 0 |
| 50 | 63 | 0 | 0 |
| 51 | 62.3333333 | 0 | 0 |
| 52 | 62.3333333 | 0 | 0 |
| 53 | 62.3333333 | 0 | 0 |
| 54 | 62.3333333 | 0 | 0 |
| 55 | 62.3333333 | 0 | 0 |
| 56 | 62.3333333 | 0 | 0 |
| 57 | 62.3333333 | 0 | 0 |
| 58 | 62.3333333 | 0 | 0 |
| 59 | 62.3333333 | 0 | 0 |
| 60 | | | |

Do not distribute

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 62.3333333 | 0 | 0 |
| 4 | 62.3333333 | 0 | 0 |
| 5 | 62.3333333 | 0 | 0 |
| 6 | 62.3333333 | 0 | 0 |
| 7 | 62.3333333 | 0 | 0 |
| 8 | 62.3333333 | 0 | 0 |
| 9 | 62.3333333 | 0 | 0 |
| 10 | 62.3333333 | 0 | 0 |
| 11 | 62.3333333 | 0 | 0 |
| 12 | 62.3333333 | 0 | 0 |
| 13 | 62.3333333 | 0 | 0 |
| 14 | 62.3333333 | 0 | 0 |
| 15 | 62.3333333 | 0 | 0 |
| 16 | 62.3333333 | 0 | 0 |
| 17 | 62.3333333 | 0 | 0 |
| 18 | 62.3333333 | 0 | 0 |
| 19 | 62.3333333 | 0 | 0 |
| 20 | 62.3333333 | 0 | 0 |
| 21 | 62.3333333 | 0 | 0 |
| 22 | 62.3333333 | 0 | 0 |
| 23 | 62.3333333 | 0 | 0 |
| 24 | 62.3333333 | 0 | 0 |
| 25 | 62.3333333 | 0 | 0 |
| 26 | 62.3333333 | 0 | 0 |
| 27 | 62.3333333 | 0 | 0 |
| 28 | 557.5 | 0 | 0 |
| 29 | | | |
| 30 | 92.8333333 | 0 | 0 |
| 31 | 92.8333333 | 0 | 0 |
| 32 | 92.8333333 | 0 | 0 |
| 33 | 92.8333333 | 0 | 0 |
| 34 | 92.8333333 | 0 | 0 |
| 35 | 92.8333333 | 0 | 0 |
| 36 | 92.8333333 | 0 | 0 |
| 37 | 92.8333333 | 0 | 0 |
| 38 | 92.8333333 | 0 | 0 |
| 39 | 92.8333333 | 0 | 0 |
| 40 | 92.8333333 | 0 | 0 |
| 41 | 92.8333333 | 0 | 0 |
| 42 | 92.8333333 | 0 | 0 |
| 43 | 92.8333333 | 0 | 0 |
| 44 | 92.8333333 | 0 | 0 |
| 45 | 92.8333333 | 0 | 0 |
| 46 | 92.8333333 | 0 | 0 |
| 47 | 92.8333333 | 0 | 0 |
| 48 | 92.8333333 | 0 | 0 |
| 49 | 92.8333333 | 0 | 0 |
| 50 | 92.8333333 | 0 | 0 |
| 51 | 92.8333333 | 0 | 0 |
| 52 | 92.8333333 | 0 | 0 |
| 53 | | | |
| 54 | 89.5 | 0 | 0 |
| 55 | 89.5 | 0 | 0 |
| 56 | 89.5 | 0 | 0 |
| 57 | 89.5 | 0 | 0 |
| 58 | 89.5 | 0 | 0 |
| 59 | 89.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 89.5 | 0 | 0 |
| 4 | 89.5 | 0 | 0 |
| 5 | 89.5 | 0 | 0 |
| 6 | 89.5 | 0 | 0 |
| 7 | 89.5 | 0 | 0 |
| 8 | 89.5 | 0 | 0 |
| 9 | 89.5 | 0 | 0 |
| 10 | 89.5 | 0 | 0 |
| 11 | 89.5 | 0 | 0 |
| 12 | 89.5 | 0 | 0 |
| 13 | 89.5 | 0 | 0 |
| 14 | 89.5 | 0 | 0 |
| 15 | 89.5 | 0 | 0 |
| 16 | 89.5 | 0 | 0 |
| 17 | 89.5 | 0 | 0 |
| 18 | 89.5 | 0 | 0 |
| 19 | 79.666667 | 0 | 0 |
| 20 | 79.666667 | 0 | 0 |
| 21 | 79.666667 | 0 | 0 |
| 22 | 79.666667 | 0 | 0 |
| 23 | 79.666667 | 0 | 0 |
| 24 | 79.666667 | 0 | 0 |
| 25 | 79.666667 | 0 | 0 |
| 26 | 79.666667 | 0 | 0 |
| 27 | 79.666667 | 0 | 0 |
| 28 | 522 | 0 | 0 |
| 29 | 522 | 0 | 0 |
| 30 | 522 | 0 | 0 |
| 31 | 161.166667 | 0 | 0 |
| 32 | 161.166667 | 0 | 0 |
| 33 | 161.166667 | 0 | 0 |
| 34 | 90 | 0 | 0 |
| 35 | 1241.16667 | 0 | 0 |
| 36 | 1240.5 | 0 | 0 |
| 37 | 1240.5 | 0 | 0 |
| 38 | 1240.5 | 0 | 0 |
| 39 | 1240.5 | 0 | 0 |
| 40 | 1240.5 | 0 | 0 |
| 41 | 1240.5 | 0 | 0 |
| 42 | 1240.5 | 0 | 0 |
| 43 | 1240.5 | 0 | 0 |
| 44 | 1240.5 | 0 | 0 |
| 45 | 1240.5 | 0 | 0 |
| 46 | 1240.5 | 0 | 0 |
| 47 | 1240.5 | 0 | 0 |
| 48 | 1240.5 | 0 | 0 |
| 49 | 1240.5 | 0 | 0 |
| 50 | 1240.5 | 0 | 0 |
| 51 | 1240.5 | 0 | 0 |
| 52 | 1240.5 | 0 | 0 |
| 53 | 1240.5 | 0 | 0 |
| 54 | 1240.5 | 0 | 0 |
| 55 | 1240.5 | 0 | 0 |
| 56 | 1240.5 | 0 | 0 |
| 57 | 1240.5 | 0 | 0 |
| 58 | 1240.5 | 0 | 0 |
| 59 | 1240.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 1240.5 | 0 | 0 |
| 4 | 1240.5 | 0 | 0 |
| 5 | 1240.5 | 0 | 0 |
| 6 | 1240.5 | 0 | 0 |
| 7 | 1240.5 | 0 | 0 |
| 8 | 1240.5 | 0 | 0 |
| 9 | 1240.5 | 0 | 0 |
| 10 | 1240.5 | 0 | 0 |
| 11 | 1240.5 | 0 | 0 |
| 12 | 1240.5 | 0 | 0 |
| 13 | 1240.5 | 0 | 0 |
| 14 | 1240.5 | 0 | 0 |
| 15 | 1240.5 | 0 | 0 |
| 16 | 1240.5 | 0 | 0 |
| 17 | 1240.5 | 0 | 0 |
| 18 | 1240.5 | 0 | 0 |
| 19 | 1240.5 | 0 | 0 |
| 20 | 1240.5 | 0 | 0 |
| 21 | 1240.5 | 0 | 0 |
| 22 | 1240.5 | 0 | 0 |
| 23 | 1240.5 | 0 | 0 |
| 24 | 1240.5 | 0 | 0 |
| 25 | 1240.5 | 0 | 0 |
| 26 | 1240.5 | 0 | 0 |
| 27 | 1240.5 | 0 | 0 |
| 28 | 1240.5 | 0 | 0 |
| 29 | 1240.5 | 0 | 0 |
| 30 | 1240.5 | 0 | 0 |
| 31 | 1240.5 | 0 | 0 |
| 32 | 1240.5 | 0 | 0 |
| 33 | 1240.5 | 0 | 0 |
| 34 | 1240.5 | 0 | 0 |
| 35 | 1240.5 | 0 | 0 |
| 36 | 1240.5 | 0 | 0 |
| 37 | 1240.5 | 0 | 0 |
| 38 | 1240.5 | 0 | 0 |
| 39 | 1240.5 | 0 | 0 |
| 40 | 1240.5 | 0 | 0 |
| 41 | 1240.5 | 0 | 0 |
| 42 | 1240.5 | 0 | 0 |
| 43 | 1240.5 | 0 | 0 |
| 44 | 1240.5 | 0 | 0 |
| 45 | 1240.5 | 0 | 0 |
| 46 | 1240.5 | 0 | 0 |
| 47 | 1240.5 | 0 | 0 |
| 48 | 501.833333 | 0 | 0 |
| 49 | 501.833333 | 0 | 0 |
| 50 | 501.833333 | 0 | 0 |
| 51 | 501.833333 | 0 | 0 |
| 52 | 501.833333 | 0 | 0 |
| 53 | 501.833333 | 0 | 0 |
| 54 | 501.833333 | 0 | 0 |
| 55 | 501.833333 | 0 | 0 |
| 56 | 501.833333 | 0 | 0 |
| 57 | 501.833333 | 0 | 0 |
| 58 | 501.833333 | 0 | 0 |
| 59 | 501.833333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 501.833333 | 0 | 0 |
| 4 | 501.833333 | 0 | 0 |
| 5 | 501.833333 | 0 | 0 |
| 6 | 501.833333 | 0 | 0 |
| 7 | 501.833333 | 0 | 0 |
| 8 | 501.833333 | 0 | 0 |
| 9 | 501.833333 | 0 | 0 |
| 10 | 501.833333 | 0 | 0 |
| 11 | 501.833333 | 0 | 0 |
| 12 | 501.833333 | 0 | 0 |
| 13 | 501.833333 | 0 | 0 |
| 14 | 501.833333 | 0 | 0 |
| 15 | 501.833333 | 0 | 0 |
| 16 | 567.5 | 0 | 0 |
| 17 | 567.333333 | 0 | 0 |
| 18 | 567.333333 | 0 | 0 |
| 19 | 567.333333 | 0 | 0 |
| 20 | 567.333333 | 0 | 0 |
| 21 | 567.333333 | 0 | 0 |
| 22 | 567.333333 | 0 | 0 |
| 23 | 567.333333 | 0 | 0 |
| 24 | 567.333333 | 0 | 0 |
| 25 | 567.333333 | 0 | 0 |
| 26 | 567.333333 | 0 | 0 |
| 27 | 567.333333 | 0 | 0 |
| 28 | 567.333333 | 0 | 0 |
| 29 | 567.333333 | 0 | 0 |
| 30 | 567.333333 | 0 | 0 |
| 31 | 567.333333 | 0 | 0 |
| 32 | 567.333333 | 0 | 0 |
| 33 | 567.333333 | 0 | 0 |
| 34 | 567.333333 | 0 | 0 |
| 35 | 567.333333 | 0 | 0 |
| 36 | 567.333333 | 0 | 0 |
| 37 | 567.333333 | 0 | 0 |
| 38 | 567.333333 | 0 | 0 |
| 39 | 567.333333 | 0 | 0 |
| 40 | 567.333333 | 0 | 0 |
| 41 | 567.333333 | 0 | 0 |
| 42 | 567.333333 | 0 | 0 |
| 43 | 567.333333 | 0 | 0 |
| 44 | 567.333333 | 0 | 0 |
| 45 | 567.333333 | 0 | 0 |
| 46 | 567.333333 | 0 | 0 |
| 47 | 567.333333 | 0 | 0 |
| 48 | 567.333333 | 0 | 0 |
| 49 | 567.333333 | 0 | 0 |
| 50 | 567.333333 | 0 | 0 |
| 51 | 567.333333 | 0 | 0 |
| 52 | 567.333333 | 0 | 0 |
| 53 | 567.333333 | 0 | 0 |
| 54 | 567.333333 | 0 | 0 |
| 55 | 567.333333 | 0 | 0 |
| 56 | 567.333333 | 0 | 0 |
| 57 | 567.333333 | 0 | 0 |
| 58 | 567.333333 | 0 | 0 |
| 59 | 567.333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 567.333333 | 0 | 0 |
| 4 | 567.333333 | 0 | 0 |
| 5 | 567.333333 | 0 | 0 |
| 6 | 567.333333 | 0 | 0 |
| 7 | 567.333333 | 0 | 0 |
| 8 | 567.333333 | 0 | 0 |
| 9 | 567.333333 | 0 | 0 |
| 10 | 567.333333 | 0 | 0 |
| 11 | 567.333333 | 0 | 0 |
| 12 | 567.333333 | 0 | 0 |
| 13 | 567.333333 | 0 | 0 |
| 14 | 567.333333 | 0 | 0 |
| 15 | 567.333333 | 0 | 0 |
| 16 | 567.333333 | 0 | 0 |
| 17 | 567.333333 | 0 | 0 |
| 18 | 567.333333 | 0 | 0 |
| 19 | 567.333333 | 0 | 0 |
| 20 | 567.333333 | 0 | 0 |
| 21 | 567.333333 | 0 | 0 |
| 22 | 567.333333 | 0 | 0 |
| 23 | 567.333333 | 0 | 0 |
| 24 | 567.333333 | 0 | 0 |
| 25 | 567.333333 | 0 | 0 |
| 26 | 567.333333 | 0 | 0 |
| 27 | 62.1666667 | 0 | 0 |
| 28 | 62.1666667 | 0 | 0 |
| 29 | 62.1666667 | 0 | 0 |
| 30 | 62.1666667 | 0 | 0 |
| 31 | 62.1666667 | 0 | 0 |
| 32 | 62.1666667 | 0 | 0 |
| 33 | 62.1666667 | 0 | 0 |
| 34 | 62.1666667 | 0 | 0 |
| 35 | 62.1666667 | 0 | 0 |
| 36 | 62.1666667 | 0 | 0 |
| 37 | 62.1666667 | 0 | 0 |
| 38 | 62.1666667 | 0 | 0 |
| 39 | 62.1666667 | 0 | 0 |
| 40 | 62.1666667 | 0 | 0 |
| 41 | 62.1666667 | 0 | 0 |
| 42 | 62.1666667 | 0 | 0 |
| 43 | 62.1666667 | 0 | 0 |
| 44 | 62.1666667 | 0 | 0 |
| 45 | 62.1666667 | 0 | 0 |
| 46 | 62.1666667 | 0 | 0 |
| 47 | 62.1666667 | 0 | 0 |
| 48 | 62.1666667 | 0 | 0 |
| 49 | 62.1666667 | 0 | 0 |
| 50 | 62.1666667 | 0 | 0 |
| 51 | 62.1666667 | 0 | 0 |
| 52 | 62.1666667 | 0 | 0 |
| 53 | 62.1666667 | 0 | 0 |
| 54 | 62.1666667 | 0 | 0 |
| 55 | 62.1666667 | 0 | 0 |
| 56 | 62.1666667 | 0 | 0 |
| 57 | 62.1666667 | 0 | 0 |
| 58 | 62.1666667 | 0 | 0 |
| 59 | 62.1666667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 62.1666667 | 0 | 0 |
| 4 | 62.1666667 | 0 | 0 |
| 5 | 62.1666667 | 0 | 0 |
| 6 | 63.3333333 | 0 | 0 |
| 7 | 150.166667 | 0 | 0 |
| 8 | 150.166667 | 0 | 0 |
| 9 | 150.166667 | 0 | 0 |
| 10 | 150.166667 | 0 | 0 |
| 11 | 150.166667 | 0 | 0 |
| 12 | 150.166667 | 0 | 0 |
| 13 | 150.166667 | 0 | 0 |
| 14 | 150.166667 | 0 | 0 |
| 15 | 150.166667 | 0 | 0 |
| 16 | 150.166667 | 0 | 0 |
| 17 | 150.166667 | 0 | 0 |
| 18 | 150.166667 | 0 | 0 |
| 19 | 150.166667 | 0 | 0 |
| 20 | 150.166667 | 0 | 0 |
| 21 | 150.166667 | 0 | 0 |
| 22 | 150.166667 | 0 | 0 |
| 23 | 150.166667 | 0 | 0 |
| 24 | 150.166667 | 0 | 0 |
| 25 | 150.166667 | 0 | 0 |
| 26 | 150.166667 | 0 | 0 |
| 27 | 150.166667 | 0 | 0 |
| 28 | 150.166667 | 0 | 0 |
| 29 | 150.166667 | 0 | 0 |
| 30 | 150.166667 | 0 | 0 |
| 31 | 150.166667 | 0 | 0 |
| 32 | 150.166667 | 0 | 0 |
| 33 | 150.166667 | 0 | 0 |
| 34 | 51.6666667 | 0 | 0 |
| 35 | 51.6666667 | 0 | 0 |
| 36 | 51.6666667 | 0 | 0 |
| 37 | 51.6666667 | 0 | 0 |
| 38 | 51.6666667 | 0 | 0 |
| 39 | 51.6666667 | 0 | 0 |
| 40 | 51.6666667 | 0 | 0 |
| 41 | 51.6666667 | 0 | 0 |
| 42 | 51.6666667 | 0 | 0 |
| 43 | 51.6666667 | 0 | 0 |
| 44 | 51.6666667 | 0 | 0 |
| 45 | 51.6666667 | 0 | 0 |
| 46 | 51.6666667 | 0 | 0 |
| 47 | 51.6666667 | 0 | 0 |
| 48 | 51.6666667 | 0 | 0 |
| 49 | 51.6666667 | 0 | 0 |
| 50 | 51.6666667 | 0 | 0 |
| 51 | 51.6666667 | 0 | 0 |
| 52 | 51.6666667 | 0 | 0 |
| 53 | 51.6666667 | 0 | 0 |
| 54 | 51.6666667 | 0 | 0 |
| 55 | 51.6666667 | 0 | 0 |
| 56 | 608.333333 | 0 | 0 |
| 57 | 608.333333 | 0 | 0 |
| 58 | 608.333333 | 0 | 0 |
| 59 | 608.333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 120.666667 | 0 | 0 |
| 4 | 120.666667 | 0 | 0 |
| 5 | 120.666667 | 0 | 0 |
| 6 | 120.666667 | 0 | 0 |
| 7 | 120.666667 | 0 | 0 |
| 8 | 120.666667 | 0 | 0 |
| 9 | 120.666667 | 0 | 0 |
| 10 | 120.666667 | 0 | 0 |
| 11 | 120.666667 | 0 | 0 |
| 12 | 120.666667 | 0 | 0 |
| 13 | 120.666667 | 0 | 0 |
| 14 | 120.666667 | 0 | 0 |
| 15 | 559 | 0 | 0 |
| 16 | 559 | 0 | 0 |
| 17 | 559 | 0 | 0 |
| 18 | 559 | 0 | 0 |
| 19 | 559 | 0 | 0 |
| 20 | 559 | 0 | 0 |
| 21 | 559 | 0 | 0 |
| 22 | 559 | 0 | 0 |
| 23 | 559 | 0 | 0 |
| 24 | 559 | 0 | 0 |
| 25 | 559 | 0 | 0 |
| 26 | 559 | 0 | 0 |
| 27 | 559 | 0 | 0 |
| 28 | 559 | 0 | 0 |
| 29 | 559 | 0 | 0 |
| 30 | 559 | 0 | 0 |
| 31 | 559 | 0 | 0 |
| 32 | 559 | 0 | 0 |
| 33 | 559 | 0 | 0 |
| 34 | 559 | 0 | 0 |
| 35 | 559 | 0 | 0 |
| 36 | 559 | 0 | 0 |
| 37 | 559 | 0 | 0 |
| 38 | 559 | 0 | 0 |
| 39 | 559 | 0 | 0 |
| 40 | 559 | 0 | 0 |
| 41 | 559 | 0 | 0 |
| 42 | 559 | 0 | 0 |
| 43 | 559 | 0 | 0 |
| 44 | 559 | 0 | 0 |
| 45 | 559.5 | 0 | 0 |
| 46 | 559.5 | 0 | 0 |
| 47 | 559.5 | 0 | 0 |
| 48 | 559.5 | 0 | 0 |
| 49 | 559.5 | 0 | 0 |
| 50 | 559.5 | 0 | 0 |
| 51 | 559.5 | 0 | 0 |
| 52 | 559.5 | 0 | 0 |
| 53 | 559.5 | 0 | 0 |
| 54 | 559.5 | 0 | 0 |
| 55 | 559.5 | 0 | 0 |
| 56 | 559.5 | 0 | 0 |
| 57 | 559.5 | 0 | 0 |
| 58 | 559.5 | 0 | 0 |
| 59 | 309.666667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 309.666667 | 0 | 0 |
| 4 | | | |
| 5 | 128.5 | 0 | 0 |
| 6 | 119.5 | 0 | 0 |
| 7 | 119.5 | 0 | 0 |
| 8 | 119.5 | 0 | 0 |
| 9 | 119.5 | 0 | 0 |
| 10 | 119.5 | 0 | 0 |
| 11 | 119.5 | 0 | 0 |
| 12 | 119.5 | 0 | 0 |
| 13 | 119.5 | 0 | 0 |
| 14 | 119.5 | 0 | 0 |
| 15 | 119.5 | 0 | 0 |
| 16 | 119.5 | 0 | 0 |
| 17 | 119.5 | 0 | 0 |
| 18 | 119.5 | 0 | 0 |
| 19 | 119.5 | 0 | 0 |
| 20 | 119.5 | 0 | 0 |
| 21 | 119.5 | 0 | 0 |
| 22 | 119.5 | 0 | 0 |
| 23 | 119.5 | 0 | 0 |
| 24 | 119.5 | 0 | 0 |
| 25 | 119.5 | 0 | 0 |
| 26 | 119.5 | 0 | 0 |
| 27 | 119.5 | 0 | 0 |
| 28 | 119.5 | 0 | 0 |
| 29 | 119.5 | 0 | 0 |
| 30 | 119.5 | 0 | 0 |
| 31 | 5138.33333 | 0 | 0 |
| 32 | 3660.83333 | 0 | 0 |
| 33 | | | |
| 34 | 169.333333 | 0 | 0 |
| 35 | 169.333333 | 0 | 0 |
| 36 | 169.333333 | 0 | 0 |
| 37 | 169.333333 | 0 | 0 |
| 38 | 169.333333 | 0 | 0 |
| 39 | 169.333333 | 0 | 0 |
| 40 | 169.333333 | 0 | 0 |
| 41 | 169.333333 | 0 | 0 |
| 42 | 148.333333 | 0 | 0 |
| 43 | 148.333333 | 0 | 0 |
| 44 | 148.333333 | 0 | 0 |
| 45 | 148.333333 | 0 | 0 |
| 46 | 148.333333 | 0 | 0 |
| 47 | 148.333333 | 0 | 0 |
| 48 | 148.333333 | 0 | 0 |
| 49 | 148.333333 | 0 | 0 |
| 50 | 148.333333 | 0 | 0 |
| 51 | 148.333333 | 0 | 0 |
| 52 | 148.333333 | 0 | 0 |
| 53 | 148.333333 | 0 | 0 |
| 54 | 148.333333 | 0 | 0 |
| 55 | 148.333333 | 0 | 0 |
| 56 | 148.333333 | 0 | 0 |
| 57 | 148.333333 | 0 | 0 |
| 58 | 148.333333 | 0 | 0 |
| 59 | 148.333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 148.333333 | 0 | 0 |
| 4 | 148.333333 | 0 | 0 |
| 5 | 148.333333 | 0 | 0 |
| 6 | 148.333333 | 0 | 0 |
| 7 | 148.333333 | 0 | 0 |
| 8 | 148.333333 | 0 | 0 |
| 9 | 148.333333 | 0 | 0 |
| 10 | 148.333333 | 0 | 0 |
| 11 | 148.333333 | 0 | 0 |
| 12 | 148.333333 | 0 | 0 |
| 13 | 148.333333 | 0 | 0 |
| 14 | 148.333333 | 0 | 0 |
| 15 | 148.333333 | 0 | 0 |
| 16 | 148.333333 | 0 | 0 |
| 17 | 148.333333 | 0 | 0 |
| 18 | 148.333333 | 0 | 0 |
| 19 | 148.333333 | 0 | 0 |
| 20 | 148.333333 | 0 | 0 |
| 21 | 148.333333 | 0 | 0 |
| 22 | 148.333333 | 0 | 0 |
| 23 | 148.333333 | 0 | 0 |
| 24 | 148.333333 | 0 | 0 |
| 25 | 148.333333 | 0 | 0 |
| 26 | 148.333333 | 0 | 0 |
| 27 | 148.333333 | 0 | 0 |
| 28 | 148.333333 | 0 | 0 |
| 29 | 148.333333 | 0 | 0 |
| 30 | 148.333333 | 0 | 0 |
| 31 | 148.333333 | 0 | 0 |
| 32 | 148.333333 | 0 | 0 |
| 33 | 148.333333 | 0 | 0 |
| 34 | 148.333333 | 0 | 0 |
| 35 | 148.333333 | 0 | 0 |
| 36 | 171.166667 | 0 | 0 |
| 37 | 54.3333333 | 0 | 0 |
| 38 | 54.3333333 | 0 | 0 |
| 39 | 54.3333333 | 0 | 0 |
| 40 | 241.333333 | 0 | 0 |
| 41 | 241.333333 | 0 | 0 |
| 42 | 241.333333 | 0 | 0 |
| 43 | 420 | 0 | 0 |
| 44 | 420 | 0 | 0 |
| 45 | 419.5 | 0 | 0 |
| 46 | 419.5 | 0 | 0 |
| 47 | 419.5 | 0 | 0 |
| 48 | 419.5 | 0 | 0 |
| 49 | 419.5 | 0 | 0 |
| 50 | 419.5 | 0 | 0 |
| 51 | 419.5 | 0 | 0 |
| 52 | 419.5 | 0 | 0 |
| 53 | 419.5 | 0 | 0 |
| 54 | 419.5 | 0 | 0 |
| 55 | 419.5 | 0 | 0 |
| 56 | 419.5 | 0 | 0 |
| 57 | 419.5 | 0 | 0 |
| 58 | 419.5 | 0 | 0 |
| 59 | 419.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|-------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 419.5 | 0 | 0 |
| 4 | 419.5 | 0 | 0 |
| 5 | 419.5 | 0 | 0 |
| 6 | 419.5 | 0 | 0 |
| 7 | 419.5 | 0 | 0 |
| 8 | 419.5 | 0 | 0 |
| 9 | 419.5 | 0 | 0 |
| 10 | 419.5 | 0 | 0 |
| 11 | 419.5 | 0 | 0 |
| 12 | 419.5 | 0 | 0 |
| 13 | 419.5 | 0 | 0 |
| 14 | 419.5 | 0 | 0 |
| 15 | 419.5 | 0 | 0 |
| 16 | 419.5 | 0 | 0 |
| 17 | 419.5 | 0 | 0 |
| 18 | 419.5 | 0 | 0 |
| 19 | 419.5 | 0 | 0 |
| 20 | 419.5 | 0 | 0 |
| 21 | 419.5 | 0 | 0 |
| 22 | 419.5 | 0 | 0 |
| 23 | 419.5 | 0 | 0 |
| 24 | 419.5 | 0 | 0 |
| 25 | 419.5 | 0 | 0 |
| 26 | 419.5 | 0 | 0 |
| 27 | 419.5 | 0 | 0 |
| 28 | 419.5 | 0 | 0 |
| 29 | 419.5 | 0 | 0 |
| 30 | 419.5 | 0 | 0 |
| 31 | 419.5 | 0 | 0 |
| 32 | 419.5 | 0 | 0 |
| 33 | 419.5 | 0 | 0 |
| 34 | 419.5 | 0 | 0 |
| 35 | 419.5 | 0 | 0 |
| 36 | 419.5 | 0 | 0 |
| 37 | 419.5 | 0 | 0 |
| 38 | 419.5 | 0 | 0 |
| 39 | 419.5 | 0 | 0 |
| 40 | 419.5 | 0 | 0 |
| 41 | 419.5 | 0 | 0 |
| 42 | 419.5 | 0 | 0 |
| 43 | 419.5 | 0 | 0 |
| 44 | 419.5 | 0 | 0 |
| 45 | 419.5 | 0 | 0 |
| 46 | 419.5 | 0 | 0 |
| 47 | 419.5 | 0 | 0 |
| 48 | 419.5 | 0 | 0 |
| 49 | 419.5 | 0 | 0 |
| 50 | 419.5 | 0 | 0 |
| 51 | 419.5 | 0 | 0 |
| 52 | 419.5 | 0 | 0 |
| 53 | 419.5 | 0 | 0 |
| 54 | 419.5 | 0 | 0 |
| 55 | 419.5 | 0 | 0 |
| 56 | 419.5 | 0 | 0 |
| 57 | 419.5 | 0 | 0 |
| 58 | 419.5 | 0 | 0 |
| 59 | 419.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 419.5 | 0 | 0 |
| 4 | 419.5 | 0 | 0 |
| 5 | 419.5 | 0 | 0 |
| 6 | 419.5 | 0 | 0 |
| 7 | 419.5 | 0 | 0 |
| 8 | 419.5 | 0 | 0 |
| 9 | 419.5 | 0 | 0 |
| 10 | 419.5 | 0 | 0 |
| 11 | 419.5 | 0 | 0 |
| 12 | 419.5 | 0 | 0 |
| 13 | 419.5 | 0 | 0 |
| 14 | 419.5 | 0 | 0 |
| 15 | 419.5 | 0 | 0 |
| 16 | 419.5 | 0 | 0 |
| 17 | 419.5 | 0 | 0 |
| 18 | 419.5 | 0 | 0 |
| 19 | 419.5 | 0 | 0 |
| 20 | 419.5 | 0 | 0 |
| 21 | 419.5 | 0 | 0 |
| 22 | 126.166667 | 0 | 0 |
| 23 | 129 | 0 | 0 |
| 24 | 3712.5 | 0 | 0 |
| 25 | 3712.5 | 0 | 0 |
| 26 | 3712.5 | 0 | 0 |
| 27 | 3712.5 | 0 | 0 |
| 28 | 3712.5 | 0 | 0 |
| 29 | 3712.5 | 0 | 0 |
| 30 | 3712.5 | 0 | 0 |
| 31 | 3712.5 | 0 | 0 |
| 32 | 3712.5 | 0 | 0 |
| 33 | 3712.5 | 0 | 0 |
| 34 | 3712.5 | 0 | 0 |
| 35 | 3712.5 | 0 | 0 |
| 36 | 269.333333 | 0 | 0 |
| 37 | 269.333333 | 0 | 0 |
| 38 | 269.333333 | 0 | 0 |
| 39 | 269.333333 | 0 | 0 |
| 40 | 269.333333 | 0 | 0 |
| 41 | 269.333333 | 0 | 0 |
| 42 | 269.333333 | 0 | 0 |
| 43 | 269.333333 | 0 | 0 |
| 44 | 269.333333 | 0 | 0 |
| 45 | 269.333333 | 0 | 0 |
| 46 | 269.333333 | 0 | 0 |
| 47 | 269.333333 | 0 | 0 |
| 48 | 269.333333 | 0 | 0 |
| 49 | 269.333333 | 0 | 0 |
| 50 | 269.333333 | 0 | 0 |
| 51 | 269.333333 | 0 | 0 |
| 52 | 269.333333 | 0 | 0 |
| 53 | 269.333333 | 0 | 0 |
| 54 | 269.333333 | 0 | 0 |
| 55 | 269.333333 | 0 | 0 |
| 56 | 269.333333 | 0 | 0 |
| 57 | 269.333333 | 0 | 0 |
| 58 | 269.333333 | 0 | 0 |
| 59 | 269.333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 269.333333 | 0 | 0 |
| 4 | 269.333333 | 0 | 0 |
| 5 | 269.333333 | 0 | 0 |
| 6 | 269.333333 | 0 | 0 |
| 7 | 269.333333 | 0 | 0 |
| 8 | 269.333333 | 0 | 0 |
| 9 | 269.333333 | 0 | 0 |
| 10 | 269.333333 | 0 | 0 |
| 11 | 269.333333 | 0 | 0 |
| 12 | 269.333333 | 0 | 0 |
| 13 | 269.333333 | 0 | 0 |
| 14 | 269.333333 | 0 | 0 |
| 15 | 269.333333 | 0 | 0 |
| 16 | 269.333333 | 0 | 0 |
| 17 | 269.333333 | 0 | 0 |
| 18 | 269.333333 | 0 | 0 |
| 19 | 269.333333 | 0 | 0 |
| 20 | 269.333333 | 0 | 0 |
| 21 | 269.333333 | 0 | 0 |
| 22 | 269.333333 | 0 | 0 |
| 23 | 269.333333 | 0 | 0 |
| 24 | 269.333333 | 0 | 0 |
| 25 | 269.333333 | 0 | 0 |
| 26 | 269.333333 | 0 | 0 |
| 27 | 269.333333 | 0 | 0 |
| 28 | 269.333333 | 0 | 0 |
| 29 | 269.333333 | 0 | 0 |
| 30 | 269.333333 | 0 | 0 |
| 31 | 269.333333 | 0 | 0 |
| 32 | 269.333333 | 0 | 0 |
| 33 | 269.333333 | 0 | 0 |
| 34 | 269.333333 | 0 | 0 |
| 35 | 269.333333 | 0 | 0 |
| 36 | 269.333333 | 0 | 0 |
| 37 | 269.333333 | 0 | 0 |
| 38 | 269.333333 | 0 | 0 |
| 39 | 269.333333 | 0 | 0 |
| 40 | 280 | 0 | 0 |
| 41 | 247.5 | 0 | 0 |
| 42 | 247.5 | 0 | 0 |
| 43 | 247.5 | 0 | 0 |
| 44 | 247.5 | 0 | 0 |
| 45 | 247.5 | 0 | 0 |
| 46 | 247.5 | 0 | 0 |
| 47 | 247.5 | 0 | 0 |
| 48 | 247.5 | 0 | 0 |
| 49 | 247.5 | 0 | 0 |
| 50 | 247.5 | 0 | 0 |
| 51 | 247.5 | 0 | 0 |
| 52 | 247.5 | 0 | 0 |
| 53 | 247.5 | 0 | 0 |
| 54 | 247.5 | 0 | 0 |
| 55 | 247.5 | 0 | 0 |
| 56 | 247.5 | 0 | 0 |
| 57 | 247.5 | 0 | 0 |
| 58 | 247.5 | 0 | 0 |
| 59 | 247.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 247.5 | 0 | 0 |
| 4 | 247.5 | 0 | 0 |
| 5 | 247.5 | 0 | 0 |
| 6 | 247.5 | 0 | 0 |
| 7 | 247.5 | 0 | 0 |
| 8 | 247.5 | 0 | 0 |
| 9 | 247.5 | 0 | 0 |
| 10 | 247.5 | 0 | 0 |
| 11 | 247.5 | 0 | 0 |
| 12 | 247.5 | 0 | 0 |
| 13 | 247.5 | 0 | 0 |
| 14 | 247.5 | 0 | 0 |
| 15 | 247.5 | 0 | 0 |
| 16 | 247.5 | 0 | 0 |
| 17 | 247.5 | 0 | 0 |
| 18 | 247.5 | 0 | 0 |
| 19 | 247.5 | 0 | 0 |
| 20 | 247.5 | 0 | 0 |
| 21 | 247.5 | 0 | 0 |
| 22 | 247.5 | 0 | 0 |
| 23 | 247.5 | 0 | 0 |
| 24 | 247.5 | 0 | 0 |
| 25 | 247.5 | 0 | 0 |
| 26 | 247.5 | 0 | 0 |
| 27 | 247.5 | 0 | 0 |
| 28 | 247.5 | 0 | 0 |
| 29 | 247.5 | 0 | 0 |
| 30 | 248.666667 | 0 | 0 |
| 31 | 215.166667 | 0 | 0 |
| 32 | 215.166667 | 0 | 0 |
| 33 | 203.166667 | 0 | 0 |
| 34 | 203.166667 | 0 | 0 |
| 35 | 203.166667 | 0 | 0 |
| 36 | 203.166667 | 0 | 0 |
| 37 | 203.166667 | 0 | 0 |
| 38 | 203.166667 | 0 | 0 |
| 39 | 203.166667 | 0 | 0 |
| 40 | 203.166667 | 0 | 0 |
| 41 | 203.166667 | 0 | 0 |
| 42 | 203.166667 | 0 | 0 |
| 43 | 203.166667 | 0 | 0 |
| 44 | 308.666667 | 0 | 0 |
| 45 | 300.333333 | 0 | 0 |
| 46 | 500.166667 | 0 | 0 |
| 47 | 500.166667 | 0 | 0 |
| 48 | 288.833333 | 0 | 0 |
| 49 | 288.833333 | 0 | 0 |
| 50 | 288.833333 | 0 | 0 |
| 51 | 288.833333 | 0 | 0 |
| 52 | 288.833333 | 0 | 0 |
| 53 | 288.5 | 0 | 0 |
| 54 | 288.5 | 0 | 0 |
| 55 | 288.5 | 0 | 0 |
| 56 | 288.5 | 0 | 0 |
| 57 | 288.5 | 0 | 0 |
| 58 | 288.5 | 0 | 0 |
| 59 | 288.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 288.5 | 0 | 0 |
| 4 | 288.5 | 0 | 0 |
| 5 | 288.5 | 0 | 0 |
| 6 | 288.5 | 0 | 0 |
| 7 | 288.5 | 0 | 0 |
| 8 | 288.5 | 0 | 0 |
| 9 | 288.5 | 0 | 0 |
| 10 | 288.5 | 0 | 0 |
| 11 | 288.5 | 0 | 0 |
| 12 | 288.5 | 0 | 0 |
| 13 | 288.5 | 0 | 0 |
| 14 | 288.5 | 0 | 0 |
| 15 | 288.5 | 0 | 0 |
| 16 | 288.5 | 0 | 0 |
| 17 | 288.5 | 0 | 0 |
| 18 | 288.5 | 0 | 0 |
| 19 | 288.5 | 0 | 0 |
| 20 | 288.5 | 0 | 0 |
| 21 | 288.5 | 0 | 0 |
| 22 | 288.5 | 0 | 0 |
| 23 | 288.5 | 0 | 0 |
| 24 | 288.5 | 0 | 0 |
| 25 | 288.5 | 0 | 0 |
| 26 | 288.5 | 0 | 0 |
| 27 | 288.5 | 0 | 0 |
| 28 | 288.5 | 0 | 0 |
| 29 | 288.5 | 0 | 0 |
| 30 | 288.5 | 0 | 0 |
| 31 | 288.5 | 0 | 0 |
| 32 | 288.5 | 0 | 0 |
| 33 | 288.5 | 0 | 0 |
| 34 | 288.5 | 0 | 0 |
| 35 | 288.5 | 0 | 0 |
| 36 | 288.5 | 0 | 0 |
| 37 | 288.5 | 0 | 0 |
| 38 | 288.5 | 0 | 0 |
| 39 | 98.666667 | 0 | 0 |
| 40 | 98.666667 | 0 | 0 |
| 41 | 228.666667 | 0 | 0 |
| 42 | 228.666667 | 0 | 0 |
| 43 | 228.666667 | 0 | 0 |
| 44 | 228.666667 | 0 | 0 |
| 45 | 228.666667 | 0 | 0 |
| 46 | 228.666667 | 0 | 0 |
| 47 | 228.666667 | 0 | 0 |
| 48 | 228.666667 | 0 | 0 |
| 49 | 228.666667 | 0 | 0 |
| 50 | 228.666667 | 0 | 0 |
| 51 | 259.5 | 0 | 0 |
| 52 | 259.5 | 0 | 0 |
| 53 | 259.5 | 0 | 0 |
| 54 | 259.5 | 0 | 0 |
| 55 | 259.5 | 0 | 0 |
| 56 | 259.5 | 0 | 0 |
| 57 | 259.5 | 0 | 0 |
| 58 | 259.5 | 0 | 0 |
| 59 | 259.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 259.5 | 0 | 0 |
| 4 | 217.833333 | 0 | 0 |
| 5 | 217.833333 | 0 | 0 |
| 6 | 217.833333 | 0 | 0 |
| 7 | 217.833333 | 0 | 0 |
| 8 | 217.833333 | 0 | 0 |
| 9 | 217.833333 | 0 | 0 |
| 10 | 217.833333 | 0 | 0 |
| 11 | 217.833333 | 0 | 0 |
| 12 | 217.833333 | 0 | 0 |
| 13 | 217.833333 | 0 | 0 |
| 14 | 217.833333 | 0 | 0 |
| 15 | 95.3333333 | 0 | 0 |
| 16 | 95.3333333 | 0 | 0 |
| 17 | 95.3333333 | 0 | 0 |
| 18 | 95.3333333 | 0 | 0 |
| 19 | 95.3333333 | 0 | 0 |
| 20 | 95.3333333 | 0 | 0 |
| 21 | 95.3333333 | 0 | 0 |
| 22 | 111.5 | 0 | 0 |
| 23 | 111.5 | 0 | 0 |
| 24 | 114.666667 | 0 | 0 |
| 25 | 83 | 0 | 0 |
| 26 | 83 | 0 | 0 |
| 27 | 83 | 0 | 0 |
| 28 | 83 | 0 | 0 |
| 29 | 83 | 0 | 0 |
| 30 | 83 | 0 | 0 |
| 31 | 83 | 0 | 0 |
| 32 | 83 | 0 | 0 |
| 33 | 83 | 0 | 0 |
| 34 | 83 | 0 | 0 |
| 35 | 83 | 0 | 0 |
| 36 | 83 | 0 | 0 |
| 37 | 83 | 0 | 0 |
| 38 | 83 | 0 | 0 |
| 39 | 177.333333 | 0 | 0 |
| 40 | 177.333333 | 0 | 0 |
| 41 | 177.333333 | 0 | 0 |
| 42 | 177.333333 | 0 | 0 |
| 43 | 177.333333 | 0 | 0 |
| 44 | 177.333333 | 0 | 0 |
| 45 | 177.333333 | 0 | 0 |
| 46 | 177.333333 | 0 | 0 |
| 47 | 177.333333 | 0 | 0 |
| 48 | 177.333333 | 0 | 0 |
| 49 | 177.333333 | 0 | 0 |
| 50 | 177.333333 | 0 | 0 |
| 51 | 177.333333 | 0 | 0 |
| 52 | 177.333333 | 0 | 0 |
| 53 | 177.333333 | 0 | 0 |
| 54 | 177.333333 | 0 | 0 |
| 55 | 177.333333 | 0 | 0 |
| 56 | 80 | 0 | 0 |
| 57 | 112.166667 | 0 | 0 |
| 58 | 112.166667 | 0 | 0 |
| 59 | 112.166667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 131 | 0 | 0 |
| 4 | 131 | 0 | 0 |
| 5 | 131 | 0 | 0 |
| 6 | 131 | 0 | 0 |
| 7 | 131 | 0 | 0 |
| 8 | 131 | 0 | 0 |
| 9 | 131 | 0 | 0 |
| 10 | 131 | 0 | 0 |
| 11 | 131 | 0 | 0 |
| 12 | 131 | 0 | 0 |
| 13 | 131 | 0 | 0 |
| 14 | 131 | 0 | 0 |
| 15 | 131 | 0 | 0 |
| 16 | 131 | 0 | 0 |
| 17 | 131 | 0 | 0 |
| 18 | 131 | 0 | 0 |
| 19 | 131 | 0 | 0 |
| 20 | 131 | 0 | 0 |
| 21 | 131 | 0 | 0 |
| 22 | 131 | 0 | 0 |
| 23 | 131 | 0 | 0 |
| 24 | 131 | 0 | 0 |
| 25 | 131 | 0 | 0 |
| 26 | 131 | 0 | 0 |
| 27 | 131 | 0 | 0 |
| 28 | 131 | 0 | 0 |
| 29 | 131 | 0 | 0 |
| 30 | 131 | 0 | 0 |
| 31 | 133.833333 | 0 | 0 |
| 32 | 115.666667 | 0 | 0 |
| 33 | 115.666667 | 0 | 0 |
| 34 | 115.666667 | 0 | 0 |
| 35 | 237.166667 | 0 | 0 |
| 36 | 322.333333 | 0 | 0 |
| 37 | 56.166667 | 0 | 0 |
| 38 | 56.166667 | 0 | 0 |
| 39 | 482.333333 | 0 | 0 |
| 40 | 482.333333 | 0 | 0 |
| 41 | 482.333333 | 0 | 0 |
| 42 | 482.333333 | 0 | 0 |
| 43 | 482.333333 | 0 | 0 |
| 44 | 63.333333 | 0 | 0 |
| 45 | 63.333333 | 0 | 0 |
| 46 | 63.333333 | 0 | 0 |
| 47 | 988467.667 | 0 | 0 |
| 48 | 988467.667 | 0 | 0 |
| 49 | 988467.667 | 0 | 0 |
| 50 | 988467.667 | 0 | 0 |
| 51 | 988467.667 | 0 | 0 |
| 52 | 988467.667 | 0 | 0 |
| 53 | 988467.667 | 0 | 0 |
| 54 | 988467.667 | 0 | 0 |
| 55 | 988467.667 | 0 | 0 |
| 56 | 988467.667 | 0 | 0 |
| 57 | 988467.667 | 0 | 0 |
| 58 | 988467.667 | 0 | 0 |
| 59 | 988467.667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 988467.667 | 0 | 0 |
| 4 | 988467.667 | 0 | 0 |
| 5 | 988467.667 | 0 | 0 |
| 6 | 988467.667 | 0 | 0 |
| 7 | 988467.667 | 0 | 0 |
| 8 | 988467.667 | 0 | 0 |
| 9 | 988467.667 | 0 | 0 |
| 10 | 988467.667 | 0 | 0 |
| 11 | 988467.667 | 0 | 0 |
| 12 | 988467.667 | 0 | 0 |
| 13 | 988467.667 | 0 | 0 |
| 14 | 988467.667 | 0 | 0 |
| 15 | 988467.667 | 0 | 0 |
| 16 | 988467.667 | 0 | 0 |
| 17 | 988467.667 | 0 | 0 |
| 18 | 988467.667 | 0 | 0 |
| 19 | 988467.667 | 0 | 0 |
| 20 | 988467.667 | 0 | 0 |
| 21 | 988467.667 | 0 | 0 |
| 22 | 988467.667 | 0 | 0 |
| 23 | 988467.667 | 0 | 0 |
| 24 | 988467.667 | 0 | 0 |
| 25 | 988467.667 | 0 | 0 |
| 26 | 988467.667 | 0 | 0 |
| 27 | 988467.667 | 0 | 0 |
| 28 | 988467.667 | 0 | 0 |
| 29 | 988467.667 | 0 | 0 |
| 30 | 17717 | 0 | 0 |
| 31 | 55.8333333 | 0 | 0 |
| 32 | 55.8333333 | 0 | 0 |
| 33 | 55.8333333 | 0 | 0 |
| 34 | 55.8333333 | 0 | 0 |
| 35 | 55.8333333 | 0 | 0 |
| 36 | 55.8333333 | 0 | 0 |
| 37 | 55.8333333 | 0 | 0 |
| 38 | 55.8333333 | 0 | 0 |
| 39 | 55.8333333 | 0 | 0 |
| 40 | 55.8333333 | 0 | 0 |
| 41 | 55.8333333 | 0 | 0 |
| 42 | 33261.3333 | 0 | 0 |
| 43 | 33261.3333 | 0 | 0 |
| 44 | 33261.3333 | 0 | 0 |
| 45 | 33261.3333 | 0 | 0 |
| 46 | 33261.3333 | 0 | 0 |
| 47 | 33261.3333 | 0 | 0 |
| 48 | 33261.3333 | 0 | 0 |
| 49 | 33261.3333 | 0 | 0 |
| 50 | 33261.3333 | 0 | 0 |
| 51 | 33261.3333 | 0 | 0 |
| 52 | 33261.3333 | 0 | 0 |
| 53 | 33261.3333 | 0 | 0 |
| 54 | 33261.3333 | 0 | 0 |
| 55 | 33261.3333 | 0 | 0 |
| 56 | 33261.3333 | 0 | 0 |
| 57 | 33261.3333 | 0 | 0 |
| 58 | 33261.3333 | 0 | 0 |
| 59 | 33261.3333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 33261.3333 | 0 | 0 |
| 4 | 33261.3333 | 0 | 0 |
| 5 | 33261.3333 | 0 | 0 |
| 6 | 33261.3333 | 0 | 0 |
| 7 | 33261.3333 | 0 | 0 |
| 8 | 6153.83333 | 0 | 0 |
| 9 | 6127.33333 | 0 | 0 |
| 10 | 6127.33333 | 0 | 0 |
| 11 | 6127.33333 | 0 | 0 |
| 12 | 6127.33333 | 0 | 0 |
| 13 | 6127.33333 | 0 | 0 |
| 14 | 6127.33333 | 0 | 0 |
| 15 | 6127.33333 | 0 | 0 |
| 16 | 6127.33333 | 0 | 0 |
| 17 | 6127.33333 | 0 | 0 |
| 18 | 6127.33333 | 0 | 0 |
| 19 | 6127.33333 | 0 | 0 |
| 20 | 6127.33333 | 0 | 0 |
| 21 | 6127.33333 | 0 | 0 |
| 22 | 6127.33333 | 0 | 0 |
| 23 | 6127.33333 | 0 | 0 |
| 24 | 6127.33333 | 0 | 0 |
| 25 | 6127.33333 | 0 | 0 |
| 26 | 6127.33333 | 0 | 0 |
| 27 | 6127.33333 | 0 | 0 |
| 28 | 6127.33333 | 0 | 0 |
| 29 | 6127.33333 | 0 | 0 |
| 30 | 6127.33333 | 0 | 0 |
| 31 | 6127.33333 | 0 | 0 |
| 32 | 6127.33333 | 0 | 0 |
| 33 | 6127.33333 | 0 | 0 |
| 34 | 6127.33333 | 0 | 0 |
| 35 | 6127.33333 | 0 | 0 |
| 36 | 6127.33333 | 0 | 0 |
| 37 | 6127.33333 | 0 | 0 |
| 38 | 6127.33333 | 0 | 0 |
| 39 | 6127.33333 | 0 | 0 |
| 40 | 6127.33333 | 0 | 0 |
| 41 | 6127.33333 | 0 | 0 |
| 42 | 6127.33333 | 0 | 0 |
| 43 | 6127.33333 | 0 | 0 |
| 44 | 6127.33333 | 0 | 0 |
| 45 | 6127.33333 | 0 | 0 |
| 46 | 6127.33333 | 0 | 0 |
| 47 | 6127.33333 | 0 | 0 |
| 48 | 6127.33333 | 0 | 0 |
| 49 | 6127.33333 | 0 | 0 |
| 50 | 6127.33333 | 0 | 0 |
| 51 | 6127.33333 | 0 | 0 |
| 52 | 6127.33333 | 0 | 0 |
| 53 | 6127.33333 | 0 | 0 |
| 54 | 6127.33333 | 0 | 0 |
| 55 | 6127.33333 | 0 | 0 |
| 56 | 6127.33333 | 0 | 0 |
| 57 | 6127.33333 | 0 | 0 |
| 58 | 6127.33333 | 0 | 0 |
| 59 | 6127.33333 | 0 | 0 |
| 60 | | | |

1
2
3 6127.33333 0 0
4 6127.33333 0 0
5 6127.33333 0 0
6 6127.33333 0 0
7 6127.33333 0 0
8 6127.33333 0 0
9 6127.33333 0 0
10 6127.33333 0 0
11 6127.33333 0 0
12 6127.33333 0 0
13 6127.33333 0 0
14 6127.33333 0 0
15 6127.33333 0 0
16 6127.33333 0 0
17 6127.33333 0 0
18 6127.33333 0 0
19 6127.33333 0 0
20 6135.33333 0 0
21 6135.33333 0 0
22 6135.33333 0 0
23 6135.33333 0 0
24 33374.3333 0 0
25 38390.8333 0 0
26 38390.8333 0 0
27 38390.8333 0 0
28 38390.8333 0 0
29 38390.8333 0 0
30 38390.8333 0 0
31 38390.8333 0 0
32 393.333333 0 0
33 393.333333 0 0
34 393.333333 0 0
35 393.333333 0 0
36 393.333333 0 0
37 393.333333 0 0
38 393.333333 0 0
39 393.333333 0 0
40 393.333333 0 0
41 393.333333 0 0
42 393.333333 0 0
43 393.333333 0 0
44 393.333333 0 0
45 393.333333 0 0
46 393.333333 0 0
47 393.333333 0 0
48 393.333333 0 0
49 393.333333 0 0
50 393.333333 0 0
51 393.333333 0 0
52 393.333333 0 0
53 393.333333 0 0
54 393.333333 0 0
55 393.333333 0 0
56 393.333333 0 0
57 393.333333 0 0
58 393.333333 0 0
59 393.333333 0 0
60

Do not distribute

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 393.333333 | 0 | 0 |
| 4 | 393.333333 | 0 | 0 |
| 5 | 393.333333 | 0 | 0 |
| 6 | 393.333333 | 0 | 0 |
| 7 | 393.333333 | 0 | 0 |
| 8 | 349.833333 | 0 | 0 |
| 9 | 349.833333 | 0 | 0 |
| 10 | 349.833333 | 0 | 0 |
| 11 | 349.833333 | 0 | 0 |
| 12 | 349.833333 | 0 | 0 |
| 13 | 349.833333 | 0 | 0 |
| 14 | 349.833333 | 0 | 0 |
| 15 | 349.833333 | 0 | 0 |
| 16 | 349.833333 | 0 | 0 |
| 17 | 349.833333 | 0 | 0 |
| 18 | 349.833333 | 0 | 0 |
| 19 | 349.833333 | 0 | 0 |
| 20 | 349.833333 | 0 | 0 |
| 21 | 349.833333 | 0 | 0 |
| 22 | 349.833333 | 0 | 0 |
| 23 | 349.833333 | 0 | 0 |
| 24 | 349.833333 | 0 | 0 |
| 25 | 349.833333 | 0 | 0 |
| 26 | 349.833333 | 0 | 0 |
| 27 | 349.833333 | 0 | 0 |
| 28 | 349.833333 | 0 | 0 |
| 29 | 349.833333 | 0 | 0 |
| 30 | 349.833333 | 0 | 0 |
| 31 | 349.833333 | 0 | 0 |
| 32 | 349.833333 | 0 | 0 |
| 33 | 349.833333 | 0 | 0 |
| 34 | 349.833333 | 0 | 0 |
| 35 | 349.833333 | 0 | 0 |
| 36 | 349.833333 | 0 | 0 |
| 37 | 349.833333 | 0 | 0 |
| 38 | 349.833333 | 0 | 0 |
| 39 | 349.833333 | 0 | 0 |
| 40 | 349.833333 | 0 | 0 |
| 41 | 349.833333 | 0 | 0 |
| 42 | 349.833333 | 0 | 0 |
| 43 | 349.833333 | 0 | 0 |
| 44 | 349.833333 | 0 | 0 |
| 45 | 249 | 0 | 0 |
| 46 | 20807.6667 | 0 | 0 |
| 47 | 20807.6667 | 0 | 0 |
| 48 | 20807.6667 | 0 | 0 |
| 49 | 20807.6667 | 0 | 0 |
| 50 | 20807.6667 | 0 | 0 |
| 51 | 20807.6667 | 0 | 0 |
| 52 | 20807.6667 | 0 | 0 |
| 53 | 20807.6667 | 0 | 0 |
| 54 | 20807.6667 | 0 | 0 |
| 55 | 20807.6667 | 0 | 0 |
| 56 | 20807.6667 | 0 | 0 |
| 57 | 20807.6667 | 0 | 0 |
| 58 | 20807.6667 | 0 | 0 |
| 59 | 20807.6667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 20807.6667 | 0 | 0 |
| 4 | 20807.6667 | 0 | 0 |
| 5 | 20807.6667 | 0 | 0 |
| 6 | 20807.6667 | 0 | 0 |
| 7 | 20807.6667 | 0 | 0 |
| 8 | 20807.6667 | 0 | 0 |
| 9 | 20807.6667 | 0 | 0 |
| 10 | 20807.6667 | 0 | 0 |
| 11 | 20807.6667 | 0 | 0 |
| 12 | 20807.6667 | 0 | 0 |
| 13 | 20807.6667 | 0 | 0 |
| 14 | 20807.6667 | 0 | 0 |
| 15 | 20807.6667 | 0 | 0 |
| 16 | 20807.6667 | 0 | 0 |
| 17 | 20807.6667 | 0 | 0 |
| 18 | 20807.6667 | 0 | 0 |
| 19 | 20807.6667 | 0 | 0 |
| 20 | 20807.6667 | 0 | 0 |
| 21 | 20807.6667 | 0 | 0 |
| 22 | 20807.6667 | 0 | 0 |
| 23 | 20807.6667 | 0 | 0 |
| 24 | 20807.6667 | 0 | 0 |
| 25 | 20807.6667 | 0 | 0 |
| 26 | 20807.6667 | 0 | 0 |
| 27 | 20807.6667 | 0 | 0 |
| 28 | 20807.6667 | 0 | 0 |
| 29 | 20807.6667 | 0 | 0 |
| 30 | 20807.6667 | 0 | 0 |
| 31 | 20807.6667 | 0 | 0 |
| 32 | 20807.6667 | 0 | 0 |
| 33 | 20807.6667 | 0 | 0 |
| 34 | 20807.6667 | 0 | 0 |
| 35 | 20807.6667 | 0 | 0 |
| 36 | 20807.6667 | 0 | 0 |
| 37 | 20807.6667 | 0 | 0 |
| 38 | 20807.6667 | 0 | 0 |
| 39 | 20807.6667 | 0 | 0 |
| 40 | 20807.6667 | 0 | 0 |
| 41 | 20807.6667 | 0 | 0 |
| 42 | 20807.6667 | 0 | 0 |
| 43 | 20807.6667 | 0 | 0 |
| 44 | 20807.6667 | 0 | 0 |
| 45 | 20807.6667 | 0 | 0 |
| 46 | 20807.6667 | 0 | 0 |
| 47 | 20807.6667 | 0 | 0 |
| 48 | 20807.6667 | 0 | 0 |
| 49 | 20807.6667 | 0 | 0 |
| 50 | 20807.6667 | 0 | 0 |
| 51 | 20807.6667 | 0 | 0 |
| 52 | 20807.6667 | 0 | 0 |
| 53 | 20807.6667 | 0 | 0 |
| 54 | 20807.6667 | 0 | 0 |
| 55 | 20807.6667 | 0 | 0 |
| 56 | 20807.6667 | 0 | 0 |
| 57 | 20807.6667 | 0 | 0 |
| 58 | 20807.6667 | 0 | 0 |
| 59 | 20807.6667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 20807.6667 | 0 | 0 |
| 4 | 20807.6667 | 0 | 0 |
| 5 | 20807.6667 | 0 | 0 |
| 6 | 20807.6667 | 0 | 0 |
| 7 | 20807.6667 | 0 | 0 |
| 8 | 20807.6667 | 0 | 0 |
| 9 | 20807.6667 | 0 | 0 |
| 10 | 20807.6667 | 0 | 0 |
| 11 | 20807.6667 | 0 | 0 |
| 12 | 20807.6667 | 0 | 0 |
| 13 | 20807.6667 | 0 | 0 |
| 14 | 20807.6667 | 0 | 0 |
| 15 | 20807.6667 | 0 | 0 |
| 16 | 20807.6667 | 0 | 0 |
| 17 | 20807.6667 | 0 | 0 |
| 18 | 20807.6667 | 0 | 0 |
| 19 | 20807.6667 | 0 | 0 |
| 20 | 20807.6667 | 0 | 0 |
| 21 | 20807.6667 | 0 | 0 |
| 22 | 20807.6667 | 0 | 0 |
| 23 | 20807.6667 | 0 | 0 |
| 24 | 20807.6667 | 0 | 0 |
| 25 | 20807.6667 | 0 | 0 |
| 26 | 20807.6667 | 0 | 0 |
| 27 | 20807.6667 | 0 | 0 |
| 28 | 20807.6667 | 0 | 0 |
| 29 | 20807.6667 | 0 | 0 |
| 30 | 20807.6667 | 0 | 0 |
| 31 | 20807.6667 | 0 | 0 |
| 32 | 20807.6667 | 0 | 0 |
| 33 | 20807.6667 | 0 | 0 |
| 34 | 20807.6667 | 0 | 0 |
| 35 | 20807.6667 | 0 | 0 |
| 36 | 20807.6667 | 0 | 0 |
| 37 | 20807.6667 | 0 | 0 |
| 38 | 20807.6667 | 0 | 0 |
| 39 | 20807.6667 | 0 | 0 |
| 40 | 20807.6667 | 0 | 0 |
| 41 | 20807.6667 | 0 | 0 |
| 42 | 20807.6667 | 0 | 0 |
| 43 | 20807.6667 | 0 | 0 |
| 44 | 20807.6667 | 0 | 0 |
| 45 | 20807.6667 | 0 | 0 |
| 46 | 20807.6667 | 0 | 0 |
| 47 | 20807.6667 | 0 | 0 |
| 48 | 20807.6667 | 0 | 0 |
| 49 | 20807.6667 | 0 | 0 |
| 50 | 20807.6667 | 0 | 0 |
| 51 | 20807.6667 | 0 | 0 |
| 52 | 20807.6667 | 0 | 0 |
| 53 | 20807.6667 | 0 | 0 |
| 54 | 20807.6667 | 0 | 0 |
| 55 | 122.5 | 0 | 0 |
| 56 | 122.5 | 0 | 0 |
| 57 | 122.5 | 0 | 0 |
| 58 | 122.5 | 0 | 0 |
| 59 | 4713.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 4713.5 | 0 | 0 |
| 4 | 12246.5 | 0 | 0 |
| 5 | 12246.5 | 0 | 0 |
| 6 | 12246.5 | 0 | 0 |
| 7 | 466.833333 | 0 | 0 |
| 8 | 466.833333 | 0 | 0 |
| 9 | 466.833333 | 0 | 0 |
| 10 | 466.833333 | 0 | 0 |
| 11 | 466.833333 | 0 | 0 |
| 12 | 466.833333 | 0 | 0 |
| 13 | 466.833333 | 0 | 0 |
| 14 | 466.833333 | 0 | 0 |
| 15 | 466.833333 | 0 | 0 |
| 16 | 377.166667 | 0 | 0 |
| 17 | 377.166667 | 0 | 0 |
| 18 | 377.166667 | 0 | 0 |
| 19 | 377.166667 | 0 | 0 |
| 20 | 377.166667 | 0 | 0 |
| 21 | 377.166667 | 0 | 0 |
| 22 | 377.166667 | 0 | 0 |
| 23 | 377.166667 | 0 | 0 |
| 24 | 377.166667 | 0 | 0 |
| 25 | 377.166667 | 0 | 0 |
| 26 | 377.166667 | 0 | 0 |
| 27 | 377.166667 | 0 | 0 |
| 28 | 377.166667 | 0 | 0 |
| 29 | 377.166667 | 0 | 0 |
| 30 | 377.166667 | 0 | 0 |
| 31 | 377.166667 | 0 | 0 |
| 32 | 377.166667 | 0 | 0 |
| 33 | 377.166667 | 0 | 0 |
| 34 | 377.166667 | 0 | 0 |
| 35 | 377.166667 | 0 | 0 |
| 36 | 377.166667 | 0 | 0 |
| 37 | 377.166667 | 0 | 0 |
| 38 | 377.166667 | 0 | 0 |
| 39 | 377.166667 | 0 | 0 |
| 40 | 377.166667 | 0 | 0 |
| 41 | 377.166667 | 0 | 0 |
| 42 | 377.166667 | 0 | 0 |
| 43 | 377.166667 | 0 | 0 |
| 44 | 377.166667 | 0 | 0 |
| 45 | 377.166667 | 0 | 0 |
| 46 | 377.166667 | 0 | 0 |
| 47 | 377.166667 | 0 | 0 |
| 48 | 377.166667 | 0 | 0 |
| 49 | 55.166667 | 0 | 0 |
| 50 | 55.166667 | 0 | 0 |
| 51 | 70.333333 | 0 | 0 |
| 52 | 70.333333 | 0 | 0 |
| 53 | 70.333333 | 0 | 0 |
| 54 | 70.333333 | 0 | 0 |
| 55 | 70.333333 | 0 | 0 |
| 56 | 70.333333 | 0 | 0 |
| 57 | 70.333333 | 0 | 0 |
| 58 | 70.333333 | 0 | 0 |
| 59 | 70.333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 70.3333333 | 0 | 0 |
| 4 | 70.3333333 | 0 | 0 |
| 5 | 70.3333333 | 0 | 0 |
| 6 | 70.3333333 | 0 | 0 |
| 7 | 70.3333333 | 0 | 0 |
| 8 | 70.3333333 | 0 | 0 |
| 9 | 70.3333333 | 0 | 0 |
| 10 | 70.3333333 | 0 | 0 |
| 11 | 70.3333333 | 0 | 0 |
| 12 | 70.3333333 | 0 | 0 |
| 13 | 70.3333333 | 0 | 0 |
| 14 | 334.833333 | 0 | 0 |
| 15 | 334.833333 | 0 | 0 |
| 16 | 334.833333 | 0 | 0 |
| 17 | 334.833333 | 0 | 0 |
| 18 | 334.833333 | 0 | 0 |
| 19 | 334.833333 | 0 | 0 |
| 20 | 174.666667 | 0 | 0 |
| 21 | 174.666667 | 0 | 0 |
| 22 | 174.666667 | 0 | 0 |
| 23 | 174.666667 | 0 | 0 |
| 24 | 174.666667 | 0 | 0 |
| 25 | 174.666667 | 0 | 0 |
| 26 | 174.666667 | 0 | 0 |
| 27 | 174.666667 | 0 | 0 |
| 28 | 174.666667 | 0 | 0 |
| 29 | 174.666667 | 0 | 0 |
| 30 | 174.666667 | 0 | 0 |
| 31 | 174.666667 | 0 | 0 |
| 32 | 174.666667 | 0 | 0 |
| 33 | 174.666667 | 0 | 0 |
| 34 | 174.666667 | 0 | 0 |
| 35 | 129156.5 | 0 | 0 |
| 36 | 129156.5 | 0 | 0 |
| 37 | 129156.5 | 0 | 0 |
| 38 | 129156.5 | 0 | 0 |
| 39 | 129156.5 | 0 | 0 |
| 40 | 129156.5 | 0 | 0 |
| 41 | 129156.5 | 0 | 0 |
| 42 | 129156.5 | 0 | 0 |
| 43 | 129156.5 | 0 | 0 |
| 44 | 129156.5 | 0 | 0 |
| 45 | 129156.5 | 0 | 0 |
| 46 | 129156.5 | 0 | 0 |
| 47 | 129156.5 | 0 | 0 |
| 48 | 129156.5 | 0 | 0 |
| 49 | 129156.5 | 0 | 0 |
| 50 | 129156.5 | 0 | 0 |
| 51 | 129156.5 | 0 | 0 |
| 52 | 129156.5 | 0 | 0 |
| 53 | 129156.5 | 0 | 0 |
| 54 | 129156.5 | 0 | 0 |
| 55 | 129156.5 | 0 | 0 |
| 56 | 129156.5 | 0 | 0 |
| 57 | 129156.5 | 0 | 0 |
| 58 | 129156.5 | 0 | 0 |
| 59 | 129156.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|----------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 129156.5 | 0 | 0 |
| 4 | 129156.5 | 0 | 0 |
| 5 | 129156.5 | 0 | 0 |
| 6 | 129156.5 | 0 | 0 |
| 7 | 129156.5 | 0 | 0 |
| 8 | 129156.5 | 0 | 0 |
| 9 | 129156.5 | 0 | 0 |
| 10 | 129156.5 | 0 | 0 |
| 11 | 129156.5 | 0 | 0 |
| 12 | 129156.5 | 0 | 0 |
| 13 | 129156.5 | 0 | 0 |
| 14 | 129156.5 | 0 | 0 |
| 15 | 129156.5 | 0 | 0 |
| 16 | 129156.5 | 0 | 0 |
| 17 | 129156.5 | 0 | 0 |
| 18 | 129156.5 | 0 | 0 |
| 19 | 129156.5 | 0 | 0 |
| 20 | 129156.5 | 0 | 0 |
| 21 | 129156.5 | 0 | 0 |
| 22 | 129156.5 | 0 | 0 |
| 23 | 129156.5 | 0 | 0 |
| 24 | 129156.5 | 0 | 0 |
| 25 | 129156.5 | 0 | 0 |
| 26 | 129156.5 | 0 | 0 |
| 27 | 129156.5 | 0 | 0 |
| 28 | 129156.5 | 0 | 0 |
| 29 | 129156.5 | 0 | 0 |
| 30 | 129156.5 | 0 | 0 |
| 31 | 129156.5 | 0 | 0 |
| 32 | 129156.5 | 0 | 0 |
| 33 | 129156.5 | 0 | 0 |
| 34 | 129156.5 | 0 | 0 |
| 35 | 129156.5 | 0 | 0 |
| 36 | 129156.5 | 0 | 0 |
| 37 | 129156.5 | 0 | 0 |
| 38 | 129156.5 | 0 | 0 |
| 39 | 129156.5 | 0 | 0 |
| 40 | 129156.5 | 0 | 0 |
| 41 | 129156.5 | 0 | 0 |
| 42 | 129156.5 | 0 | 0 |
| 43 | 129156.5 | 0 | 0 |
| 44 | 129156.5 | 0 | 0 |
| 45 | 129156.5 | 0 | 0 |
| 46 | 129156.5 | 0 | 0 |
| 47 | 129156.5 | 0 | 0 |
| 48 | 129156.5 | 0 | 0 |
| 49 | 129156.5 | 0 | 0 |
| 50 | 129156.5 | 0 | 0 |
| 51 | 129156.5 | 0 | 0 |
| 52 | 129156.5 | 0 | 0 |
| 53 | 129156.5 | 0 | 0 |
| 54 | 129156.5 | 0 | 0 |
| 55 | 129156.5 | 0 | 0 |
| 56 | 129156.5 | 0 | 0 |
| 57 | 129156.5 | 0 | 0 |
| 58 | 129156.5 | 0 | 0 |
| 59 | 129156.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 129156.5 | 0 | 0 |
| 4 | 129156.5 | 0 | 0 |
| 5 | 129156.5 | 0 | 0 |
| 6 | 129156.5 | 0 | 0 |
| 7 | 129156.5 | 0 | 0 |
| 8 | 129156.5 | 0 | 0 |
| 9 | 129156.5 | 0 | 0 |
| 10 | 129156.5 | 0 | 0 |
| 11 | 129156.5 | 0 | 0 |
| 12 | 13813.8333 | 0 | 0 |
| 13 | 13813.8333 | 0 | 0 |
| 14 | 13813.8333 | 0 | 0 |
| 15 | 13813.8333 | 0 | 0 |
| 16 | 317.833333 | 0 | 0 |
| 17 | 317.833333 | 0 | 0 |
| 18 | 317.833333 | 0 | 0 |
| 19 | 317.833333 | 0 | 0 |
| 20 | 360.833333 | 0 | 0 |
| 21 | 2265.83333 | 0 | 0 |
| 22 | 2265.83333 | 0 | 0 |
| 23 | 2265.83333 | 0 | 0 |
| 24 | 2298.66667 | 0 | 0 |
| 25 | 312.5 | 0 | 0 |
| 26 | 312.5 | 0 | 0 |
| 27 | 312.5 | 0 | 0 |
| 28 | 312.5 | 0 | 0 |
| 29 | 312.5 | 0 | 0 |
| 30 | 312.5 | 0 | 0 |
| 31 | 312.5 | 0 | 0 |
| 32 | 312.5 | 0 | 0 |
| 33 | 312.5 | 0 | 0 |
| 34 | 312.5 | 0 | 0 |
| 35 | 312.5 | 0 | 0 |
| 36 | 312.5 | 0 | 0 |
| 37 | 312.5 | 0 | 0 |
| 38 | 312.5 | 0 | 0 |
| 39 | 312.5 | 0 | 0 |
| 40 | 312.5 | 0 | 0 |
| 41 | 312.5 | 0 | 0 |
| 42 | 312.5 | 0 | 0 |
| 43 | 312.5 | 0 | 0 |
| 44 | 312.5 | 0 | 0 |
| 45 | 312.5 | 0 | 0 |
| 46 | 312.5 | 0 | 0 |
| 47 | 312.5 | 0 | 0 |
| 48 | 312.5 | 0 | 0 |
| 49 | 312.5 | 0 | 0 |
| 50 | 312.5 | 0 | 0 |
| 51 | 790.5 | 0 | 0 |
| 52 | 790.5 | 0 | 0 |
| 53 | 827 | 0 | 0 |
| 54 | 827 | 0 | 0 |
| 55 | 827 | 0 | 0 |
| 56 | 827 | 0 | 0 |
| 57 | 827 | 0 | 0 |
| 58 | 827 | 0 | 0 |
| 59 | 827 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 827 | 0 | 0 |
| 4 | 827 | 0 | 0 |
| 5 | 827 | 0 | 0 |
| 6 | 827 | 0 | 0 |
| 7 | 827 | 0 | 0 |
| 8 | 827 | 0 | 0 |
| 9 | 827 | 0 | 0 |
| 10 | 827 | 0 | 0 |
| 11 | 827 | 0 | 0 |
| 12 | 827 | 0 | 0 |
| 13 | 827 | 0 | 0 |
| 14 | 827 | 0 | 0 |
| 15 | 827 | 0 | 0 |
| 16 | 827 | 0 | 0 |
| 17 | 827 | 0 | 0 |
| 18 | 827 | 0 | 0 |
| 19 | 827 | 0 | 0 |
| 20 | 827 | 0 | 0 |
| 21 | 827 | 0 | 0 |
| 22 | 827 | 0 | 0 |
| 23 | 827 | 0 | 0 |
| 24 | 827 | 0 | 0 |
| 25 | 827 | 0 | 0 |
| 26 | 827 | 0 | 0 |
| 27 | 827 | 0 | 0 |
| 28 | 827 | 0 | 0 |
| 29 | 827 | 0 | 0 |
| 30 | 827 | 0 | 0 |
| 31 | 827 | 0 | 0 |
| 32 | 827 | 0 | 0 |
| 33 | 827 | 0 | 0 |
| 34 | 827 | 0 | 0 |
| 35 | 827 | 0 | 0 |
| 36 | 827 | 0 | 0 |
| 37 | 827 | 0 | 0 |
| 38 | 827 | 0 | 0 |
| 39 | 827 | 0 | 0 |
| 40 | 769.333333 | 0 | 0 |
| 41 | 769.333333 | 0 | 0 |
| 42 | 769.333333 | 0 | 0 |
| 43 | 769.333333 | 0 | 0 |
| 44 | 769.333333 | 0 | 0 |
| 45 | 769.333333 | 0 | 0 |
| 46 | 769.333333 | 0 | 0 |
| 47 | 769.333333 | 0 | 0 |
| 48 | 769.333333 | 0 | 0 |
| 49 | 769.333333 | 0 | 0 |
| 50 | 769.333333 | 0 | 0 |
| 51 | 769.333333 | 0 | 0 |
| 52 | 769.333333 | 0 | 0 |
| 53 | 769.333333 | 0 | 0 |
| 54 | 769.333333 | 0 | 0 |
| 55 | 769.333333 | 0 | 0 |
| 56 | 769.333333 | 0 | 0 |
| 57 | 769.333333 | 0 | 0 |
| 58 | 769.333333 | 0 | 0 |
| 59 | 769.333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 769.333333 | 0 | 0 |
| 4 | 769.333333 | 0 | 0 |
| 5 | 769.333333 | 0 | 0 |
| 6 | 769.333333 | 0 | 0 |
| 7 | 769.333333 | 0 | 0 |
| 8 | 769.333333 | 0 | 0 |
| 9 | 769.333333 | 0 | 0 |
| 10 | 769.333333 | 0 | 0 |
| 11 | 769.333333 | 0 | 0 |
| 12 | 769.333333 | 0 | 0 |
| 13 | 769.333333 | 0 | 0 |
| 14 | 769.333333 | 0 | 0 |
| 15 | 769.333333 | 0 | 0 |
| 16 | 769.333333 | 0 | 0 |
| 17 | 769.333333 | 0 | 0 |
| 18 | 769.333333 | 0 | 0 |
| 19 | 769.333333 | 0 | 0 |
| 20 | 769.333333 | 0 | 0 |
| 21 | 769.333333 | 0 | 0 |
| 22 | 769.333333 | 0 | 0 |
| 23 | 769.333333 | 0 | 0 |
| 24 | 769.333333 | 0 | 0 |
| 25 | 769.333333 | 0 | 0 |
| 26 | 769.333333 | 0 | 0 |
| 27 | 769.333333 | 0 | 0 |
| 28 | 769.333333 | 0 | 0 |
| 29 | 769.333333 | 0 | 0 |
| 30 | 769.333333 | 0 | 0 |
| 31 | 38053.5 | 0 | 0 |
| 32 | 38053.5 | 0 | 0 |
| 33 | | | |
| 34 | 37585.8333 | 0 | 0 |
| 35 | 145.833333 | 0 | 0 |
| 36 | 145.833333 | 0 | 0 |
| 37 | 145.833333 | 0 | 0 |
| 38 | 145.833333 | 0 | 0 |
| 39 | 145.833333 | 0 | 0 |
| 40 | 145.833333 | 0 | 0 |
| 41 | 145.833333 | 0 | 0 |
| 42 | 145.833333 | 0 | 0 |
| 43 | 145.833333 | 0 | 0 |
| 44 | 145.833333 | 0 | 0 |
| 45 | 145.833333 | 0 | 0 |
| 46 | 145.833333 | 0 | 0 |
| 47 | 145.833333 | 0 | 0 |
| 48 | 145.833333 | 0 | 0 |
| 49 | 145.833333 | 0 | 0 |
| 50 | 145.833333 | 0 | 0 |
| 51 | 145.833333 | 0 | 0 |
| 52 | 145.833333 | 0 | 0 |
| 53 | 145.833333 | 0 | 0 |
| 54 | 145.833333 | 0 | 0 |
| 55 | 145.833333 | 0 | 0 |
| 56 | 145.833333 | 0 | 0 |
| 57 | 145.833333 | 0 | 0 |
| 58 | 145.833333 | 0 | 0 |
| 59 | 145.833333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 84.6666667 | 0 | 0 |
| 4 | 84.6666667 | 0 | 0 |
| 5 | 84.6666667 | 0 | 0 |
| 6 | 84.6666667 | 0 | 0 |
| 7 | 84.6666667 | 0 | 0 |
| 8 | 84.6666667 | 0 | 0 |
| 9 | 84.6666667 | 0 | 0 |
| 10 | 84.6666667 | 0 | 0 |
| 11 | 84.6666667 | 0 | 0 |
| 12 | 84.6666667 | 0 | 0 |
| 13 | 84.6666667 | 0 | 0 |
| 14 | 84.6666667 | 0 | 0 |
| 15 | 84.6666667 | 0 | 0 |
| 16 | 84.6666667 | 0 | 0 |
| 17 | 84.6666667 | 0 | 0 |
| 18 | 88.8333333 | 0 | 0 |
| 19 | 8013.5 | 0 | 0 |
| 20 | 8013.5 | 0 | 0 |
| 21 | 8013.5 | 0 | 0 |
| 22 | 8013.5 | 0 | 0 |
| 23 | 8013.5 | 0 | 0 |
| 24 | 8013.5 | 0 | 0 |
| 25 | 8013.5 | 0 | 0 |
| 26 | 8013.5 | 0 | 0 |
| 27 | 8013.5 | 0 | 0 |
| 28 | 8013.5 | 0 | 0 |
| 29 | 8013.5 | 0 | 0 |
| 30 | 8013.5 | 0 | 0 |
| 31 | 8013.5 | 0 | 0 |
| 32 | 8013.5 | 0 | 0 |
| 33 | 8013.5 | 0 | 0 |
| 34 | 8013.5 | 0 | 0 |
| 35 | 8013.5 | 0 | 0 |
| 36 | 8013.5 | 0 | 0 |
| 37 | 8013.5 | 0 | 0 |
| 38 | 8013.5 | 0 | 0 |
| 39 | 8013.5 | 0 | 0 |
| 40 | 8013.5 | 0 | 0 |
| 41 | 8013.5 | 0 | 0 |
| 42 | 8013.5 | 0 | 0 |
| 43 | 8013.5 | 0 | 0 |
| 44 | 8013.5 | 0 | 0 |
| 45 | 8013.5 | 0 | 0 |
| 46 | 8013.5 | 0 | 0 |
| 47 | 8013.5 | 0 | 0 |
| 48 | 8013.5 | 0 | 0 |
| 49 | 8013.5 | 0 | 0 |
| 50 | 8013.5 | 0 | 0 |
| 51 | 8013.5 | 0 | 0 |
| 52 | 8013.5 | 0 | 0 |
| 53 | 8063.5 | 0 | 0 |
| 54 | 8063.5 | 0 | 0 |
| 55 | 8063.5 | 0 | 0 |
| 56 | 8186.33333 | 0 | 0 |
| 57 | 8186.33333 | 0 | 0 |
| 58 | 8186.33333 | 0 | 0 |
| 59 | 8186.33333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 8186.33333 | 0 | 0 |
| 4 | | | |
| 5 | 52 | 0 | 0 |
| 6 | 103.333333 | 0 | 0 |
| 7 | 103.333333 | 0 | 0 |
| 8 | | | |
| 9 | 103.333333 | 0 | 0 |
| 10 | 103.333333 | 0 | 0 |
| 11 | 103.333333 | 0 | 0 |
| 12 | | | |
| 13 | 103.333333 | 0 | 0 |
| 14 | 103.333333 | 0 | 0 |
| 15 | 103.333333 | 0 | 0 |
| 16 | 103.333333 | 0 | 0 |
| 17 | 103.333333 | 0 | 0 |
| 18 | 103.333333 | 0 | 0 |
| 19 | 103.333333 | 0 | 0 |
| 20 | 103.333333 | 0 | 0 |
| 21 | | | |
| 22 | 103.333333 | 0 | 0 |
| 23 | 103.333333 | 0 | 0 |
| 24 | 103.333333 | 0 | 0 |
| 25 | | | |
| 26 | 103.333333 | 0 | 0 |
| 27 | 103.333333 | 0 | 0 |
| 28 | 103.333333 | 0 | 0 |
| 29 | | | |
| 30 | 103.333333 | 0 | 0 |
| 31 | 5537 | 0 | 0 |
| 32 | 5537 | 0 | 0 |
| 33 | | | |
| 34 | 5537 | 0 | 0 |
| 35 | 5537 | 0 | 0 |
| 36 | 5537 | 0 | 0 |
| 37 | | | |
| 38 | 5537 | 0 | 0 |
| 39 | 5537 | 0 | 0 |
| 40 | | | |
| 41 | 5537 | 0 | 0 |
| 42 | 5537 | 0 | 0 |
| 43 | 5537 | 0 | 0 |
| 44 | 5537 | 0 | 0 |
| 45 | | | |
| 46 | 5537 | 0 | 0 |
| 47 | 5537 | 0 | 0 |
| 48 | 5537 | 0 | 0 |
| 49 | | | |
| 50 | 5537 | 0 | 0 |
| 51 | 5537 | 0 | 0 |
| 52 | 5537 | 0 | 0 |
| 53 | | | |
| 54 | 5537 | 0 | 0 |
| 55 | 5537 | 0 | 0 |
| 56 | 5537 | 0 | 0 |
| 57 | 5537 | 0 | 0 |
| 58 | 5537 | 0 | 0 |
| 59 | 5537 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 5537 | 0 | 0 |
| 4 | 5537 | 0 | 0 |
| 5 | 5537 | 0 | 0 |
| 6 | 5537 | 0 | 0 |
| 7 | 5537 | 0 | 0 |
| 8 | 5537 | 0 | 0 |
| 9 | 5537 | 0 | 0 |
| 10 | 5537 | 0 | 0 |
| 11 | 5537 | 0 | 0 |
| 12 | 5537 | 0 | 0 |
| 13 | 5537 | 0 | 0 |
| 14 | 5537 | 0 | 0 |
| 15 | 5537 | 0 | 0 |
| 16 | 5537 | 0 | 0 |
| 17 | 5537 | 0 | 0 |
| 18 | 5537 | 0 | 0 |
| 19 | 5537 | 0 | 0 |
| 20 | 5537 | 0 | 0 |
| 21 | 5537 | 0 | 0 |
| 22 | 5537 | 0 | 0 |
| 23 | 3359.83333 | 0 | 0 |
| 24 | 3359.83333 | 0 | 0 |
| 25 | 3281.83333 | 0 | 0 |
| 26 | 11173.6667 | 0 | 0 |
| 27 | 11173.6667 | 0 | 0 |
| 28 | 11173.6667 | 0 | 0 |
| 29 | 11173.6667 | 0 | 0 |
| 30 | 11173.6667 | 0 | 0 |
| 31 | 11173.6667 | 0 | 0 |
| 32 | 11173.6667 | 0 | 0 |
| 33 | 11173.6667 | 0 | 0 |
| 34 | 11173.6667 | 0 | 0 |
| 35 | 11173.6667 | 0 | 0 |
| 36 | 11173.6667 | 0 | 0 |
| 37 | 11173.6667 | 0 | 0 |
| 38 | 11173.6667 | 0 | 0 |
| 39 | 11173.6667 | 0 | 0 |
| 40 | 11173.6667 | 0 | 0 |
| 41 | 11173.6667 | 0 | 0 |
| 42 | 11173.6667 | 0 | 0 |
| 43 | 11173.6667 | 0 | 0 |
| 44 | 11173.6667 | 0 | 0 |
| 45 | 11173.6667 | 0 | 0 |
| 46 | 11173.6667 | 0 | 0 |
| 47 | 11173.6667 | 0 | 0 |
| 48 | 11173.6667 | 0 | 0 |
| 49 | 11173.6667 | 0 | 0 |
| 50 | 11173.6667 | 0 | 0 |
| 51 | 11173.6667 | 0 | 0 |
| 52 | 11173.6667 | 0 | 0 |
| 53 | 11173.6667 | 0 | 0 |
| 54 | 11173.6667 | 0 | 0 |
| 55 | 11173.6667 | 0 | 0 |
| 56 | 11173.6667 | 0 | 0 |
| 57 | 11173.6667 | 0 | 0 |
| 58 | 11173.6667 | 0 | 0 |
| 59 | 11173.6667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 11173.6667 | 0 | 0 |
| 4 | 11173.6667 | 0 | 0 |
| 5 | 11173.6667 | 0 | 0 |
| 6 | 11173.6667 | 0 | 0 |
| 7 | 11173.6667 | 0 | 0 |
| 8 | 11173.6667 | 0 | 0 |
| 9 | 11173.6667 | 0 | 0 |
| 10 | 11173.6667 | 0 | 0 |
| 11 | 11173.6667 | 0 | 0 |
| 12 | 11173.6667 | 0 | 0 |
| 13 | 11173.6667 | 0 | 0 |
| 14 | 11173.6667 | 0 | 0 |
| 15 | 11173.6667 | 0 | 0 |
| 16 | 11173.6667 | 0 | 0 |
| 17 | 11173.6667 | 0 | 0 |
| 18 | 3219.83333 | 0 | 0 |
| 19 | 3219.83333 | 0 | 0 |
| 20 | 3219.83333 | 0 | 0 |
| 21 | 3219.83333 | 0 | 0 |
| 22 | 3219.83333 | 0 | 0 |
| 23 | 3219.83333 | 0 | 0 |
| 24 | 84.6666667 | 0 | 0 |
| 25 | 84.6666667 | 0 | 0 |
| 26 | 84.6666667 | 0 | 0 |
| 27 | 952.833333 | 0 | 0 |
| 28 | 61.5 | 0 | 0 |
| 29 | 61.5 | 0 | 0 |
| 30 | 61.5 | 0 | 0 |
| 31 | 61.5 | 0 | 0 |
| 32 | 61.5 | 0 | 0 |
| 33 | 61.5 | 0 | 0 |
| 34 | 61.5 | 0 | 0 |
| 35 | 61.5 | 0 | 0 |
| 36 | 19001 | 0 | 0 |
| 37 | 19000.8333 | 0 | 0 |
| 38 | 19000.8333 | 0 | 0 |
| 39 | 19000.8333 | 0 | 0 |
| 40 | 19000.8333 | 0 | 0 |
| 41 | 19000.8333 | 0 | 0 |
| 42 | 19000.8333 | 0 | 0 |
| 43 | 19000.8333 | 0 | 0 |
| 44 | 19000.8333 | 0 | 0 |
| 45 | 19000.8333 | 0 | 0 |
| 46 | 19000.8333 | 0 | 0 |
| 47 | 18667.8333 | 0 | 0 |
| 48 | 18667.8333 | 0 | 0 |
| 49 | 18667.8333 | 0 | 0 |
| 50 | 18667.8333 | 0 | 0 |
| 51 | 18667.8333 | 0 | 0 |
| 52 | 18667.8333 | 0 | 0 |
| 53 | 18667.8333 | 0 | 0 |
| 54 | 18667.8333 | 0 | 0 |
| 55 | 18667.8333 | 0 | 0 |
| 56 | 18667.8333 | 0 | 0 |
| 57 | 18667.8333 | 0 | 0 |
| 58 | 18667.8333 | 0 | 0 |
| 59 | 18667.8333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 18667.8333 | 0 | 0 |
| 4 | 18667.8333 | 0 | 0 |
| 5 | 18667.8333 | 0 | 0 |
| 6 | 18667.8333 | 0 | 0 |
| 7 | 18667.8333 | 0 | 0 |
| 8 | 18667.8333 | 0 | 0 |
| 9 | 18667.8333 | 0 | 0 |
| 10 | 18667.8333 | 0 | 0 |
| 11 | 18667.8333 | 0 | 0 |
| 12 | 18667.8333 | 0 | 0 |
| 13 | 18667.8333 | 0 | 0 |
| 14 | 18667.8333 | 0 | 0 |
| 15 | 18667.8333 | 0 | 0 |
| 16 | 18667.8333 | 0 | 0 |
| 17 | 18667.8333 | 0 | 0 |
| 18 | 18667.8333 | 0 | 0 |
| 19 | 18667.8333 | 0 | 0 |
| 20 | 18667.8333 | 0 | 0 |
| 21 | 18667.8333 | 0 | 0 |
| 22 | 18667.8333 | 0 | 0 |
| 23 | 18667.8333 | 0 | 0 |
| 24 | 18667.8333 | 0 | 0 |
| 25 | 18667.8333 | 0 | 0 |
| 26 | 18667.8333 | 0 | 0 |
| 27 | 18667.8333 | 0 | 0 |
| 28 | 18667.8333 | 0 | 0 |
| 29 | 18667.8333 | 0 | 0 |
| 30 | 18667.8333 | 0 | 0 |
| 31 | 18667.8333 | 0 | 0 |
| 32 | 18667.8333 | 0 | 0 |
| 33 | 18667.8333 | 0 | 0 |
| 34 | 18667.8333 | 0 | 0 |
| 35 | 18667.8333 | 0 | 0 |
| 36 | 18667.8333 | 0 | 0 |
| 37 | 18667.8333 | 0 | 0 |
| 38 | 18667.8333 | 0 | 0 |
| 39 | 18667.8333 | 0 | 0 |
| 40 | 18667.8333 | 0 | 0 |
| 41 | 18667.8333 | 0 | 0 |
| 42 | 18667.8333 | 0 | 0 |
| 43 | 18667.8333 | 0 | 0 |
| 44 | 18667.8333 | 0 | 0 |
| 45 | 18667.8333 | 0 | 0 |
| 46 | 18667.8333 | 0 | 0 |
| 47 | 18667.8333 | 0 | 0 |
| 48 | 18667.8333 | 0 | 0 |
| 49 | 18667.8333 | 0 | 0 |
| 50 | 18667.8333 | 0 | 0 |
| 51 | 18667.8333 | 0 | 0 |
| 52 | 18667.8333 | 0 | 0 |
| 53 | 18667.8333 | 0 | 0 |
| 54 | 18667.8333 | 0 | 0 |
| 55 | 18667.8333 | 0 | 0 |
| 56 | 18667.8333 | 0 | 0 |
| 57 | 18667.8333 | 0 | 0 |
| 58 | 18667.8333 | 0 | 0 |
| 59 | 18667.8333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 18667.8333 | 0 | 0 |
| 4 | 18667.8333 | 0 | 0 |
| 5 | 18667.8333 | 0 | 0 |
| 6 | 18667.8333 | 0 | 0 |
| 7 | 18667.8333 | 0 | 0 |
| 8 | 18667.8333 | 0 | 0 |
| 9 | 18667.8333 | 0 | 0 |
| 10 | 18667.8333 | 0 | 0 |
| 11 | 18667.8333 | 0 | 0 |
| 12 | 18667.8333 | 0 | 0 |
| 13 | 18667.8333 | 0 | 0 |
| 14 | 18667.8333 | 0 | 0 |
| 15 | 18667.8333 | 0 | 0 |
| 16 | 18667.8333 | 0 | 0 |
| 17 | 18667.8333 | 0 | 0 |
| 18 | 18667.8333 | 0 | 0 |
| 19 | 18667.8333 | 0 | 0 |
| 20 | 18667.8333 | 0 | 0 |
| 21 | 18667.8333 | 0 | 0 |
| 22 | 18667.8333 | 0 | 0 |
| 23 | 18667.8333 | 0 | 0 |
| 24 | 18667.8333 | 0 | 0 |
| 25 | 18667.8333 | 0 | 0 |
| 26 | 18667.8333 | 0 | 0 |
| 27 | 18667.8333 | 0 | 0 |
| 28 | 18667.8333 | 0 | 0 |
| 29 | 18667.8333 | 0 | 0 |
| 30 | 18667.8333 | 0 | 0 |
| 31 | 18667.8333 | 0 | 0 |
| 32 | 18667.8333 | 0 | 0 |
| 33 | 18667.8333 | 0 | 0 |
| 34 | 18667.8333 | 0 | 0 |
| 35 | 18667.8333 | 0 | 0 |
| 36 | 18667.8333 | 0 | 0 |
| 37 | 18667.8333 | 0 | 0 |
| 38 | 18677.3333 | 0 | 0 |
| 39 | 3151.66667 | 0 | 0 |
| 40 | 18759.1667 | 0 | 0 |
| 41 | 18759.1667 | 0 | 0 |
| 42 | 18759.1667 | 0 | 0 |
| 43 | 3212.5 | 0 | 0 |
| 44 | 3212.5 | 0 | 0 |
| 45 | 3212.5 | 0 | 0 |
| 46 | 3212.5 | 0 | 0 |
| 47 | 3212.5 | 0 | 0 |
| 48 | 3212.5 | 0 | 0 |
| 49 | 3212.5 | 0 | 0 |
| 50 | 3212.5 | 0 | 0 |
| 51 | 3212.5 | 0 | 0 |
| 52 | 3212.5 | 0 | 0 |
| 53 | 18777.3333 | 0 | 0 |
| 54 | 18777.3333 | 0 | 0 |
| 55 | 18777.3333 | 0 | 0 |
| 56 | 18777.3333 | 0 | 0 |
| 57 | 18777.3333 | 0 | 0 |
| 58 | 18777.3333 | 0 | 0 |
| 59 | 18777.3333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 18777.3333 | 0 | 0 |
| 4 | 18777.3333 | 0 | 0 |
| 5 | 18777.3333 | 0 | 0 |
| 6 | 18777.3333 | 0 | 0 |
| 7 | 18777.3333 | 0 | 0 |
| 8 | 18777.3333 | 0 | 0 |
| 9 | 18777.3333 | 0 | 0 |
| 10 | 320010.667 | 0 | 0 |
| 11 | 320010.667 | 0 | 0 |
| 12 | 320010.667 | 0 | 0 |
| 13 | 320010.667 | 0 | 0 |
| 14 | 1087.33333 | 0 | 0 |
| 15 | 163.833333 | 0 | 0 |
| 16 | 163.833333 | 0 | 0 |
| 17 | 163.833333 | 0 | 0 |
| 18 | 163.833333 | 0 | 0 |
| 19 | 163.833333 | 0 | 0 |
| 20 | 163.833333 | 0 | 0 |
| 21 | 163.833333 | 0 | 0 |
| 22 | 163.833333 | 0 | 0 |
| 23 | 3197.66667 | 0 | 0 |
| 24 | 3197.66667 | 0 | 0 |
| 25 | 3197.66667 | 0 | 0 |
| 26 | 3197.66667 | 0 | 0 |
| 27 | 3197.66667 | 0 | 0 |
| 28 | 166.333333 | 0 | 0 |
| 29 | 166.333333 | 0 | 0 |
| 30 | 166.333333 | 0 | 0 |
| 31 | 166.333333 | 0 | 0 |
| 32 | 166.333333 | 0 | 0 |
| 33 | 166.333333 | 0 | 0 |
| 34 | 166.333333 | 0 | 0 |
| 35 | 166.333333 | 0 | 0 |
| 36 | 166.333333 | 0 | 0 |
| 37 | 166.333333 | 0 | 0 |
| 38 | 166.333333 | 0 | 0 |
| 39 | 166.333333 | 0 | 0 |
| 40 | 5028.66667 | 0 | 0 |
| 41 | 5028.66667 | 0 | 0 |
| 42 | 5028.66667 | 0 | 0 |
| 43 | 112 | 0 | 0 |
| 44 | 143 | 0 | 0 |
| 45 | 11530.8333 | 0 | 0 |
| 46 | 11530.8333 | 0 | 0 |
| 47 | 11530.8333 | 0 | 0 |
| 48 | 13051.5 | 0 | 0 |
| 49 | 13051.5 | 0 | 0 |
| 50 | 13051.5 | 0 | 0 |
| 51 | 13051.5 | 0 | 0 |
| 52 | 13051.5 | 0 | 0 |
| 53 | 13051.5 | 0 | 0 |
| 54 | 13051.5 | 0 | 0 |
| 55 | 13051.5 | 0 | 0 |
| 56 | 13051.5 | 0 | 0 |
| 57 | 13051.5 | 0 | 0 |
| 58 | 13051.5 | 0 | 0 |
| 59 | 13051.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 11545 | 0 | 0 |
| 4 | 11545 | 0 | 0 |
| 5 | 11559.5 | 0 | 0 |
| 6 | 11559.5 | 0 | 0 |
| 7 | 13022.1667 | 0 | 0 |
| 8 | 57 | 0 | 0 |
| 9 | 57 | 0 | 0 |
| 10 | 57 | 0 | 0 |
| 11 | 57 | 0 | 0 |
| 12 | 57 | 0 | 0 |
| 13 | 57 | 0 | 0 |
| 14 | 57 | 0 | 0 |
| 15 | 57 | 0 | 0 |
| 16 | 57 | 0 | 0 |
| 17 | 57 | 0 | 0 |
| 18 | 57 | 0 | 0 |
| 19 | 57 | 0 | 0 |
| 20 | 57 | 0 | 0 |
| 21 | 57 | 0 | 0 |
| 22 | 57 | 0 | 0 |
| 23 | 57 | 0 | 0 |
| 24 | 57 | 0 | 0 |
| 25 | 57 | 0 | 0 |
| 26 | 57 | 0 | 0 |
| 27 | 57 | 0 | 0 |
| 28 | 57 | 0 | 0 |
| 29 | 57 | 0 | 0 |
| 30 | 57 | 0 | 0 |
| 31 | 57 | 0 | 0 |
| 32 | 57 | 0 | 0 |
| 33 | 57 | 0 | 0 |
| 34 | 57 | 0 | 0 |
| 35 | 57 | 0 | 0 |
| 36 | 57 | 0 | 0 |
| 37 | 57 | 0 | 0 |
| 38 | 57 | 0 | 0 |
| 39 | 57 | 0 | 0 |
| 40 | 57 | 0 | 0 |
| 41 | 158.666667 | 0 | 0 |
| 42 | 61.8333333 | 0 | 0 |
| 43 | 61.8333333 | 0 | 0 |
| 44 | 61.8333333 | 0 | 0 |
| 45 | 61.8333333 | 0 | 0 |
| 46 | 61.8333333 | 0 | 0 |
| 47 | 61.8333333 | 0 | 0 |
| 48 | 61.8333333 | 0 | 0 |
| 49 | 61.8333333 | 0 | 0 |
| 50 | 61.8333333 | 0 | 0 |
| 51 | 61.8333333 | 0 | 0 |
| 52 | 61.8333333 | 0 | 0 |
| 53 | 61.8333333 | 0 | 0 |
| 54 | 61.8333333 | 0 | 0 |
| 55 | 61.8333333 | 0 | 0 |
| 56 | 61.8333333 | 0 | 0 |
| 57 | 61.8333333 | 0 | 0 |
| 58 | 61.8333333 | 0 | 0 |
| 59 | 61.8333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 61.8333333 | 0 | 0 |
| 4 | 61.8333333 | 0 | 0 |
| 5 | 61.8333333 | 0 | 0 |
| 6 | 61.8333333 | 0 | 0 |
| 7 | 61.8333333 | 0 | 0 |
| 8 | 61.8333333 | 0 | 0 |
| 9 | 61.8333333 | 0 | 0 |
| 10 | 61.8333333 | 0 | 0 |
| 11 | 61.8333333 | 0 | 0 |
| 12 | 61.8333333 | 0 | 0 |
| 13 | 61.8333333 | 0 | 0 |
| 14 | 61.8333333 | 0 | 0 |
| 15 | 61.8333333 | 0 | 0 |
| 16 | 61.8333333 | 0 | 0 |
| 17 | 61.8333333 | 0 | 0 |
| 18 | 61.8333333 | 0 | 0 |
| 19 | 61.8333333 | 0 | 0 |
| 20 | 61.8333333 | 0 | 0 |
| 21 | 61.8333333 | 0 | 0 |
| 22 | 61.8333333 | 0 | 0 |
| 23 | 260.166667 | 0 | 0 |
| 24 | 260.166667 | 0 | 0 |
| 25 | 246.333333 | 0 | 0 |
| 26 | 246.333333 | 0 | 0 |
| 27 | 246.333333 | 0 | 0 |
| 28 | 246.333333 | 0 | 0 |
| 29 | 246.333333 | 0 | 0 |
| 30 | 246.333333 | 0 | 0 |
| 31 | 246.333333 | 0 | 0 |
| 32 | 246.333333 | 0 | 0 |
| 33 | 246.333333 | 0 | 0 |
| 34 | 246.333333 | 0 | 0 |
| 35 | 246.333333 | 0 | 0 |
| 36 | 246.333333 | 0 | 0 |
| 37 | 246.333333 | 0 | 0 |
| 38 | 246.333333 | 0 | 0 |
| 39 | 263.5 | 0 | 0 |
| 40 | 271 | 0 | 0 |
| 41 | 271 | 0 | 0 |
| 42 | 271 | 0 | 0 |
| 43 | 271 | 0 | 0 |
| 44 | 271 | 0 | 0 |
| 45 | 271 | 0 | 0 |
| 46 | 271 | 0 | 0 |
| 47 | 271 | 0 | 0 |
| 48 | 271 | 0 | 0 |
| 49 | 271 | 0 | 0 |
| 50 | 271 | 0 | 0 |
| 51 | 271 | 0 | 0 |
| 52 | 271 | 0 | 0 |
| 53 | 271 | 0 | 0 |
| 54 | 271 | 0 | 0 |
| 55 | 1062.16667 | 0 | 0 |
| 56 | 255.666667 | 0 | 0 |
| 57 | 255.666667 | 0 | 0 |
| 58 | 255.666667 | 0 | 0 |
| 59 | 255.666667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|-------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 255.666667 | 0 | 0 |
| 4 | 255.666667 | 0 | 0 |
| 5 | 255.666667 | 0 | 0 |
| 6 | 255.666667 | 0 | 0 |
| 7 | 255.666667 | 0 | 0 |
| 8 | 255.666667 | 0 | 0 |
| 9 | 255.666667 | 0 | 0 |
| 10 | 255.666667 | 0 | 0 |
| 11 | 255.666667 | 0 | 0 |
| 12 | 255.666667 | 0 | 0 |
| 13 | 255.666667 | 0 | 0 |
| 14 | 255.666667 | 0 | 0 |
| 15 | 255.666667 | 0 | 0 |
| 16 | 255.666667 | 0 | 0 |
| 17 | 255.666667 | 0 | 0 |
| 18 | 255.666667 | 0 | 0 |
| 19 | 255.666667 | 0 | 0 |
| 20 | 255.666667 | 0 | 0 |
| 21 | 255.666667 | 0 | 0 |
| 22 | 255.666667 | 0 | 0 |
| 23 | 255.666667 | 0 | 0 |
| 24 | 255.666667 | 0 | 0 |
| 25 | 255.666667 | 0 | 0 |
| 26 | 255.666667 | 0 | 0 |
| 27 | 1211 | 0 | 0 |
| 28 | 1265.833333 | 0 | 0 |
| 29 | 1265.833333 | 0 | 0 |
| 30 | 1265.833333 | 0 | 0 |
| 31 | 1265.833333 | 0 | 0 |
| 32 | 1265.833333 | 0 | 0 |
| 33 | 1265.833333 | 0 | 0 |
| 34 | 1265.833333 | 0 | 0 |
| 35 | 1265.833333 | 0 | 0 |
| 36 | 1265.833333 | 0 | 0 |
| 37 | 1265.833333 | 0 | 0 |
| 38 | 273.333333 | 0 | 0 |
| 39 | 273.333333 | 0 | 0 |
| 40 | 273.333333 | 0 | 0 |
| 41 | 273.333333 | 0 | 0 |
| 42 | 273.333333 | 0 | 0 |
| 43 | 43858 | 0 | 0 |
| 44 | 43858 | 0 | 0 |
| 45 | 43858 | 0 | 0 |
| 46 | 43858 | 0 | 0 |
| 47 | 43858 | 0 | 0 |
| 48 | 43858 | 0 | 0 |
| 49 | 43858 | 0 | 0 |
| 50 | 43858 | 0 | 0 |
| 51 | 43858 | 0 | 0 |
| 52 | 43858 | 0 | 0 |
| 53 | 43858 | 0 | 0 |
| 54 | 43858 | 0 | 0 |
| 55 | 63 | 0 | 0 |
| 56 | 62.6666667 | 0 | 0 |
| 57 | 9693.5 | 0 | 0 |
| 58 | 9693.5 | 0 | 0 |
| 59 | 9693.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 9693.5 | 0 | 0 |
| 4 | 9693.5 | 0 | 0 |
| 5 | 9693.5 | 0 | 0 |
| 6 | 9693.5 | 0 | 0 |
| 7 | 9693.5 | 0 | 0 |
| 8 | 9693.5 | 0 | 0 |
| 9 | 9693.5 | 0 | 0 |
| 10 | 9693.5 | 0 | 0 |
| 11 | 9693.5 | 0 | 0 |
| 12 | 9693.5 | 0 | 0 |
| 13 | 9693.5 | 0 | 0 |
| 14 | 9693.5 | 0 | 0 |
| 15 | 3663.66667 | 0 | 0 |
| 16 | 3663.66667 | 0 | 0 |
| 17 | 1542.16667 | 0 | 0 |
| 18 | 351.333333 | 0 | 0 |
| 19 | 88.6666667 | 0 | 0 |
| 20 | 56.8333333 | 0 | 0 |
| 21 | 56.8333333 | 0 | 0 |
| 22 | 56.8333333 | 0 | 0 |
| 23 | 56.8333333 | 0 | 0 |
| 24 | 56.8333333 | 0 | 0 |
| 25 | 56.8333333 | 0 | 0 |
| 26 | 56.8333333 | 0 | 0 |
| 27 | 56.8333333 | 0 | 0 |
| 28 | 56.8333333 | 0 | 0 |
| 29 | 56.8333333 | 0 | 0 |
| 30 | 56.8333333 | 0 | 0 |
| 31 | 56.8333333 | 0 | 0 |
| 32 | 56.8333333 | 0 | 0 |
| 33 | 56.8333333 | 0 | 0 |
| 34 | 56.8333333 | 0 | 0 |
| 35 | 56.8333333 | 0 | 0 |
| 36 | 56.8333333 | 0 | 0 |
| 37 | 56.8333333 | 0 | 0 |
| 38 | 56.8333333 | 0 | 0 |
| 39 | 56.8333333 | 0 | 0 |
| 40 | 56.8333333 | 0 | 0 |
| 41 | 56.8333333 | 0 | 0 |
| 42 | 56.8333333 | 0 | 0 |
| 43 | 56.8333333 | 0 | 0 |
| 44 | 56.8333333 | 0 | 0 |
| 45 | 56.8333333 | 0 | 0 |
| 46 | 56.8333333 | 0 | 0 |
| 47 | 56.8333333 | 0 | 0 |
| 48 | 56.8333333 | 0 | 0 |
| 49 | 56.8333333 | 0 | 0 |
| 50 | 56.8333333 | 0 | 0 |
| 51 | 56.8333333 | 0 | 0 |
| 52 | 56.8333333 | 0 | 0 |
| 53 | 56.8333333 | 0 | 0 |
| 54 | 56.8333333 | 0 | 0 |
| 55 | 56.8333333 | 0 | 0 |
| 56 | 56.8333333 | 0 | 0 |
| 57 | 56.8333333 | 0 | 0 |
| 58 | 56.8333333 | 0 | 0 |
| 59 | 56.8333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|-------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 56.8333333 | 0 | 0 |
| 4 | 56.8333333 | 0 | 0 |
| 5 | 56.8333333 | 0 | 0 |
| 6 | 56.8333333 | 0 | 0 |
| 7 | 56.8333333 | 0 | 0 |
| 8 | 56.8333333 | 0 | 0 |
| 9 | 56.8333333 | 0 | 0 |
| 10 | 56.8333333 | 0 | 0 |
| 11 | 56.8333333 | 0 | 0 |
| 12 | 56.8333333 | 0 | 0 |
| 13 | 56.8333333 | 0 | 0 |
| 14 | 56.8333333 | 0 | 0 |
| 15 | 56.8333333 | 0 | 0 |
| 16 | 167.8333333 | 0 | 0 |
| 17 | 167.5 | 0 | 0 |
| 18 | 166.666667 | 0 | 0 |
| 19 | 166.666667 | 0 | 0 |
| 20 | 166.666667 | 0 | 0 |
| 21 | 166.666667 | 0 | 0 |
| 22 | 166.666667 | 0 | 0 |
| 23 | 166.666667 | 0 | 0 |
| 24 | 166.666667 | 0 | 0 |
| 25 | 166.666667 | 0 | 0 |
| 26 | 166.666667 | 0 | 0 |
| 27 | 166.666667 | 0 | 0 |
| 28 | 166.666667 | 0 | 0 |
| 29 | 166.666667 | 0 | 0 |
| 30 | 166.666667 | 0 | 0 |
| 31 | 166.666667 | 0 | 0 |
| 32 | 166.666667 | 0 | 0 |
| 33 | 166.666667 | 0 | 0 |
| 34 | 166.666667 | 0 | 0 |
| 35 | 166.666667 | 0 | 0 |
| 36 | 166.666667 | 0 | 0 |
| 37 | 166.666667 | 0 | 0 |
| 38 | 166.666667 | 0 | 0 |
| 39 | 166.666667 | 0 | 0 |
| 40 | 57.3333333 | 0 | 0 |
| 41 | 57.3333333 | 0 | 0 |
| 42 | 8829.66667 | 0 | 0 |
| 43 | 8766.83333 | 0 | 0 |
| 44 | 8766.83333 | 0 | 0 |
| 45 | 8766.83333 | 0 | 0 |
| 46 | 8766.83333 | 0 | 0 |
| 47 | 8766.83333 | 0 | 0 |
| 48 | 8766.83333 | 0 | 0 |
| 49 | 8766.83333 | 0 | 0 |
| 50 | 8766.83333 | 0 | 0 |
| 51 | 8766.83333 | 0 | 0 |
| 52 | 8766.83333 | 0 | 0 |
| 53 | 303.833333 | 0 | 0 |
| 54 | 303.833333 | 0 | 0 |
| 55 | 303.833333 | 0 | 0 |
| 56 | 303.833333 | 0 | 0 |
| 57 | 303.833333 | 0 | 0 |
| 58 | 303.833333 | 0 | 0 |
| 59 | 303.833333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 374.166667 | 0 | 0 |
| 4 | 374.166667 | 0 | 0 |
| 5 | 374.166667 | 0 | 0 |
| 6 | 374.166667 | 0 | 0 |
| 7 | 374.166667 | 0 | 0 |
| 8 | 132 | 0 | 0 |
| 9 | 132 | 0 | 0 |
| 10 | 132 | 0 | 0 |
| 11 | 132 | 0 | 0 |
| 12 | 132 | 0 | 0 |
| 13 | 132 | 0 | 0 |
| 14 | 132 | 0 | 0 |
| 15 | 132 | 0 | 0 |
| 16 | 132 | 0 | 0 |
| 17 | 132 | 0 | 0 |
| 18 | 132 | 0 | 0 |
| 19 | 132 | 0 | 0 |
| 20 | 132 | 0 | 0 |
| 21 | 132 | 0 | 0 |
| 22 | 132 | 0 | 0 |
| 23 | 132 | 0 | 0 |
| 24 | 132 | 0 | 0 |
| 25 | 132 | 0 | 0 |
| 26 | 132 | 0 | 0 |
| 27 | 132 | 0 | 0 |
| 28 | 132 | 0 | 0 |
| 29 | 132 | 0 | 0 |
| 30 | 132 | 0 | 0 |
| 31 | 54058.5 | 0 | 0 |
| 32 | 52422.5 | 0 | 0 |
| 33 | 52422.5 | 0 | 0 |
| 34 | 52422.5 | 0 | 0 |
| 35 | 52422.5 | 0 | 0 |
| 36 | 52422.5 | 0 | 0 |
| 37 | 52422.5 | 0 | 0 |
| 38 | 52422.5 | 0 | 0 |
| 39 | 52422.5 | 0 | 0 |
| 40 | 52422.5 | 0 | 0 |
| 41 | 52422.5 | 0 | 0 |
| 42 | 52422.5 | 0 | 0 |
| 43 | 52422.5 | 0 | 0 |
| 44 | 52422.5 | 0 | 0 |
| 45 | 52422.5 | 0 | 0 |
| 46 | 52422.5 | 0 | 0 |
| 47 | 52422.5 | 0 | 0 |
| 48 | 52422.5 | 0 | 0 |
| 49 | 52422.5 | 0 | 0 |
| 50 | 52422.5 | 0 | 0 |
| 51 | 52422.5 | 0 | 0 |
| 52 | 52422.5 | 0 | 0 |
| 53 | 52422.5 | 0 | 0 |
| 54 | 52422.5 | 0 | 0 |
| 55 | 52422.5 | 0 | 0 |
| 56 | 52422.5 | 0 | 0 |
| 57 | 52422.5 | 0 | 0 |
| 58 | 52422.5 | 0 | 0 |
| 59 | 52422.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|---------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 52422.5 | 0 | 0 |
| 4 | 52422.5 | 0 | 0 |
| 5 | 52422.5 | 0 | 0 |
| 6 | 52422.5 | 0 | 0 |
| 7 | 52422.5 | 0 | 0 |
| 8 | 52422.5 | 0 | 0 |
| 9 | 52422.5 | 0 | 0 |
| 10 | 52422.5 | 0 | 0 |
| 11 | 52422.5 | 0 | 0 |
| 12 | 52422.5 | 0 | 0 |
| 13 | 52422.5 | 0 | 0 |
| 14 | 52422.5 | 0 | 0 |
| 15 | 52422.5 | 0 | 0 |
| 16 | 52422.5 | 0 | 0 |
| 17 | 52422.5 | 0 | 0 |
| 18 | 52422.5 | 0 | 0 |
| 19 | 52422.5 | 0 | 0 |
| 20 | 52422.5 | 0 | 0 |
| 21 | 52422.5 | 0 | 0 |
| 22 | 52422.5 | 0 | 0 |
| 23 | 52422.5 | 0 | 0 |
| 24 | 52422.5 | 0 | 0 |
| 25 | 52422.5 | 0 | 0 |
| 26 | 52422.5 | 0 | 0 |
| 27 | 52422.5 | 0 | 0 |
| 28 | 52422.5 | 0 | 0 |
| 29 | 52422.5 | 0 | 0 |
| 30 | 52422.5 | 0 | 0 |
| 31 | 52422.5 | 0 | 0 |
| 32 | 52422.5 | 0 | 0 |
| 33 | 52422.5 | 0 | 0 |
| 34 | 52422.5 | 0 | 0 |
| 35 | 52422.5 | 0 | 0 |
| 36 | 52422.5 | 0 | 0 |
| 37 | 52422.5 | 0 | 0 |
| 38 | 52422.5 | 0 | 0 |
| 39 | 52422.5 | 0 | 0 |
| 40 | 52422.5 | 0 | 0 |
| 41 | 52422.5 | 0 | 0 |
| 42 | 52422.5 | 0 | 0 |
| 43 | 52422.5 | 0 | 0 |
| 44 | 52422.5 | 0 | 0 |
| 45 | 52422.5 | 0 | 0 |
| 46 | 52422.5 | 0 | 0 |
| 47 | 52422.5 | 0 | 0 |
| 48 | 52422.5 | 0 | 0 |
| 49 | 52422.5 | 0 | 0 |
| 50 | 52422.5 | 0 | 0 |
| 51 | 52422.5 | 0 | 0 |
| 52 | 52422.5 | 0 | 0 |
| 53 | 52422.5 | 0 | 0 |
| 54 | 52422.5 | 0 | 0 |
| 55 | 52422.5 | 0 | 0 |
| 56 | 52422.5 | 0 | 0 |
| 57 | 52422.5 | 0 | 0 |
| 58 | 52422.5 | 0 | 0 |
| 59 | 52422.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|---------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 52422.5 | 0 | 0 |
| 4 | 52422.5 | 0 | 0 |
| 5 | 52422.5 | 0 | 0 |
| 6 | 52422.5 | 0 | 0 |
| 7 | 52422.5 | 0 | 0 |
| 8 | 52422.5 | 0 | 0 |
| 9 | 52422.5 | 0 | 0 |
| 10 | 52422.5 | 0 | 0 |
| 11 | 52422.5 | 0 | 0 |
| 12 | 52422.5 | 0 | 0 |
| 13 | 52422.5 | 0 | 0 |
| 14 | 52422.5 | 0 | 0 |
| 15 | 52422.5 | 0 | 0 |
| 16 | 52422.5 | 0 | 0 |
| 17 | 52422.5 | 0 | 0 |
| 18 | 52422.5 | 0 | 0 |
| 19 | 52422.5 | 0 | 0 |
| 20 | 52422.5 | 0 | 0 |
| 21 | 52422.5 | 0 | 0 |
| 22 | 52422.5 | 0 | 0 |
| 23 | 52422.5 | 0 | 0 |
| 24 | 52422.5 | 0 | 0 |
| 25 | 52422.5 | 0 | 0 |
| 26 | 52422.5 | 0 | 0 |
| 27 | 52422.5 | 0 | 0 |
| 28 | 52422.5 | 0 | 0 |
| 29 | 52422.5 | 0 | 0 |
| 30 | 52422.5 | 0 | 0 |
| 31 | 52422.5 | 0 | 0 |
| 32 | 52422.5 | 0 | 0 |
| 33 | 52422.5 | 0 | 0 |
| 34 | 52422.5 | 0 | 0 |
| 35 | 52422.5 | 0 | 0 |
| 36 | 52422.5 | 0 | 0 |
| 37 | 52422.5 | 0 | 0 |
| 38 | 52422.5 | 0 | 0 |
| 39 | 52422.5 | 0 | 0 |
| 40 | 52422.5 | 0 | 0 |
| 41 | 52422.5 | 0 | 0 |
| 42 | 52422.5 | 0 | 0 |
| 43 | 52422.5 | 0 | 0 |
| 44 | 52422.5 | 0 | 0 |
| 45 | 52422.5 | 0 | 0 |
| 46 | 52422.5 | 0 | 0 |
| 47 | 52422.5 | 0 | 0 |
| 48 | 52422.5 | 0 | 0 |
| 49 | 52422.5 | 0 | 0 |
| 50 | 52422.5 | 0 | 0 |
| 51 | 52422.5 | 0 | 0 |
| 52 | 52422.5 | 0 | 0 |
| 53 | 52422.5 | 0 | 0 |
| 54 | 52422.5 | 0 | 0 |
| 55 | 52422.5 | 0 | 0 |
| 56 | 52422.5 | 0 | 0 |
| 57 | 52422.5 | 0 | 0 |
| 58 | 52422.5 | 0 | 0 |
| 59 | 52422.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|---------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 52422.5 | 0 | 0 |
| 4 | 52422.5 | 0 | 0 |
| 5 | 52422.5 | 0 | 0 |
| 6 | 52422.5 | 0 | 0 |
| 7 | 52422.5 | 0 | 0 |
| 8 | 52422.5 | 0 | 0 |
| 9 | 52422.5 | 0 | 0 |
| 10 | 52422.5 | 0 | 0 |
| 11 | 52422.5 | 0 | 0 |
| 12 | 52422.5 | 0 | 0 |
| 13 | 52422.5 | 0 | 0 |
| 14 | 52422.5 | 0 | 0 |
| 15 | 52422.5 | 0 | 0 |
| 16 | 52422.5 | 0 | 0 |
| 17 | 52422.5 | 0 | 0 |
| 18 | 52422.5 | 0 | 0 |
| 19 | 52422.5 | 0 | 0 |
| 20 | 52422.5 | 0 | 0 |
| 21 | 52422.5 | 0 | 0 |
| 22 | 52422.5 | 0 | 0 |
| 23 | 52422.5 | 0 | 0 |
| 24 | 52422.5 | 0 | 0 |
| 25 | 52422.5 | 0 | 0 |
| 26 | 52422.5 | 0 | 0 |
| 27 | 52422.5 | 0 | 0 |
| 28 | 52422.5 | 0 | 0 |
| 29 | 52422.5 | 0 | 0 |
| 30 | 52422.5 | 0 | 0 |
| 31 | 52422.5 | 0 | 0 |
| 32 | 52422.5 | 0 | 0 |
| 33 | 52422.5 | 0 | 0 |
| 34 | 52422.5 | 0 | 0 |
| 35 | 52422.5 | 0 | 0 |
| 36 | 52422.5 | 0 | 0 |
| 37 | 52422.5 | 0 | 0 |
| 38 | 52422.5 | 0 | 0 |
| 39 | 52422.5 | 0 | 0 |
| 40 | 52422.5 | 0 | 0 |
| 41 | 52422.5 | 0 | 0 |
| 42 | 52422.5 | 0 | 0 |
| 43 | 52422.5 | 0 | 0 |
| 44 | 52422.5 | 0 | 0 |
| 45 | 52422.5 | 0 | 0 |
| 46 | 52422.5 | 0 | 0 |
| 47 | 52422.5 | 0 | 0 |
| 48 | 52422.5 | 0 | 0 |
| 49 | 52422.5 | 0 | 0 |
| 50 | 52422.5 | 0 | 0 |
| 51 | 52422.5 | 0 | 0 |
| 52 | 52422.5 | 0 | 0 |
| 53 | 52422.5 | 0 | 0 |
| 54 | 52422.5 | 0 | 0 |
| 55 | 52422.5 | 0 | 0 |
| 56 | 52422.5 | 0 | 0 |
| 57 | 52422.5 | 0 | 0 |
| 58 | 52422.5 | 0 | 0 |
| 59 | 52422.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 52422.5 | 0 | 0 |
| 4 | 52422.5 | 0 | 0 |
| 5 | 52422.5 | 0 | 0 |
| 6 | 52422.5 | 0 | 0 |
| 7 | 52422.5 | 0 | 0 |
| 8 | 52422.5 | 0 | 0 |
| 9 | 52422.5 | 0 | 0 |
| 10 | 52422.5 | 0 | 0 |
| 11 | 52422.5 | 0 | 0 |
| 12 | 52422.5 | 0 | 0 |
| 13 | 52422.5 | 0 | 0 |
| 14 | 52422.5 | 0 | 0 |
| 15 | 52422.5 | 0 | 0 |
| 16 | 52422.5 | 0 | 0 |
| 17 | 52422.5 | 0 | 0 |
| 18 | 52422.5 | 0 | 0 |
| 19 | 52422.5 | 0 | 0 |
| 20 | 52422.5 | 0 | 0 |
| 21 | 52422.5 | 0 | 0 |
| 22 | 52422.5 | 0 | 0 |
| 23 | 52422.5 | 0 | 0 |
| 24 | 52422.5 | 0 | 0 |
| 25 | 52422.5 | 0 | 0 |
| 26 | 52422.5 | 0 | 0 |
| 27 | 52422.5 | 0 | 0 |
| 28 | 52422.5 | 0 | 0 |
| 29 | 52422.5 | 0 | 0 |
| 30 | 52443.1667 | 0 | 0 |
| 31 | 52443.1667 | 0 | 0 |
| 32 | 52443.1667 | 0 | 0 |
| 33 | 52443.1667 | 0 | 0 |
| 34 | 52443.1667 | 0 | 0 |
| 35 | 52443.1667 | 0 | 0 |
| 36 | 52660.5 | 0 | 0 |
| 37 | 52660.5 | 0 | 0 |
| 38 | 52660.5 | 0 | 0 |
| 39 | 52660.5 | 0 | 0 |
| 40 | 67163.6667 | 0 | 0 |
| 41 | 67031.1667 | 0 | 0 |
| 42 | 67031.1667 | 0 | 0 |
| 43 | 67031.1667 | 0 | 0 |
| 44 | 67031.1667 | 0 | 0 |
| 45 | 67031.1667 | 0 | 0 |
| 46 | 67031.1667 | 0 | 0 |
| 47 | 67031.1667 | 0 | 0 |
| 48 | 67031.1667 | 0 | 0 |
| 49 | 67031.1667 | 0 | 0 |
| 50 | 67031.1667 | 0 | 0 |
| 51 | 67031.1667 | 0 | 0 |
| 52 | 67031.1667 | 0 | 0 |
| 53 | 67031.1667 | 0 | 0 |
| 54 | 67031.1667 | 0 | 0 |
| 55 | 67031.1667 | 0 | 0 |
| 56 | 67031.1667 | 0 | 0 |
| 57 | 67031.1667 | 0 | 0 |
| 58 | 67031.1667 | 0 | 0 |
| 59 | 67031.1667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 67031.1667 | 0 | 0 |
| 4 | 67031.1667 | 0 | 0 |
| 5 | 67031.1667 | 0 | 0 |
| 6 | 67031.1667 | 0 | 0 |
| 7 | 67031.1667 | 0 | 0 |
| 8 | 67031.1667 | 0 | 0 |
| 9 | 67031.1667 | 0 | 0 |
| 10 | 67031.1667 | 0 | 0 |
| 11 | 67031.1667 | 0 | 0 |
| 12 | 67031.1667 | 0 | 0 |
| 13 | 67031.1667 | 0 | 0 |
| 14 | 67031.1667 | 0 | 0 |
| 15 | 67031.1667 | 0 | 0 |
| 16 | 67031.1667 | 0 | 0 |
| 17 | 67031.1667 | 0 | 0 |
| 18 | 67031.1667 | 0 | 0 |
| 19 | 67031.1667 | 0 | 0 |
| 20 | 67031.1667 | 0 | 0 |
| 21 | 67031.1667 | 0 | 0 |
| 22 | 67031.1667 | 0 | 0 |
| 23 | 67031.1667 | 0 | 0 |
| 24 | 67031.1667 | 0 | 0 |
| 25 | 67031.1667 | 0 | 0 |
| 26 | 67031.1667 | 0 | 0 |
| 27 | 67031.1667 | 0 | 0 |
| 28 | 32271.5 | 0 | 0 |
| 29 | 32271.5 | 0 | 0 |
| 30 | 32271.5 | 0 | 0 |
| 31 | 32271.5 | 0 | 0 |
| 32 | 32271.5 | 0 | 0 |
| 33 | 32271.5 | 0 | 0 |
| 34 | 32271.5 | 0 | 0 |
| 35 | 32271.5 | 0 | 0 |
| 36 | 32271.5 | 0 | 0 |
| 37 | 32271.5 | 0 | 0 |
| 38 | 32271.5 | 0 | 0 |
| 39 | 32271.5 | 0 | 0 |
| 40 | 32271.5 | 0 | 0 |
| 41 | 32271.5 | 0 | 0 |
| 42 | 32271.5 | 0 | 0 |
| 43 | 32271.5 | 0 | 0 |
| 44 | 14421.3333 | 0 | 0 |
| 45 | 14421.3333 | 0 | 0 |
| 46 | 1609.33333 | 0 | 0 |
| 47 | 1609.33333 | 0 | 0 |
| 48 | 1609.33333 | 0 | 0 |
| 49 | 1609.33333 | 0 | 0 |
| 50 | 1609.33333 | 0 | 0 |
| 51 | 1609.33333 | 0 | 0 |
| 52 | 1609.33333 | 0 | 0 |
| 53 | 1609.33333 | 0 | 0 |
| 54 | 1609.33333 | 0 | 0 |
| 55 | 1609.33333 | 0 | 0 |
| 56 | 1609.33333 | 0 | 0 |
| 57 | 1609.33333 | 0 | 0 |
| 58 | 1609.33333 | 0 | 0 |
| 59 | 1609.33333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 1609.33333 | 0 | 0 |
| 4 | 1609.33333 | 0 | 0 |
| 5 | 1609.33333 | 0 | 0 |
| 6 | 1609.33333 | 0 | 0 |
| 7 | 1609.33333 | 0 | 0 |
| 8 | 1609.33333 | 0 | 0 |
| 9 | 1609.33333 | 0 | 0 |
| 10 | 1609.33333 | 0 | 0 |
| 11 | 1609.33333 | 0 | 0 |
| 12 | 1609.33333 | 0 | 0 |
| 13 | 1609.33333 | 0 | 0 |
| 14 | 1609.33333 | 0 | 0 |
| 15 | 1609.33333 | 0 | 0 |
| 16 | 1609.33333 | 0 | 0 |
| 17 | 1609.33333 | 0 | 0 |
| 18 | 1609.33333 | 0 | 0 |
| 19 | 1609.33333 | 0 | 0 |
| 20 | 1609.33333 | 0 | 0 |
| 21 | 1609.33333 | 0 | 0 |
| 22 | 1609.33333 | 0 | 0 |
| 23 | 1609.33333 | 0 | 0 |
| 24 | 1609.33333 | 0 | 0 |
| 25 | 1609.33333 | 0 | 0 |
| 26 | 1609.33333 | 0 | 0 |
| 27 | 1609.33333 | 0 | 0 |
| 28 | 1609.33333 | 0 | 0 |
| 29 | 1609.33333 | 0 | 0 |
| 30 | 1609.33333 | 0 | 0 |
| 31 | 1609.33333 | 0 | 0 |
| 32 | 1609.33333 | 0 | 0 |
| 33 | 1609.33333 | 0 | 0 |
| 34 | 1609.33333 | 0 | 0 |
| 35 | 1609.33333 | 0 | 0 |
| 36 | 1609.33333 | 0 | 0 |
| 37 | 1609.33333 | 0 | 0 |
| 38 | 1609.33333 | 0 | 0 |
| 39 | 1609.33333 | 0 | 0 |
| 40 | 1609.33333 | 0 | 0 |
| 41 | 1609.33333 | 0 | 0 |
| 42 | 1609.33333 | 0 | 0 |
| 43 | 1609.33333 | 0 | 0 |
| 44 | 1609.33333 | 0 | 0 |
| 45 | 1609.33333 | 0 | 0 |
| 46 | 1609.33333 | 0 | 0 |
| 47 | 1609.33333 | 0 | 0 |
| 48 | 1609.33333 | 0 | 0 |
| 49 | 1609.33333 | 0 | 0 |
| 50 | 1609.33333 | 0 | 0 |
| 51 | 1609.33333 | 0 | 0 |
| 52 | 1609.33333 | 0 | 0 |
| 53 | 1609.33333 | 0 | 0 |
| 54 | 1609.33333 | 0 | 0 |
| 55 | 1609.33333 | 0 | 0 |
| 56 | 1609.33333 | 0 | 0 |
| 57 | 1609.33333 | 0 | 0 |
| 58 | 1609.33333 | 0 | 0 |
| 59 | 1953 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 375.833333 | 0 | 0 |
| 4 | 59.5 | 0 | 0 |
| 5 | | | |
| 6 | 8251.83333 | 0 | 0 |
| 7 | 8251.83333 | 0 | 0 |
| 8 | | | |
| 9 | 8251.83333 | 0 | 0 |
| 10 | 8251.83333 | 0 | 0 |
| 11 | 8251.83333 | 0 | 0 |
| 12 | | | |
| 13 | 8251.83333 | 0 | 0 |
| 14 | 8251.83333 | 0 | 0 |
| 15 | 8251.83333 | 0 | 0 |
| 16 | | | |
| 17 | 8251.83333 | 0 | 0 |
| 18 | 8251.83333 | 0 | 0 |
| 19 | 8251.83333 | 0 | 0 |
| 20 | | | |
| 21 | 8251.83333 | 0 | 0 |
| 22 | 8251.83333 | 0 | 0 |
| 23 | 8251.83333 | 0 | 0 |
| 24 | | | |
| 25 | 8251.83333 | 0 | 0 |
| 26 | 8251.83333 | 0 | 0 |
| 27 | 98.666667 | 0 | 0 |
| 28 | | | |
| 29 | 13406 | 0 | 0 |
| 30 | 13406 | 0 | 0 |
| 31 | 599.666667 | 0 | 0 |
| 32 | 599.666667 | 0 | 0 |
| 33 | | | |
| 34 | 599.666667 | 0 | 0 |
| 35 | 599.666667 | 0 | 0 |
| 36 | | | |
| 37 | 599.666667 | 0 | 0 |
| 38 | 599.666667 | 0 | 0 |
| 39 | 599.666667 | 0 | 0 |
| 40 | | | |
| 41 | 599.666667 | 0 | 0 |
| 42 | 599.666667 | 0 | 0 |
| 43 | 599.666667 | 0 | 0 |
| 44 | | | |
| 45 | 599.666667 | 0 | 0 |
| 46 | 599.666667 | 0 | 0 |
| 47 | 599.666667 | 0 | 0 |
| 48 | | | |
| 49 | 599.666667 | 0 | 0 |
| 50 | 599.666667 | 0 | 0 |
| 51 | 599.666667 | 0 | 0 |
| 52 | | | |
| 53 | 599.666667 | 0 | 0 |
| 54 | 599.666667 | 0 | 0 |
| 55 | 599.666667 | 0 | 0 |
| 56 | | | |
| 57 | 599.666667 | 0 | 0 |
| 58 | 599.666667 | 0 | 0 |
| 59 | 599.666667 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 599.666667 | 0 | 0 |
| 4 | 599.666667 | 0 | 0 |
| 5 | 599.666667 | 0 | 0 |
| 6 | 599.666667 | 0 | 0 |
| 7 | 599.666667 | 0 | 0 |
| 8 | 599.666667 | 0 | 0 |
| 9 | 599.666667 | 0 | 0 |
| 10 | 599.666667 | 0 | 0 |
| 11 | 599.666667 | 0 | 0 |
| 12 | 599.666667 | 0 | 0 |
| 13 | 599.666667 | 0 | 0 |
| 14 | 599.666667 | 0 | 0 |
| 15 | 599.666667 | 0 | 0 |
| 16 | 599.666667 | 0 | 0 |
| 17 | 599.666667 | 0 | 0 |
| 18 | 599.666667 | 0 | 0 |
| 19 | 599.666667 | 0 | 0 |
| 20 | 599.666667 | 0 | 0 |
| 21 | 599.666667 | 0 | 0 |
| 22 | 599.666667 | 0 | 0 |
| 23 | 599.666667 | 0 | 0 |
| 24 | 599.666667 | 0 | 0 |
| 25 | 599.666667 | 0 | 0 |
| 26 | 599.666667 | 0 | 0 |
| 27 | 599.666667 | 0 | 0 |
| 28 | 599.666667 | 0 | 0 |
| 29 | 599.666667 | 0 | 0 |
| 30 | 600.5 | 0 | 0 |
| 31 | 70561 | 0 | 0 |
| 32 | 70561 | 0 | 0 |
| 33 | 70561 | 0 | 0 |
| 34 | 70561 | 0 | 0 |
| 35 | 70561 | 0 | 0 |
| 36 | 141.5 | 0 | 0 |
| 37 | 8733.66667 | 0 | 0 |
| 38 | 8733.66667 | 0 | 0 |
| 39 | 8733.66667 | 0 | 0 |
| 40 | 8727.5 | 0 | 0 |
| 41 | 8727.5 | 0 | 0 |
| 42 | 8727.5 | 0 | 0 |
| 43 | 8727.5 | 0 | 0 |
| 44 | 8727.5 | 0 | 0 |
| 45 | 8727.5 | 0 | 0 |
| 46 | 8727.5 | 0 | 0 |
| 47 | 8727.5 | 0 | 0 |
| 48 | 8727.5 | 0 | 0 |
| 49 | 8727.5 | 0 | 0 |
| 50 | 8727.5 | 0 | 0 |
| 51 | 8727.5 | 0 | 0 |
| 52 | 8727.5 | 0 | 0 |
| 53 | 8727.5 | 0 | 0 |
| 54 | 8727.5 | 0 | 0 |
| 55 | 8727.5 | 0 | 0 |
| 56 | 8727.5 | 0 | 0 |
| 57 | 8727.5 | 0 | 0 |
| 58 | 8727.5 | 0 | 0 |
| 59 | 8727.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|--------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 8727.5 | 0 | 0 |
| 4 | 8727.5 | 0 | 0 |
| 5 | 8727.5 | 0 | 0 |
| 6 | 8727.5 | 0 | 0 |
| 7 | 8727.5 | 0 | 0 |
| 8 | 8727.5 | 0 | 0 |
| 9 | 8727.5 | 0 | 0 |
| 10 | 8727.5 | 0 | 0 |
| 11 | 8727.5 | 0 | 0 |
| 12 | 8727.5 | 0 | 0 |
| 13 | 8727.5 | 0 | 0 |
| 14 | 8727.5 | 0 | 0 |
| 15 | 8727.5 | 0 | 0 |
| 16 | 8727.5 | 0 | 0 |
| 17 | 8727.5 | 0 | 0 |
| 18 | 8727.5 | 0 | 0 |
| 19 | 8727.5 | 0 | 0 |
| 20 | 8727.5 | 0 | 0 |
| 21 | 8727.5 | 0 | 0 |
| 22 | 8727.5 | 0 | 0 |
| 23 | 8727.5 | 0 | 0 |
| 24 | 8727.5 | 0 | 0 |
| 25 | 8727.5 | 0 | 0 |
| 26 | 8727.5 | 0 | 0 |
| 27 | 8727.5 | 0 | 0 |
| 28 | 8727.5 | 0 | 0 |
| 29 | 8727.5 | 0 | 0 |
| 30 | 8727.5 | 0 | 0 |
| 31 | 8727.5 | 0 | 0 |
| 32 | 8727.5 | 0 | 0 |
| 33 | 8727.5 | 0 | 0 |
| 34 | 8727.5 | 0 | 0 |
| 35 | 8727.5 | 0 | 0 |
| 36 | 8727.5 | 0 | 0 |
| 37 | 8727.5 | 0 | 0 |
| 38 | 8727.5 | 0 | 0 |
| 39 | 8727.5 | 0 | 0 |
| 40 | 8727.5 | 0 | 0 |
| 41 | 8727.5 | 0 | 0 |
| 42 | 8727.5 | 0 | 0 |
| 43 | 8727.5 | 0 | 0 |
| 44 | 8727.5 | 0 | 0 |
| 45 | 8727.5 | 0 | 0 |
| 46 | 8727.5 | 0 | 0 |
| 47 | 8727.5 | 0 | 0 |
| 48 | 8727.5 | 0 | 0 |
| 49 | 8727.5 | 0 | 0 |
| 50 | 8727.5 | 0 | 0 |
| 51 | 8727.5 | 0 | 0 |
| 52 | 8727.5 | 0 | 0 |
| 53 | 8727.5 | 0 | 0 |
| 54 | 8727.5 | 0 | 0 |
| 55 | 8727.5 | 0 | 0 |
| 56 | 8727.5 | 0 | 0 |
| 57 | 8727.5 | 0 | 0 |
| 58 | 8727.5 | 0 | 0 |
| 59 | 8727.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 8727.5 | 0 | 0 |
| 4 | 8727.5 | 0 | 0 |
| 5 | 8727.5 | 0 | 0 |
| 6 | 8727.5 | 0 | 0 |
| 7 | 8727.5 | 0 | 0 |
| 8 | 8727.5 | 0 | 0 |
| 9 | 8727.5 | 0 | 0 |
| 10 | 8727.5 | 0 | 0 |
| 11 | 8727.5 | 0 | 0 |
| 12 | 8727.5 | 0 | 0 |
| 13 | 8727.5 | 0 | 0 |
| 14 | 8727.5 | 0 | 0 |
| 15 | 8727.5 | 0 | 0 |
| 16 | 8727.5 | 0 | 0 |
| 17 | 8727.5 | 0 | 0 |
| 18 | 8727.5 | 0 | 0 |
| 19 | 8727.5 | 0 | 0 |
| 20 | 8727.5 | 0 | 0 |
| 21 | 8727.5 | 0 | 0 |
| 22 | 143 | 0 | 0 |
| 23 | 143 | 0 | 0 |
| 24 | 139.833333 | 0 | 0 |
| 25 | 1750.83333 | 0 | 0 |
| 26 | 10607.6667 | 0 | 0 |
| 27 | 10607.6667 | 0 | 0 |
| 28 | 10607.6667 | 0 | 0 |
| 29 | 10607.6667 | 0 | 0 |
| 30 | 10607.6667 | 0 | 0 |
| 31 | 10607.6667 | 0 | 0 |
| 32 | 10607.6667 | 0 | 0 |
| 33 | 10607.6667 | 0 | 0 |
| 34 | 10607.6667 | 0 | 0 |
| 35 | 10607.6667 | 0 | 0 |
| 36 | 10607.6667 | 0 | 0 |
| 37 | 10607.6667 | 0 | 0 |
| 38 | 10607.6667 | 0 | 0 |
| 39 | 10607.6667 | 0 | 0 |
| 40 | 10607.6667 | 0 | 0 |
| 41 | 10607.6667 | 0 | 0 |
| 42 | 10607.6667 | 0 | 0 |
| 43 | 10607.6667 | 0 | 0 |
| 44 | 10607.6667 | 0 | 0 |
| 45 | 10607.6667 | 0 | 0 |
| 46 | 10607.6667 | 0 | 0 |
| 47 | 10607.6667 | 0 | 0 |
| 48 | 10607.6667 | 0 | 0 |
| 49 | 10607.6667 | 0 | 0 |
| 50 | 10607.6667 | 0 | 0 |
| 51 | 10607.6667 | 0 | 0 |
| 52 | 10607.6667 | 0 | 0 |
| 53 | 10607.6667 | 0 | 0 |
| 54 | 10607.6667 | 0 | 0 |
| 55 | 10607.6667 | 0 | 0 |
| 56 | 10607.6667 | 0 | 0 |
| 57 | 649.333333 | 0 | 0 |
| 58 | 528.333333 | 0 | 0 |
| 59 | | | |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 361.5 | 0 | 0 |
| 4 | 361.5 | 0 | 0 |
| 5 | 361.5 | 0 | 0 |
| 6 | 361.5 | 0 | 0 |
| 7 | 361.5 | 0 | 0 |
| 8 | 361.5 | 0 | 0 |
| 9 | 361.5 | 0 | 0 |
| 10 | 361.5 | 0 | 0 |
| 11 | 361.5 | 0 | 0 |
| 12 | 361.5 | 0 | 0 |
| 13 | 361.5 | 0 | 0 |
| 14 | 361.5 | 0 | 0 |
| 15 | 361.5 | 0 | 0 |
| 16 | 361.5 | 0 | 0 |
| 17 | 361.5 | 0 | 0 |
| 18 | 361.5 | 0 | 0 |
| 19 | 361.5 | 0 | 0 |
| 20 | 361.5 | 0 | 0 |
| 21 | 361.5 | 0 | 0 |
| 22 | 15201.3333 | 0 | 0 |
| 23 | 51.8333333 | 0 | 0 |
| 24 | 2493.5 | 0 | 0 |
| 25 | 2416.83333 | 0 | 0 |
| 26 | 2416.83333 | 0 | 0 |
| 27 | 2416.83333 | 0 | 0 |
| 28 | 2370.83333 | 0 | 0 |
| 29 | 2370.83333 | 0 | 0 |
| 30 | 2370.83333 | 0 | 0 |
| 31 | 2370.83333 | 0 | 0 |
| 32 | 2370.83333 | 0 | 0 |
| 33 | 2370.83333 | 0 | 0 |
| 34 | 2370.83333 | 0 | 0 |
| 35 | 2370.83333 | 0 | 0 |
| 36 | 2370.83333 | 0 | 0 |
| 37 | 2370.83333 | 0 | 0 |
| 38 | 2370.83333 | 0 | 0 |
| 39 | 2370.83333 | 0 | 0 |
| 40 | 75.8333333 | 0 | 0 |
| 41 | 75.8333333 | 0 | 0 |
| 42 | 75.8333333 | 0 | 0 |
| 43 | 448.333333 | 0 | 0 |
| 44 | 448.333333 | 0 | 0 |
| 45 | 448.333333 | 0 | 0 |
| 46 | 448.333333 | 0 | 0 |
| 47 | 448.333333 | 0 | 0 |
| 48 | 448.333333 | 0 | 0 |
| 49 | 448.333333 | 0 | 0 |
| 50 | 448.333333 | 0 | 0 |
| 51 | 448.333333 | 0 | 0 |
| 52 | 448.333333 | 0 | 0 |
| 53 | 448.333333 | 0 | 0 |
| 54 | 448.333333 | 0 | 0 |
| 55 | 448.333333 | 0 | 0 |
| 56 | 448.333333 | 0 | 0 |
| 57 | 448.333333 | 0 | 0 |
| 58 | 448.333333 | 0 | 0 |
| 59 | 448.333333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|-------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 448.333333 | 0 | 0 |
| 4 | 448.333333 | 0 | 0 |
| 5 | 448.333333 | 0 | 0 |
| 6 | 448.333333 | 0 | 0 |
| 7 | 448.333333 | 0 | 0 |
| 8 | 448.333333 | 0 | 0 |
| 9 | 448.333333 | 0 | 0 |
| 10 | 448.333333 | 0 | 0 |
| 11 | 448.333333 | 0 | 0 |
| 12 | 448.333333 | 0 | 0 |
| 13 | 448.333333 | 0 | 0 |
| 14 | 448.333333 | 0 | 0 |
| 15 | 448.333333 | 0 | 0 |
| 16 | 481.666667 | 0 | 0 |
| 17 | 2345 | 0 | 0 |
| 18 | 407.666667 | 0 | 0 |
| 19 | 406.833333 | 0 | 0 |
| 20 | 406.833333 | 0 | 0 |
| 21 | 406.833333 | 0 | 0 |
| 22 | 60.5 | 0 | 0 |
| 23 | 60.5 | 0 | 0 |
| 24 | 60.5 | 0 | 0 |
| 25 | 60.5 | 0 | 0 |
| 26 | 60.5 | 0 | 0 |
| 27 | 60.5 | 0 | 0 |
| 28 | 60.5 | 0 | 0 |
| 29 | 6764.5 | 0 | 0 |
| 30 | 6764.5 | 0 | 0 |
| 31 | 6764.5 | 0 | 0 |
| 32 | 6764.5 | 0 | 0 |
| 33 | 6764.5 | 0 | 0 |
| 34 | 6764.5 | 0 | 0 |
| 35 | 6764.5 | 0 | 0 |
| 36 | 6764.5 | 0 | 0 |
| 37 | 6764.5 | 0 | 0 |
| 38 | 6764.5 | 0 | 0 |
| 39 | 6764.5 | 0 | 0 |
| 40 | 6764.5 | 0 | 0 |
| 41 | 6764.5 | 0 | 0 |
| 42 | 6764.5 | 0 | 0 |
| 43 | 6764.5 | 0 | 0 |
| 44 | 6764.5 | 0 | 0 |
| 45 | 6764.5 | 0 | 0 |
| 46 | 6764.5 | 0 | 0 |
| 47 | 6764.5 | 0 | 0 |
| 48 | 6764.5 | 0 | 0 |
| 49 | 6764.5 | 0 | 0 |
| 50 | 6764.5 | 0 | 0 |
| 51 | 6764.5 | 0 | 0 |
| 52 | 6764.5 | 0 | 0 |
| 53 | 6764.5 | 0 | 0 |
| 54 | 6764.5 | 0 | 0 |
| 55 | 3555.833333 | 0 | 0 |
| 56 | 3555.833333 | 0 | 0 |
| 57 | 11827.1667 | 0 | 0 |
| 58 | 3559.5 | 0 | 0 |
| 59 | | | |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 3559.5 | 0 | 0 |
| 4 | 5266.5 | 0 | 0 |
| 5 | 5266.5 | 0 | 0 |
| 6 | 5266.5 | 0 | 0 |
| 7 | 5266.5 | 0 | 0 |
| 8 | 5584.5 | 0 | 0 |
| 9 | 5584.5 | 0 | 0 |
| 10 | 5584.5 | 0 | 0 |
| 11 | 5584.5 | 0 | 0 |
| 12 | 5584.5 | 0 | 0 |
| 13 | 5584.5 | 0 | 0 |
| 14 | 5584.5 | 0 | 0 |
| 15 | 5584.5 | 0 | 0 |
| 16 | 5584.5 | 0 | 0 |
| 17 | 5584.5 | 0 | 0 |
| 18 | 11680.3333 | 0 | 0 |
| 19 | 11680.3333 | 0 | 0 |
| 20 | 11680.3333 | 0 | 0 |
| 21 | 11680.3333 | 0 | 0 |
| 22 | 11680.3333 | 0 | 0 |
| 23 | 11680.3333 | 0 | 0 |
| 24 | 11680.3333 | 0 | 0 |
| 25 | 11680.3333 | 0 | 0 |
| 26 | 11680.3333 | 0 | 0 |
| 27 | 11680.3333 | 0 | 0 |
| 28 | 11680.3333 | 0 | 0 |
| 29 | 11680.3333 | 0 | 0 |
| 30 | 11680.3333 | 0 | 0 |
| 31 | 11680.3333 | 0 | 0 |
| 32 | 11680.3333 | 0 | 0 |
| 33 | 11680.3333 | 0 | 0 |
| 34 | 11680.3333 | 0 | 0 |
| 35 | 11680.3333 | 0 | 0 |
| 36 | 11680.3333 | 0 | 0 |
| 37 | 11680.3333 | 0 | 0 |
| 38 | 11680.3333 | 0 | 0 |
| 39 | 11680.3333 | 0 | 0 |
| 40 | 11680.3333 | 0 | 0 |
| 41 | 11680.3333 | 0 | 0 |
| 42 | 11680.3333 | 0 | 0 |
| 43 | 11680.3333 | 0 | 0 |
| 44 | 11680.3333 | 0 | 0 |
| 45 | 11680.3333 | 0 | 0 |
| 46 | 11680.3333 | 0 | 0 |
| 47 | 11680.3333 | 0 | 0 |
| 48 | 11680.3333 | 0 | 0 |
| 49 | 11680.3333 | 0 | 0 |
| 50 | 11680.3333 | 0 | 0 |
| 51 | 11680.3333 | 0 | 0 |
| 52 | 11680.3333 | 0 | 0 |
| 53 | 11680.3333 | 0 | 0 |
| 54 | 11680.3333 | 0 | 0 |
| 55 | 11680.3333 | 0 | 0 |
| 56 | 11680.3333 | 0 | 0 |
| 57 | 11680.3333 | 0 | 0 |
| 58 | 11680.3333 | 0 | 0 |
| 59 | 11680.3333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 11680.3333 | 0 | 0 |
| 4 | 11680.3333 | 0 | 0 |
| 5 | 11680.3333 | 0 | 0 |
| 6 | 11680.3333 | 0 | 0 |
| 7 | 11680.3333 | 0 | 0 |
| 8 | 11680.3333 | 0 | 0 |
| 9 | 11680.3333 | 0 | 0 |
| 10 | 11680.3333 | 0 | 0 |
| 11 | 11680.3333 | 0 | 0 |
| 12 | 11680.3333 | 0 | 0 |
| 13 | 11680.3333 | 0 | 0 |
| 14 | 11680.3333 | 0 | 0 |
| 15 | 11680.3333 | 0 | 0 |
| 16 | 11680.3333 | 0 | 0 |
| 17 | 11680.3333 | 0 | 0 |
| 18 | 11680.3333 | 0 | 0 |
| 19 | 11680.3333 | 0 | 0 |
| 20 | 11680.3333 | 0 | 0 |
| 21 | 11680.3333 | 0 | 0 |
| 22 | 11680.3333 | 0 | 0 |
| 23 | 11680.3333 | 0 | 0 |
| 24 | 11680.3333 | 0 | 0 |
| 25 | 11680.3333 | 0 | 0 |
| 26 | 11680.3333 | 0 | 0 |
| 27 | 11680.3333 | 0 | 0 |
| 28 | 11680.3333 | 0 | 0 |
| 29 | 11680.3333 | 0 | 0 |
| 30 | 11680.3333 | 0 | 0 |
| 31 | 11680.3333 | 0 | 0 |
| 32 | 11680.3333 | 0 | 0 |
| 33 | 11680.3333 | 0 | 0 |
| 34 | 11680.3333 | 0 | 0 |
| 35 | 11680.3333 | 0 | 0 |
| 36 | 11715 | 0 | 0 |
| 37 | 773.333333 | 0 | 0 |
| 38 | 773.333333 | 0 | 0 |
| 39 | 773.333333 | 0 | 0 |
| 40 | 773.333333 | 0 | 0 |
| 41 | 775.333333 | 0 | 0 |
| 42 | 775.333333 | 0 | 0 |
| 43 | 6238 | 0 | 0 |
| 44 | 6238 | 0 | 0 |
| 45 | 6194 | 0 | 0 |
| 46 | 6194 | 0 | 0 |
| 47 | 6194 | 0 | 0 |
| 48 | 6194 | 0 | 0 |
| 49 | 6194 | 0 | 0 |
| 50 | 6194 | 0 | 0 |
| 51 | 6194 | 0 | 0 |
| 52 | 6194 | 0 | 0 |
| 53 | 6194 | 0 | 0 |
| 54 | 6194 | 0 | 0 |
| 55 | 6194 | 0 | 0 |
| 56 | 6194 | 0 | 0 |
| 57 | 6194 | 0 | 0 |
| 58 | 6194 | 0 | 0 |
| 59 | 6194 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 6194 | 0 | 0 |
| 4 | 6194 | 0 | 0 |
| 5 | 6194 | 0 | 0 |
| 6 | 6194 | 0 | 0 |
| 7 | 6194 | 0 | 0 |
| 8 | 6194 | 0 | 0 |
| 9 | 6194 | 0 | 0 |
| 10 | 6194 | 0 | 0 |
| 11 | 6194 | 0 | 0 |
| 12 | 6194 | 0 | 0 |
| 13 | 6194 | 0 | 0 |
| 14 | 6194 | 0 | 0 |
| 15 | 6194 | 0 | 0 |
| 16 | 6194 | 0 | 0 |
| 17 | 6194 | 0 | 0 |
| 18 | 6194 | 0 | 0 |
| 19 | 6194 | 0 | 0 |
| 20 | 6194 | 0 | 0 |
| 21 | 6194 | 0 | 0 |
| 22 | 6194 | 0 | 0 |
| 23 | 6194 | 0 | 0 |
| 24 | 6194 | 0 | 0 |
| 25 | 6194 | 0 | 0 |
| 26 | 6194 | 0 | 0 |
| 27 | 6194 | 0 | 0 |
| 28 | 6194 | 0 | 0 |
| 29 | 6194 | 0 | 0 |
| 30 | 6194 | 0 | 0 |
| 31 | 6194 | 0 | 0 |
| 32 | 6194 | 0 | 0 |
| 33 | 6194 | 0 | 0 |
| 34 | 6194 | 0 | 0 |
| 35 | 6194 | 0 | 0 |
| 36 | 6194 | 0 | 0 |
| 37 | 6194 | 0 | 0 |
| 38 | 6194 | 0 | 0 |
| 39 | 6194 | 0 | 0 |
| 40 | 6194 | 0 | 0 |
| 41 | 6194 | 0 | 0 |
| 42 | 372.833333 | 0 | 0 |
| 43 | 372.833333 | 0 | 0 |
| 44 | 372.833333 | 0 | 0 |
| 45 | 372.833333 | 0 | 0 |
| 46 | 372.833333 | 0 | 0 |
| 47 | 372.833333 | 0 | 0 |
| 48 | 372.833333 | 0 | 0 |
| 49 | 2077.5 | 0 | 0 |
| 50 | 2077.5 | 0 | 0 |
| 51 | 2077.5 | 0 | 0 |
| 52 | 2077.5 | 0 | 0 |
| 53 | 2077.5 | 0 | 0 |
| 54 | 2077.5 | 0 | 0 |
| 55 | 2077.5 | 0 | 0 |
| 56 | 2077.5 | 0 | 0 |
| 57 | 2077.5 | 0 | 0 |
| 58 | 2077.5 | 0 | 0 |
| 59 | 2077.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|--------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 2077.5 | 0 | 0 |
| 4 | 2077.5 | 0 | 0 |
| 5 | 2077.5 | 0 | 0 |
| 6 | 2077.5 | 0 | 0 |
| 7 | 2077.5 | 0 | 0 |
| 8 | 2077.5 | 0 | 0 |
| 9 | 2077.5 | 0 | 0 |
| 10 | 2077.5 | 0 | 0 |
| 11 | 2077.5 | 0 | 0 |
| 12 | 2077.5 | 0 | 0 |
| 13 | 2077.5 | 0 | 0 |
| 14 | 2077.5 | 0 | 0 |
| 15 | 2077.5 | 0 | 0 |
| 16 | 2077.5 | 0 | 0 |
| 17 | 2077.5 | 0 | 0 |
| 18 | 2077.5 | 0 | 0 |
| 19 | 2077.5 | 0 | 0 |
| 20 | 2077.5 | 0 | 0 |
| 21 | 2077.5 | 0 | 0 |
| 22 | 2077.5 | 0 | 0 |
| 23 | 2077.5 | 0 | 0 |
| 24 | 2077.5 | 0 | 0 |
| 25 | 2077.5 | 0 | 0 |
| 26 | 2077.5 | 0 | 0 |
| 27 | 2077.5 | 0 | 0 |
| 28 | 2077.5 | 0 | 0 |
| 29 | 2077.5 | 0 | 0 |
| 30 | 2077.5 | 0 | 0 |
| 31 | 2077.5 | 0 | 0 |
| 32 | 2077.5 | 0 | 0 |
| 33 | 2077.5 | 0 | 0 |
| 34 | 2077.5 | 0 | 0 |
| 35 | 2077.5 | 0 | 0 |
| 36 | 2077.5 | 0 | 0 |
| 37 | 2077.5 | 0 | 0 |
| 38 | 2077.5 | 0 | 0 |
| 39 | 2077.5 | 0 | 0 |
| 40 | 2077.5 | 0 | 0 |
| 41 | 2077.5 | 0 | 0 |
| 42 | 2077.5 | 0 | 0 |
| 43 | 2077.5 | 0 | 0 |
| 44 | 2077.5 | 0 | 0 |
| 45 | 2077.5 | 0 | 0 |
| 46 | 2077.5 | 0 | 0 |
| 47 | 2077.5 | 0 | 0 |
| 48 | 2077.5 | 0 | 0 |
| 49 | 2077.5 | 0 | 0 |
| 50 | 2077.5 | 0 | 0 |
| 51 | 2077.5 | 0 | 0 |
| 52 | 2077.5 | 0 | 0 |
| 53 | 2077.5 | 0 | 0 |
| 54 | 2077.5 | 0 | 0 |
| 55 | 2077.5 | 0 | 0 |
| 56 | 2077.5 | 0 | 0 |
| 57 | 2077.5 | 0 | 0 |
| 58 | 2077.5 | 0 | 0 |
| 59 | 2077.5 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 2077.5 | 0 | 0 |
| 4 | 2077.5 | 0 | 0 |
| 5 | 2077.5 | 0 | 0 |
| 6 | 2077.5 | 0 | 0 |
| 7 | 2077.5 | 0 | 0 |
| 8 | 2077.5 | 0 | 0 |
| 9 | 2077.5 | 0 | 0 |
| 10 | 2077.5 | 0 | 0 |
| 11 | 2077.5 | 0 | 0 |
| 12 | 2077.5 | 0 | 0 |
| 13 | 2077.5 | 0 | 0 |
| 14 | 2077.5 | 0 | 0 |
| 15 | 2077.5 | 0 | 0 |
| 16 | 2077.5 | 0 | 0 |
| 17 | 2077.5 | 0 | 0 |
| 18 | 2077.5 | 0 | 0 |
| 19 | 2077.5 | 0 | 0 |
| 20 | 2077.5 | 0 | 0 |
| 21 | 2077.5 | 0 | 0 |
| 22 | 2077.5 | 0 | 0 |
| 23 | 131.166667 | 0 | 0 |
| 24 | 480.5 | 0 | 0 |
| 25 | 59.6666667 | 0 | 0 |
| 26 | 435.333333 | 0 | 0 |
| 27 | 217.333333 | 0 | 0 |
| 28 | 217.333333 | 0 | 0 |
| 29 | 217.333333 | 0 | 0 |
| 30 | 217.333333 | 0 | 0 |
| 31 | 217.333333 | 0 | 0 |
| 32 | 1611.83333 | 0 | 0 |
| 33 | 1611.83333 | 0 | 0 |
| 34 | 1611.83333 | 0 | 0 |
| 35 | 1611.83333 | 0 | 0 |
| 36 | 1611.83333 | 0 | 0 |
| 37 | 1611.83333 | 0 | 0 |
| 38 | 1611.83333 | 0 | 0 |
| 39 | 1611.83333 | 0 | 0 |
| 40 | 1611.83333 | 0 | 0 |
| 41 | 1611.83333 | 0 | 0 |
| 42 | 1611.83333 | 0 | 0 |
| 43 | 1611.83333 | 0 | 0 |
| 44 | 1611.83333 | 0 | 0 |
| 45 | 1611.83333 | 0 | 0 |
| 46 | 1611.83333 | 0 | 0 |
| 47 | 1618.5 | 0 | 0 |
| 48 | 480.5 | 0 | 0 |
| 49 | 480.5 | 0 | 0 |
| 50 | 480.5 | 0 | 0 |
| 51 | 480.5 | 0 | 0 |
| 52 | 480.5 | 0 | 0 |
| 53 | 480.5 | 0 | 0 |
| 54 | 480.5 | 0 | 0 |
| 55 | 480.5 | 0 | 0 |
| 56 | 218.833333 | 0 | 0 |
| 57 | 103.833333 | 0 | 0 |
| 58 | 103.833333 | 0 | 0 |
| 59 | 103.833333 | 0 | 0 |
| 60 | | | |

| | | | |
|----|------------|---|---|
| 1 | | | |
| 2 | | | |
| 3 | 103.833333 | 0 | 0 |
| 4 | 103.833333 | 0 | 0 |
| 5 | 103.833333 | 0 | 0 |
| 6 | 103.833333 | 0 | 0 |
| 7 | 103.833333 | 0 | 0 |
| 8 | 103.833333 | 0 | 0 |
| 9 | 103.833333 | 0 | 0 |
| 10 | 103.833333 | 0 | 0 |
| 11 | 103.833333 | 0 | 0 |
| 12 | 103.833333 | 0 | 0 |
| 13 | 103.833333 | 0 | 0 |
| 14 | 103.833333 | 0 | 0 |
| 15 | 103.833333 | 0 | 0 |
| 16 | 103.833333 | 0 | 0 |
| 17 | 103.833333 | 0 | 0 |
| 18 | 105.5 | 0 | 0 |
| 19 | 105.5 | 0 | 0 |
| 20 | 105.5 | 0 | 0 |
| 21 | | | |
| 22 | 61.333333 | 0 | 0 |
| 23 | 61.333333 | 0 | 0 |
| 24 | 61.333333 | 0 | 0 |
| 25 | 61.333333 | 0 | 0 |
| 26 | 61.333333 | 0 | 0 |
| 27 | 61.333333 | 0 | 0 |
| 28 | 61.333333 | 0 | 0 |
| 29 | 61.333333 | 0 | 0 |
| 30 | 61.333333 | 0 | 0 |
| 31 | 61.333333 | 0 | 0 |
| 32 | 61.333333 | 0 | 0 |
| 33 | 61.333333 | 0 | 0 |
| 34 | 61.333333 | 0 | 0 |
| 35 | 61.333333 | 0 | 0 |
| 36 | 61.333333 | 0 | 0 |
| 37 | 61.333333 | 0 | 0 |
| 38 | 61.333333 | 0 | 0 |
| 39 | 61.333333 | 0 | 0 |
| 40 | 61.333333 | 0 | 0 |
| 41 | 61.333333 | 0 | 0 |
| 42 | 61.333333 | 0 | 0 |
| 43 | 61.333333 | 0 | 0 |
| 44 | 61.333333 | 0 | 0 |
| 45 | 61.333333 | 0 | 0 |
| 46 | 61.333333 | 0 | 0 |
| 47 | 61.333333 | 0 | 0 |
| 48 | 61.333333 | 0 | 0 |
| 49 | 61.333333 | 0 | 0 |
| 50 | 61.333333 | 0 | 0 |
| 51 | 61.333333 | 0 | 0 |
| 52 | 61.333333 | 0 | 0 |
| 53 | 61.333333 | 0 | 0 |
| 54 | 61.333333 | 0 | 0 |
| 55 | 61.333333 | 0 | 0 |
| 56 | 61.333333 | 0 | 0 |
| 57 | 61.333333 | 0 | 0 |
| 58 | 61.333333 | 0 | 0 |
| 59 | 61.333333 | 0 | 0 |
| 60 | | | |

| miRNA_Acc. | Target_Acc. | Expectation | UPE\$ | miRNA_start |
|-------------------------|--------------------|-------------|-------|-------------|
| aggcaagaugcuggcauagcugu | Phvul.007G103100.1 | 2 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.007G103100.1 | 2 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.009G006000.3 | 2.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.009G006000.2 | 2.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.009G006000.1 | 2.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.002G198200.1 | 2.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.009G006000.3 | 2.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.009G006000.2 | 2.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.009G006000.1 | 2.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.002G198200.1 | 2.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.001G214600.7 | 3 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.009G150800.1 | 3 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.002G261000.1 | 3 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.001G214600.7 | 3 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.009G150800.1 | 3 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.002G261000.1 | 3 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.001G022900.1 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.008G128900.1 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.001G219900.4 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.001G219900.3 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.001G219900.1 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.001G219900.2 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.003G174100.1 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.008G040500.1 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.004G018100.1 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.008G290000.1 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.005G040800.1 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.010G000700.3 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.010G000700.1 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.010G000700.2 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.001G022900.1 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.008G128900.1 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.001G219900.4 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.001G219900.3 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.001G219900.1 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.001G219900.2 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.003G174100.1 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.008G040500.1 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.004G018100.1 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.008G290000.1 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.005G040800.1 | 3.5 | -1 | 1 |
| aggcaagaugcuggcauagcugu | Phvul.010G000700.3 | 3.5 | -1 | 1 |

| | | | | | |
|----|-------------------------|--------------------|-----|----|---|
| 1 | | | | | |
| 2 | | | | | |
| 3 | aggcaagaugcuggcauagcugu | Phvul.010G000700.1 | 3.5 | -1 | 1 |
| 4 | aggcaagaugcuggcauagcugu | Phvul.010G000700.2 | 3.5 | -1 | 1 |
| 5 | aggcaagaugcuggcauagcugu | Phvul.009G032100.1 | 4 | -1 | 1 |
| 6 | aggcaagaugcuggcauagcugu | Phvul.009G243500.2 | 4 | -1 | 1 |
| 7 | aggcaagaugcuggcauagcugu | Phvul.002G061200.1 | 4 | -1 | 1 |
| 8 | aggcaagaugcuggcauagcugu | Phvul.008G061900.3 | 4 | -1 | 1 |
| 9 | aggcaagaugcuggcauagcugu | Phvul.008G061900.2 | 4 | -1 | 1 |
| 10 | aggcaagaugcuggcauagcugu | Phvul.008G061900.1 | 4 | -1 | 1 |
| 11 | aggcaagaugcuggcauagcugu | Phvul.009G226500.1 | 4 | -1 | 1 |
| 12 | aggcaagaugcuggcauagcugu | Phvul.009G226500.2 | 4 | -1 | 1 |
| 13 | aggcaagaugcuggcauagcugu | Phvul.009G242900.3 | 4 | -1 | 1 |
| 14 | aggcaagaugcuggcauagcugu | Phvul.009G242900.4 | 4 | -1 | 1 |
| 15 | aggcaagaugcuggcauagcugu | Phvul.009G242900.2 | 4 | -1 | 1 |
| 16 | aggcaagaugcuggcauagcugu | Phvul.009G242900.1 | 4 | -1 | 1 |
| 17 | aggcaagaugcuggcauagcugu | Phvul.002G133900.2 | 4 | -1 | 1 |
| 18 | aggcaagaugcuggcauagcugu | Phvul.009G106900.1 | 4 | -1 | 1 |
| 19 | aggcaagaugcuggcauagcugu | Phvul.009G036300.1 | 4 | -1 | 1 |
| 20 | aggcaagaugcuggcauagcugu | Phvul.009G192300.1 | 4 | -1 | 1 |
| 21 | aggcaagaugcuggcauagcugu | Phvul.003G112400.1 | 4 | -1 | 1 |
| 22 | aggcaagaugcuggcauagcugu | Phvul.009G032100.1 | 4 | -1 | 1 |
| 23 | aggcaagaugcuggcauagcugu | Phvul.009G243500.2 | 4 | -1 | 1 |
| 24 | aggcaagaugcuggcauagcugu | Phvul.002G061200.1 | 4 | -1 | 1 |
| 25 | aggcaagaugcuggcauagcugu | Phvul.008G061900.3 | 4 | -1 | 1 |
| 26 | aggcaagaugcuggcauagcugu | Phvul.008G061900.2 | 4 | -1 | 1 |
| 27 | aggcaagaugcuggcauagcugu | Phvul.008G061900.1 | 4 | -1 | 1 |
| 28 | aggcaagaugcuggcauagcugu | Phvul.009G226500.1 | 4 | -1 | 1 |
| 29 | aggcaagaugcuggcauagcugu | Phvul.009G226500.2 | 4 | -1 | 1 |
| 30 | aggcaagaugcuggcauagcugu | Phvul.009G242900.3 | 4 | -1 | 1 |
| 31 | aggcaagaugcuggcauagcugu | Phvul.009G242900.4 | 4 | -1 | 1 |
| 32 | aggcaagaugcuggcauagcugu | Phvul.009G242900.2 | 4 | -1 | 1 |
| 33 | aggcaagaugcuggcauagcugu | Phvul.009G242900.1 | 4 | -1 | 1 |
| 34 | aggcaagaugcuggcauagcugu | Phvul.002G133900.2 | 4 | -1 | 1 |
| 35 | aggcaagaugcuggcauagcugu | Phvul.009G106900.1 | 4 | -1 | 1 |
| 36 | aggcaagaugcuggcauagcugu | Phvul.009G036300.1 | 4 | -1 | 1 |
| 37 | aggcaagaugcuggcauagcugu | Phvul.009G192300.1 | 4 | -1 | 1 |
| 38 | aggcaagaugcuggcauagcugu | Phvul.003G112400.1 | 4 | -1 | 1 |
| 39 | aggcaagaugcuggcauagcugu | Phvul.009G032100.1 | 4 | -1 | 1 |
| 40 | aggcaagaugcuggcauagcugu | Phvul.009G243500.2 | 4 | -1 | 1 |
| 41 | aggcaagaugcuggcauagcugu | Phvul.002G061200.1 | 4 | -1 | 1 |
| 42 | aggcaagaugcuggcauagcugu | Phvul.008G061900.3 | 4 | -1 | 1 |
| 43 | aggcaagaugcuggcauagcugu | Phvul.008G061900.2 | 4 | -1 | 1 |
| 44 | aggcaagaugcuggcauagcugu | Phvul.008G061900.1 | 4 | -1 | 1 |
| 45 | aggcaagaugcuggcauagcugu | Phvul.009G226500.1 | 4 | -1 | 1 |
| 46 | aggcaagaugcuggcauagcugu | Phvul.009G226500.2 | 4 | -1 | 1 |
| 47 | aggcaagaugcuggcauagcugu | Phvul.009G242900.3 | 4 | -1 | 1 |
| 48 | aggcaagaugcuggcauagcugu | Phvul.009G242900.4 | 4 | -1 | 1 |
| 49 | aggcaagaugcuggcauagcugu | Phvul.009G242900.2 | 4 | -1 | 1 |
| 50 | aggcaagaugcuggcauagcugu | Phvul.009G242900.1 | 4 | -1 | 1 |
| 51 | aggcaagaugcuggcauagcugu | Phvul.002G133900.2 | 4 | -1 | 1 |
| 52 | aggcaagaugcuggcauagcugu | Phvul.009G106900.1 | 4 | -1 | 1 |
| 53 | aggcaagaugcuggcauagcugu | Phvul.009G036300.1 | 4 | -1 | 1 |
| 54 | aggcaagaugcuggcauagcugu | Phvul.009G192300.1 | 4 | -1 | 1 |
| 55 | aggcaagaugcuggcauagcugu | Phvul.003G112400.1 | 4 | -1 | 1 |
| 56 | aggcaagaugcuggcauagcugu | Phvul.006G151200.1 | 4.5 | -1 | 1 |
| 57 | aggcaagaugcuggcauagcugu | Phvul.006G104300.2 | 4.5 | -1 | 1 |
| 58 | aggcaagaugcuggcauagcugu | Phvul.006G104300.1 | 4.5 | -1 | 1 |
| 59 | aggcaagaugcuggcauagcugu | Phvul.011G033500.1 | 4.5 | -1 | 1 |
| 60 | aggcaagaugcuggcauagcugu | Phvul.008G038200.1 | 4.5 | -1 | 1 |
| | aggcaagaugcuggcauagcugu | Phvul.002G022400.1 | 4.5 | -1 | 1 |
| | aggcaagaugcuggcauagcugu | Phvul.L001644.1 | 4.5 | -1 | 1 |

| | | | | | |
|----|-------------------------|--------------------|-----|----|---|
| 1 | | | | | |
| 2 | | | | | |
| 3 | aggcaagaugcuggcauagcugu | Phvul.001G264132.1 | 4.5 | -1 | 1 |
| 4 | aggcaagaugcuggcauagcugu | Phvul.009G019100.1 | 4.5 | -1 | 1 |
| 5 | aggcaagaugcuggcauagcugu | Phvul.009G073900.1 | 4.5 | -1 | 1 |
| 6 | aggcaagaugcuggcauagcugu | Phvul.003G159700.1 | 4.5 | -1 | 1 |
| 7 | aggcaagaugcuggcauagcugu | Phvul.006G151200.1 | 4.5 | -1 | 1 |
| 8 | aggcaagaugcuggcauagcugu | Phvul.006G104300.2 | 4.5 | -1 | 1 |
| 9 | aggcaagaugcuggcauagcugu | Phvul.006G104300.1 | 4.5 | -1 | 1 |
| 10 | aggcaagaugcuggcauagcugu | Phvul.011G033500.1 | 4.5 | -1 | 1 |
| 11 | aggcaagaugcuggcauagcugu | Phvul.008G038200.1 | 4.5 | -1 | 1 |
| 12 | aggcaagaugcuggcauagcugu | Phvul.002G022400.1 | 4.5 | -1 | 1 |
| 13 | aggcaagaugcuggcauagcugu | Phvul.L001644.1 | 4.5 | -1 | 1 |
| 14 | aggcaagaugcuggcauagcugu | Phvul.001G264132.1 | 4.5 | -1 | 1 |
| 15 | aggcaagaugcuggcauagcugu | Phvul.009G019100.1 | 4.5 | -1 | 1 |
| 16 | aggcaagaugcuggcauagcugu | Phvul.009G073900.1 | 4.5 | -1 | 1 |
| 17 | aggcaagaugcuggcauagcugu | Phvul.003G159700.1 | 4.5 | -1 | 1 |
| 18 | aggcaagaugcuggcauagcugu | Phvul.001G214600.7 | 5 | -1 | 1 |
| 19 | aggcaagaugcuggcauagcugu | Phvul.009G228600.1 | 5 | -1 | 1 |
| 20 | aggcaagaugcuggcauagcugu | Phvul.009G035800.1 | 5 | -1 | 1 |
| 21 | aggcaagaugcuggcauagcugu | Phvul.011G134100.1 | 5 | -1 | 1 |
| 22 | aggcaagaugcuggcauagcugu | Phvul.011G134000.1 | 5 | -1 | 1 |
| 23 | aggcaagaugcuggcauagcugu | Phvul.011G130800.1 | 5 | -1 | 1 |
| 24 | aggcaagaugcuggcauagcugu | Phvul.011G081100.1 | 5 | -1 | 1 |
| 25 | aggcaagaugcuggcauagcugu | Phvul.011G133300.1 | 5 | -1 | 1 |
| 26 | aggcaagaugcuggcauagcugu | Phvul.007G247800.1 | 5 | -1 | 1 |
| 27 | aggcaagaugcuggcauagcugu | Phvul.004G172000.1 | 5 | -1 | 1 |
| 28 | aggcaagaugcuggcauagcugu | Phvul.010G031700.2 | 5 | -1 | 1 |
| 29 | aggcaagaugcuggcauagcugu | Phvul.010G031700.3 | 5 | -1 | 1 |
| 30 | aggcaagaugcuggcauagcugu | Phvul.005G105800.1 | 5 | -1 | 1 |
| 31 | aggcaagaugcuggcauagcugu | Phvul.009G021200.1 | 5 | -1 | 1 |
| 32 | aggcaagaugcuggcauagcugu | Phvul.009G226800.1 | 5 | -1 | 1 |
| 33 | aggcaagaugcuggcauagcugu | Phvul.006G162000.1 | 5 | -1 | 1 |
| 34 | aggcaagaugcuggcauagcugu | Phvul.002G038300.1 | 5 | -1 | 1 |
| 35 | aggcaagaugcuggcauagcugu | Phvul.007G188300.1 | 5 | -1 | 1 |
| 36 | aggcaagaugcuggcauagcugu | Phvul.004G084688.1 | 5 | -1 | 1 |
| 37 | aggcaagaugcuggcauagcugu | Phvul.L001859.1 | 5 | -1 | 1 |
| 38 | aggcaagaugcuggcauagcugu | Phvul.002G027900.1 | 5 | -1 | 1 |
| 39 | aggcaagaugcuggcauagcugu | Phvul.005G180700.1 | 5 | -1 | 1 |
| 40 | aggcaagaugcuggcauagcugu | Phvul.004G153700.1 | 5 | -1 | 1 |
| 41 | aggcaagaugcuggcauagcugu | Phvul.001G214600.7 | 5 | -1 | 1 |
| 42 | aggcaagaugcuggcauagcugu | Phvul.009G228600.1 | 5 | -1 | 1 |
| 43 | aggcaagaugcuggcauagcugu | Phvul.009G035800.1 | 5 | -1 | 1 |
| 44 | aggcaagaugcuggcauagcugu | Phvul.011G134100.1 | 5 | -1 | 1 |
| 45 | aggcaagaugcuggcauagcugu | Phvul.011G134000.1 | 5 | -1 | 1 |
| 46 | aggcaagaugcuggcauagcugu | Phvul.011G130800.1 | 5 | -1 | 1 |
| 47 | aggcaagaugcuggcauagcugu | Phvul.011G081100.1 | 5 | -1 | 1 |
| 48 | aggcaagaugcuggcauagcugu | Phvul.011G133300.1 | 5 | -1 | 1 |
| 49 | aggcaagaugcuggcauagcugu | Phvul.007G247800.1 | 5 | -1 | 1 |
| 50 | aggcaagaugcuggcauagcugu | Phvul.004G172000.1 | 5 | -1 | 1 |
| 51 | aggcaagaugcuggcauagcugu | Phvul.010G031700.2 | 5 | -1 | 1 |
| 52 | aggcaagaugcuggcauagcugu | Phvul.010G031700.3 | 5 | -1 | 1 |
| 53 | aggcaagaugcuggcauagcugu | Phvul.005G105800.1 | 5 | -1 | 1 |
| 54 | aggcaagaugcuggcauagcugu | Phvul.009G021200.1 | 5 | -1 | 1 |
| 55 | aggcaagaugcuggcauagcugu | Phvul.009G226800.1 | 5 | -1 | 1 |
| 56 | aggcaagaugcuggcauagcugu | Phvul.006G162000.1 | 5 | -1 | 1 |
| 57 | aggcaagaugcuggcauagcugu | Phvul.002G038300.1 | 5 | -1 | 1 |
| 58 | aggcaagaugcuggcauagcugu | Phvul.007G188300.1 | 5 | -1 | 1 |
| 59 | aggcaagaugcuggcauagcugu | Phvul.004G084688.1 | 5 | -1 | 1 |
| 60 | aggcaagaugcuggcauagcugu | Phvul.L001859.1 | 5 | -1 | 1 |

| | | | | | |
|----|-------------------------|--------------------|---|----|---|
| 1 | | | | | |
| 2 | | | | | |
| 3 | aggcaagaugcuggcauagcugu | Phvul.011G130800.1 | 5 | -1 | 1 |
| 4 | aggcaagaugcuggcauagcugu | Phvul.011G081100.1 | 5 | -1 | 1 |
| 5 | aggcaagaugcuggcauagcugu | Phvul.011G133300.1 | 5 | -1 | 1 |
| 6 | aggcaagaugcuggcauagcugu | Phvul.007G247800.1 | 5 | -1 | 1 |
| 7 | aggcaagaugcuggcauagcugu | Phvul.004G172000.1 | 5 | -1 | 1 |
| 8 | aggcaagaugcuggcauagcugu | Phvul.010G031700.2 | 5 | -1 | 1 |
| 9 | aggcaagaugcuggcauagcugu | Phvul.010G031700.3 | 5 | -1 | 1 |
| 10 | aggcaagaugcuggcauagcugu | Phvul.005G105800.1 | 5 | -1 | 1 |
| 11 | aggcaagaugcuggcauagcugu | Phvul.009G021200.1 | 5 | -1 | 1 |
| 12 | aggcaagaugcuggcauagcugu | Phvul.009G226800.1 | 5 | -1 | 1 |
| 13 | aggcaagaugcuggcauagcugu | Phvul.006G162000.1 | 5 | -1 | 1 |
| 14 | aggcaagaugcuggcauagcugu | Phvul.002G038300.1 | 5 | -1 | 1 |
| 15 | aggcaagaugcuggcauagcugu | Phvul.007G188300.1 | 5 | -1 | 1 |
| 16 | aggcaagaugcuggcauagcugu | Phvul.004G084688.1 | 5 | -1 | 1 |
| 17 | aggcaagaugcuggcauagcugu | Phvul.L001859.1 | 5 | -1 | 1 |
| 18 | aggcaagaugcuggcauagcugu | Phvul.002G027900.1 | 5 | -1 | 1 |
| 19 | aggcaagaugcuggcauagcugu | Phvul.005G180700.1 | 5 | -1 | 1 |
| 20 | aggcaagaugcuggcauagcugu | Phvul.004G153700.1 | 5 | -1 | 1 |
| 21 | | | | | |
| 22 | | | | | |
| 23 | | | | | |
| 24 | | | | | |
| 25 | | | | | |
| 26 | | | | | |
| 27 | | | | | |
| 28 | | | | | |
| 29 | | | | | |
| 30 | | | | | |
| 31 | | | | | |
| 32 | | | | | |
| 33 | | | | | |
| 34 | | | | | |
| 35 | | | | | |
| 36 | | | | | |
| 37 | | | | | |
| 38 | | | | | |
| 39 | | | | | |
| 40 | | | | | |
| 41 | | | | | |
| 42 | | | | | |
| 43 | | | | | |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| miRNA_end | Target_start | Target_end | miRNA_alignment | Target_alignment | Inhibition |
|-----------|--------------|------------|-----------------|-------------------|------------|
| 23 | 1845 | 1867 | AGGCAAGAU(|UGGAUUAUG | Cleavage |
| 23 | 1845 | 1867 | AGGCAAGAU(|UGGAUUAUG | Cleavage |
| 23 | 1031 | 1053 | AGGCAAGAU(|:CAAGCUAUG(| Cleavage |
| 23 | 1656 | 1678 | AGGCAAGAU(|:CAAGCUAUG(| Cleavage |
| 23 | 1656 | 1678 | AGGCAAGAU(|:CAAGCUAUG(| Cleavage |
| 23 | 775 | 797 | AGGCAAGAU(|:AAACUUAUG(| Cleavage |
| 23 | 1031 | 1053 | AGGCAAGAU(|:CAAGCUAUG(| Cleavage |
| 23 | 1656 | 1678 | AGGCAAGAU(|:CAAGCUAUG(| Cleavage |
| 23 | 1656 | 1678 | AGGCAAGAU(|:CAAGCUAUG(| Cleavage |
| 23 | 775 | 797 | AGGCAAGAU(|:AAACUUAUG(| Cleavage |
| 23 | 1055 | 1077 | AGGCAAGAU(|:UCAUCUAUG(| Cleavage |
| 23 | 1403 | 1425 | AGGCAAGAU(|:AGAACUCUG(| Cleavage |
| 23 | 1694 | 1716 | AGGCAAGAU(|:UCUCCUUUG(| Cleavage |
| 23 | 1055 | 1077 | AGGCAAGAU(|:UCAUCUAUG(| Cleavage |
| 23 | 1403 | 1425 | AGGCAAGAU(|:AGAACUCUG(| Cleavage |
| 23 | 1694 | 1716 | AGGCAAGAU(|:UCUCCUUUG(| Cleavage |
| 23 | 94 | 116 | AGGCAAGAU(|:ACAACUGUG(| Cleavage |
| 23 | 798 | 820 | AGGCAAGAU(|:CCAACUGUG(| Cleavage |
| 23 | 573 | 595 | AGGCAAGAU(|:GCUGAUUAU(| Cleavage |
| 23 | 573 | 595 | AGGCAAGAU(|:GCUGAUUAU(| Cleavage |
| 23 | 1468 | 1490 | AGGCAAGAU(|:GCUGAUUAU(| Cleavage |
| 23 | 1468 | 1490 | AGGCAAGAU(|:GCUGAUUAU(| Cleavage |
| 23 | 2981 | 3002 | AGGCAAGAU(|:GCACCUAU-C(| Cleavage |
| 23 | 1638 | 1660 | AGGCAAGAU(|:GAAACUAUG(| Cleavage |
| 23 | 1884 | 1906 | AGGCAAGAU(|:AGCAUUAUG(| Cleavage |
| 23 | 1140 | 1162 | AGGCAAGAU(|:ACUUCAGUG(| Cleavage |
| 23 | 1074 | 1096 | AGGCAAGAU(|:UAACCUCUG(| Cleavage |
| 23 | 1003 | 1025 | AGGCAAGAU(|:CAUUCUAUG(| Cleavage |
| 23 | 1003 | 1025 | AGGCAAGAU(|:CAUUCUAUG(| Cleavage |
| 23 | 1003 | 1025 | AGGCAAGAU(|:CAUUCUAUG(| Cleavage |
| 23 | 94 | 116 | AGGCAAGAU(|:ACAACUGUG(| Cleavage |
| 23 | 798 | 820 | AGGCAAGAU(|:CCAACUGUG(| Cleavage |
| 23 | 573 | 595 | AGGCAAGAU(|:GCUGAUUAU(| Cleavage |
| 23 | 573 | 595 | AGGCAAGAU(|:GCUGAUUAU(| Cleavage |
| 23 | 1468 | 1490 | AGGCAAGAU(|:GCUGAUUAU(| Cleavage |
| 23 | 1468 | 1490 | AGGCAAGAU(|:GCUGAUUAU(| Cleavage |
| 23 | 2981 | 3002 | AGGCAAGAU(|:GCACCUAU-C(| Cleavage |
| 23 | 1638 | 1660 | AGGCAAGAU(|:GAAACUAUG(| Cleavage |
| 23 | 1884 | 1906 | AGGCAAGAU(|:AGCAUUAUG(| Cleavage |
| 23 | 1140 | 1162 | AGGCAAGAU(|:ACUUCAGUG(| Cleavage |
| 23 | 1074 | 1096 | AGGCAAGAU(|:UAACCUCUG(| Cleavage |
| 23 | 1003 | 1025 | AGGCAAGAU(|:CAUUCUAUG(| Cleavage |

| | | | |
|----|----|------|---|
| 1 | | | |
| 2 | | | |
| 3 | | | |
| 4 | 23 | 1000 | 1022 AGGCAAGAU(:..... :..... :AUAGCUAUG) Cleavage |
| 5 | 23 | 1064 | 1086 AGGCAAGAU(:... :..... :AUAGCAAUG) Cleavage |
| 6 | 23 | 1000 | 1022 AGGCAAGAU(:..... :..... :AUAGCUAUG) Cleavage |
| 7 | 23 | 1232 | 1255 AGGCAAGAU(:..... :..... :CAAGCUAUG) Translation |
| 8 | 23 | 1770 | 1792 AGGCAAGAU(:... :..... :...UCAGUUUUG) Cleavage |
| 9 | 23 | 2276 | 2298 AGGCAAGAU(:... :..... :GCAGUUUCG) Cleavage |
| 10 | 23 | 2353 | 2375 AGGCAAGAU(:... :..... :GCAGUUUCG) Cleavage |
| 11 | 23 | 2353 | 2375 AGGCAAGAU(:... :..... :GCAGUUUCG) Cleavage |
| 12 | 23 | 1513 | 1535 AGGCAAGAU(:... :..... :...AUAGCACUG) Cleavage |
| 13 | 23 | 733 | 755 AGGCAAGAU(:... :..... :UUAGUAAUG) Translation |
| 14 | 23 | 809 | 831 AGGCAAGAU(:... :... :..... :ACUGCUAAG) Cleavage |
| 15 | 23 | 1197 | 1220 AGGCA-AGAU :..... :..... :GGUGCUAUG) Cleavage |
| 16 | 23 | 1385 | 1407 AGGCAAGAU(:... :..... :..... :AUUGCUAUG) Cleavage |
| 17 | 23 | 277 | 299 AGGCAAGAU(:... :..... :..... :ACACCCGUG) Cleavage |
| 18 | 23 | 2137 | 2159 AGGCAAGAU(:..... :..... :UUGGUUGUG) Cleavage |
| 19 | 23 | 693 | 716 AGGCAAGAU(:... :..... :..... :UUAUCUGUG) Translation |
| 20 | 23 | 34 | 56 AGGCAAGAU(:... :... :..... :AAAGCUUUG) Translation |
| 21 | 23 | 1702 | 1724 AGGCAAGAU(:... :... :..... :AUGGAUUUG) Cleavage |
| 22 | 23 | 606 | 628 AGGCAAGAU(:... :..... :...UGAGCAAUG) Cleavage |
| 23 | | | |
| 24 | | | |
| 25 | | | |
| 26 | | | |
| 27 | | | |
| 28 | | | |
| 29 | | | |
| 30 | | | |
| 31 | | | |
| 32 | | | |
| 33 | | | |
| 34 | | | |
| 35 | | | |
| 36 | | | |
| 37 | | | |
| 38 | | | |
| 39 | | | |
| 40 | | | |
| 41 | | | |
| 42 | | | |
| 43 | | | |
| 44 | | | |
| 45 | | | |
| 46 | | | |
| 47 | | | |
| 48 | | | |
| 49 | | | |
| 50 | | | |
| 51 | | | |
| 52 | | | |
| 53 | | | |
| 54 | | | |
| 55 | | | |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

| | Target_Desc. | Multiplicity | Target_Acc. | locusName | Pfam | |
|----|--------------|--------------|------------------|------------------|--------------|---|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | | | | | | |
| 4 | | | | | | |
| 5 | pacid=371666 | 1 | Phvul.007G103100 | Phvul.007G103100 | PF02127 | |
| 6 | pacid=371666 | 1 | Phvul.007G103100 | Phvul.007G103100 | PF02127 | |
| 7 | pacid=371508 | 1 | Phvul.009G006000 | Phvul.009G006000 | PF00650 | |
| 8 | pacid=371508 | 1 | Phvul.009G006000 | Phvul.009G006000 | PF00650 | |
| 9 | pacid=371508 | 1 | Phvul.009G006000 | Phvul.009G006000 | PF00650 | |
| 10 | pacid=371508 | 1 | Phvul.009G006000 | Phvul.009G006000 | PF00650 | |
| 11 | pacid=371750 | 1 | Phvul.002G198200 | Phvul.002G198200 | PF12847 | |
| 12 | pacid=371508 | 1 | Phvul.009G006000 | Phvul.009G006000 | PF00650 | |
| 13 | pacid=371508 | 1 | Phvul.009G006000 | Phvul.009G006000 | PF00650 | |
| 14 | pacid=371508 | 1 | Phvul.009G006000 | Phvul.009G006000 | PF00650 | |
| 15 | pacid=371508 | 1 | Phvul.009G006000 | Phvul.009G006000 | PF00650 | |
| 16 | pacid=371750 | 1 | Phvul.002G198200 | Phvul.002G198200 | PF12847 | |
| 17 | pacid=371692 | 2 | Phvul.001G214600 | Phvul.001G214600 | | 0 |
| 18 | pacid=371516 | 1 | Phvul.009G150800 | Phvul.009G150800 | PF03151 | |
| 19 | pacid=371743 | 1 | Phvul.002G261000 | Phvul.002G261000 | PF12070 | |
| 20 | pacid=371692 | 2 | Phvul.001G214600 | Phvul.001G214600 | | 0 |
| 21 | pacid=371516 | 1 | Phvul.009G150800 | Phvul.009G150800 | PF03151 | |
| 22 | pacid=371743 | 1 | Phvul.002G261000 | Phvul.002G261000 | PF12070 | |
| 23 | pacid=371685 | 1 | Phvul.001G022900 | Phvul.001G022900 | PF00447 | |
| 24 | pacid=371580 | 1 | Phvul.008G128900 | Phvul.008G128900 | PF00097 | |
| 25 | pacid=371709 | 1 | Phvul.001G219900 | Phvul.001G219900 | PF00483 | |
| 26 | pacid=371709 | 1 | Phvul.001G219900 | Phvul.001G219900 | PF00483 | |
| 27 | pacid=371709 | 1 | Phvul.001G219900 | Phvul.001G219900 | PF00483 | |
| 28 | pacid=371709 | 1 | Phvul.001G219900 | Phvul.001G219900 | PF00483 | |
| 29 | pacid=371478 | 1 | Phvul.003G174100 | Phvul.003G174100 | PF03144,PF00 | |
| 30 | pacid=371593 | 1 | Phvul.008G040500 | Phvul.008G040500 | PF00854 | |
| 31 | pacid=371633 | 1 | Phvul.004G018100 | Phvul.004G018100 | PF02705 | |
| 32 | pacid=371602 | 1 | Phvul.008G290000 | Phvul.008G290000 | PF00627,PF00 | |
| 33 | pacid=371525 | 1 | Phvul.005G040800 | Phvul.005G040800 | PF04652 | |
| 34 | pacid=371440 | 1 | Phvul.010G000700 | Phvul.010G000700 | PF12295,PF11 | |
| 35 | pacid=371440 | 1 | Phvul.010G000700 | Phvul.010G000700 | PF12295,PF11 | |
| 36 | pacid=371440 | 1 | Phvul.010G000700 | Phvul.010G000700 | PF12295,PF11 | |
| 37 | pacid=371685 | 1 | Phvul.001G022900 | Phvul.001G022900 | PF00447 | |
| 38 | pacid=371580 | 1 | Phvul.008G128900 | Phvul.008G128900 | PF00097 | |
| 39 | pacid=371709 | 1 | Phvul.001G219900 | Phvul.001G219900 | PF00483 | |
| 40 | pacid=371709 | 1 | Phvul.001G219900 | Phvul.001G219900 | PF00483 | |
| 41 | pacid=371709 | 1 | Phvul.001G219900 | Phvul.001G219900 | PF00483 | |
| 42 | pacid=371709 | 1 | Phvul.001G219900 | Phvul.001G219900 | PF00483 | |
| 43 | pacid=371478 | 1 | Phvul.003G174100 | Phvul.003G174100 | PF03144,PF00 | |
| 44 | pacid=371593 | 1 | Phvul.008G040500 | Phvul.008G040500 | PF00854 | |
| 45 | pacid=371633 | 1 | Phvul.004G018100 | Phvul.004G018100 | PF02705 | |
| 46 | pacid=371602 | 1 | Phvul.008G290000 | Phvul.008G290000 | PF00627,PF00 | |
| 47 | pacid=371525 | 1 | Phvul.005G040800 | Phvul.005G040800 | PF04652 | |
| 48 | pacid=371440 | 1 | Phvul.010G000700 | Phvul.010G000700 | PF12295,PF11 | |
| 49 | pacid=371440 | 1 | Phvul.010G000700 | Phvul.010G000700 | PF12295,PF11 | |
| 50 | pacid=371440 | 1 | Phvul.010G000700 | Phvul.010G000700 | PF12295,PF11 | |
| 51 | pacid=371685 | 1 | Phvul.001G022900 | Phvul.001G022900 | PF00447 | |
| 52 | pacid=371580 | 1 | Phvul.008G128900 | Phvul.008G128900 | PF00097 | |
| 53 | pacid=371709 | 1 | Phvul.001G219900 | Phvul.001G219900 | PF00483 | |
| 54 | pacid=371709 | 1 | Phvul.001G219900 | Phvul.001G219900 | PF00483 | |
| 55 | pacid=371709 | 1 | Phvul.001G219900 | Phvul.001G219900 | PF00483 | |
| 56 | pacid=371709 | 1 | Phvul.001G219900 | Phvul.001G219900 | PF00483 | |
| 57 | pacid=371478 | 1 | Phvul.003G174100 | Phvul.003G174100 | PF03144,PF00 | |
| 58 | pacid=371593 | 1 | Phvul.008G040500 | Phvul.008G040500 | PF00854 | |
| 59 | pacid=371633 | 1 | Phvul.004G018100 | Phvul.004G018100 | PF02705 | |
| 60 | pacid=371602 | 1 | Phvul.008G290000 | Phvul.008G290000 | PF00627,PF00 | |
| 61 | pacid=371525 | 1 | Phvul.005G040800 | Phvul.005G040800 | PF04652 | |
| 62 | pacid=371440 | 1 | Phvul.010G000700 | Phvul.010G000700 | PF12295,PF11 | |

| | | | | |
|----|--------------|--------------------|------------------|--------------|
| 1 | | | | |
| 2 | | | | |
| 3 | | | | |
| 4 | pacid=371440 | 1 Phvul.010G000700 | Phvul.010G000700 | PF12295,PF11 |
| 5 | pacid=371440 | 1 Phvul.010G000700 | Phvul.010G000700 | PF12295,PF11 |
| 6 | pacid=371489 | 1 Phvul.009G032100 | Phvul.009G032100 | PF04674 |
| 7 | pacid=371515 | 1 Phvul.009G243500 | Phvul.009G243500 | PF00856 |
| 8 | pacid=371751 | 1 Phvul.002G061200 | Phvul.002G061200 | PF08244,PF11 |
| 9 | pacid=371613 | 1 Phvul.008G061900 | Phvul.008G061900 | PF07690 |
| 10 | pacid=371613 | 1 Phvul.008G061900 | Phvul.008G061900 | PF07690 |
| 11 | pacid=371613 | 1 Phvul.008G061900 | Phvul.008G061900 | PF07690 |
| 12 | pacid=371613 | 1 Phvul.008G061900 | Phvul.008G061900 | PF07690 |
| 13 | pacid=371514 | 1 Phvul.009G226500 | Phvul.009G226500 | PF16124,PF00 |
| 14 | pacid=371514 | 1 Phvul.009G226500 | Phvul.009G226500 | PF16124,PF00 |
| 15 | pacid=371506 | 1 Phvul.009G242900 | Phvul.009G242900 | PF07687,PF01 |
| 16 | pacid=371506 | 1 Phvul.009G242900 | Phvul.009G242900 | PF07687,PF01 |
| 17 | pacid=371506 | 1 Phvul.009G242900 | Phvul.009G242900 | PF07687,PF01 |
| 18 | pacid=371505 | 1 Phvul.009G242900 | Phvul.009G242900 | PF07687,PF01 |
| 19 | pacid=371505 | 1 Phvul.009G242900 | Phvul.009G242900 | PF07687,PF01 |
| 20 | pacid=371774 | 1 Phvul.002G133900 | Phvul.002G133900 | 0 |
| 21 | pacid=371497 | 1 Phvul.009G106900 | Phvul.009G106900 | PF10255 |
| 22 | pacid=371504 | 1 Phvul.009G036300 | Phvul.009G036300 | PF00249 |
| 23 | pacid=371489 | 1 Phvul.009G192300 | Phvul.009G192300 | PF13414 |
| 24 | pacid=371446 | 1 Phvul.003G112400 | Phvul.003G112400 | PF04802 |
| 25 | pacid=371489 | 1 Phvul.009G032100 | Phvul.009G032100 | PF04674 |
| 26 | pacid=371515 | 1 Phvul.009G243500 | Phvul.009G243500 | PF00856 |
| 27 | pacid=371751 | 1 Phvul.002G061200 | Phvul.002G061200 | PF08244,PF11 |
| 28 | pacid=371613 | 1 Phvul.008G061900 | Phvul.008G061900 | PF07690 |
| 29 | pacid=371613 | 1 Phvul.008G061900 | Phvul.008G061900 | PF07690 |
| 30 | pacid=371613 | 1 Phvul.008G061900 | Phvul.008G061900 | PF07690 |
| 31 | pacid=371514 | 1 Phvul.009G226500 | Phvul.009G226500 | PF16124,PF00 |
| 32 | pacid=371514 | 1 Phvul.009G226500 | Phvul.009G226500 | PF16124,PF00 |
| 33 | pacid=371506 | 1 Phvul.009G242900 | Phvul.009G242900 | PF07687,PF01 |
| 34 | pacid=371506 | 1 Phvul.009G242900 | Phvul.009G242900 | PF07687,PF01 |
| 35 | pacid=371506 | 1 Phvul.009G242900 | Phvul.009G242900 | PF07687,PF01 |
| 36 | pacid=371505 | 1 Phvul.009G242900 | Phvul.009G242900 | PF07687,PF01 |
| 37 | pacid=371774 | 1 Phvul.002G133900 | Phvul.002G133900 | 0 |
| 38 | pacid=371497 | 1 Phvul.009G106900 | Phvul.009G106900 | PF10255 |
| 39 | pacid=371504 | 1 Phvul.009G036300 | Phvul.009G036300 | PF00249 |
| 40 | pacid=371489 | 1 Phvul.009G192300 | Phvul.009G192300 | PF13414 |
| 41 | pacid=371446 | 1 Phvul.003G112400 | Phvul.003G112400 | PF04802 |
| 42 | pacid=371734 | 1 Phvul.006G151200 | Phvul.006G151200 | PF00849 |
| 43 | pacid=371721 | 1 Phvul.006G104300 | Phvul.006G104300 | PF06101 |
| 44 | pacid=371721 | 1 Phvul.006G104300 | Phvul.006G104300 | PF06101 |
| 45 | pacid=371563 | 1 Phvul.011G033500 | Phvul.011G033500 | PF01535,PF13 |
| 46 | pacid=371588 | 1 Phvul.008G038200 | Phvul.008G038200 | PF00249 |
| 47 | pacid=371787 | 1 Phvul.002G022400 | Phvul.002G022400 | PF01535,PF13 |
| 48 | pacid=371742 | 1 Phvul.L001644 | Phvul.L001644 | PF14432,PF01 |
| 49 | | | | |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

| | | | | |
|----|--------------|--------------------|------------------|--------------|
| 1 | | | | |
| 2 | | | | |
| 3 | | | | |
| 4 | pacid=371686 | 1 Phvul.001G264132 | Phvul.001G264132 | PF00270 |
| 5 | pacid=371502 | 1 Phvul.009G019100 | Phvul.009G019100 | PF01399,PF08 |
| 6 | pacid=371514 | 1 Phvul.009G073900 | Phvul.009G073900 | 0 |
| 7 | pacid=371469 | 1 Phvul.003G159700 | Phvul.003G159700 | PF08263,PF13 |
| 8 | pacid=371734 | 1 Phvul.006G151200 | Phvul.006G151200 | PF00849 |
| 9 | pacid=371721 | 1 Phvul.006G104300 | Phvul.006G104300 | PF06101 |
| 10 | pacid=371721 | 1 Phvul.006G104300 | Phvul.006G104300 | PF06101 |
| 11 | pacid=371563 | 1 Phvul.011G033500 | Phvul.011G033500 | PF01535,PF13 |
| 12 | pacid=371588 | 1 Phvul.008G038200 | Phvul.008G038200 | PF00249 |
| 13 | pacid=371787 | 1 Phvul.002G022400 | Phvul.002G022400 | PF01535,PF13 |
| 14 | pacid=371742 | 1 Phvul.L001644 | Phvul.L001644 | PF14432,PF01 |
| 15 | pacid=371686 | 1 Phvul.001G264132 | Phvul.001G264132 | PF00270 |
| 16 | pacid=371502 | 1 Phvul.009G019100 | Phvul.009G019100 | PF01399,PF08 |
| 17 | pacid=371514 | 1 Phvul.009G073900 | Phvul.009G073900 | 0 |
| 18 | pacid=371469 | 1 Phvul.003G159700 | Phvul.003G159700 | PF08263,PF13 |
| 19 | pacid=371692 | 2 Phvul.001G214600 | Phvul.001G214600 | 0 |
| 20 | pacid=371486 | 1 Phvul.009G228600 | Phvul.009G228600 | PF06596 |
| 21 | pacid=371491 | 1 Phvul.009G035800 | Phvul.009G035800 | PF07714,PF14 |
| 22 | pacid=371564 | 1 Phvul.011G134100 | Phvul.011G134100 | PF08246,PF00 |
| 23 | pacid=371557 | 1 Phvul.011G134000 | Phvul.011G134000 | PF08246,PF00 |
| 24 | pacid=371547 | 1 Phvul.011G130800 | Phvul.011G130800 | PF08246,PF00 |
| 25 | pacid=371568 | 1 Phvul.011G081100 | Phvul.011G081100 | PF08246,PF00 |
| 26 | pacid=371571 | 1 Phvul.011G133300 | Phvul.011G133300 | PF08246,PF00 |
| 27 | pacid=371674 | 1 Phvul.007G247800 | Phvul.007G247800 | PF12922,PF12 |
| 28 | pacid=371622 | 1 Phvul.004G172000 | Phvul.004G172000 | 0 |
| 29 | pacid=371435 | 1 Phvul.010G031700 | Phvul.010G031700 | PF04130 |
| 30 | pacid=371435 | 1 Phvul.010G031700 | Phvul.010G031700 | PF04130 |
| 31 | pacid=371533 | 1 Phvul.005G105800 | Phvul.005G105800 | PF05623 |
| 32 | pacid=371519 | 1 Phvul.009G021200 | Phvul.009G021200 | 0 |
| 33 | pacid=371493 | 1 Phvul.009G226800 | Phvul.009G226800 | PF04525 |
| 34 | pacid=371719 | 1 Phvul.006G162000 | Phvul.006G162000 | PF00097,PF05 |
| 35 | pacid=371757 | 1 Phvul.002G038300 | Phvul.002G038300 | PF06101 |
| 36 | pacid=371658 | 1 Phvul.007G188300 | Phvul.007G188300 | PF11721,PF07 |
| 37 | pacid=371636 | 1 Phvul.004G084688 | Phvul.004G084688 | PF08263,PF00 |
| 38 | pacid=371521 | 1 Phvul.L001859 | Phvul.L001859 | 0 |
| 39 | pacid=371753 | 1 Phvul.002G027900 | Phvul.002G027900 | PF00190 |
| 40 | pacid=371530 | 1 Phvul.005G180700 | Phvul.005G180700 | PF00690,PF00 |
| 41 | pacid=371631 | 1 Phvul.004G153700 | Phvul.004G153700 | PF13041,PF01 |
| 42 | pacid=371692 | 2 Phvul.001G214600 | Phvul.001G214600 | 0 |
| 43 | pacid=371486 | 1 Phvul.009G228600 | Phvul.009G228600 | PF06596 |
| 44 | pacid=371491 | 1 Phvul.009G035800 | Phvul.009G035800 | PF07714,PF14 |
| 45 | pacid=371564 | 1 Phvul.011G134100 | Phvul.011G134100 | PF08246,PF00 |
| 46 | pacid=371557 | 1 Phvul.011G134000 | Phvul.011G134000 | PF08246,PF00 |
| 47 | | | | |
| 48 | | | | |
| 49 | | | | |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

| | | | | |
|----|--------------|--------------------|------------------|--------------|
| 1 | | | | |
| 2 | | | | |
| 3 | pacid=371547 | 1 Phvul.011G130800 | Phvul.011G130800 | PF08246,PF00 |
| 4 | pacid=371568 | 1 Phvul.011G081100 | Phvul.011G081100 | PF08246,PF00 |
| 5 | pacid=371571 | 1 Phvul.011G133300 | Phvul.011G133300 | PF08246,PF00 |
| 6 | pacid=371674 | 1 Phvul.007G247800 | Phvul.007G247800 | PF12922,PF12 |
| 7 | pacid=371622 | 1 Phvul.004G172000 | Phvul.004G172000 | 0 |
| 8 | pacid=371435 | 1 Phvul.010G031700 | Phvul.010G031700 | PF04130 |
| 9 | pacid=371435 | 1 Phvul.010G031700 | Phvul.010G031700 | PF04130 |
| 10 | pacid=371533 | 1 Phvul.005G105800 | Phvul.005G105800 | PF05623 |
| 11 | pacid=371519 | 1 Phvul.009G021200 | Phvul.009G021200 | 0 |
| 12 | pacid=371493 | 1 Phvul.009G226800 | Phvul.009G226800 | PF04525 |
| 13 | pacid=371719 | 1 Phvul.006G162000 | Phvul.006G162000 | PF00097,PF05 |
| 14 | pacid=371757 | 1 Phvul.002G038300 | Phvul.002G038300 | PF06101 |
| 15 | pacid=371658 | 1 Phvul.007G188300 | Phvul.007G188300 | PF11721,PF07 |
| 16 | pacid=371636 | 1 Phvul.004G084688 | Phvul.004G084688 | PF08263,PF00 |
| 17 | pacid=371521 | 1 Phvul.L001859 | Phvul.L001859 | 0 |
| 18 | pacid=371753 | 1 Phvul.002G027900 | Phvul.002G027900 | PF00190 |
| 19 | pacid=371530 | 1 Phvul.005G180700 | Phvul.005G180700 | PF00690,PF00 |
| 20 | pacid=371631 | 1 Phvul.004G153700 | Phvul.004G153700 | PF13041,PF01 |
| 21 | | | | |
| 22 | | | | |
| 23 | | | | |
| 24 | | | | |
| 25 | | | | |
| 26 | | | | |
| 27 | | | | |
| 28 | | | | |
| 29 | | | | |
| 30 | | | | |
| 31 | | | | |
| 32 | | | | |
| 33 | | | | |
| 34 | | | | |
| 35 | | | | |
| 36 | | | | |
| 37 | | | | |
| 38 | | | | |
| 39 | | | | |
| 40 | | | | |
| 41 | | | | |
| 42 | | | | |
| 43 | | | | |
| 44 | | | | |
| 45 | | | | |
| 46 | | | | |
| 47 | | | | |
| 48 | | | | |
| 49 | | | | |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| Panther | KOG | KEGG | KOG | GO | Best-hit-arabi-arabi-symbol |
|--------------------------|---------|-------------|----------|----------------|-----------------------------|
| PTHR28570,P ⁻ | | 0 3.4.11.21 | K01267 | GO:0008270,(| AT5G04710.1 0 |
| PTHR28570,P ⁻ | | 0 3.4.11.21 | K01267 | GO:0008270,(| AT5G04710.1 0 |
| PTHR23324,P ⁻ | | 0 | 0 | 0 | 0 AT4G39170.1 0 |
| PTHR23324,P ⁻ | | 0 | 0 | 0 | 0 AT4G39170.1 0 |
| PTHR23324,P ⁻ | | 0 | 0 | 0 | 0 AT4G39170.1 0 |
| PTHR21404 | KOG1045 | | 0 | 0 GO:0008173,(| AT4G20910.1 CRM2,HEN1 |
| PTHR23324,P ⁻ | | 0 | 0 | 0 | 0 AT4G39170.1 0 |
| PTHR23324,P ⁻ | | 0 | 0 | 0 | 0 AT4G39170.1 0 |
| PTHR23324,P ⁻ | | 0 | 0 | 0 | 0 AT4G39170.1 0 |
| PTHR21404 | KOG1045 | | 0 | 0 GO:0008173,(| AT4G20910.1 CRM2,HEN1 |
| PTHR34210,P ⁻ | | 0 | 0 | 0 | 0 AT3G62330.1 0 |
| PTHR11132,P ⁻ | KOG1444 | | 0 K15356 | | 0 AT2G13650.1 GONST1 |
| PTHR21243,P ⁻ | | 0 | 0 | 0 GO:0006351,(| AT4G40050.1 0 |
| PTHR34210,P ⁻ | | 0 | 0 | 0 | 0 AT3G62330.1 0 |
| PTHR11132,P ⁻ | KOG1444 | | 0 K15356 | | 0 AT2G13650.1 GONST1 |
| PTHR21243,P ⁻ | | 0 | 0 | 0 GO:0006351,(| AT4G40050.1 0 |
| PTHR10015,P ⁻ | | 0 | 0 K09419 | GO:0043565,(| AT1G46264.1 AT-HSFB4,HSF |
| PTHR10825,P ⁻ | | 0 6.3.2.19 | K10695 | GO:0046872 | AT5G44280.1 ATRING1A,RIM |
| PTHR22572,P ⁻ | KOG1322 | 2.7.7.27 | | 0 GO:0016779,(| AT1G27680.1 APL2 |
| PTHR22572,P ⁻ | KOG1322 | 2.7.7.27 | | 0 GO:0016779,(| AT1G27680.1 APL2 |
| PTHR22572,P ⁻ | KOG1322 | 2.7.7.27 | | 0 GO:0016779,(| AT1G27680.1 APL2 |
| PTHR22572,P ⁻ | KOG1322 | 2.7.7.27 | | 0 GO:0016779,(| AT1G27680.1 APL2 |
| PTHR23115,P ⁻ | | 0 3.6.5.3 | K12852 | GO:0005525 | AT1G06220.1 CLO,GFA1,ME |
| PTHR11654,P ⁻ | | 0 | 0 | 0 GO:0016020,(| AT1G32450.1 NRT1.5 |
| PTHR30540,P ⁻ | | 0 | 0 K03549 | GO:0071805,(| AT5G14880.1 0 |
| PTHR13779,P ⁻ | | 0 3.6.1.3 | K07478 | GO:0005524 | AT1G24290.1 0 |
| PTHR12741,P ⁻ | | 0 2.4.1.34 | K11000 | GO:0003843 | AT2G31960.2 ATGSL03,ATG: |
| PTHR15245,P ⁻ | KOG1895 | | 0 | 0 | 0 AT5G01400.1 ESP4 |
| PTHR15245,P ⁻ | KOG1895 | | 0 | 0 | 0 AT5G01400.1 ESP4 |
| PTHR15245,P ⁻ | KOG1895 | | 0 | 0 | 0 AT5G01400.1 ESP4 |
| PTHR10015,P ⁻ | | 0 | 0 K09419 | GO:0043565,(| AT1G46264.1 AT-HSFB4,HSF |
| PTHR10825,P ⁻ | | 0 6.3.2.19 | K10695 | GO:0046872 | AT5G44280.1 ATRING1A,RIM |
| PTHR22572,P ⁻ | KOG1322 | 2.7.7.27 | | 0 GO:0016779,(| AT1G27680.1 APL2 |
| PTHR22572,P ⁻ | KOG1322 | 2.7.7.27 | | 0 GO:0016779,(| AT1G27680.1 APL2 |
| PTHR22572,P ⁻ | KOG1322 | 2.7.7.27 | | 0 GO:0016779,(| AT1G27680.1 APL2 |
| PTHR22572,P ⁻ | KOG1322 | 2.7.7.27 | | 0 GO:0016779,(| AT1G27680.1 APL2 |
| PTHR23115,P ⁻ | | 0 3.6.5.3 | K12852 | GO:0005525 | AT1G06220.1 CLO,GFA1,ME |
| PTHR11654,P ⁻ | | 0 | 0 | 0 GO:0016020,(| AT1G32450.1 NRT1.5 |
| PTHR30540,P ⁻ | | 0 | 0 K03549 | GO:0071805,(| AT5G14880.1 0 |
| PTHR13779,P ⁻ | | 0 3.6.1.3 | K07478 | GO:0005524 | AT1G24290.1 0 |
| PTHR12741,P ⁻ | | 0 2.4.1.34 | K11000 | GO:0003843 | AT2G31960.2 ATGSL03,ATG: |
| PTHR15245,P ⁻ | KOG1895 | | 0 | 0 | 0 AT5G01400.1 ESP4 |

| | | | | | | | | | |
|----|--------------------------|---------|-----------|-----------|--------|--------------|-------------|---------------|---|
| 1 | | | | | | | | | |
| 2 | | | | | | | | | |
| 3 | PTHR15245,P ⁻ | KOG1895 | 0 | 0 | 0 | AT5G01400.1 | ESP4 | | |
| 4 | PTHR15245,P ⁻ | KOG1895 | 0 | 0 | 0 | AT5G01400.1 | ESP4 | | |
| 5 | PTHR31279,P ⁻ | | 0 | 0 | 0 | AT4G08950.1 | EXO | | |
| 6 | PTHR13271,P ⁻ | | 0 | 2.1.1.127 | 0 | GO:0005515 | AT4G20130.1 | PTAC14 | |
| 7 | PTHR31953,P ⁻ | | 0 | 3.2.1.26 | K01193 | GO:0004575,(| AT1G12240.1 | ATBETAFRUCT | |
| 8 | PTHR11662,P ⁻ | KOG2532 | 0 | | 0 | GO:0055085,(| AT4G00370.1 | ANTR2,PHT4;4 | |
| 9 | PTHR11662,P ⁻ | KOG2532 | 0 | | 0 | GO:0055085,(| AT4G00370.1 | ANTR2,PHT4;4 | |
| 10 | PTHR11662,P ⁻ | KOG2532 | 0 | | 0 | GO:0055085,(| AT4G00370.1 | ANTR2,PHT4;4 | |
| 11 | PTHR13710,P ⁻ | KOG0352 | 3.6.4.12 | K10901 | 0 | GO:0005524,(| AT4G35740.1 | ATRECCQ3,Recl | |
| 12 | PTHR13710,P ⁻ | KOG0352 | 3.6.4.12 | K10901 | 0 | GO:0005524,(| AT4G35740.1 | ATRECCQ3,Recl | |
| 13 | PTHR32494,P ⁻ | | 0 | 3.5.3.9 | 0 | GO:0016787,(| AT4G20070.1 | AAH,ATAAH | |
| 14 | PTHR32494,P ⁻ | | 0 | 3.5.3.9 | 0 | GO:0016787,(| AT4G20070.1 | AAH,ATAAH | |
| 15 | PTHR32494,P ⁻ | | 0 | 3.5.3.9 | 0 | GO:0016787,(| AT4G20070.1 | AAH,ATAAH | |
| 16 | PTHR32494,P ⁻ | | 0 | 3.5.3.9 | 0 | GO:0016787,(| AT4G20070.1 | AAH,ATAAH | |
| 17 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 18 | PTHR13242 | KOG3677 | 0 | K15029 | 0 | GO:0005852,(| AT5G25754.1 | | 0 |
| 19 | PTHR21717,P ⁻ | | 0 | 0 | 0 | 0 | AT1G09710.2 | | 0 |
| 20 | PTHR16193 | KOG1128 | 0 | 0 | 0 | 0 | AT5G17270.1 | | 0 |
| 21 | PTHR23318,P ⁻ | KOG2175 | 0 | K17491 | 0 | 0 | AT3G06670.1 | | 0 |
| 22 | PTHR31279,P ⁻ | | 0 | 0 | 0 | 0 | AT4G08950.1 | EXO | |
| 23 | PTHR13271,P ⁻ | | 0 | 2.1.1.127 | 0 | GO:0005515 | AT4G20130.1 | PTAC14 | |
| 24 | PTHR31953,P ⁻ | | 0 | 3.2.1.26 | K01193 | GO:0004575,(| AT1G12240.1 | ATBETAFRUCT | |
| 25 | PTHR11662,P ⁻ | KOG2532 | 0 | | 0 | GO:0055085,(| AT4G00370.1 | ANTR2,PHT4;4 | |
| 26 | PTHR11662,P ⁻ | KOG2532 | 0 | | 0 | GO:0055085,(| AT4G00370.1 | ANTR2,PHT4;4 | |
| 27 | PTHR11662,P ⁻ | KOG2532 | 0 | | 0 | GO:0055085,(| AT4G00370.1 | ANTR2,PHT4;4 | |
| 28 | PTHR13710,P ⁻ | KOG0352 | 3.6.4.12 | K10901 | 0 | GO:0005524,(| AT4G35740.1 | ATRECCQ3,Recl | |
| 29 | PTHR13710,P ⁻ | KOG0352 | 3.6.4.12 | K10901 | 0 | GO:0005524,(| AT4G35740.1 | ATRECCQ3,Recl | |
| 30 | PTHR32494,P ⁻ | | 0 | 3.5.3.9 | 0 | GO:0016787,(| AT4G20070.1 | AAH,ATAAH | |
| 31 | PTHR32494,P ⁻ | | 0 | 3.5.3.9 | 0 | GO:0016787,(| AT4G20070.1 | AAH,ATAAH | |
| 32 | PTHR32494,P ⁻ | | 0 | 3.5.3.9 | 0 | GO:0016787,(| AT4G20070.1 | AAH,ATAAH | |
| 33 | PTHR32494,P ⁻ | | 0 | 3.5.3.9 | 0 | GO:0016787,(| AT4G20070.1 | AAH,ATAAH | |
| 34 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 35 | PTHR13242 | KOG3677 | 0 | K15029 | 0 | GO:0005852,(| AT5G25754.1 | | 0 |
| 36 | PTHR21717,P ⁻ | | 0 | 0 | 0 | 0 | AT1G09710.2 | | 0 |
| 37 | PTHR16193 | KOG1128 | 0 | 0 | 0 | 0 | AT5G17270.1 | | 0 |
| 38 | PTHR23318,P ⁻ | KOG2175 | 0 | K17491 | 0 | 0 | AT3G06670.1 | | 0 |
| 39 | PTHR31279,P ⁻ | | 0 | 0 | 0 | 0 | AT4G08950.1 | EXO | |
| 40 | PTHR13271,P ⁻ | | 0 | 2.1.1.127 | 0 | GO:0005515 | AT4G20130.1 | PTAC14 | |
| 41 | PTHR31953,P ⁻ | | 0 | 3.2.1.26 | K01193 | GO:0004575,(| AT1G12240.1 | ATBETAFRUCT | |
| 42 | PTHR11662,P ⁻ | KOG2532 | 0 | | 0 | GO:0055085,(| AT4G00370.1 | ANTR2,PHT4;4 | |
| 43 | PTHR11662,P ⁻ | KOG2532 | 0 | | 0 | GO:0055085,(| AT4G00370.1 | ANTR2,PHT4;4 | |
| 44 | PTHR11662,P ⁻ | KOG2532 | 0 | | 0 | GO:0055085,(| AT4G00370.1 | ANTR2,PHT4;4 | |
| 45 | PTHR13710,P ⁻ | KOG0352 | 3.6.4.12 | K10901 | 0 | GO:0005524,(| AT4G35740.1 | ATRECCQ3,Recl | |
| 46 | PTHR13710,P ⁻ | KOG0352 | 3.6.4.12 | K10901 | 0 | GO:0005524,(| AT4G35740.1 | ATRECCQ3,Recl | |
| 47 | PTHR32494,P ⁻ | | 0 | 3.5.3.9 | 0 | GO:0016787,(| AT4G20070.1 | AAH,ATAAH | |
| 48 | PTHR32494,P ⁻ | | 0 | 3.5.3.9 | 0 | GO:0016787,(| AT4G20070.1 | AAH,ATAAH | |
| 49 | PTHR32494,P ⁻ | | 0 | 3.5.3.9 | 0 | GO:0016787,(| AT4G20070.1 | AAH,ATAAH | |
| 50 | PTHR32494,P ⁻ | | 0 | 3.5.3.9 | 0 | GO:0016787,(| AT4G20070.1 | AAH,ATAAH | |
| 51 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 52 | PTHR13242 | KOG3677 | 0 | K15029 | 0 | GO:0005852,(| AT5G25754.1 | | 0 |
| 53 | PTHR21717,P ⁻ | | 0 | 0 | 0 | 0 | AT1G09710.2 | | 0 |
| 54 | PTHR16193 | KOG1128 | 0 | 0 | 0 | 0 | AT5G17270.1 | | 0 |
| 55 | PTHR23318,P ⁻ | KOG2175 | 0 | K17491 | 0 | 0 | AT3G06670.1 | | 0 |
| 56 | PTHR11079,P ⁻ | KOG1919 | 5.4.99.24 | | 0 | GO:0009982,(| AT4G21770.1 | | 0 |
| 57 | PTHR17204,P ⁻ | | 0 | 0 | 0 | 0 | AT3G04350.1 | | 0 |
| 58 | PTHR17204,P ⁻ | | 0 | 0 | 0 | 0 | AT3G04350.1 | | 0 |
| 59 | PTHR24015,P ⁻ | | 0 | 0 | 0 | 0 | AT2G21090.1 | | 0 |
| 60 | PTHR10641,P ⁻ | | 0 | 0 | 0 | 0 | AT1G66370.1 | AtMYB113,M | |
| 61 | PTHR24015,P ⁻ | | 0 | 0 | 0 | 0 | AT3G50420.1 | | 0 |
| 62 | PTHR24015,P ⁻ | | 0 | 0 | 0 | 0 | AT1G25360.1 | | 0 |

| | | | | | |
|----|----------------------------------|------------|----------|------------------------------------|---|
| 1 | | | | | |
| 2 | | | | | |
| 3 | PTHR18934,P ⁻ | 0 3.6.4.13 | | 0 GO:0005524,(AT3G26560.1 | 0 |
| 4 | PTHR10758,P ⁻ | 0 | 0 K03033 | GO:0005515,(AT1G20200.1 EMB2719,HA | |
| 5 | PTHR37613 | 0 | 0 | 0 0 0 | 0 |
| 6 | | | | | |
| 7 | PTHR27008,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT2G26730.1 | 0 |
| 8 | | | | | |
| 9 | PTHR11079,P ⁻ KOG1919 | 5.4.99.24 | | 0 GO:0009982,(AT4G21770.1 | 0 |
| 10 | PTHR17204,P ⁻ | 0 | 0 | 0 0 AT3G04350.1 | 0 |
| 11 | PTHR17204,P ⁻ | 0 | 0 | 0 0 AT3G04350.1 | 0 |
| 12 | PTHR24015,P ⁻ | 0 | 0 | 0 0 AT2G21090.1 | 0 |
| 13 | | | | | |
| 14 | PTHR10641,P ⁻ | 0 | 0 | 0 0 AT1G66370.1 AtMYB113,M | |
| 15 | PTHR24015,P ⁻ | 0 | 0 | 0 0 AT3G50420.1 | 0 |
| 16 | PTHR24015,P ⁻ | 0 | 0 | 0 0 AT1G25360.1 | 0 |
| 17 | | | | | |
| 18 | PTHR18934,P ⁻ | 0 3.6.4.13 | | 0 GO:0005524,(AT3G26560.1 | 0 |
| 19 | PTHR10758,P ⁻ | 0 | 0 K03033 | GO:0005515,(AT1G20200.1 EMB2719,HA | |
| 20 | PTHR37613 | 0 | 0 | 0 0 0 | 0 |
| 21 | | | | | |
| 22 | PTHR27008,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0005515,(AT2G26730.1 | 0 |
| 23 | PTHR34210,P ⁻ | 0 | 0 | 0 0 AT3G62330.1 | 0 |
| 24 | PTHR34455,P ⁻ | 0 | 0 | 0 GO:0016020,(AT2G06520.1 PSBX | |
| 25 | | | | | |
| 26 | PTHR23257,P ⁻ KOG0192 | 2.7.11.1 | | 0 GO:0006468,(AT4G24480.1 | 0 |
| 27 | PTHR12411,P ⁻ KOG1543 | 3.4.22.33 | | 0 GO:0008234,(AT5G45890.1 SAG12 | |
| 28 | PTHR12411,P ⁻ KOG1543 | 3.4.22.33 | | 0 GO:0008234,(AT5G45890.1 SAG12 | |
| 29 | PTHR12411,P ⁻ KOG1543 | 3.4.22.33 | | 0 GO:0008234,(AT5G45890.1 SAG12 | |
| 30 | PTHR12411,P ⁻ KOG1543 | 3.4.22.33 | | 0 GO:0008234,(AT5G45890.1 SAG12 | |
| 31 | PTHR12411,P ⁻ KOG1543 | 3.4.22.33 | | 0 GO:0008234,(AT5G45890.1 SAG12 | |
| 32 | PTHR12411,P ⁻ KOG1543 | 3.4.22.33 | | 0 GO:0008234,(AT5G45890.1 SAG12 | |
| 33 | | | | | |
| 34 | PTHR14222,P ⁻ | 0 | 0 K06677 | GO:0007076 AT3G57060.2 | 0 |
| 35 | PTHR35505,P ⁻ | 0 | 0 | 0 0 AT5G11780.1 | 0 |
| 36 | PTHR19302,P ⁻ | 0 | 0 K16569 | GO:0005815,(AT5G17410.2 | 0 |
| 37 | PTHR19302,P ⁻ | 0 | 0 K16569 | GO:0005815,(AT5G17410.2 | 0 |
| 38 | PTHR31343,P ⁻ | 0 | 0 | 0 0 AT4G03420.1 | 0 |
| 39 | PTHR34936,P ⁻ | 0 | 0 | 0 0 AT1G20460.1 | 0 |
| 40 | PTHR31087,P ⁻ | 0 | 0 | 0 0 AT2G05910.1 | 0 |
| 41 | | | | | |
| 42 | PTHR21319,P ⁻ KOG1940 | 6.3.2.19 | K10144 | GO:0046872,(AT5G18650.1 | 0 |
| 43 | PTHR17204,P ⁻ | 0 | 0 | 0 0 AT5G43950.1 | 0 |
| 44 | PTHR27003,P ⁻ KOG1187 | 2.7.11.1 | | 0 GO:0006468,(AT5G28680.1 ANX2 | |
| 45 | PTHR27000,P ⁻ KOG1187 | 2.7.10.1 | | 0 GO:0005515,(AT1G34420.1 | 0 |
| 46 | | | | | |
| 47 | 0 | 0 | 0 | 0 0 0 | 0 |
| 48 | | | | | |
| 49 | PTHR31189,P ⁻ | 0 | 0 | 0 GO:0045735 AT2G18540.1 | 0 |
| 50 | PTHR24093,P ⁻ | 0 3.6.3.6 | K01535 | GO:0046872,(AT1G80660.1 AHA9,HA9 | |
| 51 | PTHR24015,P ⁻ | 0 | 0 | 0 0 AT5G66520.1 | 0 |
| 52 | PTHR34210,P ⁻ | 0 | 0 | 0 0 AT3G62330.1 | 0 |
| 53 | PTHR34455,P ⁻ | 0 | 0 | 0 GO:0016020,(AT2G06520.1 PSBX | |
| 54 | | | | | |
| 55 | PTHR23257,P ⁻ KOG0192 | 2.7.11.1 | | 0 GO:0006468,(AT4G24480.1 | 0 |
| 56 | PTHR12411,P ⁻ KOG1543 | 3.4.22.33 | | 0 GO:0008234,(AT5G45890.1 SAG12 | |
| 57 | PTHR12411,P ⁻ KOG1543 | 3.4.22.33 | | 0 GO:0008234,(AT5G45890.1 SAG12 | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | | |
|----|----------------------------------|-----------|----------|----------------------------------|-------------------------------|---|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | PTHR12411,P ⁻ KOG1543 | 3.4.22.33 | | 0 | GO:0008234,(AT5G45890.1 SAG12 | |
| 4 | PTHR12411,P ⁻ KOG1543 | 3.4.22.33 | | 0 | GO:0008234,(AT5G45890.1 SAG12 | |
| 5 | PTHR12411,P ⁻ KOG1543 | 3.4.22.33 | | 0 | GO:0008234,(AT5G45890.1 SAG12 | |
| 6 | PTHR12411,P ⁻ KOG1543 | 3.4.22.33 | | 0 | GO:0008234,(AT5G45890.1 SAG12 | |
| 7 | PTHR14222,P ⁻ | 0 | 0 K06677 | GO:0007076 | AT3G57060.2 | 0 |
| 8 | PTHR35505,P ⁻ | 0 | 0 | 0 | AT5G11780.1 | 0 |
| 9 | PTHR19302,P ⁻ | 0 | 0 K16569 | GO:0005815,(AT5G17410.2 | | 0 |
| 10 | PTHR19302,P ⁻ | 0 | 0 K16569 | GO:0005815,(AT5G17410.2 | | 0 |
| 11 | PTHR19302,P ⁻ | 0 | 0 K16569 | GO:0005815,(AT5G17410.2 | | 0 |
| 12 | PTHR31343,P ⁻ | 0 | 0 | 0 | AT4G03420.1 | 0 |
| 13 | PTHR34936,P ⁻ | 0 | 0 | 0 | AT1G20460.1 | 0 |
| 14 | PTHR34936,P ⁻ | 0 | 0 | 0 | AT1G20460.1 | 0 |
| 15 | PTHR31087,P ⁻ | 0 | 0 | 0 | AT2G05910.1 | 0 |
| 16 | PTHR31087,P ⁻ | 0 | 0 | 0 | AT2G05910.1 | 0 |
| 17 | PTHR21319,P ⁻ KOG1940 | 6.3.2.19 | K10144 | GO:0046872,(AT5G18650.1 | | 0 |
| 18 | PTHR17204,P ⁻ | 0 | 0 | 0 | AT5G43950.1 | 0 |
| 19 | PTHR27003,P ⁻ KOG1187 | 2.7.11.1 | | 0 | GO:0006468,(AT5G28680.1 ANX2 | |
| 20 | PTHR27000,P ⁻ KOG1187 | 2.7.10.1 | | 0 | GO:0005515,(AT1G34420.1 | 0 |
| 21 | PTHR27000,P ⁻ KOG1187 | 2.7.10.1 | | 0 | GO:0005515,(AT1G34420.1 | 0 |
| 22 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | PTHR31189,P ⁻ | 0 | 0 | 0 | GO:0045735 AT2G18540.1 | 0 |
| 24 | PTHR24093,P ⁻ | 0 3.6.3.6 | K01535 | GO:0046872,(AT1G80660.1 AHA9,HA9 | | |
| 25 | PTHR24093,P ⁻ | 0 3.6.3.6 | K01535 | GO:0046872,(AT1G80660.1 AHA9,HA9 | | |
| 26 | PTHR24015,P ⁻ | 0 | 0 | 0 | AT5G66520.1 | 0 |
| 27 | | | | | | |
| 28 | | | | | | |
| 29 | | | | | | |
| 30 | | | | | | |
| 31 | | | | | | |
| 32 | | | | | | |
| 33 | | | | | | |
| 34 | | | | | | |
| 35 | | | | | | |
| 36 | | | | | | |
| 37 | | | | | | |
| 38 | | | | | | |
| 39 | | | | | | |
| 40 | | | | | | |
| 41 | | | | | | |
| 42 | | | | | | |
| 43 | | | | | | |
| 44 | | | | | | |
| 45 | | | | | | |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| arabi-defline | ID | Annot_defline | IDENTIFIER |
|---|---------------------------|---------------|----------------|
| Zn-dependent exopeptidases superfamily prot | Phvul.007G10PTHR28570: | SI | Phvul.007G10 |
| Zn-dependent exopeptidases superfamily prot | Phvul.007G10PTHR28570: | SI | Phvul.007G10 |
| Sec14p-like phosphatidylinositol transfer famil | Phvul.009G00PTHR23324: | SI | Phvul.009G00 |
| Sec14p-like phosphatidylinositol transfer famil | Phvul.009G00PTHR23324: | SI | Phvul.009G00 |
| Sec14p-like phosphatidylinositol transfer famil | Phvul.009G00PTHR23324: | SI | Phvul.009G00 |
| double-stranded RNA binding protein-related , | Phvul.002G19PTHR21404 - I | | Phvul.002G19 |
| Sec14p-like phosphatidylinositol transfer famil | Phvul.009G00PTHR23324: | SI | Phvul.009G00 |
| Sec14p-like phosphatidylinositol transfer famil | Phvul.009G00PTHR23324: | SI | Phvul.009G00 |
| Sec14p-like phosphatidylinositol transfer famil | Phvul.009G00PTHR23324: | SI | Phvul.009G00 |
| double-stranded RNA binding protein-related , | Phvul.002G19PTHR21404 - I | | Phvul.002G19 |
| Zinc knuckle (CCHC-type) family protein | | 0 | 0 Phvul.001G21 |
| golgi nucleotide sugar transporter 1 | Phvul.009G15K15356 - GDP | | Phvul.009G15 |
| Protein of unknown function (DUF3550/UPF0€ | Phvul.002G26PF12070 - Pro | | Phvul.002G26 |
| Zinc knuckle (CCHC-type) family protein | | 0 | 0 Phvul.001G21 |
| golgi nucleotide sugar transporter 1 | Phvul.009G15K15356 - GDP | | Phvul.009G15 |
| Protein of unknown function (DUF3550/UPF0€ | Phvul.002G26PF12070 - Pro | | Phvul.002G26 |
| heat shock transcription factor B4 | Phvul.001G02PTHR10015: | SI | Phvul.001G02 |
| RING 1A | Phvul.008G12PTHR10825: | SI | Phvul.008G12 |
| ADPGLC-PPase large subunit | Phvul.001G21PTHR22572//I | | Phvul.001G21 |
| ADPGLC-PPase large subunit | Phvul.001G21PTHR22572//I | | Phvul.001G21 |
| ADPGLC-PPase large subunit | Phvul.001G21PTHR22572//I | | Phvul.001G21 |
| ADPGLC-PPase large subunit | Phvul.001G21PTHR22572//I | | Phvul.001G21 |
| Ribosomal protein S5/Elongation factor G/III/v | Phvul.003G17K12852 - 116 | | Phvul.003G17 |
| nitrate transporter 1.5 | Phvul.008G04PTHR11654: | SI | Phvul.008G04 |
| Potassium transporter family protein | Phvul.004G01PTHR30540: | SI | Phvul.004G01 |
| AAA-type ATPase family protein | Phvul.008G29K07478 - puta | | Phvul.008G29 |
| glucan synthase-like 3 | Phvul.005G04PTHR12741: | SI | Phvul.005G04 |
| HEAT repeat-containing protein | Phvul.010G00PTHR15245//I | | Phvul.010G00 |
| HEAT repeat-containing protein | Phvul.010G00PTHR15245//I | | Phvul.010G00 |
| HEAT repeat-containing protein | Phvul.010G00PTHR15245//I | | Phvul.010G00 |
| heat shock transcription factor B4 | Phvul.001G02PTHR10015: | SI | Phvul.001G02 |
| RING 1A | Phvul.008G12PTHR10825: | SI | Phvul.008G12 |
| ADPGLC-PPase large subunit | Phvul.001G21PTHR22572//I | | Phvul.001G21 |
| ADPGLC-PPase large subunit | Phvul.001G21PTHR22572//I | | Phvul.001G21 |
| ADPGLC-PPase large subunit | Phvul.001G21PTHR22572//I | | Phvul.001G21 |
| ADPGLC-PPase large subunit | Phvul.001G21PTHR22572//I | | Phvul.001G21 |
| Ribosomal protein S5/Elongation factor G/III/v | Phvul.003G17K12852 - 116 | | Phvul.003G17 |
| nitrate transporter 1.5 | Phvul.008G04PTHR11654: | SI | Phvul.008G04 |
| Potassium transporter family protein | Phvul.004G01PTHR30540: | SI | Phvul.004G01 |
| AAA-type ATPase family protein | Phvul.008G29K07478 - puta | | Phvul.008G29 |
| glucan synthase-like 3 | Phvul.005G04PTHR12741: | SI | Phvul.005G04 |
| HEAT repeat-containing protein | Phvul.010G00PTHR15245//I | | Phvul.010G00 |

| | | | |
|----|--|--------------------------------------|--------------|
| 1 | | | |
| 2 | | | |
| 3 | HEAT repeat-containing protein | Phvul.010G00PTHR15245//IPhvul.010G00 | |
| 4 | HEAT repeat-containing protein | Phvul.010G00PTHR15245//IPhvul.010G00 | |
| 5 | Phosphate-responsive 1 family protein | Phvul.009G03PTHR31279:SI | Phvul.009G03 |
| 6 | plastid transcriptionally active 14 | Phvul.009G24PTHR13271:SI | Phvul.009G24 |
| 7 | plastid transcriptionally active 14 | Phvul.009G24PTHR13271:SI | Phvul.009G24 |
| 8 | Glycosyl hydrolases family 32 protein | Phvul.002G06PTHR31953:SI | Phvul.002G06 |
| 9 | Glycosyl hydrolases family 32 protein | Phvul.002G06PTHR31953:SI | Phvul.002G06 |
| 10 | Major facilitator superfamily protein | Phvul.008G06PTHR11662:SI | Phvul.008G06 |
| 11 | Major facilitator superfamily protein | Phvul.008G06PTHR11662:SI | Phvul.008G06 |
| 12 | Major facilitator superfamily protein | Phvul.008G06PTHR11662:SI | Phvul.008G06 |
| 13 | Major facilitator superfamily protein | Phvul.008G06PTHR11662:SI | Phvul.008G06 |
| 14 | DEAD/DEAH box RNA helicase family protein | Phvul.009G22PTHR13710:SI | Phvul.009G22 |
| 15 | DEAD/DEAH box RNA helicase family protein | Phvul.009G22PTHR13710:SI | Phvul.009G22 |
| 16 | DEAD/DEAH box RNA helicase family protein | Phvul.009G22PTHR13710:SI | Phvul.009G22 |
| 17 | allantoate amidohydrolase | Phvul.009G24K02083 - allan | Phvul.009G24 |
| 18 | allantoate amidohydrolase | Phvul.009G24K02083 - allan | Phvul.009G24 |
| 19 | allantoate amidohydrolase | Phvul.009G24K02083 - allan | Phvul.009G24 |
| 20 | allantoate amidohydrolase | Phvul.009G24K02083 - allan | Phvul.009G24 |
| 21 | allantoate amidohydrolase | Phvul.009G24K02083 - allan | Phvul.009G24 |
| 22 | | 0 | 0 |
| 23 | RNA polymerase I-associated factor PAF67 | Phvul.009G10K15029 - tran: | Phvul.009G10 |
| 24 | Homeodomain-like superfamily protein | Phvul.009G03PTHR21717:SI | Phvul.009G03 |
| 25 | Homeodomain-like superfamily protein | Phvul.009G03PTHR21717:SI | Phvul.009G03 |
| 26 | Protein prenyltransferase superfamily protei | Phvul.009G19KOG1128 - Un | Phvul.009G19 |
| 27 | binding | Phvul.003G11K17491 - prot: | Phvul.003G11 |
| 28 | Phosphate-responsive 1 family protein | Phvul.009G03PTHR31279:SI | Phvul.009G03 |
| 29 | Phosphate-responsive 1 family protein | Phvul.009G03PTHR31279:SI | Phvul.009G03 |
| 30 | plastid transcriptionally active 14 | Phvul.009G24PTHR13271:SI | Phvul.009G24 |
| 31 | plastid transcriptionally active 14 | Phvul.009G24PTHR13271:SI | Phvul.009G24 |
| 32 | Glycosyl hydrolases family 32 protein | Phvul.002G06PTHR31953:SI | Phvul.002G06 |
| 33 | Glycosyl hydrolases family 32 protein | Phvul.002G06PTHR31953:SI | Phvul.002G06 |
| 34 | Major facilitator superfamily protein | Phvul.008G06PTHR11662:SI | Phvul.008G06 |
| 35 | Major facilitator superfamily protein | Phvul.008G06PTHR11662:SI | Phvul.008G06 |
| 36 | Major facilitator superfamily protein | Phvul.008G06PTHR11662:SI | Phvul.008G06 |
| 37 | Major facilitator superfamily protein | Phvul.008G06PTHR11662:SI | Phvul.008G06 |
| 38 | DEAD/DEAH box RNA helicase family protein | Phvul.009G22PTHR13710:SI | Phvul.009G22 |
| 39 | DEAD/DEAH box RNA helicase family protein | Phvul.009G22PTHR13710:SI | Phvul.009G22 |
| 40 | DEAD/DEAH box RNA helicase family protein | Phvul.009G22PTHR13710:SI | Phvul.009G22 |
| 41 | allantoate amidohydrolase | Phvul.009G24K02083 - allan | Phvul.009G24 |
| 42 | allantoate amidohydrolase | Phvul.009G24K02083 - allan | Phvul.009G24 |
| 43 | allantoate amidohydrolase | Phvul.009G24K02083 - allan | Phvul.009G24 |
| 44 | allantoate amidohydrolase | Phvul.009G24K02083 - allan | Phvul.009G24 |
| 45 | | 0 | 0 |
| 46 | RNA polymerase I-associated factor PAF67 | Phvul.009G10K15029 - tran: | Phvul.009G10 |
| 47 | Homeodomain-like superfamily protein | Phvul.009G03PTHR21717:SI | Phvul.009G03 |
| 48 | Homeodomain-like superfamily protein | Phvul.009G03PTHR21717:SI | Phvul.009G03 |
| 49 | Protein prenyltransferase superfamily protei | Phvul.009G19KOG1128 - Un | Phvul.009G19 |
| 50 | binding | Phvul.003G11K17491 - prot: | Phvul.003G11 |
| 51 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SI | Phvul.006G15 |
| 52 | Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SI | Phvul.006G15 |
| 53 | Plant protein of unknown function (DUF946) | Phvul.006G10PTHR17204//IPhvul.006G10 | |
| 54 | Plant protein of unknown function (DUF946) | Phvul.006G10PTHR17204//IPhvul.006G10 | |
| 55 | Pentatricopeptide repeat (PPR-like) superfamil | Phvul.011G03PF01535//PF1 | Phvul.011G03 |
| 56 | myb domain protein 113 | Phvul.008G03PTHR10641:SI | Phvul.008G03 |
| 57 | myb domain protein 113 | Phvul.008G03PTHR10641:SI | Phvul.008G03 |
| 58 | Pentatricopeptide repeat (PPR) superfamily pr | Phvul.002G02PF01535//PF1 | Phvul.002G02 |
| 59 | Pentatricopeptide repeat (PPR) superfamily pr | Phvul.L00164PF01535//PF1 | Phvul.L00164 |
| 60 | Pentatricopeptide repeat (PPR) superfamily pr | Phvul.L00164PF01535//PF1 | Phvul.L00164 |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | |
|---|------------------------------|----------------|
| ATP-dependent RNA helicase, putative | Phvul.001G26PTHR18934//IPhvu | l.001G26 |
| PAM domain (PCI/PINT associated module) prc | Phvul.009G01K03033 - 26S | lPhvul.009G01 |
| | 0 | 0 Phvul.009G07 |
| Leucine-rich repeat protein kinase family prote | Phvul.003G15PF00069//PFC | Phvul.003G15 |
| Pseudouridine synthase family protein | Phvul.006G15PTHR11079:SI | Phvul.006G15 |
| Plant protein of unknown function (DUF946) | Phvul.006G10PTHR17204//IPhvu | l.006G10 |
| Plant protein of unknown function (DUF946) | Phvul.006G10PTHR17204//IPhvu | l.006G10 |
| Pentatricopeptide repeat (PPR-like) superfamil | Phvul.011G03PF01535//PF1 | Phvul.011G03 |
| myb domain protein 113 | Phvul.008G03PTHR10641:SI | Phvul.008G03 |
| Pentatricopeptide repeat (PPR) superfamily pr | Phvul.002G02PF01535//PF1 | Phvul.002G02 |
| Pentatricopeptide repeat (PPR) superfamily pr | Phvul.L00164PF01535//PF1 | Phvul.L00164 |
| ATP-dependent RNA helicase, putative | Phvul.001G26PTHR18934//IPhvu | l.001G26 |
| PAM domain (PCI/PINT associated module) prc | Phvul.009G01K03033 - 26S | lPhvul.009G01 |
| | 0 | 0 Phvul.009G07 |
| Leucine-rich repeat protein kinase family prote | Phvul.003G15PF00069//PFC | Phvul.003G15 |
| Zinc knuckle (CCHC-type) family protein | 0 | 0 Phvul.001G21 |
| photosystem II subunit X | Phvul.009G22PTHR34455:SI | Phvul.009G22 |
| Protein kinase superfamily protein | Phvul.009G03PTHR23257:SI | Phvul.009G03 |
| senescence-associated gene 12 | Phvul.011G13PTHR12411:SI | Phvul.011G13 |
| senescence-associated gene 12 | Phvul.011G13PTHR12411:SI | Phvul.011G13 |
| senescence-associated gene 12 | Phvul.011G13PTHR12411:SI | Phvul.011G13 |
| senescence-associated gene 12 | Phvul.011G08PTHR12411//IPhvu | l.011G08 |
| senescence-associated gene 12 | Phvul.011G13PTHR12411:SI | Phvul.011G13 |
| binding | Phvul.007G24K06677 - conc | Phvul.007G24 |
| | 0 | 0 Phvul.004G17 |
| Spc97 / Spc98 family of spindle pole body (SBP | Phvul.010G03K16569 - gam | Phvul.010G03 |
| Spc97 / Spc98 family of spindle pole body (SBP | Phvul.010G03K16569 - gam | Phvul.010G03 |
| Protein of unknown function (DUF789) | Phvul.005G10PTHR31343:SI | Phvul.005G10 |
| | 0 | 0 Phvul.009G02 |
| Protein of unknown function (DUF567) | Phvul.009G22PTHR31087:SI | Phvul.009G22 |
| CHY-type/CTCHY-type/RING-type Zinc finger p | Phvul.006G16PTHR21319//IPhvu | l.006G16 |
| Plant protein of unknown function (DUF946) | Phvul.002G03PTHR17204//IPhvu | l.002G03 |
| Malectin/receptor-like protein kinase family pi | Phvul.007G18PTHR27003:SI | Phvul.007G18 |
| leucine-rich repeat transmembrane protein kir | Phvul.004G08PTHR27000:SI | Phvul.004G08 |
| | 0 | 0 Phvul.L00185 |
| RmlC-like cupins superfamily protein | Phvul.002G02PTHR31189:SI | Phvul.002G02 |
| H(+)-ATPase 9 | Phvul.005G18PTHR24093:SI | Phvul.005G18 |
| Tetratricopeptide repeat (TPR)-like superfamil | Phvul.004G15PF01535//PF1 | Phvul.004G15 |
| Zinc knuckle (CCHC-type) family protein | 0 | 0 Phvul.001G21 |
| photosystem II subunit X | Phvul.009G22PTHR34455:SI | Phvul.009G22 |
| Protein kinase superfamily protein | Phvul.009G03PTHR23257:SI | Phvul.009G03 |
| senescence-associated gene 12 | Phvul.011G13PTHR12411:SI | Phvul.011G13 |
| senescence-associated gene 12 | Phvul.011G13PTHR12411:SI | Phvul.011G13 |

1
2
3 senescence-associated gene 12 Phvul.011G13PTHR12411:SI Phvul.011G13
4 senescence-associated gene 12 Phvul.011G08PTHR12411//I Phvul.011G08
5 senescence-associated gene 12 Phvul.011G13PTHR12411:SI Phvul.011G13
6 binding Phvul.007G24K06677 - conc Phvul.007G24
7 0 0 0 Phvul.004G17
8
9 Spc97 / Spc98 family of spindle pole body (SBP Phvul.010G03K16569 - gam Phvul.010G03
10 Spc97 / Spc98 family of spindle pole body (SBP Phvul.010G03K16569 - gam Phvul.010G03
11 Protein of unknown function (DUF789) Phvul.005G10PTHR31343:SI Phvul.005G10
12 0 0 0 Phvul.009G02
13 Protein of unknown function (DUF567) Phvul.009G22PTHR31087:SI Phvul.009G22
14 CHY-type/CTCHY-type/RING-type Zinc finger p Phvul.006G16PTHR21319//I Phvul.006G16
15 Plant protein of unknown function (DUF946) Phvul.002G03PTHR17204//I Phvul.002G03
16 Malectin/receptor-like protein kinase family p Phvul.007G18PTHR27003:SI Phvul.007G18
17 leucine-rich repeat transmembrane protein kir Phvul.004G08PTHR27000:SI Phvul.004G08
18 0 0 0 Phvul.L00185
19 RmlC-like cupins superfamily protein Phvul.002G02PTHR31189:SI Phvul.002G02
20 H(+)-ATPase 9 Phvul.005G18PTHR24093:SI Phvul.005G18
21 Tetratricopeptide repeat (TPR)-like superfamil Phvul.004G15PF01535//PF1 Phvul.004G15
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| NAME | DESCRIPTION |
|------|-------------|
|------|-------------|

| | |
|----------------|---|
| Protein home | M18-class aspartyl aminopeptidase (DAP) (original description: pacid=37166631 tran |
| Protein home | M18-class aspartyl aminopeptidase (DAP) (original description: pacid=37166631 tran |
| not assigned.ε | (original description: pacid=37150821 transcript=Phvul.009G006000.3 locus=Phvul.C |
| not assigned.ε | (original description: pacid=37150821 transcript=Phvul.009G006000.3 locus=Phvul.C |
| not assigned.ε | (original description: pacid=37150821 transcript=Phvul.009G006000.3 locus=Phvul.C |
| RNA processir | miRNA/siRNA methyltransferase (HEN1) (original description: pacid=37175057 transi |
| not assigned.ε | (original description: pacid=37150821 transcript=Phvul.009G006000.3 locus=Phvul.C |
| not assigned.ε | (original description: pacid=37150821 transcript=Phvul.009G006000.3 locus=Phvul.C |
| not assigned.ε | (original description: pacid=37150821 transcript=Phvul.009G006000.3 locus=Phvul.C |
| RNA processir | miRNA/siRNA methyltransferase (HEN1) (original description: pacid=37175057 transi |
| not assigned.r | no hits & (original description: pacid=37169210 transcript=Phvul.001G214600.7 locu |
| Solute transp | nucleotide sugar transporter (GONST1 2 3 4) (original description: pacid=37151677 |
| not assigned.r | no hits & (original description: pacid=37174363 transcript=Phvul.002G261000.1 locu |
| not assigned.r | no hits & (original description: pacid=37169210 transcript=Phvul.001G214600.7 locu |
| Solute transp | nucleotide sugar transporter (GONST1 2 3 4) (original description: pacid=37151677 |
| not assigned.r | no hits & (original description: pacid=37174363 transcript=Phvul.002G261000.1 locu |
| RNA biosynth | transcription factor (HSF) (original description: pacid=37168548 transcript=Phvul.001 |
| Chromatin or | ε modification writer component RING1 of modification writer protein components (o |
| Carbohydrate | ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph |
| Carbohydrate | ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph |
| Carbohydrate | ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph |
| Carbohydrate | ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph |
| RNA processir | protein factor SNU114/U5-116kDa of U5 small nuclear ribonucleoprotein particle (sn |
| Solute transp | anion transporter (NRT1/PTR) (original description: pacid=37159373 transcript=Phvu |
| Solute transp | potassium cation transporter (HAK/KUP/KT) (original description: pacid=37163324 tr |
| not assigned.r | no hits & (original description: pacid=37160223 transcript=Phvul.008G290000.1 locu |
| not assigned.ε | (original description: pacid=37152506 transcript=Phvul.005G040800.1 locus=Phvul.C |
| RNA processir | component Symplekin/Pta1 of Cleavage and Polyadenylation Specificity Factor (CPSF |
| RNA processir | component Symplekin/Pta1 of Cleavage and Polyadenylation Specificity Factor (CPSF |
| RNA processir | component Symplekin/Pta1 of Cleavage and Polyadenylation Specificity Factor (CPSF |
| RNA biosynth | transcription factor (HSF) (original description: pacid=37168548 transcript=Phvul.001 |
| Chromatin or | ε modification writer component RING1 of modification writer protein components (o |
| Carbohydrate | ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph |
| Carbohydrate | ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph |
| Carbohydrate | ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph |
| Carbohydrate | ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph |
| RNA processir | protein factor SNU114/U5-116kDa of U5 small nuclear ribonucleoprotein particle (sn |
| Solute transp | anion transporter (NRT1/PTR) (original description: pacid=37159373 transcript=Phvu |
| Solute transp | potassium cation transporter (HAK/KUP/KT) (original description: pacid=37163324 tr |
| not assigned.r | no hits & (original description: pacid=37160223 transcript=Phvul.008G290000.1 locu |
| not assigned.ε | (original description: pacid=37152506 transcript=Phvul.005G040800.1 locus=Phvul.C |
| RNA processir | component Symplekin/Pta1 of Cleavage and Polyadenylation Specificity Factor (CPSF |

1
2
3 RNA processir component Symplekin/Pta1 of Cleavage and Polyadenylation Specificity Factor (CPSF
4 RNA processir component Symplekin/Pta1 of Cleavage and Polyadenylation Specificity Factor (CPSF
5 not assigned.ε (original description: pacid=37148991 transcript=Phvul.009G032100.1 locus=Phvul.C
6 RNA biosynth PAP7/TAC14 cofactor of plastid-encoded RNA polymerase (original description: pacid
7 Carbohydrate acid beta-fructofuranosidase (VIN) (original description: pacid=37175113 transcript=
8 Solute transp phosphate transporter (PHT4) (original description: pacid=37161312 transcript=Phvu
9 Solute transp phosphate transporter (PHT4) (original description: pacid=37161312 transcript=Phvu
10 Solute transp phosphate transporter (PHT4) (original description: pacid=37161312 transcript=Phvu
11 not assigned.ε (original description: pacid=37151468 transcript=Phvul.009G226500.2 locus=Phvul.C
12 not assigned.ε (original description: pacid=37151468 transcript=Phvul.009G226500.2 locus=Phvul.C
13 Nucleotide mεallantoate amidohydrolase (original description: pacid=37150600 transcript=Phvul.O
14 Nucleotide mεallantoate amidohydrolase (original description: pacid=37150600 transcript=Phvul.O
15 Nucleotide mεallantoate amidohydrolase (original description: pacid=37150600 transcript=Phvul.O
16 Nucleotide mεallantoate amidohydrolase (original description: pacid=37150600 transcript=Phvul.O
17 not assigned.r no hits & (original description: pacid=37177485 transcript=Phvul.002G133900.2 locu
18 Protein biosyr component eIF3I of eIF3 mRNA-to-PIC binding complex (original description: pacid=3
19 RNA biosynth transcription factor (MYB-related) (original description: pacid=37150497 transcript=F
20 not assigned.r no hits & (original description: pacid=37148905 transcript=Phvul.009G192300.1 locu
21 Protein modif regulatory component PP4R3 of PP4 phosphatase complex (original description: paci
22 not assigned.ε (original description: pacid=37148991 transcript=Phvul.009G032100.1 locus=Phvul.C
23 RNA biosynth PAP7/TAC14 cofactor of plastid-encoded RNA polymerase (original description: pacid
24 Carbohydrate acid beta-fructofuranosidase (VIN) (original description: pacid=37175113 transcript=
25 Solute transp phosphate transporter (PHT4) (original description: pacid=37161312 transcript=Phvu
26 Solute transp phosphate transporter (PHT4) (original description: pacid=37161312 transcript=Phvu
27 Solute transp phosphate transporter (PHT4) (original description: pacid=37161312 transcript=Phvu
28 not assigned.ε (original description: pacid=37151468 transcript=Phvul.009G226500.2 locus=Phvul.C
29 not assigned.ε (original description: pacid=37151468 transcript=Phvul.009G226500.2 locus=Phvul.C
30 Nucleotide mεallantoate amidohydrolase (original description: pacid=37150600 transcript=Phvul.O
31 Nucleotide mεallantoate amidohydrolase (original description: pacid=37150600 transcript=Phvul.O
32 Nucleotide mεallantoate amidohydrolase (original description: pacid=37150600 transcript=Phvul.O
33 not assigned.r no hits & (original description: pacid=37177485 transcript=Phvul.002G133900.2 locu
34 Protein biosyr component eIF3I of eIF3 mRNA-to-PIC binding complex (original description: pacid=3
35 RNA biosynth transcription factor (MYB-related) (original description: pacid=37150497 transcript=F
36 not assigned.r no hits & (original description: pacid=37148905 transcript=Phvul.009G192300.1 locu
37 Protein modif regulatory component PP4R3 of PP4 phosphatase complex (original description: paci
38 not assigned.ε (original description: pacid=37173420 transcript=Phvul.006G151200.1 locus=Phvul.C
39 not assigned.r no hits & (original description: pacid=37172154 transcript=Phvul.006G104300.2 locu
40 not assigned.r no hits & (original description: pacid=37172154 transcript=Phvul.006G104300.2 locu
41 not assigned.ε (original description: pacid=37156354 transcript=Phvul.011G033500.1 locus=Phvul.C
42 RNA biosynth transcription factor (MYB) (original description: pacid=37158898 transcript=Phvul.00
43 not assigned.ε (original description: pacid=37178778 transcript=Phvul.002G022400.1 locus=Phvul.C
44 not assigned.ε (original description: pacid=37174264 transcript=Phvul.L001644.1 locus=Phvul.L001
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3 not assigned.ã (original description: pacid=37168645 transcript=Phvul.001G264132.1 locus=Phvul.C
4 Protein home regulatory component RPN3 of 26S proteasome (original description: pacid=371502C
5 not assigned.r no hits & (original description: pacid=37151497 transcript=Phvul.009G073900.1 locu
6 Protein modif protein kinase (LRR-III) (original description: pacid=37146991 transcript=Phvul.003G:
7 not assigned.ã (original description: pacid=37173420 transcript=Phvul.006G151200.1 locus=Phvul.C
8 not assigned.r no hits & (original description: pacid=37172154 transcript=Phvul.006G104300.2 locu
9 not assigned.r no hits & (original description: pacid=37172154 transcript=Phvul.006G104300.2 locu
10 not assigned.ã (original description: pacid=37156354 transcript=Phvul.011G033500.1 locus=Phvul.C
11 RNA biosynthetranscription factor (MYB) (original description: pacid=37158898 transcript=Phvul.00
12 not assigned.ã (original description: pacid=37178778 transcript=Phvul.002G022400.1 locus=Phvul.C
13 not assigned.ã (original description: pacid=37174264 transcript=Phvul.L001644.1 locus=Phvul.L001
14 not assigned.ã (original description: pacid=37168645 transcript=Phvul.001G264132.1 locus=Phvul.C
15 Protein home regulatory component RPN3 of 26S proteasome (original description: pacid=371502C
16 not assigned.r no hits & (original description: pacid=37151497 transcript=Phvul.009G073900.1 locu
17 Protein modif protein kinase (LRR-III) (original description: pacid=37146991 transcript=Phvul.003G:
18 not assigned.r no hits & (original description: pacid=37169210 transcript=Phvul.001G214600.7 locu
19 Photosynthesicomponent PsbX of PS-II complex (original description: pacid=37148668 transcript=P
20 Protein modif protein kinase (MAP3K-RAF) (original description: pacid=37149156 transcript=Phvul.
21 Protein home protease (Papain) (original description: pacid=37156473 transcript=Phvul.011G1341C
22 Protein home protease (Papain) (original description: pacid=37155727 transcript=Phvul.011G1340C
23 Protein home protease (Papain) (original description: pacid=37154718 transcript=Phvul.011G1308C
24 Protein home protease (Papain) (original description: pacid=37156814 transcript=Phvul.011G0811C
25 Protein home protease (Papain) (original description: pacid=37157156 transcript=Phvul.011G1333C
26 Cell cycle orgã component CAP-D2A of condensin I complex (original description: pacid=37167459 t
27 not assigned.r no hits & (original description: pacid=37162297 transcript=Phvul.004G172000.1 locu
28 Cytoskeleton component GCP2 of gamma-Tubulin ring complex (gamma-TuRC) (original descriptio
29 Cytoskeleton component GCP2 of gamma-Tubulin ring complex (gamma-TuRC) (original descriptio
30 not assigned.r no hits & (original description: pacid=37153352 transcript=Phvul.005G105800.1 locu
31 not assigned.r no hits & (original description: pacid=37151943 transcript=Phvul.009G021200.1 locu
32 not assigned.ã (original description: pacid=37149394 transcript=Phvul.009G226800.1 locus=Phvul.C
33 not assigned.ã (original description: pacid=37171980 transcript=Phvul.006G162000.1 locus=Phvul.C
34 not assigned.r no hits & (original description: pacid=37175715 transcript=Phvul.002G038300.1 locu
35 Protein modif protein kinase (CrIRL1) (original description: pacid=37165831 transcript=Phvul.007C
36 Protein modif protein kinase (LRR-Xc) (original description: pacid=37163699 transcript=Phvul.004G
37 not assigned.r no hits & (original description: pacid=37152177 transcript=Phvul.L001859.1 locus=Pl
38 not assigned.ã (original description: pacid=37175319 transcript=Phvul.002G027900.2 locus=Phvul.C
39 Solute transpã P3A-type proton-translocating ATPase (AHA) (original description: pacid=37153023 t
40 not assigned.ã (original description: pacid=37163120 transcript=Phvul.004G153700.1 locus=Phvul.C
41 not assigned.r no hits & (original description: pacid=37169210 transcript=Phvul.001G214600.7 locu
42 Photosynthesicomponent PsbX of PS-II complex (original description: pacid=37148668 transcript=P
43 Protein modif protein kinase (MAP3K-RAF) (original description: pacid=37149156 transcript=Phvul.
44 Protein home protease (Papain) (original description: pacid=37156473 transcript=Phvul.011G1341C
45 Protein home protease (Papain) (original description: pacid=37155727 transcript=Phvul.011G1340C
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3 Protein homeoprotease (Papain) (original description: pacid=37154718 transcript=Phvul.011G1308
4 Protein homeoprotease (Papain) (original description: pacid=37156814 transcript=Phvul.011G0811
5 Protein homeoprotease (Papain) (original description: pacid=37157156 transcript=Phvul.011G1333
6 Cell cycle orga component CAP-D2A of condensin I complex (original description: pacid=37167459 t
7 not assigned.r no hits & (original description: pacid=37162297 transcript=Phvul.004G172000.1 locu
8 Cytoskeleton component GCP2 of gamma-Tubulin ring complex (gamma-TuRC) (original descriptio
9 Cytoskeleton component GCP2 of gamma-Tubulin ring complex (gamma-TuRC) (original descriptio
10 not assigned.r no hits & (original description: pacid=37153352 transcript=Phvul.005G105800.1 locu
11 not assigned.r no hits & (original description: pacid=37151943 transcript=Phvul.009G021200.1 locu
12 not assigned.ε (original description: pacid=37149394 transcript=Phvul.009G226800.1 locus=Phvul.C
13 not assigned.ε (original description: pacid=37171980 transcript=Phvul.006G162000.1 locus=Phvul.C
14 not assigned.r no hits & (original description: pacid=37175715 transcript=Phvul.002G038300.1 locu
15 Protein modif protein kinase (CrRLK1) (original description: pacid=37165831 transcript=Phvul.007C
16 Protein modif protein kinase (LRR-Xc) (original description: pacid=37163699 transcript=Phvul.004G
17 not assigned.r no hits & (original description: pacid=37152177 transcript=Phvul.L001859.1 locus=Pl
18 not assigned.ε (original description: pacid=37175319 transcript=Phvul.002G027900.2 locus=Phvul.C
19 Solute transp P3A-type proton-translocating ATPase (AHA) (original description: pacid=37153023 t
20 not assigned.ε (original description: pacid=37163120 transcript=Phvul.004G153700.1 locus=Phvul.C
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5 rscript=Phvul.007G103100.1 locus=Phvul.007G103100 ID=Phvul.007G103100.1.v2.1 annot-version=
6 rscript=Phvul.007G103100.1 locus=Phvul.007G103100 ID=Phvul.007G103100.1.v2.1 annot-version=
7 J09G006000 ID=Phvul.009G006000.3.v2.1 annot-version=v2.1) & Phosphatidylinositol/phosphatidy
8 J09G006000 ID=Phvul.009G006000.3.v2.1 annot-version=v2.1) & Phosphatidylinositol/phosphatidy
9 J09G006000 ID=Phvul.009G006000.3.v2.1 annot-version=v2.1) & Phosphatidylinositol/phosphatidy
10 rcript=Phvul.002G198200.1 locus=Phvul.002G198200 ID=Phvul.002G198200.1.v2.1 annot-version=v
11 J09G006000 ID=Phvul.009G006000.3.v2.1 annot-version=v2.1) & Phosphatidylinositol/phosphatidy
12 J09G006000 ID=Phvul.009G006000.3.v2.1 annot-version=v2.1) & Phosphatidylinositol/phosphatidy
13 J09G006000 ID=Phvul.009G006000.3.v2.1 annot-version=v2.1) & Phosphatidylinositol/phosphatidy
14 rcript=Phvul.002G198200.1 locus=Phvul.002G198200 ID=Phvul.002G198200.1.v2.1 annot-version=v
15 rscript=Phvul.001G214600 ID=Phvul.001G214600.7.v2.1 annot-version=v2.1)
16
17 r transcript=Phvul.009G150800.1 locus=Phvul.009G150800 ID=Phvul.009G150800.1.v2.1 annot-vers
18 rscript=Phvul.002G261000 ID=Phvul.002G261000.1.v2.1 annot-version=v2.1)
19 rscript=Phvul.001G214600 ID=Phvul.001G214600.7.v2.1 annot-version=v2.1)
20
21 r transcript=Phvul.009G150800.1 locus=Phvul.009G150800 ID=Phvul.009G150800.1.v2.1 annot-vers
22 rscript=Phvul.002G261000 ID=Phvul.002G261000.1.v2.1 annot-version=v2.1)
23
24 1G022900.1 locus=Phvul.001G022900 ID=Phvul.001G022900.1.v2.1 annot-version=v2.1) &
25 original description: pacid=37158087 transcript=Phvul.008G128900.1 locus=Phvul.008G128900 ID=P
26 h
27 v.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
28 v.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
29 v.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
30 v.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
31 v.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
32 v.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
33 v.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
34 rRNP) (original description: pacid=37147800 transcript=Phvul.003G174100.1 locus=Phvul.003G1741
35 il.008G040500.1 locus=Phvul.008G040500 ID=Phvul.008G040500.1.v2.1 annot-version=v2.1) &
36 ranscript=Phvul.004G018100.1 locus=Phvul.004G018100 ID=Phvul.004G018100.1.v2.1 annot-versio
37 rscript=Phvul.008G290000 ID=Phvul.008G290000.1.v2.1 annot-version=v2.1)
38 J05G040800 ID=Phvul.005G040800.1.v2.1 annot-version=v2.1) & Callose synthase 2 OS=Arabidopsi
39 r) complex (original description: pacid=37144029 transcript=Phvul.010G000700.3 locus=Phvul.010G
40 r) complex (original description: pacid=37144029 transcript=Phvul.010G000700.3 locus=Phvul.010G
41 r) complex (original description: pacid=37144029 transcript=Phvul.010G000700.3 locus=Phvul.010G
42 r) complex (original description: pacid=37144029 transcript=Phvul.010G000700.3 locus=Phvul.010G
43 1G022900.1 locus=Phvul.001G022900 ID=Phvul.001G022900.1.v2.1 annot-version=v2.1) &
44 original description: pacid=37158087 transcript=Phvul.008G128900.1 locus=Phvul.008G128900 ID=P
45 h
46 v.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
47 v.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
48 v.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
49 v.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
50 v.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
51 v.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
52 v.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
53 v.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
54 rRNP) (original description: pacid=37147800 transcript=Phvul.003G174100.1 locus=Phvul.003G1741
55 il.008G040500.1 locus=Phvul.008G040500 ID=Phvul.008G040500.1.v2.1 annot-version=v2.1) &
56 ranscript=Phvul.004G018100.1 locus=Phvul.004G018100 ID=Phvul.004G018100.1.v2.1 annot-versio
57 rscript=Phvul.008G290000 ID=Phvul.008G290000.1.v2.1 annot-version=v2.1)
58 J05G040800 ID=Phvul.005G040800.1.v2.1 annot-version=v2.1) & Callose synthase 2 OS=Arabidopsi
59 r) complex (original description: pacid=37144029 transcript=Phvul.010G000700.3 locus=Phvul.010G
60

1
2
3 J01G264132 ID=Phvul.001G264132.1.v2.1 annot-version=v2.1) & Probable pre-mRNA-splicing facto
4 J2 transcript=Phvul.009G019100.1 locus=Phvul.009G019100 ID=Phvul.009G019100.1.v2.1 annot-ve
5 js=Phvul.009G073900 ID=Phvul.009G073900.1.v2.1 annot-version=v2.1)
6 159700.1 locus=Phvul.003G159700 ID=Phvul.003G159700.1.v2.1 annot-version=v2.1) &
7 J06G151200 ID=Phvul.006G151200.1.v2.1 annot-version=v2.1) & RNA pseudouridine synthase 6, cf
8 js=Phvul.006G104300 ID=Phvul.006G104300.2.v2.1 annot-version=v2.1)
9 js=Phvul.006G104300 ID=Phvul.006G104300.2.v2.1 annot-version=v2.1)
10 J11G033500 ID=Phvul.011G033500.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
11 J8G038200.1 locus=Phvul.008G038200 ID=Phvul.008G038200.1.v2.1 annot-version=v2.1) &
12 J02G022400 ID=Phvul.002G022400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
13 644 ID=Phvul.L001644.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containing protein A
14 J01G264132 ID=Phvul.001G264132.1.v2.1 annot-version=v2.1) & Probable pre-mRNA-splicing facto
15 J2 transcript=Phvul.009G019100.1 locus=Phvul.009G019100 ID=Phvul.009G019100.1.v2.1 annot-ve
16 js=Phvul.009G073900 ID=Phvul.009G073900.1.v2.1 annot-version=v2.1)
17 159700.1 locus=Phvul.003G159700 ID=Phvul.003G159700.1.v2.1 annot-version=v2.1) &
18 js=Phvul.001G214600 ID=Phvul.001G214600.7.v2.1 annot-version=v2.1)
19 hvul.009G228600.1 locus=Phvul.009G228600 ID=Phvul.009G228600.1.v2.1 annot-version=v2.1) &
20 009G035800.1 locus=Phvul.009G035800 ID=Phvul.009G035800.1.v2.1 annot-version=v2.1) &
21 00.1 locus=Phvul.011G134100 ID=Phvul.011G134100.1.v2.1 annot-version=v2.1) &
22 00.1 locus=Phvul.011G134000 ID=Phvul.011G134000.1.v2.1 annot-version=v2.1) &
23 00.1 locus=Phvul.011G130800 ID=Phvul.011G130800.1.v2.1 annot-version=v2.1) &
24 00.1 locus=Phvul.011G081100 ID=Phvul.011G081100.1.v2.1 annot-version=v2.1) &
25 00.1 locus=Phvul.011G133300 ID=Phvul.011G133300.1.v2.1 annot-version=v2.1) &
26 ranscript=Phvul.007G247800.1 locus=Phvul.007G247800 ID=Phvul.007G247800.1.v2.1 annot-versic
27 js=Phvul.004G172000 ID=Phvul.004G172000.1.v2.1 annot-version=v2.1)
28 in: pacid=37143582 transcript=Phvul.010G031700.5 locus=Phvul.010G031700 ID=Phvul.010G03170
29 in: pacid=37143582 transcript=Phvul.010G031700.5 locus=Phvul.010G031700 ID=Phvul.010G03170
30 js=Phvul.005G105800 ID=Phvul.005G105800.1.v2.1 annot-version=v2.1)
31 js=Phvul.009G021200 ID=Phvul.009G021200.1.v2.1 annot-version=v2.1)
32 J09G226800 ID=Phvul.009G226800.1.v2.1 annot-version=v2.1) & Protein LURP-one-related 6 OS=A
33 J06G162000 ID=Phvul.006G162000.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase MIEL1
34 js=Phvul.002G038300 ID=Phvul.002G038300.1.v2.1 annot-version=v2.1)
35 G188300.1 locus=Phvul.007G188300 ID=Phvul.007G188300.1.v2.1 annot-version=v2.1) &
36 i084688.1 locus=Phvul.004G084688 ID=Phvul.004G084688.1.v2.1 annot-version=v2.1) &
37 hvul.L001859 ID=Phvul.L001859.1.v2.1 annot-version=v2.1)
38 J02G027900 ID=Phvul.002G027900.2.v2.1 annot-version=v2.1) & Vicilin-like seed storage protein A
39 ranscript=Phvul.005G180700.1 locus=Phvul.005G180700 ID=Phvul.005G180700.1.v2.1 annot-versic
40 J04G153700 ID=Phvul.004G153700.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
41 js=Phvul.001G214600 ID=Phvul.001G214600.7.v2.1 annot-version=v2.1)
42 hvul.009G228600.1 locus=Phvul.009G228600 ID=Phvul.009G228600.1.v2.1 annot-version=v2.1) &
43 009G035800.1 locus=Phvul.009G035800 ID=Phvul.009G035800.1.v2.1 annot-version=v2.1) &
44 00.1 locus=Phvul.011G134100 ID=Phvul.011G134100.1.v2.1 annot-version=v2.1) &
45 00.1 locus=Phvul.011G134000 ID=Phvul.011G134000.1.v2.1 annot-version=v2.1) &
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3 00.1 locus=Phvul.011G130800 ID=Phvul.011G130800.1.v2.1 annot-version=v2.1) &
4 00.1 locus=Phvul.011G081100 ID=Phvul.011G081100.1.v2.1 annot-version=v2.1) &
5 00.1 locus=Phvul.011G133300 ID=Phvul.011G133300.1.v2.1 annot-version=v2.1) &
6 :ranscript=Phvul.007G247800.1 locus=Phvul.007G247800 ID=Phvul.007G247800.1.v2.1 annot-versic
7
8 :s=Phvul.004G172000 ID=Phvul.004G172000.1.v2.1 annot-version=v2.1)
9
10 in: pacid=37143582 transcript=Phvul.010G031700.5 locus=Phvul.010G031700 ID=Phvul.010G03170
11 in: pacid=37143582 transcript=Phvul.010G031700.5 locus=Phvul.010G031700 ID=Phvul.010G03170
12 :s=Phvul.005G105800 ID=Phvul.005G105800.1.v2.1 annot-version=v2.1)
13 :s=Phvul.009G021200 ID=Phvul.009G021200.1.v2.1 annot-version=v2.1)
14 009G226800 ID=Phvul.009G226800.1.v2.1 annot-version=v2.1) & Protein LURP-one-related 6 OS=A
15 006G162000 ID=Phvul.006G162000.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase MIEL1
16 :s=Phvul.002G038300 ID=Phvul.002G038300.1.v2.1 annot-version=v2.1)
17
18 0188300.1 locus=Phvul.007G188300 ID=Phvul.007G188300.1.v2.1 annot-version=v2.1) &
19 0084688.1 locus=Phvul.004G084688 ID=Phvul.004G084688.1.v2.1 annot-version=v2.1) &
20
21 hvul.L001859 ID=Phvul.L001859.1.v2.1 annot-version=v2.1)
22
23 002G027900 ID=Phvul.002G027900.2.v2.1 annot-version=v2.1) & Vicilin-like seed storage protein A
24 :ranscript=Phvul.005G180700.1 locus=Phvul.005G180700 ID=Phvul.005G180700.1.v2.1 annot-versic
25
26 004G153700 ID=Phvul.004G153700.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5 =v2.1) &
6 =v2.1) &
7 /lcholine transfer protein SFH8 OS=Arabidopsis thaliana (sp|f4ihj0|sfh8_arath : 681.0)
8 /lcholine transfer protein SFH8 OS=Arabidopsis thaliana (sp|f4ihj0|sfh8_arath : 681.0)
9 /lcholine transfer protein SFH8 OS=Arabidopsis thaliana (sp|f4ihj0|sfh8_arath : 681.0)
10
11 .2.1) &
12 /lcholine transfer protein SFH8 OS=Arabidopsis thaliana (sp|f4ihj0|sfh8_arath : 681.0)
13 /lcholine transfer protein SFH8 OS=Arabidopsis thaliana (sp|f4ihj0|sfh8_arath : 681.0)
14 /lcholine transfer protein SFH8 OS=Arabidopsis thaliana (sp|f4ihj0|sfh8_arath : 681.0)
15 /lcholine transfer protein SFH8 OS=Arabidopsis thaliana (sp|f4ihj0|sfh8_arath : 681.0)
16
17 .2.1) &
18
19 sion=v2.1) &
20
21
22
23 sion=v2.1) &
24
25
26
27 Phvul.008G128900.1.v2.1 annot-version=v2.1) &
28
29
30
31
32
33
34 100 ID=Phvul.003G174100.1.v2.1 annot-version=v2.1) &
35
36 n=v2.1) &
37
38
39 is thaliana (sp|q9sl03|cals2_arath : 318.0)
40 i000700 ID=Phvul.010G000700.3.v2.1 annot-version=v2.1) &
41 i000700 ID=Phvul.010G000700.3.v2.1 annot-version=v2.1) &
42 i000700 ID=Phvul.010G000700.3.v2.1 annot-version=v2.1) &
43 i000700 ID=Phvul.010G000700.3.v2.1 annot-version=v2.1) &
44
45 Phvul.008G128900.1.v2.1 annot-version=v2.1) &
46
47
48
49
50
51
52 100 ID=Phvul.003G174100.1.v2.1 annot-version=v2.1) &
53
54 n=v2.1) &
55
56
57 is thaliana (sp|q9sl03|cals2_arath : 318.0)
58 i000700 ID=Phvul.010G000700.3.v2.1 annot-version=v2.1) &
59
60

1
2
3 ;000700 ID=Phvul.010G000700.3.v2.1 annot-version=v2.1) &
4 ;000700 ID=Phvul.010G000700.3.v2.1 annot-version=v2.1) &
5 sis thaliana (sp|q9zpe7|exo_arath : 404.0)
6 1 annot-version=v2.1) &
7
8
9

10
11
12
13
14 ke 3 OS=Arabidopsis thaliana (sp|q9ft72|rql3_arath : 811.0)
15 ke 3 OS=Arabidopsis thaliana (sp|q9ft72|rql3_arath : 811.0)
16
17
18
19
20
21
22

23 nnot-version=v2.1) &
24
25
26

27 .1 annot-version=v2.1) &
28 sis thaliana (sp|q9zpe7|exo_arath : 404.0)
29 1 annot-version=v2.1) &
30
31
32
33
34
35

36 ke 3 OS=Arabidopsis thaliana (sp|q9ft72|rql3_arath : 811.0)
37 ke 3 OS=Arabidopsis thaliana (sp|q9ft72|rql3_arath : 811.0)
38
39
40
41
42
43
44

45 nnot-version=v2.1) &
46
47
48
49

50 .1 annot-version=v2.1) &
51 nloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
52
53
54

55 ing protein At2g21090 OS=Arabidopsis thaliana (sp|q9skq4|pp167_arath : 607.0)
56
57

58 ing protein At3g50420 OS=Arabidopsis thaliana (sp|q9sct2|pp277_arath : 413.0)
59 t1g25360 OS=Arabidopsis thaliana (sp|q9fri5|ppr57_arath : 1008.0)
60

1
2
3 or ATP-dependent RNA helicase DEAH5 OS=Arabidopsis thaliana (sp|q38953|deah5_arath : 438.0)
4 version=v2.1) &

5
6
7
8 chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
9

10
11
12 binding protein At2g21090 OS=Arabidopsis thaliana (sp|q9skq4|pp167_arath : 607.0)
13

14
15 binding protein At3g50420 OS=Arabidopsis thaliana (sp|q9sct2|pp277_arath : 413.0)

16 At1g25360 OS=Arabidopsis thaliana (sp|q9fri5|ppr57_arath : 1008.0)

17
18 or ATP-dependent RNA helicase DEAH5 OS=Arabidopsis thaliana (sp|q38953|deah5_arath : 438.0)
19 version=v2.1) &

20
21
22
23
24
25
26
27
28
29
30
31
32
33
34 on=v2.1) &

35
36)0.5.v2.1 annot-version=v2.1) &

37)0.5.v2.1 annot-version=v2.1) &

38
39
40
41 Arabidopsis thaliana (sp|q9zuf7|lor6_arath : 232.0)

42 OS=Arabidopsis thaliana (sp|q8vzk0|miel1_arath : 409.0)
43
44
45
46
47
48

49 At2g18540 OS=Arabidopsis thaliana (sp|f4iqk5|vcl21_arath : 226.0)

50 on=v2.1) &

51 binding protein At5g66520 OS=Arabidopsis thaliana (sp|q9fjy7|pp449_arath : 417.0)
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7 on=v2.1) &
8
9

10)0.5.v2.1 annot-version=v2.1) &

11)0.5.v2.1 annot-version=v2.1) &
12
13
14

15 rabidopsis thaliana (sp|q9zuf7|lor6_arath : 232.0)

16 OS=Arabidopsis thaliana (sp|q8vzk0|miel1_arath : 409.0)
17
18
19

20
21
22
23 .t2g18540 OS=Arabidopsis thaliana (sp|f4iqk5|vcl21_arath : 226.0)

24 on=v2.1) &
25

26 ing protein At5g66520 OS=Arabidopsis thaliana (sp|q9fjy7|pp449_arath : 417.0)
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | miRNA_Acc. | Target_Acc. | Expectation | UPE\$ | miRNA_start | miRNA_end |
|----|--------------|--------------------|-------------|-------|-------------|-----------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | aaaccguuacca | Phvul.004G064100.1 | 3 | -1 | 1 | 22 |
| 4 | aaaccguuacca | Phvul.009G096000.1 | 3 | -1 | 1 | 22 |
| 5 | aaaccguuacca | Phvul.008G049000.1 | 3 | -1 | 1 | 22 |
| 6 | aaaccguuacca | Phvul.004G064100.1 | 3 | -1 | 1 | 23 |
| 7 | aaaccguuacca | Phvul.009G096000.1 | 3 | -1 | 1 | 23 |
| 8 | aaaccguuacca | Phvul.004G064100.1 | 3 | -1 | 1 | 23 |
| 9 | aaaccguuacca | Phvul.009G096000.1 | 3 | -1 | 1 | 23 |
| 10 | aaaccguuacca | Phvul.004G064100.1 | 3 | -1 | 1 | 23 |
| 11 | aaaccguuacca | Phvul.009G096000.1 | 3 | -1 | 1 | 23 |
| 12 | aaaccguuacca | Phvul.009G196100.1 | 3.5 | -1 | 1 | 22 |
| 13 | aaaccguuacca | Phvul.008G199900.1 | 3.5 | -1 | 1 | 22 |
| 14 | aaaccguuacca | Phvul.007G157000.1 | 3.5 | -1 | 1 | 22 |
| 15 | aaaccguuacca | Phvul.009G104850.1 | 3.5 | -1 | 1 | 22 |
| 16 | aaaccguuacca | Phvul.004G038100.1 | 3.5 | -1 | 1 | 22 |
| 17 | aaaccguuacca | Phvul.011G073600.2 | 3.5 | -1 | 1 | 22 |
| 18 | aaaccguuacca | Phvul.011G073600.1 | 3.5 | -1 | 1 | 22 |
| 19 | aaaccguuacca | Phvul.L001604.3 | 3.5 | -1 | 1 | 22 |
| 20 | aaaccguuacca | Phvul.L001604.2 | 3.5 | -1 | 1 | 22 |
| 21 | aaaccguuacca | Phvul.L001604.1 | 3.5 | -1 | 1 | 22 |
| 22 | aaaccguuacca | Phvul.004G160700.1 | 3.5 | -1 | 1 | 22 |
| 23 | aaaccguuacca | Phvul.011G152300.3 | 3.5 | -1 | 1 | 22 |
| 24 | aaaccguuacca | Phvul.011G152300.2 | 3.5 | -1 | 1 | 22 |
| 25 | aaaccguuacca | Phvul.011G152300.1 | 3.5 | -1 | 1 | 22 |
| 26 | aaaccguuacca | Phvul.003G229300.1 | 3.5 | -1 | 1 | 22 |
| 27 | aaaccguuacca | Phvul.003G229300.2 | 3.5 | -1 | 1 | 22 |
| 28 | aaaccguuacca | Phvul.003G178200.1 | 3.5 | -1 | 1 | 22 |
| 29 | aaaccguuacca | Phvul.009G196100.1 | 3.5 | -1 | 1 | 23 |
| 30 | aaaccguuacca | Phvul.008G199900.1 | 3.5 | -1 | 1 | 23 |
| 31 | aaaccguuacca | Phvul.007G157000.1 | 3.5 | -1 | 1 | 23 |
| 32 | aaaccguuacca | Phvul.004G160700.1 | 3.5 | -1 | 1 | 23 |
| 33 | aaaccguuacca | Phvul.009G104850.1 | 3.5 | -1 | 1 | 23 |
| 34 | aaaccguuacca | Phvul.L001604.3 | 3.5 | -1 | 1 | 23 |
| 35 | aaaccguuacca | Phvul.L001604.2 | 3.5 | -1 | 1 | 23 |
| 36 | aaaccguuacca | Phvul.L001604.1 | 3.5 | -1 | 1 | 23 |
| 37 | aaaccguuacca | Phvul.004G038100.1 | 3.5 | -1 | 1 | 23 |
| 38 | aaaccguuacca | Phvul.011G073600.2 | 3.5 | -1 | 1 | 23 |
| 39 | aaaccguuacca | Phvul.011G073600.1 | 3.5 | -1 | 1 | 23 |
| 40 | aaaccguuacca | Phvul.009G196100.1 | 3.5 | -1 | 1 | 23 |
| 41 | aaaccguuacca | Phvul.008G199900.1 | 3.5 | -1 | 1 | 23 |
| 42 | aaaccguuacca | Phvul.007G157000.1 | 3.5 | -1 | 1 | 23 |
| 43 | aaaccguuacca | Phvul.004G160700.1 | 3.5 | -1 | 1 | 23 |
| 44 | aaaccguuacca | Phvul.009G104850.1 | 3.5 | -1 | 1 | 23 |
| 45 | aaaccguuacca | Phvul.L001604.3 | 3.5 | -1 | 1 | 23 |
| 46 | aaaccguuacca | Phvul.L001604.2 | 3.5 | -1 | 1 | 23 |
| 47 | aaaccguuacca | Phvul.L001604.1 | 3.5 | -1 | 1 | 23 |
| 48 | aaaccguuacca | Phvul.004G038100.1 | 3.5 | -1 | 1 | 23 |
| 49 | aaaccguuacca | Phvul.011G073600.2 | 3.5 | -1 | 1 | 23 |
| 50 | aaaccguuacca | Phvul.011G073600.1 | 3.5 | -1 | 1 | 23 |
| 51 | aaaccguuacca | Phvul.009G196100.1 | 3.5 | -1 | 1 | 23 |
| 52 | aaaccguuacca | Phvul.008G199900.1 | 3.5 | -1 | 1 | 23 |
| 53 | aaaccguuacca | Phvul.007G157000.1 | 3.5 | -1 | 1 | 23 |
| 54 | aaaccguuacca | Phvul.004G160700.1 | 3.5 | -1 | 1 | 23 |
| 55 | aaaccguuacca | Phvul.009G104850.1 | 3.5 | -1 | 1 | 23 |
| 56 | aaaccguuacca | Phvul.L001604.3 | 3.5 | -1 | 1 | 23 |
| 57 | aaaccguuacca | Phvul.L001604.2 | 3.5 | -1 | 1 | 23 |
| 58 | aaaccguuacca | Phvul.L001604.1 | 3.5 | -1 | 1 | 23 |
| 59 | aaaccguuacca | Phvul.004G038100.1 | 3.5 | -1 | 1 | 23 |
| 60 | aaaccguuacca | Phvul.011G073600.2 | 3.5 | -1 | 1 | 23 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | aaaccguuacca Phvul.011G073600.1 | 3.5 | -1 | 1 | 23 |
| 3 | aaaccguuacca Phvul.002G289600.3 | 4 | -1 | 1 | 22 |
| 4 | aaaccguuacca Phvul.002G289600.1 | 4 | -1 | 1 | 22 |
| 5 | aaaccguuacca Phvul.002G289600.2 | 4 | -1 | 1 | 22 |
| 6 | aaaccguuacca Phvul.002G041900.1 | 4 | -1 | 1 | 22 |
| 7 | aaaccguuacca Phvul.010G108300.1 | 4 | -1 | 1 | 22 |
| 8 | aaaccguuacca Phvul.006G148800.1 | 4 | -1 | 1 | 22 |
| 9 | aaaccguuacca Phvul.006G214700.4 | 4 | -1 | 1 | 22 |
| 10 | aaaccguuacca Phvul.006G214700.3 | 4 | -1 | 1 | 22 |
| 11 | aaaccguuacca Phvul.006G214700.2 | 4 | -1 | 1 | 22 |
| 12 | aaaccguuacca Phvul.006G214700.1 | 4 | -1 | 1 | 22 |
| 13 | aaaccguuacca Phvul.002G231800.1 | 4 | -1 | 1 | 22 |
| 14 | aaaccguuacca Phvul.005G137000.3 | 4 | -1 | 1 | 22 |
| 15 | aaaccguuacca Phvul.005G137000.1 | 4 | -1 | 1 | 22 |
| 16 | aaaccguuacca Phvul.005G137000.4 | 4 | -1 | 1 | 22 |
| 17 | aaaccguuacca Phvul.005G137000.6 | 4 | -1 | 1 | 22 |
| 18 | aaaccguuacca Phvul.002G226900.1 | 4 | -1 | 1 | 22 |
| 19 | aaaccguuacca Phvul.005G137000.5 | 4 | -1 | 1 | 22 |
| 20 | aaaccguuacca Phvul.005G137000.2 | 4 | -1 | 1 | 22 |
| 21 | aaaccguuacca Phvul.007G222000.1 | 4 | -1 | 1 | 22 |
| 22 | aaaccguuacca Phvul.007G029200.1 | 4 | -1 | 1 | 22 |
| 23 | aaaccguuacca Phvul.003G058400.1 | 4 | -1 | 1 | 22 |
| 24 | aaaccguuacca Phvul.002G250000.1 | 4 | -1 | 1 | 22 |
| 25 | aaaccguuacca Phvul.004G028100.1 | 4 | -1 | 1 | 22 |
| 26 | aaaccguuacca Phvul.008G216700.1 | 4 | -1 | 1 | 22 |
| 27 | aaaccguuacca Phvul.008G216700.1 | 4 | -1 | 1 | 22 |
| 28 | aaaccguuacca Phvul.002G190100.1 | 4 | -1 | 1 | 22 |
| 29 | aaaccguuacca Phvul.004G087000.1 | 4 | -1 | 1 | 22 |
| 30 | aaaccguuacca Phvul.001G036500.1 | 4 | -1 | 1 | 22 |
| 31 | aaaccguuacca Phvul.005G102100.2 | 4 | -1 | 1 | 22 |
| 32 | aaaccguuacca Phvul.005G102100.1 | 4 | -1 | 1 | 22 |
| 33 | aaaccguuacca Phvul.002G289600.3 | 4 | -1 | 1 | 23 |
| 34 | aaaccguuacca Phvul.002G289600.1 | 4 | -1 | 1 | 23 |
| 35 | aaaccguuacca Phvul.002G289600.2 | 4 | -1 | 1 | 23 |
| 36 | aaaccguuacca Phvul.002G041900.1 | 4 | -1 | 1 | 23 |
| 37 | aaaccguuacca Phvul.006G148800.1 | 4 | -1 | 1 | 23 |
| 38 | aaaccguuacca Phvul.010G108300.1 | 4 | -1 | 1 | 23 |
| 39 | aaaccguuacca Phvul.006G214700.2 | 4 | -1 | 1 | 23 |
| 40 | aaaccguuacca Phvul.006G214700.1 | 4 | -1 | 1 | 23 |
| 41 | aaaccguuacca Phvul.006G214700.4 | 4 | -1 | 1 | 23 |
| 42 | aaaccguuacca Phvul.006G214700.3 | 4 | -1 | 1 | 23 |
| 43 | aaaccguuacca Phvul.008G216700.1 | 4 | -1 | 1 | 23 |
| 44 | aaaccguuacca Phvul.008G216700.1 | 4 | -1 | 1 | 23 |
| 45 | aaaccguuacca Phvul.001G036500.1 | 4 | -1 | 1 | 23 |
| 46 | aaaccguuacca Phvul.002G289600.3 | 4 | -1 | 1 | 23 |
| 47 | aaaccguuacca Phvul.002G289600.1 | 4 | -1 | 1 | 23 |
| 48 | aaaccguuacca Phvul.002G289600.2 | 4 | -1 | 1 | 23 |
| 49 | aaaccguuacca Phvul.001G036500.1 | 4 | -1 | 1 | 23 |
| 50 | aaaccguuacca Phvul.002G289600.3 | 4 | -1 | 1 | 23 |
| 51 | aaaccguuacca Phvul.002G289600.1 | 4 | -1 | 1 | 23 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | aaaccguuacca Phvul.002G289600.2 | 4 | -1 | 1 | 23 |
| 3 | aaaccguuacca Phvul.002G041900.1 | 4 | -1 | 1 | 23 |
| 4 | aaaccguuacca Phvul.006G148800.1 | 4 | -1 | 1 | 23 |
| 5 | aaaccguuacca Phvul.010G108300.1 | 4 | -1 | 1 | 23 |
| 6 | aaaccguuacca Phvul.006G214700.2 | 4 | -1 | 1 | 23 |
| 7 | aaaccguuacca Phvul.006G214700.1 | 4 | -1 | 1 | 23 |
| 8 | aaaccguuacca Phvul.006G214700.4 | 4 | -1 | 1 | 23 |
| 9 | aaaccguuacca Phvul.006G214700.3 | 4 | -1 | 1 | 23 |
| 10 | aaaccguuacca Phvul.008G216700.1 | 4 | -1 | 1 | 23 |
| 11 | aaaccguuacca Phvul.008G216700.1 | 4 | -1 | 1 | 23 |
| 12 | aaaccguuacca Phvul.001G036500.1 | 4 | -1 | 1 | 23 |
| 13 | aaaccguuacca Phvul.001G052300.1 | 4.5 | -1 | 1 | 22 |
| 14 | aaaccguuacca Phvul.010G110700.2 | 4.5 | -1 | 1 | 22 |
| 15 | aaaccguuacca Phvul.010G110700.1 | 4.5 | -1 | 1 | 22 |
| 16 | aaaccguuacca Phvul.009G100000.5 | 4.5 | -1 | 1 | 22 |
| 17 | aaaccguuacca Phvul.009G100000.4 | 4.5 | -1 | 1 | 22 |
| 18 | aaaccguuacca Phvul.009G100000.3 | 4.5 | -1 | 1 | 22 |
| 19 | aaaccguuacca Phvul.009G100000.2 | 4.5 | -1 | 1 | 22 |
| 20 | aaaccguuacca Phvul.001G073300.1 | 4.5 | -1 | 1 | 22 |
| 21 | aaaccguuacca Phvul.008G279750.1 | 4.5 | -1 | 1 | 22 |
| 22 | aaaccguuacca Phvul.010G152600.1 | 4.5 | -1 | 1 | 22 |
| 23 | aaaccguuacca Phvul.006G021500.1 | 4.5 | -1 | 1 | 22 |
| 24 | aaaccguuacca Phvul.009G177300.1 | 4.5 | -1 | 1 | 22 |
| 25 | aaaccguuacca Phvul.007G147400.1 | 4.5 | -1 | 1 | 22 |
| 26 | aaaccguuacca Phvul.003G178100.1 | 4.5 | -1 | 1 | 22 |
| 27 | aaaccguuacca Phvul.011G102400.1 | 4.5 | -1 | 1 | 22 |
| 28 | aaaccguuacca Phvul.001G106800.1 | 4.5 | -1 | 1 | 22 |
| 29 | aaaccguuacca Phvul.007G261100.2 | 4.5 | -1 | 1 | 22 |
| 30 | aaaccguuacca Phvul.007G261100.1 | 4.5 | -1 | 1 | 22 |
| 31 | aaaccguuacca Phvul.011G187600.1 | 4.5 | -1 | 1 | 22 |
| 32 | aaaccguuacca Phvul.006G148800.1 | 4.5 | -1 | 1 | 22 |
| 33 | aaaccguuacca Phvul.006G148800.1 | 4.5 | -1 | 1 | 22 |
| 34 | aaaccguuacca Phvul.002G044500.1 | 4.5 | -1 | 1 | 22 |
| 35 | aaaccguuacca Phvul.007G113300.1 | 4.5 | -1 | 1 | 22 |
| 36 | aaaccguuacca Phvul.006G206800.1 | 4.5 | -1 | 1 | 22 |
| 37 | aaaccguuacca Phvul.010G144900.1 | 4.5 | -1 | 1 | 22 |
| 38 | aaaccguuacca Phvul.002G083800.1 | 4.5 | -1 | 1 | 22 |
| 39 | aaaccguuacca Phvul.001G067500.3 | 4.5 | -1 | 1 | 22 |
| 40 | aaaccguuacca Phvul.001G067500.2 | 4.5 | -1 | 1 | 22 |
| 41 | aaaccguuacca Phvul.001G067500.1 | 4.5 | -1 | 1 | 22 |
| 42 | aaaccguuacca Phvul.006G045600.1 | 4.5 | -1 | 1 | 22 |
| 43 | aaaccguuacca Phvul.010G156000.1 | 4.5 | -1 | 1 | 22 |
| 44 | aaaccguuacca Phvul.007G055500.1 | 4.5 | -1 | 1 | 22 |
| 45 | aaaccguuacca Phvul.007G055500.1 | 4.5 | -1 | 1 | 22 |
| 46 | aaaccguuacca Phvul.005G154600.1 | 4.5 | -1 | 1 | 22 |
| 47 | aaaccguuacca Phvul.005G154600.3 | 4.5 | -1 | 1 | 22 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | aaaccguuacca Phvul.007G055200.1 | 4.5 | -1 | 1 | 22 |
| 3 | aaaccguuacca Phvul.007G055200.1 | 4.5 | -1 | 1 | 22 |
| 4 | aaaccguuacca Phvul.005G154600.2 | 4.5 | -1 | 1 | 22 |
| 5 | aaaccguuacca Phvul.008G273100.1 | 4.5 | -1 | 1 | 22 |
| 6 | aaaccguuacca Phvul.008G216700.1 | 4.5 | -1 | 1 | 22 |
| 7 | aaaccguuacca Phvul.010G121200.1 | 4.5 | -1 | 1 | 22 |
| 8 | aaaccguuacca Phvul.010G121200.2 | 4.5 | -1 | 1 | 22 |
| 9 | aaaccguuacca Phvul.007G270500.1 | 4.5 | -1 | 1 | 22 |
| 10 | aaaccguuacca Phvul.004G125900.1 | 4.5 | -1 | 1 | 22 |
| 11 | aaaccguuacca Phvul.005G027200.1 | 4.5 | -1 | 1 | 22 |
| 12 | aaaccguuacca Phvul.010G110700.2 | 4.5 | -1 | 1 | 23 |
| 13 | aaaccguuacca Phvul.010G110700.1 | 4.5 | -1 | 1 | 23 |
| 14 | aaaccguuacca Phvul.001G052300.1 | 4.5 | -1 | 1 | 23 |
| 15 | aaaccguuacca Phvul.008G279750.1 | 4.5 | -1 | 1 | 23 |
| 16 | aaaccguuacca Phvul.009G100000.5 | 4.5 | -1 | 1 | 23 |
| 17 | aaaccguuacca Phvul.009G100000.4 | 4.5 | -1 | 1 | 23 |
| 18 | aaaccguuacca Phvul.009G100000.3 | 4.5 | -1 | 1 | 23 |
| 19 | aaaccguuacca Phvul.009G100000.2 | 4.5 | -1 | 1 | 23 |
| 20 | aaaccguuacca Phvul.001G073300.1 | 4.5 | -1 | 1 | 23 |
| 21 | aaaccguuacca Phvul.010G152600.1 | 4.5 | -1 | 1 | 23 |
| 22 | aaaccguuacca Phvul.011G102400.1 | 4.5 | -1 | 1 | 23 |
| 23 | aaaccguuacca Phvul.006G148800.1 | 4.5 | -1 | 1 | 23 |
| 24 | aaaccguuacca Phvul.006G148800.1 | 4.5 | -1 | 1 | 23 |
| 25 | aaaccguuacca Phvul.010G121200.1 | 4.5 | -1 | 1 | 23 |
| 26 | aaaccguuacca Phvul.010G121200.2 | 4.5 | -1 | 1 | 23 |
| 27 | aaaccguuacca Phvul.004G125900.1 | 4.5 | -1 | 1 | 23 |
| 28 | aaaccguuacca Phvul.002G044500.1 | 4.5 | -1 | 1 | 23 |
| 29 | aaaccguuacca Phvul.007G113300.1 | 4.5 | -1 | 1 | 23 |
| 30 | aaaccguuacca Phvul.006G021500.1 | 4.5 | -1 | 1 | 23 |
| 31 | aaaccguuacca Phvul.009G177300.1 | 4.5 | -1 | 1 | 23 |
| 32 | aaaccguuacca Phvul.007G147400.1 | 4.5 | -1 | 1 | 23 |
| 33 | aaaccguuacca Phvul.003G178100.1 | 4.5 | -1 | 1 | 23 |
| 34 | aaaccguuacca Phvul.005G154600.1 | 4.5 | -1 | 1 | 23 |
| 35 | aaaccguuacca Phvul.005G154600.3 | 4.5 | -1 | 1 | 23 |
| 36 | aaaccguuacca Phvul.001G106800.1 | 4.5 | -1 | 1 | 23 |
| 37 | aaaccguuacca Phvul.007G261100.2 | 4.5 | -1 | 1 | 23 |
| 38 | aaaccguuacca Phvul.007G261100.1 | 4.5 | -1 | 1 | 23 |
| 39 | aaaccguuacca Phvul.011G187600.1 | 4.5 | -1 | 1 | 23 |
| 40 | aaaccguuacca Phvul.005G154600.2 | 4.5 | -1 | 1 | 23 |
| 41 | aaaccguuacca Phvul.008G273100.1 | 4.5 | -1 | 1 | 23 |
| 42 | aaaccguuacca Phvul.005G065300.1 | 4.5 | -1 | 1 | 23 |
| 43 | aaaccguuacca Phvul.006G206800.1 | 4.5 | -1 | 1 | 23 |
| 44 | aaaccguuacca Phvul.006G045600.1 | 4.5 | -1 | 1 | 23 |
| 45 | aaaccguuacca Phvul.008G216700.1 | 4.5 | -1 | 1 | 23 |
| 46 | aaaccguuacca Phvul.011G111800.1 | 4.5 | -1 | 1 | 23 |
| 47 | aaaccguuacca Phvul.010G144900.1 | 4.5 | -1 | 1 | 23 |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | aaaccguuacca Phvul.002G083800.1 | 4.5 | -1 | 1 | 23 |
| 3 | aaaccguuacca Phvul.007G270500.1 | 4.5 | -1 | 1 | 23 |
| 4 | aaaccguuacca Phvul.001G067500.3 | 4.5 | -1 | 1 | 23 |
| 5 | aaaccguuacca Phvul.010G110700.2 | 4.5 | -1 | 1 | 23 |
| 6 | aaaccguuacca Phvul.010G110700.1 | 4.5 | -1 | 1 | 23 |
| 7 | aaaccguuacca Phvul.001G052300.1 | 4.5 | -1 | 1 | 23 |
| 8 | aaaccguuacca Phvul.008G279750.1 | 4.5 | -1 | 1 | 23 |
| 9 | aaaccguuacca Phvul.009G100000.5 | 4.5 | -1 | 1 | 23 |
| 10 | aaaccguuacca Phvul.009G100000.4 | 4.5 | -1 | 1 | 23 |
| 11 | aaaccguuacca Phvul.009G100000.3 | 4.5 | -1 | 1 | 23 |
| 12 | aaaccguuacca Phvul.009G100000.2 | 4.5 | -1 | 1 | 23 |
| 13 | aaaccguuacca Phvul.001G073300.1 | 4.5 | -1 | 1 | 23 |
| 14 | aaaccguuacca Phvul.010G152600.1 | 4.5 | -1 | 1 | 23 |
| 15 | aaaccguuacca Phvul.011G102400.1 | 4.5 | -1 | 1 | 23 |
| 16 | aaaccguuacca Phvul.006G148800.1 | 4.5 | -1 | 1 | 23 |
| 17 | aaaccguuacca Phvul.006G148800.1 | 4.5 | -1 | 1 | 23 |
| 18 | aaaccguuacca Phvul.010G121200.1 | 4.5 | -1 | 1 | 23 |
| 19 | aaaccguuacca Phvul.010G121200.2 | 4.5 | -1 | 1 | 23 |
| 20 | aaaccguuacca Phvul.004G125900.1 | 4.5 | -1 | 1 | 23 |
| 21 | aaaccguuacca Phvul.002G044500.1 | 4.5 | -1 | 1 | 23 |
| 22 | aaaccguuacca Phvul.007G113300.1 | 4.5 | -1 | 1 | 23 |
| 23 | aaaccguuacca Phvul.006G021500.1 | 4.5 | -1 | 1 | 23 |
| 24 | aaaccguuacca Phvul.009G177300.1 | 4.5 | -1 | 1 | 23 |
| 25 | aaaccguuacca Phvul.007G147400.1 | 4.5 | -1 | 1 | 23 |
| 26 | aaaccguuacca Phvul.003G178100.1 | 4.5 | -1 | 1 | 23 |
| 27 | aaaccguuacca Phvul.005G154600.1 | 4.5 | -1 | 1 | 23 |
| 28 | aaaccguuacca Phvul.005G154600.3 | 4.5 | -1 | 1 | 23 |
| 29 | aaaccguuacca Phvul.001G106800.1 | 4.5 | -1 | 1 | 23 |
| 30 | aaaccguuacca Phvul.007G261100.2 | 4.5 | -1 | 1 | 23 |
| 31 | aaaccguuacca Phvul.007G261100.1 | 4.5 | -1 | 1 | 23 |
| 32 | aaaccguuacca Phvul.011G187600.1 | 4.5 | -1 | 1 | 23 |
| 33 | aaaccguuacca Phvul.005G154600.2 | 4.5 | -1 | 1 | 23 |
| 34 | aaaccguuacca Phvul.008G273100.1 | 4.5 | -1 | 1 | 23 |
| 35 | aaaccguuacca Phvul.005G065300.1 | 4.5 | -1 | 1 | 23 |
| 36 | aaaccguuacca Phvul.006G206800.1 | 4.5 | -1 | 1 | 23 |
| 37 | aaaccguuacca Phvul.006G045600.1 | 4.5 | -1 | 1 | 23 |
| 38 | aaaccguuacca Phvul.008G216700.1 | 4.5 | -1 | 1 | 23 |
| 39 | aaaccguuacca Phvul.011G111800.1 | 4.5 | -1 | 1 | 23 |
| 40 | aaaccguuacca Phvul.010G144900.1 | 4.5 | -1 | 1 | 23 |
| 41 | aaaccguuacca Phvul.002G083800.1 | 4.5 | -1 | 1 | 23 |
| 42 | aaaccguuacca Phvul.007G270500.1 | 4.5 | -1 | 1 | 23 |
| 43 | aaaccguuacca Phvul.001G067500.3 | 4.5 | -1 | 1 | 23 |
| 44 | aaaccguuacca Phvul.001G067500.2 | 4.5 | -1 | 1 | 23 |
| 45 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 22 |
| 46 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 22 |
| 47 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 22 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 22 |
| 3 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 22 |
| 4 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 22 |
| 5 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 22 |
| 6 | aaaccguuacca Phvul.004G019300.2 | 5 | -1 | 1 | 22 |
| 7 | aaaccguuacca Phvul.004G019300.1 | 5 | -1 | 1 | 22 |
| 8 | aaaccguuacca Phvul.009G104850.1 | 5 | -1 | 1 | 22 |
| 9 | aaaccguuacca Phvul.009G104850.1 | 5 | -1 | 1 | 22 |
| 10 | aaaccguuacca Phvul.009G104850.1 | 5 | -1 | 1 | 22 |
| 11 | aaaccguuacca Phvul.009G104850.1 | 5 | -1 | 1 | 22 |
| 12 | aaaccguuacca Phvul.003G158800.1 | 5 | -1 | 1 | 22 |
| 13 | aaaccguuacca Phvul.006G173500.1 | 5 | -1 | 1 | 22 |
| 14 | aaaccguuacca Phvul.006G173500.1 | 5 | -1 | 1 | 22 |
| 15 | aaaccguuacca Phvul.002G183700.1 | 5 | -1 | 1 | 22 |
| 16 | aaaccguuacca Phvul.011G102400.1 | 5 | -1 | 1 | 22 |
| 17 | aaaccguuacca Phvul.007G027000.1 | 5 | -1 | 1 | 22 |
| 18 | aaaccguuacca Phvul.007G027000.1 | 5 | -1 | 1 | 22 |
| 19 | aaaccguuacca Phvul.005G043000.2 | 5 | -1 | 1 | 22 |
| 20 | aaaccguuacca Phvul.006G148800.1 | 5 | -1 | 1 | 22 |
| 21 | aaaccguuacca Phvul.006G148800.1 | 5 | -1 | 1 | 22 |
| 22 | aaaccguuacca Phvul.011G069000.1 | 5 | -1 | 1 | 22 |
| 23 | aaaccguuacca Phvul.006G206800.1 | 5 | -1 | 1 | 22 |
| 24 | aaaccguuacca Phvul.005G054600.1 | 5 | -1 | 1 | 22 |
| 25 | aaaccguuacca Phvul.005G054600.1 | 5 | -1 | 1 | 22 |
| 26 | aaaccguuacca Phvul.001G024200.1 | 5 | -1 | 1 | 22 |
| 27 | aaaccguuacca Phvul.008G060700.1 | 5 | -1 | 1 | 22 |
| 28 | aaaccguuacca Phvul.004G147900.1 | 5 | -1 | 1 | 22 |
| 29 | aaaccguuacca Phvul.004G147900.1 | 5 | -1 | 1 | 22 |
| 30 | aaaccguuacca Phvul.001G057200.1 | 5 | -1 | 1 | 22 |
| 31 | aaaccguuacca Phvul.009G046200.1 | 5 | -1 | 1 | 22 |
| 32 | aaaccguuacca Phvul.011G133400.1 | 5 | -1 | 1 | 22 |
| 33 | aaaccguuacca Phvul.008G111100.1 | 5 | -1 | 1 | 22 |
| 34 | aaaccguuacca Phvul.008G111100.1 | 5 | -1 | 1 | 22 |
| 35 | aaaccguuacca Phvul.006G070000.2 | 5 | -1 | 1 | 22 |
| 36 | aaaccguuacca Phvul.L001687.1 | 5 | -1 | 1 | 22 |
| 37 | aaaccguuacca Phvul.008G033500.1 | 5 | -1 | 1 | 22 |
| 38 | aaaccguuacca Phvul.008G033500.1 | 5 | -1 | 1 | 22 |
| 39 | aaaccguuacca Phvul.008G036100.2 | 5 | -1 | 1 | 22 |
| 40 | aaaccguuacca Phvul.008G036100.2 | 5 | -1 | 1 | 22 |
| 41 | aaaccguuacca Phvul.009G198900.1 | 5 | -1 | 1 | 22 |
| 42 | aaaccguuacca Phvul.008G036100.1 | 5 | -1 | 1 | 22 |
| 43 | aaaccguuacca Phvul.006G037000.1 | 5 | -1 | 1 | 22 |
| 44 | aaaccguuacca Phvul.006G037000.1 | 5 | -1 | 1 | 22 |
| 45 | aaaccguuacca Phvul.001G205600.1 | 5 | -1 | 1 | 22 |
| 46 | aaaccguuacca Phvul.011G159400.1 | 5 | -1 | 1 | 22 |
| 47 | aaaccguuacca Phvul.004G061900.1 | 5 | -1 | 1 | 22 |
| 48 | aaaccguuacca Phvul.006G048000.1 | 5 | -1 | 1 | 22 |
| 49 | aaaccguuacca Phvul.006G048000.1 | 5 | -1 | 1 | 22 |
| 50 | aaaccguuacca Phvul.009G007900.1 | 5 | -1 | 1 | 22 |
| 51 | aaaccguuacca Phvul.009G007900.1 | 5 | -1 | 1 | 22 |
| 52 | aaaccguuacca Phvul.005G067950.1 | 5 | -1 | 1 | 22 |
| 53 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 23 |
| 54 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 23 |
| 55 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 23 |
| 56 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 23 |
| 57 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 23 |
| 58 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 23 |
| 59 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 23 |
| 60 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 23 |
| | aaaccguuacca Phvul.006G173500.1 | 5 | -1 | 1 | 23 |
| | aaaccguuacca Phvul.002G183700.1 | 5 | -1 | 1 | 23 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | aaaccguuacca Phvul.005G043000.2 | 5 | -1 | 1 | 23 |
| 3 | aaaccguuacca Phvul.004G019300.2 | 5 | -1 | 1 | 23 |
| 4 | aaaccguuacca Phvul.004G019300.1 | 5 | -1 | 1 | 23 |
| 5 | aaaccguuacca Phvul.011G069000.1 | 5 | -1 | 1 | 23 |
| 6 | aaaccguuacca Phvul.002G231800.1 | 5 | -1 | 1 | 23 |
| 7 | aaaccguuacca Phvul.L001687.1 | 5 | -1 | 1 | 23 |
| 8 | aaaccguuacca Phvul.L001687.1 | 5 | -1 | 1 | 23 |
| 9 | aaaccguuacca Phvul.L001687.1 | 5 | -1 | 1 | 23 |
| 10 | aaaccguuacca Phvul.011G102400.1 | 5 | -1 | 1 | 23 |
| 11 | aaaccguuacca Phvul.006G037000.1 | 5 | -1 | 1 | 23 |
| 12 | aaaccguuacca Phvul.009G104850.1 | 5 | -1 | 1 | 23 |
| 13 | aaaccguuacca Phvul.009G104850.1 | 5 | -1 | 1 | 23 |
| 14 | aaaccguuacca Phvul.009G104850.1 | 5 | -1 | 1 | 23 |
| 15 | aaaccguuacca Phvul.009G104850.1 | 5 | -1 | 1 | 23 |
| 16 | aaaccguuacca Phvul.003G158800.1 | 5 | -1 | 1 | 23 |
| 17 | aaaccguuacca Phvul.003G158800.1 | 5 | -1 | 1 | 23 |
| 18 | aaaccguuacca Phvul.001G057200.1 | 5 | -1 | 1 | 23 |
| 19 | aaaccguuacca Phvul.004G057900.1 | 5 | -1 | 1 | 23 |
| 20 | aaaccguuacca Phvul.007G027000.1 | 5 | -1 | 1 | 23 |
| 21 | aaaccguuacca Phvul.007G027000.1 | 5 | -1 | 1 | 23 |
| 22 | aaaccguuacca Phvul.009G063500.1 | 5 | -1 | 1 | 23 |
| 23 | aaaccguuacca Phvul.009G063500.1 | 5 | -1 | 1 | 23 |
| 24 | aaaccguuacca Phvul.008G060700.1 | 5 | -1 | 1 | 23 |
| 25 | aaaccguuacca Phvul.011G110000.1 | 5 | -1 | 1 | 23 |
| 26 | aaaccguuacca Phvul.010G003800.1 | 5 | -1 | 1 | 23 |
| 27 | aaaccguuacca Phvul.009G063500.2 | 5 | -1 | 1 | 23 |
| 28 | aaaccguuacca Phvul.009G063500.2 | 5 | -1 | 1 | 23 |
| 29 | aaaccguuacca Phvul.006G206800.1 | 5 | -1 | 1 | 23 |
| 30 | aaaccguuacca Phvul.005G054600.1 | 5 | -1 | 1 | 23 |
| 31 | aaaccguuacca Phvul.005G054600.1 | 5 | -1 | 1 | 23 |
| 32 | aaaccguuacca Phvul.001G024200.1 | 5 | -1 | 1 | 23 |
| 33 | aaaccguuacca Phvul.006G098000.1 | 5 | -1 | 1 | 23 |
| 34 | aaaccguuacca Phvul.006G098000.1 | 5 | -1 | 1 | 23 |
| 35 | aaaccguuacca Phvul.008G033500.1 | 5 | -1 | 1 | 23 |
| 36 | aaaccguuacca Phvul.011G028900.1 | 5 | -1 | 1 | 23 |
| 37 | aaaccguuacca Phvul.011G028900.1 | 5 | -1 | 1 | 23 |
| 38 | aaaccguuacca Phvul.008G036100.2 | 5 | -1 | 1 | 23 |
| 39 | aaaccguuacca Phvul.008G036100.1 | 5 | -1 | 1 | 23 |
| 40 | aaaccguuacca Phvul.004G061900.1 | 5 | -1 | 1 | 23 |
| 41 | aaaccguuacca Phvul.004G061900.1 | 5 | -1 | 1 | 23 |
| 42 | aaaccguuacca Phvul.006G048000.1 | 5 | -1 | 1 | 23 |
| 43 | aaaccguuacca Phvul.007G156900.1 | 5 | -1 | 1 | 23 |
| 44 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 23 |
| 45 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 23 |
| 46 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 23 |
| 47 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 23 |
| 48 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 23 |
| 49 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 23 |
| 50 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 23 |
| 51 | aaaccguuacca Phvul.011G133575.1 | 5 | -1 | 1 | 23 |
| 52 | aaaccguuacca Phvul.006G173500.1 | 5 | -1 | 1 | 23 |
| 53 | aaaccguuacca Phvul.002G183700.1 | 5 | -1 | 1 | 23 |
| 54 | aaaccguuacca Phvul.002G183700.1 | 5 | -1 | 1 | 23 |
| 55 | aaaccguuacca Phvul.005G043000.2 | 5 | -1 | 1 | 23 |
| 56 | aaaccguuacca Phvul.004G019300.2 | 5 | -1 | 1 | 23 |
| 57 | aaaccguuacca Phvul.004G019300.1 | 5 | -1 | 1 | 23 |
| 58 | aaaccguuacca Phvul.004G019300.1 | 5 | -1 | 1 | 23 |
| 59 | aaaccguuacca Phvul.011G069000.1 | 5 | -1 | 1 | 23 |
| 60 | aaaccguuacca Phvul.002G231800.1 | 5 | -1 | 1 | 23 |
| | aaaccguuacca Phvul.L001687.1 | 5 | -1 | 1 | 23 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | aaaccguuacca Phvul.011G102400.1 | 5 | -1 | 1 | 23 |
| 3 | aaaccguuacca Phvul.006G037000.1 | 5 | -1 | 1 | 23 |
| 4 | aaaccguuacca Phvul.009G104850.1 | 5 | -1 | 1 | 23 |
| 5 | aaaccguuacca Phvul.009G104850.1 | 5 | -1 | 1 | 23 |
| 6 | aaaccguuacca Phvul.009G104850.1 | 5 | -1 | 1 | 23 |
| 7 | aaaccguuacca Phvul.009G104850.1 | 5 | -1 | 1 | 23 |
| 8 | aaaccguuacca Phvul.003G158800.1 | 5 | -1 | 1 | 23 |
| 9 | aaaccguuacca Phvul.001G057200.1 | 5 | -1 | 1 | 23 |
| 10 | aaaccguuacca Phvul.001G057200.1 | 5 | -1 | 1 | 23 |
| 11 | aaaccguuacca Phvul.004G057900.1 | 5 | -1 | 1 | 23 |
| 12 | aaaccguuacca Phvul.007G027000.1 | 5 | -1 | 1 | 23 |
| 13 | aaaccguuacca Phvul.007G027000.1 | 5 | -1 | 1 | 23 |
| 14 | aaaccguuacca Phvul.009G063500.1 | 5 | -1 | 1 | 23 |
| 15 | aaaccguuacca Phvul.009G063500.1 | 5 | -1 | 1 | 23 |
| 16 | aaaccguuacca Phvul.008G060700.1 | 5 | -1 | 1 | 23 |
| 17 | aaaccguuacca Phvul.011G110000.1 | 5 | -1 | 1 | 23 |
| 18 | aaaccguuacca Phvul.010G003800.1 | 5 | -1 | 1 | 23 |
| 19 | aaaccguuacca Phvul.009G063500.2 | 5 | -1 | 1 | 23 |
| 20 | aaaccguuacca Phvul.006G206800.1 | 5 | -1 | 1 | 23 |
| 21 | aaaccguuacca Phvul.006G206800.1 | 5 | -1 | 1 | 23 |
| 22 | aaaccguuacca Phvul.005G054600.1 | 5 | -1 | 1 | 23 |
| 23 | aaaccguuacca Phvul.005G054600.1 | 5 | -1 | 1 | 23 |
| 24 | aaaccguuacca Phvul.001G024200.1 | 5 | -1 | 1 | 23 |
| 25 | aaaccguuacca Phvul.006G098000.1 | 5 | -1 | 1 | 23 |
| 26 | aaaccguuacca Phvul.006G098000.1 | 5 | -1 | 1 | 23 |
| 27 | aaaccguuacca Phvul.008G033500.1 | 5 | -1 | 1 | 23 |
| 28 | aaaccguuacca Phvul.011G028900.1 | 5 | -1 | 1 | 23 |
| 29 | aaaccguuacca Phvul.011G028900.1 | 5 | -1 | 1 | 23 |
| 30 | aaaccguuacca Phvul.008G036100.2 | 5 | -1 | 1 | 23 |
| 31 | aaaccguuacca Phvul.008G036100.1 | 5 | -1 | 1 | 23 |
| 32 | aaaccguuacca Phvul.008G036100.1 | 5 | -1 | 1 | 23 |
| 33 | aaaccguuacca Phvul.004G061900.1 | 5 | -1 | 1 | 23 |
| 34 | aaaccguuacca Phvul.006G048000.1 | 5 | -1 | 1 | 23 |
| 35 | aaaccguuacca Phvul.007G156900.1 | 5 | -1 | 1 | 23 |
| 36 | | | | | |
| 37 | | | | | |
| 38 | | | | | |
| 39 | | | | | |
| 40 | | | | | |
| 41 | | | | | |
| 42 | | | | | |
| 43 | | | | | |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | Target_start | Target_end | miRNA_align | alignment | Target_align | Inhibition | Target_Desc. |
|----|--------------|------------|-------------|------------|-----------------------|--------------|--------------|
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | | 119 | 140 | AAACCGUUAC | :: :: :::::GCCUUUGUC | /Cleavage | pacid=371619 |
| 4 | | 646 | 667 | AAACCGUUAC | :: ::::: :::AUUUUAAUA | /Cleavage | pacid=371509 |
| 5 | | | | | | | |
| 6 | | 1051 | 1072 | AAACCGUUAC | :: :::::UCGUGAAUA | /Cleavage | pacid=371614 |
| 7 | | 118 | 140 | AAACCGUUAC | :: :: :::::GGCCUUUGU | /Cleavage | pacid=371619 |
| 8 | | | | | | | |
| 9 | | 645 | 667 | AAACCGUUAC | :: ::::: :::UAUUUAAU | /Cleavage | pacid=371509 |
| 10 | | 118 | 140 | AAACCGUUAC | :: :: :::::GGCCUUUGU | /Cleavage | pacid=371619 |
| 11 | | 645 | 667 | AAACCGUUAC | :: ::::: :::UAUUUAAU | /Cleavage | pacid=371509 |
| 12 | | 138 | 159 | AAACCGUUAC | :: ::::: AAUUCAGUA | (Translation | pacid=371489 |
| 13 | | | | | | | |
| 14 | | 645 | 666 | AAACCGUUAC | :: ::::: :::GGCUCAGUA | /Translation | pacid=371593 |
| 15 | | 1217 | 1238 | AAACCGUUAC | :: :::::ACCACAGUAA | Cleavage | pacid=371664 |
| 16 | | 193 | 214 | AAACCGUUAC | :: :::::GUUUUGGUG | Cleavage | pacid=371513 |
| 17 | | | | | | | |
| 18 | | 1819 | 1840 | AAACCGUUAC | :: :::::UUCUCAGAA | /Translation | pacid=371635 |
| 19 | | 2711 | 2732 | AAACCGUUAC | :: :::::AUAAUGGUG | /Cleavage | pacid=371550 |
| 20 | | 2714 | 2735 | AAACCGUUAC | :: :::::AUAAUGGUG | /Cleavage | pacid=371550 |
| 21 | | | | | | | |
| 22 | | 321 | 342 | AAACCGUUAC | :: :::::GUUUCAGAA | (Cleavage | pacid=371574 |
| 23 | | 298 | 319 | AAACCGUUAC | :: :::::GUUUCAGAA | (Cleavage | pacid=371574 |
| 24 | | 316 | 337 | AAACCGUUAC | :: :::::GUUUCAGAA | (Cleavage | pacid=371574 |
| 25 | | | | | | | |
| 26 | | 28 | 49 | AAACCGUUAC | :: :::::GAGACAGCA | /Cleavage | pacid=371620 |
| 27 | | 1182 | 1203 | AAACCGUUAC | :: :::::AUUUCAGAG | /Cleavage | pacid=371556 |
| 28 | | 1264 | 1285 | AAACCGUUAC | :: :::::AUUUCAGAG | /Cleavage | pacid=371556 |
| 29 | | | | | | | |
| 30 | | 1264 | 1285 | AAACCGUUAC | :: :::::AUUUCAGAG | /Cleavage | pacid=371556 |
| 31 | | 43 | 64 | AAACCGUUAC | :: :::::GUUUUGAUG | Cleavage | pacid=371470 |
| 32 | | 43 | 64 | AAACCGUUAC | :: :::::GUUUUGAUG | Cleavage | pacid=371470 |
| 33 | | | | | | | |
| 34 | | 121 | 142 | AAACCGUUAC | :: :::::CCAUCAGCAA | Cleavage | pacid=371453 |
| 35 | | 137 | 159 | AAACCGUUAC | :: :::::CAAUUCAGU | /Translation | pacid=371489 |
| 36 | | 644 | 666 | AAACCGUUAC | :: :::::GGGCUCAGU | /Translation | pacid=371593 |
| 37 | | | | | | | |
| 38 | | 1216 | 1238 | AAACCGUUAC | :: :::::AACCACAGUA | Cleavage | pacid=371664 |
| 39 | | 27 | 49 | AAACCGUUAC | :: :::::AGAGACAGCA | /Cleavage | pacid=371620 |
| 40 | | 192 | 214 | AAACCGUUAC | :: :::::GGUUUUGGU | Cleavage | pacid=371513 |
| 41 | | 320 | 342 | AAACCGUUAC | :: :::::AGUUUCAGA | /Cleavage | pacid=371574 |
| 42 | | | | | | | |
| 43 | | 297 | 319 | AAACCGUUAC | :: :::::AGUUUCAGA | /Cleavage | pacid=371574 |
| 44 | | 315 | 337 | AAACCGUUAC | :: :::::AGUUUCAGA | /Cleavage | pacid=371574 |
| 45 | | | | | | | |
| 46 | | 1818 | 1840 | AAACCGUUAC | :: :::::GUUCUCAGA | /Translation | pacid=371635 |
| 47 | | 2710 | 2732 | AAACCGUUAC | :: :::::AAUAAUGGU | (Cleavage | pacid=371550 |
| 48 | | 2713 | 2735 | AAACCGUUAC | :: :::::AAUAAUGGU | (Cleavage | pacid=371550 |
| 49 | | | | | | | |
| 50 | | 137 | 159 | AAACCGUUAC | :: :::::CAAUUCAGU | /Translation | pacid=371489 |
| 51 | | 644 | 666 | AAACCGUUAC | :: :::::GGGCUCAGU | /Translation | pacid=371593 |
| 52 | | 1216 | 1238 | AAACCGUUAC | :: :::::AACCACAGUA | Cleavage | pacid=371664 |
| 53 | | | | | | | |
| 54 | | 27 | 49 | AAACCGUUAC | :: :::::AGAGACAGCA | /Cleavage | pacid=371620 |
| 55 | | 192 | 214 | AAACCGUUAC | :: :::::GGUUUUGGU | Cleavage | pacid=371513 |
| 56 | | 320 | 342 | AAACCGUUAC | :: :::::AGUUUCAGA | /Cleavage | pacid=371574 |
| 57 | | | | | | | |
| 58 | | 297 | 319 | AAACCGUUAC | :: :::::AGUUUCAGA | /Cleavage | pacid=371574 |
| 59 | | 315 | 337 | AAACCGUUAC | :: :::::AGUUUCAGA | /Cleavage | pacid=371574 |
| 60 | | | | | | | |
| | | 1818 | 1840 | AAACCGUUAC | :: :::::GUUCUCAGA | /Translation | pacid=371635 |
| | | 2710 | 2732 | AAACCGUUAC | :: :::::AAUAAUGGU | (Cleavage | pacid=371550 |

| | | | | |
|----|------|-------------------|------------------------------|--------------|
| 1 | | | | |
| 2 | 2713 | 2735 AAACCGUUAC |: AAUAAUGGU/Cleavage | pacid=371550 |
| 3 | 1940 | 1961 AAACCGUUAC:: |: AAAUUAGUA/Cleavage | pacid=371781 |
| 4 | 1944 | 1965 AAACCGUUAC:: |: AAAUUAGUA/Cleavage | pacid=371781 |
| 5 | | | | |
| 6 | 1972 | 1993 AAACCGUUAC:: |: AAAUUAGUA/Cleavage | pacid=371781 |
| 7 | 156 | 177 AAACCGUUAC |: GUUUGAGUA Cleavage | pacid=371748 |
| 8 | 1163 | 1184 AAACCGUUAC: |: AUCUCGGUC/Cleavage | pacid=371440 |
| 9 | | | | |
| 10 | 1130 | 1151 AAACCGUUAC:: |: GACAAGGUC/Cleavage | pacid=371723 |
| 11 | 968 | 989 AAACCGUUAC: |: AUCAUAGUG/Translation | pacid=371726 |
| 12 | 968 | 989 AAACCGUUAC: |: AUCAUAGUG/Translation | pacid=371726 |
| 13 | 968 | 989 AAACCGUUAC: |: AUCAUAGUG/Translation | pacid=371726 |
| 14 | 968 | 989 AAACCGUUAC: |: AUCAUAGUG/Translation | pacid=371726 |
| 15 | 968 | 989 AAACCGUUAC: |: AUCAUAGUG/Translation | pacid=371726 |
| 16 | 711 | 732 AAACCGUUAC |: AUGCAAGUA/Cleavage | pacid=371777 |
| 17 | | | | |
| 18 | 2616 | 2637 AAACCGUUAC |: GUGGCAGUA/Cleavage | pacid=371537 |
| 19 | 2616 | 2637 AAACCGUUAC |: GUGGCAGUA/Cleavage | pacid=371537 |
| 20 | 2616 | 2637 AAACCGUUAC |: GUGGCAGUA/Cleavage | pacid=371537 |
| 21 | 2616 | 2637 AAACCGUUAC |: GUGGCAGUA/Cleavage | pacid=371537 |
| 22 | 2616 | 2637 AAACCGUUAC |: GUGGCAGUA/Cleavage | pacid=371537 |
| 23 | 3174 | 3195 AAACCGUUAC |: UCUUUGGUA Cleavage | pacid=371783 |
| 24 | 2616 | 2637 AAACCGUUAC |: GUGGCAGUA/Cleavage | pacid=371537 |
| 25 | 2616 | 2637 AAACCGUUAC |: GUGGCAGUA/Cleavage | pacid=371537 |
| 26 | 2616 | 2637 AAACCGUUAC |: GUGGCAGUA/Cleavage | pacid=371537 |
| 27 | 724 | 745 AAACCGUUAC |: CAGGUGGUG/Cleavage | pacid=371648 |
| 28 | 702 | 723 AAACCGUUAC |: CCGUCAGUG/Cleavage | pacid=371659 |
| 29 | | | | |
| 30 | 1489 | 1510 AAACCGUUAC |: CAUUAACUA/Cleavage | pacid=371463 |
| 31 | 1252 | 1273 AAACCGUUAC |: UUAACAGUG/Translation | pacid=371746 |
| 32 | 503 | 524 AAACCGUUAC |: GUAGUAGUA/Translation | pacid=371631 |
| 33 | 240 | 261 AAACCGUUAC |: GUUUCCUG/Cleavage | pacid=371598 |
| 34 | 342 | 363 AAACCGUUAC |: GUUUCCUG/Cleavage | pacid=371598 |
| 35 | 990 | 1011 AAACCGUUAC: |: GAAUUAGCA/Cleavage | pacid=371773 |
| 36 | 1310 | 1331 AAACCGUUAC |: GGUUCAACA/Cleavage | pacid=371619 |
| 37 | 381 | 402 AAACCGUUAC: |: GAAUCAGAA/Translation | pacid=371707 |
| 38 | 1572 | 1593 AAACCGUUAC |: CUUUGAGUA/Cleavage | pacid=371530 |
| 39 | 1575 | 1596 AAACCGUUAC |: CUUUGAGUA/Cleavage | pacid=371530 |
| 40 | 1939 | 1961 AAACCGUUAC:: |: AAAUUAGU/Cleavage | pacid=371781 |
| 41 | 1943 | 1965 AAACCGUUAC:: |: AAAUUAGU/Cleavage | pacid=371781 |
| 42 | 1971 | 1993 AAACCGUUAC:: |: AAAUUAGU/Cleavage | pacid=371781 |
| 43 | 155 | 177 AAACCGUUAC: |: AGUUUGAGU Cleavage | pacid=371748 |
| 44 | 1129 | 1151 AAACCGUUAC:: |: GGACAAGGU/Cleavage | pacid=371723 |
| 45 | 1162 | 1184 AAACCGUUAC: |: CAUCUCGGUC/Cleavage | pacid=371440 |
| 46 | 967 | 989 AAACCGUUAC: |: CAUCAUAGU/Translation | pacid=371726 |
| 47 | 967 | 989 AAACCGUUAC: |: CAUCAUAGU/Translation | pacid=371726 |
| 48 | 967 | 989 AAACCGUUAC: |: CAUCAUAGU/Translation | pacid=371726 |
| 49 | 967 | 989 AAACCGUUAC: |: CAUCAUAGU/Translation | pacid=371726 |
| 50 | 239 | 261 AAACCGUUAC |: GGUUCCCU/Cleavage | pacid=371598 |
| 51 | 341 | 363 AAACCGUUAC |: GGUUCCCU/Cleavage | pacid=371598 |
| 52 | 380 | 402 AAACCGUUAC: |: GGAAUCAGA/Translation | pacid=371707 |
| 53 | 1939 | 1961 AAACCGUUAC:: |: AAAUUAGU/Cleavage | pacid=371781 |
| 54 | 1943 | 1965 AAACCGUUAC:: |: AAAUUAGU/Cleavage | pacid=371781 |

| | | | |
|----|------|--|--------------|
| 1 | | | |
| 2 | 1971 | 1993 AAACCGUUAC:: :::: :::: ::::AAAUUAGU/Cleavage | pacid=371781 |
| 3 | 155 | 177 AAACCGUUAC: . : :::: :::: ::::AGUUUGAGU Cleavage | pacid=371748 |
| 4 | 1129 | 1151 AAACCGUUAC.: : : : :::: :::: ::::GGACAAGGU(Cleavage | pacid=371723 |
| 5 | 1162 | 1184 AAACCGUUAC : : : : :::: :::: ::::CAUCUCGGU(Cleavage | pacid=371440 |
| 6 | 967 | 989 AAACCGUUAC : : : : :::: :::: ::::CAUCAUAGU(Translation | pacid=371726 |
| 7 | 967 | 989 AAACCGUUAC : : : : :::: :::: ::::CAUCAUAGU(Translation | pacid=371726 |
| 8 | 967 | 989 AAACCGUUAC : : : : :::: :::: ::::CAUCAUAGU(Translation | pacid=371726 |
| 9 | 967 | 989 AAACCGUUAC : : : : :::: :::: ::::CAUCAUAGU(Translation | pacid=371726 |
| 10 | 967 | 989 AAACCGUUAC : : : : :::: :::: ::::CAUCAUAGU(Translation | pacid=371726 |
| 11 | 967 | 989 AAACCGUUAC : : : : :::: :::: ::::CAUCAUAGU(Translation | pacid=371726 |
| 12 | 239 | 261 AAACCGUUAC : : : : :::: :::: ::::GGUUUCCCU(Cleavage | pacid=371598 |
| 13 | 341 | 363 AAACCGUUAC : : : : :::: :::: ::::GGUUUCCCU(Cleavage | pacid=371598 |
| 14 | 380 | 402 AAACCGUUAC.: : : : :::: :::: ::::GGAAUCAGA/Translation | pacid=371707 |
| 15 | 520 | 541 AAACCGUUAC:: : : : :::: :::: :::: AACACAGUG(Cleavage | pacid=371712 |
| 16 | 188 | 209 AAACCGUUAC:: : : : :::: :::: :::: AAUUUAGUG.Cleavage | pacid=371425 |
| 17 | 188 | 209 AAACCGUUAC:: : : : :::: :::: :::: AAUUUAGUG.Cleavage | pacid=371425 |
| 18 | 550 | 571 AAACCGUUAC:: : : : :::: :::: :::: AAUUUAGUG.Cleavage | pacid=371425 |
| 19 | 550 | 571 AAACCGUUAC:: : : : :::: :::: :::: AAUUUAGUG.Cleavage | pacid=371425 |
| 20 | 1347 | 1370 AAACCGUUAC.: : : : :::: :::: ::::GACUGACAGI Cleavage | pacid=371501 |
| 21 | 1394 | 1417 AAACCGUUAC.: : : : :::: :::: ::::GACUGACAGI Cleavage | pacid=371501 |
| 22 | 1475 | 1498 AAACCGUUAC.: : : : :::: :::: ::::GACUGACAGI Cleavage | pacid=371501 |
| 23 | 1480 | 1503 AAACCGUUAC.: : : : :::: :::: ::::GACUGACAGI Cleavage | pacid=371501 |
| 24 | 1480 | 1503 AAACCGUUAC.: : : : :::: :::: ::::GACUGACAGI Cleavage | pacid=371501 |
| 25 | 593 | 614 AAACCGUUAC.: : : : :::: :::: :::: AAUACAGUG(Cleavage | pacid=371679 |
| 26 | 593 | 614 AAACCGUUAC.: : : : :::: :::: :::: AAUACAGUG(Cleavage | pacid=371679 |
| 27 | 1109 | 1130 AAACCGUUAC.: : : : :::: :::: :::: AACUUCAUG(Cleavage | pacid=371611 |
| 28 | 224 | 245 AAACCGUUAC.: : : : :::: :::: :::: GAUUCAGUA(Cleavage | pacid=371431 |
| 29 | 224 | 245 AAACCGUUAC.: : : : :::: :::: :::: GAUUCAGUA(Cleavage | pacid=371431 |
| 30 | 1397 | 1418 AAACCGUUAC : : : : :::: :::: :::: UACUCAGCA Cleavage | pacid=371726 |
| 31 | 676 | 697 AAACCGUUAC : : : : :::: :::: :::: AUGACAGUG/Cleavage | pacid=371501 |
| 32 | 676 | 697 AAACCGUUAC : : : : :::: :::: :::: AUGACAGUG/Cleavage | pacid=371501 |
| 33 | 789 | 810 AAACCGUUAC : : : : :::: :::: :::: CUUUUAGUA(Cleavage | pacid=371645 |
| 34 | 820 | 841 AAACCGUUAC : : : : :::: :::: :::: UUACUAGAG/Cleavage | pacid=371457 |
| 35 | 820 | 841 AAACCGUUAC : : : : :::: :::: :::: UUACUAGAG/Cleavage | pacid=371457 |
| 36 | 665 | 686 AAACCGUUAC : : : : :::: :::: :::: GUGGUGGUG Cleavage | pacid=371548 |
| 37 | 6 | 27 AAACCGUUAC.: : : : :::: :::: :::: AAU AUUGUG Cleavage | pacid=371690 |
| 38 | 868 | 889 AAACCGUUAC : : : : :::: :::: :::: GUAGUAGUA.Cleavage | pacid=371654 |
| 39 | 868 | 889 AAACCGUUAC : : : : :::: :::: :::: GUAGUAGUA.Cleavage | pacid=371654 |
| 40 | 868 | 889 AAACCGUUAC : : : : :::: :::: :::: GUAGUAGUA.Cleavage | pacid=371654 |
| 41 | 495 | 516 AAACCGUUAC : : : : :::: :::: :::: CAAUCGGUG(Cleavage | pacid=371552 |
| 42 | 1238 | 1259 AAACCGUUAC.: : : : :::: :::: :::: GACAAGGUC/Cleavage | pacid=371723 |
| 43 | 1031 | 1052 AAACCGUUAC.: : : : :::: :::: :::: GGCAAGGUC/Cleavage | pacid=371723 |
| 44 | 791 | 812 AAACCGUUAC.: : : : :::: :::: :::: AGUUCAUUA/Translation | pacid=371763 |
| 45 | 988 | 1009 AAACCGUUAC.: : : : :::: :::: :::: GACACAUUG(Cleavage | pacid=371655 |
| 46 | 988 | 1009 AAACCGUUAC.: : : : :::: :::: :::: GACACAUUG(Cleavage | pacid=371655 |
| 47 | 584 | 605 AAACCGUUAC : : : : :::: :::: :::: AUAAUGGUA/Cleavage | pacid=371741 |
| 48 | 1386 | 1407 AAACCGUUAC : : : : :::: :::: :::: CUAUCAGUG/Cleavage | pacid=371423 |
| 49 | 160 | 181 AAACCGUUAC : : : : :::: :::: :::: CACUAUGUA/Cleavage | pacid=371773 |
| 50 | 160 | 181 AAACCGUUAC : : : : :::: :::: :::: CACUAUGUA/Cleavage | pacid=371773 |
| 51 | 448 | 469 AAACCGUUAC : : : : :::: :::: :::: AUGUCAGUG/Cleavage | pacid=371702 |
| 52 | 501 | 522 AAACCGUUAC : : : : :::: :::: :::: AUGUCAGUG/Cleavage | pacid=371702 |
| 53 | 517 | 538 AAACCGUUAC : : : : :::: :::: :::: AUGUCAGUG/Cleavage | pacid=371702 |
| 54 | 517 | 538 AAACCGUUAC : : : : :::: :::: :::: AUGUCAGUG/Cleavage | pacid=371702 |
| 55 | 3048 | 3069 AAACCGUUAC : : : : :::: :::: :::: UGUUCAGUG.Translation | pacid=371717 |
| 56 | 814 | 835 AAACCGUUAC : : : : :::: :::: :::: UGUUCGGUG.Translation | pacid=371439 |
| 57 | 814 | 835 AAACCGUUAC : : : : :::: :::: :::: UGUUCGGUG.Translation | pacid=371439 |
| 58 | 443 | 464 AAACCGUUAC : : : : :::: :::: :::: UGCUCGGUU(Cleavage | pacid=371670 |
| 59 | 1174 | 1195 AAACCGUUAC : : : : :::: :::: :::: GUGUUGGUG Cleavage | pacid=371670 |
| 60 | 32 | 53 AAACCGUUAC.: : : : :::: :::: :::: AAAUUGGUG/Cleavage | pacid=371540 |
| 60 | 37 | 58 AAACCGUUAC.: : : : :::: :::: :::: AAAUUGGUG/Cleavage | pacid=371540 |

| | | | |
|----|------|-------------------|------------------------------------|
| 1 | | | |
| 2 | 442 | 463 AAACCGUUAC | UGCUCGGUU Cleavage pacid=371668 |
| 3 | 1173 | 1194 AAACCGUUAC | :GUGUUGGUG Cleavage pacid=371668 |
| 4 | 41 | 62 AAACCGUUAC:: | AAAAUGGUG Cleavage pacid=371540 |
| 5 | 113 | 134 AAACCGUUAC:: | AAAUUAGUU Translation pacid=371600 |
| 6 | 291 | 312 AAACCGUUAC:: | GAAUUUCCUG Cleavage pacid=371598 |
| 7 | 278 | 299 AAACCGUUAC:: | GAAUUAGUA Translation pacid=371432 |
| 8 | 278 | 299 AAACCGUUAC:: | GAAUUAGUA Translation pacid=371432 |
| 9 | 1831 | 1852 AAACCGUUAC:: | AAGUUAAUG Cleavage pacid=371641 |
| 10 | 1059 | 1080 AAACCGUUAC | :ACAGCAGUAC Cleavage pacid=371626 |
| 11 | 2504 | 2525 AAACCGUUAC:: | AAAUCAGAA Translation pacid=371527 |
| 12 | 187 | 209 AAACCGUUAC:: | AAAUUUAGU Cleavage pacid=371425 |
| 13 | 549 | 571 AAACCGUUAC:: | AAAUUUAGU Cleavage pacid=371425 |
| 14 | 519 | 541 AAACCGUUAC | :UACACAGU Cleavage pacid=371712 |
| 15 | 1108 | 1130 AAACCGUUAC:: | GAACUUCAU Cleavage pacid=371611 |
| 16 | 1346 | 1370 AAACCGUUAC | :CGACUGACAC Cleavage pacid=371501 |
| 17 | 1393 | 1417 AAACCGUUAC | :CGACUGACAC Cleavage pacid=371501 |
| 18 | 1474 | 1498 AAACCGUUAC | :CGACUGACAC Cleavage pacid=371501 |
| 19 | 1479 | 1503 AAACCGUUAC | :CGACUGACAC Cleavage pacid=371501 |
| 20 | 592 | 614 AAACCGUUAC | :CAAUACAGU Cleavage pacid=371679 |
| 21 | 223 | 245 AAACCGUUAC | :UGAUUCAGU Cleavage pacid=371431 |
| 22 | 664 | 686 AAACCGUUAC | :GGUGGUGGU Cleavage pacid=371548 |
| 23 | 1237 | 1259 AAACCGUUAC:: | GGACAAGGU Cleavage pacid=371723 |
| 24 | 1030 | 1052 AAACCGUUAC:: | GGGCAAGGU Cleavage pacid=371723 |
| 25 | 277 | 299 AAACCGUUAC:: | AGAAUUAGU Translation pacid=371432 |
| 26 | 277 | 299 AAACCGUUAC:: | AGAAUUAGU Translation pacid=371432 |
| 27 | 1058 | 1080 AAACCGUUAC | :AACAGCAGU Cleavage pacid=371626 |
| 28 | 790 | 812 AAACCGUUAC:: | GAGUUCAUU Translation pacid=371763 |
| 29 | 987 | 1009 AAACCGUUAC:: | GGACACAUU Cleavage pacid=371655 |
| 30 | 1396 | 1418 AAACCGUUAC | :UUACUCAGC Cleavage pacid=371726 |
| 31 | 675 | 697 AAACCGUUAC | :UAUGACAGU Cleavage pacid=371501 |
| 32 | 788 | 810 AAACCGUUAC | :ACUUUUAGU Cleavage pacid=371645 |
| 33 | 819 | 841 AAACCGUUAC | :UUUACUAGA Cleavage pacid=371457 |
| 34 | 31 | 53 AAACCGUUAC:: | GAAAAUGGU Cleavage pacid=371540 |
| 35 | 36 | 58 AAACCGUUAC:: | GAAAAUGGU Cleavage pacid=371540 |
| 36 | 5 | 27 AAACCGUUAC | :CAAUAUUGU Cleavage pacid=371690 |
| 37 | 867 | 889 AAACCGUUAC | :AGUAGUAGU Cleavage pacid=371654 |
| 38 | 867 | 889 AAACCGUUAC | :AGUAGUAGU Cleavage pacid=371654 |
| 39 | 494 | 516 AAACCGUUAC | :GCAAUCGGU Cleavage pacid=371552 |
| 40 | 40 | 62 AAACCGUUAC:: | GAAAAUGGU Cleavage pacid=371540 |
| 41 | 112 | 134 AAACCGUUAC:: | GAAUUUAGU Translation pacid=371600 |
| 42 | 343 | 365 AAACCGUUAC:: | AACUUCAGU Cleavage pacid=371523 |
| 43 | 583 | 605 AAACCGUUAC | :UAUAAUGGU Cleavage pacid=371741 |
| 44 | 3047 | 3069 AAACCGUUAC:: | AUGUUCAGU Translation pacid=371717 |
| 45 | 290 | 312 AAACCGUUAC:: | GGAUUUCCU Cleavage pacid=371598 |
| 46 | 323 | 345 AAACCGUUAC:: | AAGGACAGU Cleavage pacid=371570 |
| 47 | 1385 | 1407 AAACCGUUAC | :ACUAUCAGU Cleavage pacid=371423 |

| | | | |
|----|------|--|--------------|
| 1 | | | |
| 2 | 159 | 181 AAACCGUUAC :: ::::: GCACUAUGU/Cleavage | pacid=371773 |
| 3 | 1830 | 1852 AAACCGUUAC:: :: ::::: GAAGUUAUU/Cleavage | pacid=371641 |
| 4 | 447 | 469 AAACCGUUAC ::::: GAUGUCAGU/Cleavage | pacid=371702 |
| 5 | 187 | 209 AAACCGUUAC::: ::::: AAAUUUAGU/Cleavage | pacid=371425 |
| 6 | 549 | 571 AAACCGUUAC::: ::::: AAAUUUAGU/Cleavage | pacid=371425 |
| 7 | 519 | 541 AAACCGUUAC ::::: UAACACAGU/Cleavage | pacid=371712 |
| 8 | | | |
| 9 | 1108 | 1130 AAACCGUUAC::: ::::: GAACUUCAU/Cleavage | pacid=371611 |
| 10 | 1346 | 1370 AAACCGUUAC ::::: CGACUGACAC/Cleavage | pacid=371501 |
| 11 | 1393 | 1417 AAACCGUUAC ::::: CGACUGACAC/Cleavage | pacid=371501 |
| 12 | 1474 | 1498 AAACCGUUAC ::::: CGACUGACAC/Cleavage | pacid=371501 |
| 13 | 1479 | 1503 AAACCGUUAC ::::: CGACUGACAC/Cleavage | pacid=371501 |
| 14 | 592 | 614 AAACCGUUAC ::::: CAAUACAGU/Cleavage | pacid=371679 |
| 15 | 223 | 245 AAACCGUUAC ::::: UGAUUCAGU/Cleavage | pacid=371431 |
| 16 | 664 | 686 AAACCGUUAC ::::: GGUGGUGGU/Cleavage | pacid=371548 |
| 17 | 1237 | 1259 AAACCGUUAC::: ::::: GGACAAGGU/Cleavage | pacid=371723 |
| 18 | 1030 | 1052 AAACCGUUAC::: ::::: GGGCAAGGU/Cleavage | pacid=371723 |
| 19 | 277 | 299 AAACCGUUAC::: ::::: AGAAUUAGU/Translation | pacid=371432 |
| 20 | 277 | 299 AAACCGUUAC::: ::::: AGAAUUAGU/Translation | pacid=371432 |
| 21 | 1058 | 1080 AAACCGUUAC ::::: AACAGCAGU/Cleavage | pacid=371626 |
| 22 | 790 | 812 AAACCGUUAC::: ::::: GAGUUCAUU/Translation | pacid=371763 |
| 23 | 987 | 1009 AAACCGUUAC::: ::::: GGACACAUU/Cleavage | pacid=371655 |
| 24 | 1396 | 1418 AAACCGUUAC ::::: UUACUCAGC/Cleavage | pacid=371726 |
| 25 | 675 | 697 AAACCGUUAC ::::: UAUGACAGU/Cleavage | pacid=371501 |
| 26 | 788 | 810 AAACCGUUAC ::::: ACUUUUAGU/Cleavage | pacid=371645 |
| 27 | 819 | 841 AAACCGUUAC ::::: UUUACUAGA/Cleavage | pacid=371457 |
| 28 | 31 | 53 AAACCGUUAC::: ::::: GAAAUGGU/Cleavage | pacid=371540 |
| 29 | 36 | 58 AAACCGUUAC::: ::::: GAAAUGGU/Cleavage | pacid=371540 |
| 30 | 5 | 27 AAACCGUUAC ::::: CAAUAUUGU/Cleavage | pacid=371690 |
| 31 | 867 | 889 AAACCGUUAC ::::: AGUAGUAGU/Cleavage | pacid=371654 |
| 32 | 867 | 889 AAACCGUUAC ::::: AGUAGUAGU/Cleavage | pacid=371654 |
| 33 | 494 | 516 AAACCGUUAC ::::: GCAAUCGGU/Cleavage | pacid=371552 |
| 34 | 40 | 62 AAACCGUUAC::: ::::: GAAAUGGU/Cleavage | pacid=371540 |
| 35 | 112 | 134 AAACCGUUAC::: ::::: GAAAUUAGU/Translation | pacid=371600 |
| 36 | 343 | 365 AAACCGUUAC::: ::::: AACUUCAGU/Cleavage | pacid=371523 |
| 37 | 583 | 605 AAACCGUUAC ::::: UAUAAUGGU/Cleavage | pacid=371741 |
| 38 | 3047 | 3069 AAACCGUUAC::: ::::: AUGUUCAGU/Translation | pacid=371717 |
| 39 | 290 | 312 AAACCGUUAC::: ::::: GGAUUUCCU/Cleavage | pacid=371598 |
| 40 | 323 | 345 AAACCGUUAC::: ::::: AAGGACAGU/Cleavage | pacid=371570 |
| 41 | 1385 | 1407 AAACCGUUAC ::::: ACUAUCAGU/Cleavage | pacid=371423 |
| 42 | 159 | 181 AAACCGUUAC ::::: GCACUAUGU/Cleavage | pacid=371773 |
| 43 | 1830 | 1852 AAACCGUUAC::: ::::: GAAGUUAUU/Cleavage | pacid=371641 |
| 44 | 447 | 469 AAACCGUUAC ::::: GAUGUCAGU/Cleavage | pacid=371702 |
| 45 | 500 | 522 AAACCGUUAC ::::: GAUGUCAGU/Cleavage | pacid=371702 |
| 46 | 1264 | 1285 AAACCGUUAC::: ::::: GAUUCGGUG/Cleavage | pacid=371548 |
| 47 | 514 | 535 AAACCGUUAC::: ::::: GAAUUGGCA/Cleavage | pacid=371548 |
| 48 | 838 | 859 AAACCGUUAC::: ::::: GAAUUGGCA/Cleavage | pacid=371548 |

| | | | |
|----|------|---|--------------|
| 1 | | | |
| 2 | 904 | 925 AAACCGUUAC:: :...:: :GAAUUGGCA/Cleavage | pacid=371548 |
| 3 | 1102 | 1123 AAACCGUUAC:: :...:: :GAAUUGGCA/Cleavage | pacid=371548 |
| 4 | 1054 | 1075 AAACCGUUAC : :...:: :GUUUAGGUG Cleavage | pacid=371548 |
| 5 | 1535 | 1556 AAACCGUUAC:: :...:: :AACACAGUAA Cleavage | pacid=371621 |
| 6 | 1540 | 1561 AAACCGUUAC:: :...:: :AACACAGUAA Cleavage | pacid=371621 |
| 7 | | | |
| 8 | 625 | 646 AAACCGUUAC :...:: :GAGCAGGUG/Cleavage | pacid=371513 |
| 9 | 715 | 736 AAACCGUUAC :...:: :GAGCAGGUG/Cleavage | pacid=371513 |
| 10 | 859 | 880 AAACCGUUAC :...:: :GAGCAGGUG/Cleavage | pacid=371513 |
| 11 | 958 | 979 AAACCGUUAC:: :...:: :GACCCGUAA Cleavage | pacid=371460 |
| 12 | 509 | 530 AAACCGUUAC:: :...:: :AGCGUGGUG Cleavage | pacid=371718 |
| 13 | 522 | 543 AAACCGUUAC:: :...:: :AACUCACAAA Cleavage | pacid=371779 |
| 14 | 311 | 332 AAACCGUUAC:: :...:: :GAUUUGGUG Cleavage | pacid=371548 |
| 15 | 328 | 349 AAACCGUUAC:: :...:: :AAUGCAGUG/Cleavage | pacid=371642 |
| 16 | 132 | 153 AAACCGUUAC:: :...:: :AACACAGCAA Cleavage | pacid=371533 |
| 17 | 1460 | 1481 AAACCGUUAC :...:: :GUCAUGGUU Cleavage | pacid=371723 |
| 18 | 1020 | 1041 AAACCGUUAC:: :...:: :GGCUUGGUG Translation | pacid=371550 |
| 19 | 608 | 629 AAACCGUUAC :...:: :AUUAUGGUU Cleavage | pacid=371741 |
| 20 | 3142 | 3163 AAACCGUUAC :...:: :UAUUCAGCAC Cleavage | pacid=371544 |
| 21 | 2698 | 2719 AAACCGUUAC:: :...:: :AAUUCACUAC Cleavage | pacid=371680 |
| 22 | 1224 | 1245 AAACCGUUAC :...:: :UAUUCAGUG/ Translation | pacid=371578 |
| 23 | 155 | 176 AAACCGUUAC :...:: :UUCUUGGUC Cleavage | pacid=371617 |
| 24 | 210 | 231 AAACCGUUAC :...:: :GUUUCAGUG Cleavage | pacid=371708 |
| 25 | 797 | 818 AAACCGUUAC :...:: :GUUUUGGUA Translation | pacid=371501 |
| 26 | 361 | 382 AAACCGUUAC :...:: :GUGGCGGUA Cleavage | pacid=371573 |
| 27 | 788 | 809 AAACCGUUAC :...:: :GGAGUGGUA Cleavage | pacid=371583 |
| 28 | 682 | 703 AAACCGUUAC :...:: :GGAGUGGUA Cleavage | pacid=371731 |
| 29 | 350 | 371 AAACCGUUAC:: :...:: :GACUCCUGC Cleavage | pacid=371712 |
| 30 | 550 | 571 AAACCGUUAC:: :...:: :GGUUUGGUG Cleavage | pacid=371609 |
| 31 | 2 | 23 AAACCGUUAC:: :...:: :AACACAUAGA Cleavage | pacid=371609 |
| 32 | 1144 | 1165 AAACCGUUAC:: :...:: :AUCUUAGUG Cleavage | pacid=371512 |
| 33 | 2 | 23 AAACCGUUAC:: :...:: :AACACAUAGA Cleavage | pacid=371609 |
| 34 | 419 | 440 AAACCGUUAC:: :...:: :GACUCCUGC Cleavage | pacid=371741 |
| 35 | 712 | 733 AAACCGUUAC :...:: :CAAUAGUG Cleavage | pacid=371699 |
| 36 | 1245 | 1266 AAACCGUUAC :...:: :GUCUUAGUG Cleavage | pacid=371562 |
| 37 | 265 | 286 AAACCGUUAC:: :...:: :AGUUCAGAA Cleavage | pacid=371626 |
| 38 | 445 | 466 AAACCGUUAC:: :...:: :AGUUAGGUG Cleavage | pacid=371737 |
| 39 | 1970 | 1991 AAACCGUUAC :...:: :UGUUUACUA Cleavage | pacid=371509 |
| 40 | 1324 | 1345 AAACCGUUAC :...:: :GCUAUGGUA Cleavage | pacid=371526 |
| 41 | 1263 | 1285 AAACCGUUAC:: :...:: :GGAUUCGGU Cleavage | pacid=371548 |
| 42 | 513 | 535 AAACCGUUAC:: :...:: :GGAAUUGGC Cleavage | pacid=371548 |
| 43 | 837 | 859 AAACCGUUAC:: :...:: :GGAAUUGGC Cleavage | pacid=371548 |
| 44 | 903 | 925 AAACCGUUAC:: :...:: :GGAAUUGGC Cleavage | pacid=371548 |
| 45 | 1101 | 1123 AAACCGUUAC:: :...:: :GGAAUUGGC Cleavage | pacid=371548 |
| 46 | 1053 | 1075 AAACCGUUAC :...:: :GGUUUAGGU Cleavage | pacid=371548 |
| 47 | 508 | 530 AAACCGUUAC:: :...:: :AAGCGUGGU Cleavage | pacid=371718 |
| 48 | 521 | 543 AAACCGUUAC:: :...:: :AACUCACAA Cleavage | pacid=371779 |
| 49 | | | |
| 50 | | | |
| 51 | | | |
| 52 | | | |
| 53 | | | |
| 54 | | | |
| 55 | | | |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

| | | | |
|----|------|---|--------------|
| 1 | | | |
| 2 | 131 | 153 AAACCGUUAC:::: :: ::::: :AAACACAGCA Cleavage | pacid=371533 |
| 3 | 1534 | 1556 AAACCGUUAC:::: ::::: : GAACACAGUA Cleavage | pacid=371621 |
| 4 | 1539 | 1561 AAACCGUUAC:::: ::::: : GAACACAGUA Cleavage | pacid=371621 |
| 5 | | | |
| 6 | 1019 | 1041 AAACCGUUAC:::: ::::: : :::::AGGCUUGGU Translation | pacid=371550 |
| 7 | 709 | 732 AAACCGUUAC:::: :: ::::: : ::::AAAUGCAAGL Cleavage | pacid=371777 |
| 8 | 349 | 371 AAACCGUUAC::::: : ::::: : :AGACUCCCUC Cleavage | pacid=371712 |
| 9 | | | |
| 10 | 310 | 332 AAACCGUUAC::::: : ::::: : :GGAUUUGGU Cleavage | pacid=371548 |
| 11 | 418 | 440 AAACCGUUAC::::: : ::::: : :AGACUCCCUC Cleavage | pacid=371741 |
| 12 | | | |
| 13 | 714 | 736 AAACCGUUAC ::::: : :GGAGCAGGU Cleavage | pacid=371513 |
| 14 | 858 | 880 AAACCGUUAC ::::: : :GGAGCAGGU Cleavage | pacid=371513 |
| 15 | 624 | 646 AAACCGUUAC ::::: : :GGAGCAGGU Cleavage | pacid=371513 |
| 16 | 957 | 979 AAACCGUUAC :: ::::: : :UGACCCGGU Cleavage | pacid=371460 |
| 17 | | | |
| 18 | 209 | 231 AAACCGUUAC: ::::: : :AGUUUCAGU Cleavage | pacid=371708 |
| 19 | 2329 | 2350 AAACCGUUAC::::: : ::::: : :AGAUUCAGU Cleavage | pacid=371623 |
| 20 | 327 | 349 AAACCGUUAC :: ::::: : : :CAAUGCAGU Cleavage | pacid=371642 |
| 21 | | | |
| 22 | 818 | 840 AAACCGUUAC: ::::: : : :AACCUCAUUC Cleavage | pacid=371492 |
| 23 | 1223 | 1245 AAACCGUUAC: ::::: : : :AUAUUCAGU Translation | pacid=371578 |
| 24 | 736 | 758 AAACCGUUAC::::: : ::::: : :AGGCUCACCA Cleavage | pacid=371570 |
| 25 | | | |
| 26 | 331 | 353 AAACCGUUAC: ::::: : : :AGAAUCAGU Cleavage | pacid=371433 |
| 27 | 740 | 762 AAACCGUUAC: ::::: : : :AACCUCAUUC Cleavage | pacid=371492 |
| 28 | 607 | 629 AAACCGUUAC: ::::: : : :GAUUAUGGU Cleavage | pacid=371741 |
| 29 | | | |
| 30 | 3141 | 3163 AAACCGUUAC ::::: : : :GUAUUCAGC Cleavage | pacid=371544 |
| 31 | 2697 | 2719 AAACCGUUAC ::::: : : : :UAAUUCACU Cleavage | pacid=371680 |
| 32 | 154 | 176 AAACCGUUAC: ::::: : : : :AAGAUUAGU Translation | pacid=371718 |
| 33 | 295 | 317 AAACCGUUAC :: ::::: : : :UCAGUCUGU Cleavage | pacid=371718 |
| 34 | | | |
| 35 | 549 | 571 AAACCGUUAC::::: : ::::: : :GGGUUUGGU Cleavage | pacid=371609 |
| 36 | 1176 | 1198 AAACCGUUAC: ::::: : : : :AAGUACACU Cleavage | pacid=371552 |
| 37 | | | |
| 38 | 1 | 23 AAACCGUUAC::::: : ::::: : :GAACACAUAC Cleavage | pacid=371609 |
| 39 | 1 | 23 AAACCGUUAC::::: : ::::: : :GAACACAUAC Cleavage | pacid=371609 |
| 40 | 264 | 286 AAACCGUUAC::::: : ::::: : :GAGUUCAGA Cleavage | pacid=371626 |
| 41 | 444 | 466 AAACCGUUAC: ::::: : : :GAGUUAGGU Cleavage | pacid=371737 |
| 42 | | | |
| 43 | 1325 | 1347 AAACCGUUAC: ::::: : : : :AACCACAGUA Cleavage | pacid=371640 |
| 44 | 1263 | 1285 AAACCGUUAC::::: : ::::: : :GGAUUCGGU Cleavage | pacid=371548 |
| 45 | 513 | 535 AAACCGUUAC: ::::: : : : :GGAAUUGGC Cleavage | pacid=371548 |
| 46 | 837 | 859 AAACCGUUAC: ::::: : : : :GGAAUUGGC Cleavage | pacid=371548 |
| 47 | 903 | 925 AAACCGUUAC: ::::: : : : :GGAAUUGGC Cleavage | pacid=371548 |
| 48 | | | |
| 49 | 1101 | 1123 AAACCGUUAC: ::::: : : : :GGAAUUGGC Cleavage | pacid=371548 |
| 50 | 1053 | 1075 AAACCGUUAC ::::: : : : :GGUUUAGGU Cleavage | pacid=371548 |
| 51 | 508 | 530 AAACCGUUAC: ::::: : : : :AAGCGUGGU Cleavage | pacid=371718 |
| 52 | 521 | 543 AAACCGUUAC::::: : ::::: : :AAACUCACAA Cleavage | pacid=371779 |
| 53 | | | |
| 54 | 131 | 153 AAACCGUUAC::::: : ::::: : :AAACACAGCA Cleavage | pacid=371533 |
| 55 | 1534 | 1556 AAACCGUUAC::::: : ::::: : :GAACACAGUA Cleavage | pacid=371621 |
| 56 | 1539 | 1561 AAACCGUUAC::::: : ::::: : :GAACACAGUA Cleavage | pacid=371621 |
| 57 | | | |
| 58 | 1019 | 1041 AAACCGUUAC::::: : ::::: : : :AGGCUUGGU Translation | pacid=371550 |
| 59 | 709 | 732 AAACCGUUAC::::: : ::::: : : :AAAUGCAAGL Cleavage | pacid=371777 |
| 60 | 349 | 371 AAACCGUUAC::::: : ::::: : :AGACUCCCUC Cleavage | pacid=371712 |

| | | | |
|----|------|---|--------------|
| 1 | | | |
| 2 | 310 | 332 AAACCGUUAC.....: GGAAUUUGGU Cleavage | pacid=371548 |
| 3 | 418 | 440 AAACCGUUAC:..... :AGACUCCCUC Cleavage | pacid=371741 |
| 4 | 714 | 736 AAACCGUUAC: GGAGCAGGU Cleavage | pacid=371513 |
| 5 | 858 | 880 AAACCGUUAC: GGAGCAGGU Cleavage | pacid=371513 |
| 6 | 624 | 646 AAACCGUUAC: GGAGCAGGU Cleavage | pacid=371513 |
| 7 | 957 | 979 AAACCGUUAC : : : : :UGACCCGGU Cleavage | pacid=371460 |
| 8 | 209 | 231 AAACCGUUAC:.....: AGUUUCAGU Cleavage | pacid=371708 |
| 9 | 2329 | 2350 AAACCGUUAC:.....: : : : :AGAUUCAGU Cleavage | pacid=371623 |
| 10 | 327 | 349 AAACCGUUAC : : : : : : : : : :CAAUGCAGU Cleavage | pacid=371642 |
| 11 | 818 | 840 AAACCGUUAC: : : : : : : : : :AACCUCAUUC Cleavage | pacid=371492 |
| 12 | 1223 | 1245 AAACCGUUAC:.....: : : : : :AUAUUCAGU Translation | pacid=371578 |
| 13 | 736 | 758 AAACCGUUAC:.....: : : : : :AGGCUCACCA Cleavage | pacid=371570 |
| 14 | 331 | 353 AAACCGUUAC: : : : : : : : : :AGAAUCAGU Cleavage | pacid=371433 |
| 15 | 740 | 762 AAACCGUUAC: : : : : : : : : :AACCUCAUUC Cleavage | pacid=371492 |
| 16 | 607 | 629 AAACCGUUAC: . . . : : : : : : :GAUUAUGGU Cleavage | pacid=371741 |
| 17 | 3141 | 3163 AAACCGUUAC : : : : : : : : : :GUAUUCAGC Cleavage | pacid=371544 |
| 18 | 2697 | 2719 AAACCGUUAC : : : : : : : : : :UAAUUCACU Cleavage | pacid=371680 |
| 19 | 154 | 176 AAACCGUUAC: : : : : : : : : :AAGAUUAGU Translation | pacid=371718 |
| 20 | 295 | 317 AAACCGUUAC : : : : : : : : : :UCAGUCUGU Cleavage | pacid=371718 |
| 21 | 549 | 571 AAACCGUUAC.....: : : : : : : : : :GGGUUUGGU Cleavage | pacid=371609 |
| 22 | 1176 | 1198 AAACCGUUAC:.. : : : : : : : : :AAGUACACU Cleavage | pacid=371552 |
| 23 | 1 | 23 AAACCGUUAC: : : : : : : : : :GAACACAUAC Cleavage | pacid=371609 |
| 24 | 1 | 23 AAACCGUUAC: : : : : : : : : :GAACACAUAC Cleavage | pacid=371609 |
| 25 | 264 | 286 AAACCGUUAC:.....: : : : : : : : : :GAGUUCAGA Cleavage | pacid=371626 |
| 26 | 444 | 466 AAACCGUUAC:.. : : : : : : : : :GAGUUAGGU Cleavage | pacid=371737 |
| 27 | 1325 | 1347 AAACCGUUAC: : : : : : : : : :AACCACAGUA Cleavage | pacid=371640 |
| 28 | | | |
| 29 | | | |
| 30 | | | |
| 31 | | | |
| 32 | | | |
| 33 | | | |
| 34 | | | |
| 35 | | | |
| 36 | | | |
| 37 | | | |
| 38 | | | |
| 39 | | | |
| 40 | | | |
| 41 | | | |
| 42 | | | |
| 43 | | | |
| 44 | | | |
| 45 | | | |
| 46 | | | |
| 47 | | | |
| 48 | | | |
| 49 | | | |
| 50 | | | |
| 51 | | | |
| 52 | | | |
| 53 | | | |
| 54 | | | |
| 55 | | | |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

| | Multiplicity | peptideName | locusName | Pfam | Panther | KOG |
|----|--------------|------------------|------------------|-------------------------|---------------|---------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | 1 | Phvul.004G064100 | Phvul.004G064100 | PF00445 | PTHR11240,P | KOG1642 |
| 4 | 1 | Phvul.009G096000 | Phvul.009G096000 | PF03330 | PTHR22595,P | 0 |
| 5 | 1 | Phvul.008G049000 | Phvul.008G049000 | PF00793 | PTHR21057,P | 0 |
| 6 | 1 | Phvul.004G064100 | Phvul.004G064100 | PF00445 | PTHR11240,P | KOG1642 |
| 7 | 1 | Phvul.009G096000 | Phvul.009G096000 | PF03330 | PTHR22595,P | 0 |
| 8 | 1 | Phvul.004G064100 | Phvul.004G064100 | PF00445 | PTHR11240,P | KOG1642 |
| 9 | 1 | Phvul.009G096000 | Phvul.009G096000 | PF03330 | PTHR22595,P | 0 |
| 10 | 1 | Phvul.004G064100 | Phvul.004G064100 | PF00445 | PTHR11240,P | KOG1642 |
| 11 | 1 | Phvul.009G096000 | Phvul.009G096000 | PF03330 | PTHR22595,P | 0 |
| 12 | 1 | Phvul.009G196100 | Phvul.009G196100 | | 0 PTHR33494,P | 0 |
| 13 | 1 | Phvul.008G199900 | Phvul.008G199900 | PF05653 | PTHR12570,P | KOG2922 |
| 14 | 1 | Phvul.007G157000 | Phvul.007G157000 | | 0 PTHR33981,P | 0 |
| 15 | 4 | Phvul.009G104850 | Phvul.009G104850 | | 0 | 0 |
| 16 | 1 | Phvul.004G038100 | Phvul.004G038100 | PF10250 | PTHR36050,P | 0 |
| 17 | 1 | Phvul.011G073600 | Phvul.011G073600 | PF02309,PF02PTHR31384,P | | 0 |
| 18 | 1 | Phvul.011G073600 | Phvul.011G073600 | PF02309,PF02PTHR31384,P | | 0 |
| 19 | 1 | Phvul.L001604 | Phvul.L001604 | | 0 PTHR36390 | 0 |
| 20 | 1 | Phvul.L001604 | Phvul.L001604 | | 0 PTHR36390 | 0 |
| 21 | 1 | Phvul.L001604 | Phvul.L001604 | | 0 PTHR36390 | 0 |
| 22 | 1 | Phvul.004G160700 | Phvul.004G160700 | PF00293,PF15PTHR13622,P | | KOG4313 |
| 23 | 1 | Phvul.011G152300 | Phvul.011G152300 | PF08276,PF00PTHR27002,P | | KOG1187 |
| 24 | 1 | Phvul.011G152300 | Phvul.011G152300 | PF08276,PF00PTHR27002,P | | KOG1187 |
| 25 | 1 | Phvul.011G152300 | Phvul.011G152300 | PF08276,PF00PTHR27002,P | | KOG1187 |
| 26 | 1 | Phvul.003G229300 | Phvul.003G229300 | PF10260 | PTHR13527,P | KOG3249 |
| 27 | 1 | Phvul.003G229300 | Phvul.003G229300 | PF10260 | PTHR13527,P | KOG3249 |
| 28 | 1 | Phvul.003G178200 | Phvul.003G178200 | PF02153 | PTHR11811,P | 0 |
| 29 | 1 | Phvul.009G196100 | Phvul.009G196100 | | 0 PTHR33494,P | 0 |
| 30 | 1 | Phvul.008G199900 | Phvul.008G199900 | PF05653 | PTHR12570,P | KOG2922 |
| 31 | 1 | Phvul.007G157000 | Phvul.007G157000 | | 0 PTHR33981,P | 0 |
| 32 | 1 | Phvul.004G160700 | Phvul.004G160700 | PF00293,PF15PTHR13622,P | | KOG4313 |
| 33 | 4 | Phvul.009G104850 | Phvul.009G104850 | | 0 | 0 |
| 34 | 1 | Phvul.L001604 | Phvul.L001604 | | 0 PTHR36390 | 0 |
| 35 | 1 | Phvul.L001604 | Phvul.L001604 | | 0 PTHR36390 | 0 |
| 36 | 1 | Phvul.L001604 | Phvul.L001604 | | 0 PTHR36390 | 0 |
| 37 | 1 | Phvul.004G038100 | Phvul.004G038100 | PF10250 | PTHR36050,P | 0 |
| 38 | 1 | Phvul.011G073600 | Phvul.011G073600 | PF02309,PF02PTHR31384,P | | 0 |
| 39 | 1 | Phvul.011G073600 | Phvul.011G073600 | PF02309,PF02PTHR31384,P | | 0 |
| 40 | 1 | Phvul.009G196100 | Phvul.009G196100 | | 0 PTHR33494,P | 0 |
| 41 | 1 | Phvul.008G199900 | Phvul.008G199900 | PF05653 | PTHR12570,P | KOG2922 |
| 42 | 1 | Phvul.007G157000 | Phvul.007G157000 | | 0 PTHR33981,P | 0 |
| 43 | 1 | Phvul.004G160700 | Phvul.004G160700 | PF00293,PF15PTHR13622,P | | KOG4313 |
| 44 | 4 | Phvul.009G104850 | Phvul.009G104850 | | 0 | 0 |
| 45 | 1 | Phvul.L001604 | Phvul.L001604 | | 0 PTHR36390 | 0 |
| 46 | 1 | Phvul.L001604 | Phvul.L001604 | | 0 PTHR36390 | 0 |
| 47 | 1 | Phvul.L001604 | Phvul.L001604 | | 0 PTHR36390 | 0 |
| 48 | 1 | Phvul.004G038100 | Phvul.004G038100 | PF10250 | PTHR36050,P | 0 |
| 49 | 1 | Phvul.011G073600 | Phvul.011G073600 | PF02309,PF02PTHR31384,P | | 0 |
| 50 | 1 | Phvul.011G073600 | Phvul.011G073600 | PF02309,PF02PTHR31384,P | | 0 |
| 51 | 1 | Phvul.009G196100 | Phvul.009G196100 | | 0 PTHR33494,P | 0 |
| 52 | 1 | Phvul.008G199900 | Phvul.008G199900 | PF05653 | PTHR12570,P | KOG2922 |
| 53 | 1 | Phvul.007G157000 | Phvul.007G157000 | | 0 PTHR33981,P | 0 |
| 54 | 1 | Phvul.004G160700 | Phvul.004G160700 | PF00293,PF15PTHR13622,P | | KOG4313 |
| 55 | 4 | Phvul.009G104850 | Phvul.009G104850 | | 0 | 0 |
| 56 | 1 | Phvul.L001604 | Phvul.L001604 | | 0 PTHR36390 | 0 |
| 57 | 1 | Phvul.L001604 | Phvul.L001604 | | 0 PTHR36390 | 0 |
| 58 | 1 | Phvul.L001604 | Phvul.L001604 | | 0 PTHR36390 | 0 |
| 59 | 1 | Phvul.004G038100 | Phvul.004G038100 | PF10250 | PTHR36050,P | 0 |
| 60 | 1 | Phvul.011G073600 | Phvul.011G073600 | PF02309,PF02PTHR31384,P | | 0 |

| | | | | | |
|----|--------------------|------------------|--------------------------------------|---------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.011G073600 | Phvul.011G073600 | PF02309,PF02PTHR31384,P ⁻ | | 0 |
| 3 | 1 Phvul.002G289600 | Phvul.002G289600 | PF00153 PTHR24089,P ⁻ | | 0 |
| 4 | 1 Phvul.002G289600 | Phvul.002G289600 | PF00153 PTHR24089,P ⁻ | | 0 |
| 5 | 1 Phvul.002G289600 | Phvul.002G289600 | PF00153 PTHR24089,P ⁻ | | 0 |
| 6 | 1 Phvul.002G289600 | Phvul.002G289600 | PF00153 PTHR24089,P ⁻ | | 0 |
| 7 | 1 Phvul.002G041900 | Phvul.002G041900 | 0 PTHR35105,P ⁻ | | 0 |
| 8 | 1 Phvul.010G108300 | Phvul.010G108300 | PF01176 PTHR21668,P ⁻ | KOG3403 | |
| 9 | 4 Phvul.006G148800 | Phvul.006G148800 | 0 | 0 | 0 |
| 10 | 1 Phvul.006G214700 | Phvul.006G214700 | PF02493,PF01PTHR23086,P ⁻ | | KOG0229 |
| 11 | 1 Phvul.006G214700 | Phvul.006G214700 | PF02493,PF01PTHR23086,P ⁻ | | KOG0229 |
| 12 | 1 Phvul.006G214700 | Phvul.006G214700 | PF02493,PF01PTHR23086,P ⁻ | | KOG0229 |
| 13 | 1 Phvul.006G214700 | Phvul.006G214700 | PF02493,PF01PTHR23086,P ⁻ | | KOG0229 |
| 14 | 1 Phvul.006G214700 | Phvul.006G214700 | PF02493,PF01PTHR23086,P ⁻ | | KOG0229 |
| 15 | 1 Phvul.002G231800 | Phvul.002G231800 | PF00011 PTHR11527,P ⁻ | | KOG0710 |
| 16 | 1 Phvul.005G137000 | Phvul.005G137000 | PF02037,PF02PTHR10782,P ⁻ | | KOG2169 |
| 17 | 1 Phvul.005G137000 | Phvul.005G137000 | PF02037,PF02PTHR10782,P ⁻ | | KOG2169 |
| 18 | 1 Phvul.005G137000 | Phvul.005G137000 | PF02037,PF02PTHR10782,P ⁻ | | KOG2169 |
| 19 | 1 Phvul.005G137000 | Phvul.005G137000 | PF02037,PF02PTHR10782,P ⁻ | | KOG2169 |
| 20 | 1 Phvul.005G137000 | Phvul.005G137000 | PF02037,PF02PTHR10782,P ⁻ | | KOG2169 |
| 21 | 1 Phvul.005G137000 | Phvul.005G137000 | PF02037,PF02PTHR10782,P ⁻ | | KOG2169 |
| 22 | 1 Phvul.002G226900 | Phvul.002G226900 | PF03031,PF00PTHR23081,P ⁻ | | KOG0323 |
| 23 | 1 Phvul.005G137000 | Phvul.005G137000 | PF02037,PF02PTHR10782,P ⁻ | | KOG2169 |
| 24 | 1 Phvul.005G137000 | Phvul.005G137000 | PF02037,PF02PTHR10782,P ⁻ | | KOG2169 |
| 25 | 1 Phvul.005G137000 | Phvul.005G137000 | PF02037,PF02PTHR10782,P ⁻ | | KOG2169 |
| 26 | 1 Phvul.007G222000 | Phvul.007G222000 | 0 | 0 | 0 |
| 27 | 1 Phvul.007G029200 | Phvul.007G029200 | PF07797 PTHR33130,P ⁻ | | 0 |
| 28 | 1 Phvul.003G058400 | Phvul.003G058400 | PF14416,PF13PTHR32285,P ⁻ | | 0 |
| 29 | 1 Phvul.002G250000 | Phvul.002G250000 | PF02493,PF01PTHR23086,P ⁻ | | 0 |
| 30 | 1 Phvul.004G028100 | Phvul.004G028100 | PF00271,PF12PTHR12131,P ⁻ | | 0 |
| 31 | 3 Phvul.008G216700 | Phvul.008G216700 | 0 | 0 | 0 |
| 32 | 3 Phvul.008G216700 | Phvul.008G216700 | 0 | 0 | 0 |
| 33 | 1 Phvul.002G190100 | Phvul.002G190100 | PF00467,PF01PTHR10497 | | KOG3418 |
| 34 | 1 Phvul.004G087000 | Phvul.004G087000 | PF07731,PF07PTHR11709,P ⁻ | | KOG1263 |
| 35 | 1 Phvul.001G036500 | Phvul.001G036500 | 0 PTHR10593,P ⁻ | | 0 |
| 36 | 1 Phvul.005G102100 | Phvul.005G102100 | PF13639 PTHR22763,P ⁻ | | 0 |
| 37 | 1 Phvul.005G102100 | Phvul.005G102100 | PF13639 PTHR22763,P ⁻ | | 0 |
| 38 | 1 Phvul.002G289600 | Phvul.002G289600 | PF00153 PTHR24089,P ⁻ | | 0 |
| 39 | 1 Phvul.002G289600 | Phvul.002G289600 | PF00153 PTHR24089,P ⁻ | | 0 |
| 40 | 1 Phvul.002G289600 | Phvul.002G289600 | PF00153 PTHR24089,P ⁻ | | 0 |
| 41 | 1 Phvul.002G289600 | Phvul.002G289600 | PF00153 PTHR24089,P ⁻ | | 0 |
| 42 | 1 Phvul.002G041900 | Phvul.002G041900 | 0 PTHR35105,P ⁻ | | 0 |
| 43 | 3 Phvul.006G148800 | Phvul.006G148800 | 0 | 0 | 0 |
| 44 | 1 Phvul.010G108300 | Phvul.010G108300 | PF01176 PTHR21668,P ⁻ | | KOG3403 |
| 45 | 1 Phvul.006G214700 | Phvul.006G214700 | PF02493,PF01PTHR23086,P ⁻ | | KOG0229 |
| 46 | 1 Phvul.006G214700 | Phvul.006G214700 | PF02493,PF01PTHR23086,P ⁻ | | KOG0229 |
| 47 | 1 Phvul.006G214700 | Phvul.006G214700 | PF02493,PF01PTHR23086,P ⁻ | | KOG0229 |
| 48 | 1 Phvul.006G214700 | Phvul.006G214700 | PF02493,PF01PTHR23086,P ⁻ | | KOG0229 |
| 49 | 3 Phvul.008G216700 | Phvul.008G216700 | 0 | 0 | 0 |
| 50 | 3 Phvul.008G216700 | Phvul.008G216700 | 0 | 0 | 0 |
| 51 | 1 Phvul.001G036500 | Phvul.001G036500 | 0 PTHR10593,P ⁻ | | 0 |
| 52 | 1 Phvul.002G289600 | Phvul.002G289600 | PF00153 PTHR24089,P ⁻ | | 0 |
| 53 | 1 Phvul.002G289600 | Phvul.002G289600 | PF00153 PTHR24089,P ⁻ | | 0 |

| | | | | | |
|----|---------------------------|-------------------------|--------------------------------------|----------------------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.002G289600 | Phvul.002G289600 | PF00153 | PTHR24089,P ⁻ | 0 |
| 3 | 1 Phvul.002G041900 | Phvul.002G041900 | | 0 PTHR35105,P ⁻ | 0 |
| 4 | 3 Phvul.006G148800 | Phvul.006G148800 | 0 | 0 | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.010G108300 | Phvul.010G108300 | PF01176 | PTHR21668,P ⁻ | KOG3403 |
| 7 | 1 Phvul.006G214700 | Phvul.006G214700 | PF02493,PF01PTHR23086,P ⁻ | | KOG0229 |
| 8 | 1 Phvul.006G214700 | Phvul.006G214700 | PF02493,PF01PTHR23086,P ⁻ | | KOG0229 |
| 9 | | | | | |
| 10 | 1 Phvul.006G214700 | Phvul.006G214700 | PF02493,PF01PTHR23086,P ⁻ | | KOG0229 |
| 11 | 1 Phvul.006G214700 | Phvul.006G214700 | PF02493,PF01PTHR23086,P ⁻ | | KOG0229 |
| 12 | 3 Phvul.008G216700 | Phvul.008G216700 | 0 | 0 | 0 |
| 13 | | | | | |
| 14 | 3 Phvul.008G216700 | Phvul.008G216700 | 0 | 0 | 0 |
| 15 | 1 Phvul.001G036500 | Phvul.001G036500 | 0 | PTHR10593,P ⁻ | 0 |
| 16 | 1 Phvul.001G052300 | Phvul.001G052300 | 0 | PTHR35697,P ⁻ | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.010G110700 | Phvul.010G110700 | PF08167 | PTHR34105 | 0 |
| 19 | 1 Phvul.010G110700 | Phvul.010G110700 | PF08167 | PTHR34105 | 0 |
| 20 | 1 Phvul.009G100000 | Phvul.009G100000 | PF00240,PF13PTHR24006 | KOG1863 | |
| 21 | | | | | |
| 22 | 1 Phvul.009G100000 | Phvul.009G100000 | PF00240,PF13PTHR24006 | | KOG1863 |
| 23 | 1 Phvul.009G100000 | Phvul.009G100000 | PF00240,PF13PTHR24006 | | KOG1863 |
| 24 | 1 Phvul.009G100000 | Phvul.009G100000 | PF00240,PF13PTHR24006 | | KOG1863 |
| 25 | | | | | |
| 26 | 1 Phvul.001G073300 | Phvul.001G073300 | | 0 PTHR35697,P ⁻ | 0 |
| 27 | 1 Phvul.008G279750 | Phvul.008G279750 | PF03552 | PTHR13301,P ⁻ | 0 |
| 28 | 1 Phvul.010G152600 | Phvul.010G152600 | PF11145 | PTHR33389,P ⁻ | 0 |
| 29 | | | | | |
| 30 | 1 Phvul.006G021500 | Phvul.006G021500 | PF14577,PF14PTHR33232,P ⁻ | | 0 |
| 31 | 1 Phvul.009G177300 | Phvul.009G177300 | PF00787,PF13PTHR12326,P ⁻ | | 0 |
| 32 | 1 Phvul.007G147400 | Phvul.007G147400 | PF00005,PF00PTHR24221,P ⁻ | | 0 |
| 33 | | | | | |
| 34 | 1 Phvul.003G178100 | Phvul.003G178100 | PF00226,PF01PTHR24078,P ⁻ | | KOG0714 |
| 35 | 2 Phvul.011G102400 | Phvul.011G102400 | 0 | 0 | 0 |
| 36 | 1 Phvul.001G106800 | Phvul.001G106800 | PF00249 | PTHR10641,P ⁻ | KOG0048 |
| 37 | 1 Phvul.007G261100 | Phvul.007G261100 | PF08327,PF09PTHR13009,P ⁻ | | KOG2936 |
| 38 | 1 Phvul.007G261100 | Phvul.007G261100 | PF08327,PF09PTHR13009,P ⁻ | | KOG2936 |
| 39 | 1 Phvul.011G187600 | Phvul.011G187600 | PF11605,PF04PTHR13128,P ⁻ | | KOG2760 |
| 40 | | | | | |
| 41 | 4 Phvul.006G148800 | Phvul.006G148800 | 0 | 0 | 0 |
| 42 | | | | | |
| 43 | 4 Phvul.006G148800 | Phvul.006G148800 | 0 | 0 | 0 |
| 44 | 1 Phvul.002G044500 | Phvul.002G044500 | PF14432,PF13PTHR24015,P ⁻ | | 0 |
| 45 | 1 Phvul.007G113300 | Phvul.007G113300 | PF08031,PF01PTHR32448,P ⁻ | | 0 |
| 46 | | | | | |
| 47 | 2 Phvul.006G206800 | Phvul.006G206800 | PF00806 | PTHR12537,P ⁻ | 0 |
| 48 | 1 Phvul.010G144900 | Phvul.010G144900 | PF00349,PF03PTHR19443,P ⁻ | | 0 |
| 49 | 1 Phvul.002G083800 | Phvul.002G083800 | PF00249 | PTHR10641,P ⁻ | 0 |
| 50 | | | | | |
| 51 | 1 Phvul.001G067500 | Phvul.001G067500 | | 0 PTHR34194,P ⁻ | 0 |
| 52 | 1 Phvul.001G067500 | Phvul.001G067500 | | 0 PTHR34194,P ⁻ | 0 |
| 53 | 1 Phvul.001G067500 | Phvul.001G067500 | | 0 PTHR34194,P ⁻ | 0 |
| 54 | | | | | |
| 55 | 1 Phvul.006G045600 | Phvul.006G045600 | PF00439 | PTHR22881,P ⁻ | 0 |
| 56 | 1 Phvul.010G156000 | Phvul.010G156000 | PF04525 | PTHR31087,P ⁻ | 0 |
| 57 | 2 Phvul.007G055500 | Phvul.007G055500 | PF07690 | PTHR23500,P ⁻ | KOG0254 |
| 58 | 2 Phvul.007G055500 | Phvul.007G055500 | PF07690 | PTHR23500,P ⁻ | KOG0254 |
| 59 | 1 Phvul.005G154600 | Phvul.005G154600 | PF04266 | PTHR34204,P ⁻ | 0 |
| 60 | 1 Phvul.005G154600 | Phvul.005G154600 | PF04266 | PTHR34204,P ⁻ | 0 |

| | | | | | | | | |
|----|---|------------------|------------------|--------------|---------------|---------|---|--|
| 1 | | | | | | | | |
| 2 | 2 | Phvul.007G055200 | Phvul.007G055200 | PF07690 | PTHR23500,P | KOG0254 | | |
| 3 | 2 | Phvul.007G055200 | Phvul.007G055200 | PF07690 | PTHR23500,P | KOG0254 | | |
| 4 | 1 | Phvul.005G154600 | Phvul.005G154600 | PF04266 | PTHR34204,P | | 0 | |
| 5 | 1 | Phvul.008G273100 | Phvul.008G273100 | PF00149 | PTHR11668,P | | 0 | |
| 6 | 3 | Phvul.008G216700 | Phvul.008G216700 | | 0 | 0 | 0 | |
| 7 | 1 | Phvul.010G121200 | Phvul.010G121200 | PF03372 | PTHR12121,P | KOG2338 | | |
| 8 | 1 | Phvul.010G121200 | Phvul.010G121200 | PF03372 | PTHR12121,P | KOG2338 | | |
| 9 | 1 | Phvul.007G270500 | Phvul.007G270500 | PF00400,PF08 | PTHR22840 | | 0 | |
| 10 | 1 | Phvul.004G125900 | Phvul.004G125900 | PF00999 | PTHR16254,P | KOG1650 | | |
| 11 | 1 | Phvul.005G027200 | Phvul.005G027200 | PF00931 | PTHR23155,P | KOG4658 | | |
| 12 | 1 | Phvul.010G110700 | Phvul.010G110700 | PF08167 | PTHR34105 | | 0 | |
| 13 | 1 | Phvul.010G110700 | Phvul.010G110700 | PF08167 | PTHR34105 | | 0 | |
| 14 | 1 | Phvul.001G052300 | Phvul.001G052300 | | 0 PTHR35697,P | | 0 | |
| 15 | 1 | Phvul.008G279750 | Phvul.008G279750 | PF03552 | PTHR13301,P | | 0 | |
| 16 | 1 | Phvul.009G100000 | Phvul.009G100000 | PF00240,PF13 | PTHR24006 | KOG1863 | | |
| 17 | 1 | Phvul.009G100000 | Phvul.009G100000 | PF00240,PF13 | PTHR24006 | KOG1863 | | |
| 18 | 1 | Phvul.009G100000 | Phvul.009G100000 | PF00240,PF13 | PTHR24006 | KOG1863 | | |
| 19 | 1 | Phvul.009G100000 | Phvul.009G100000 | PF00240,PF13 | PTHR24006 | KOG1863 | | |
| 20 | 1 | Phvul.001G073300 | Phvul.001G073300 | | 0 PTHR35697,P | | 0 | |
| 21 | 1 | Phvul.010G152600 | Phvul.010G152600 | PF11145 | PTHR33389,P | | 0 | |
| 22 | 2 | Phvul.011G102400 | Phvul.011G102400 | | 0 | 0 | 0 | |
| 23 | 3 | Phvul.006G148800 | Phvul.006G148800 | | 0 | 0 | 0 | |
| 24 | 3 | Phvul.006G148800 | Phvul.006G148800 | | 0 | 0 | 0 | |
| 25 | 1 | Phvul.010G121200 | Phvul.010G121200 | PF03372 | PTHR12121,P | KOG2338 | | |
| 26 | 1 | Phvul.010G121200 | Phvul.010G121200 | PF03372 | PTHR12121,P | KOG2338 | | |
| 27 | 1 | Phvul.004G125900 | Phvul.004G125900 | PF00999 | PTHR16254,P | KOG1650 | | |
| 28 | 1 | Phvul.002G044500 | Phvul.002G044500 | PF14432,PF13 | PTHR24015,P | | 0 | |
| 29 | 1 | Phvul.007G113300 | Phvul.007G113300 | PF08031,PF01 | PTHR32448,P | | 0 | |
| 30 | 1 | Phvul.006G021500 | Phvul.006G021500 | PF14577,PF14 | PTHR33232,P | | 0 | |
| 31 | 1 | Phvul.009G177300 | Phvul.009G177300 | PF00787,PF13 | PTHR12326,P | | 0 | |
| 32 | 1 | Phvul.007G147400 | Phvul.007G147400 | PF00005,PF00 | PTHR24221,P | | 0 | |
| 33 | 1 | Phvul.003G178100 | Phvul.003G178100 | PF00226,PF01 | PTHR24078,P | KOG0714 | | |
| 34 | 1 | Phvul.005G154600 | Phvul.005G154600 | PF04266 | PTHR34204,P | | 0 | |
| 35 | 1 | Phvul.005G154600 | Phvul.005G154600 | PF04266 | PTHR34204,P | | 0 | |
| 36 | 1 | Phvul.001G106800 | Phvul.001G106800 | PF00249 | PTHR10641,P | KOG0048 | | |
| 37 | 1 | Phvul.007G261100 | Phvul.007G261100 | PF08327,PF09 | PTHR13009,P | KOG2936 | | |
| 38 | 1 | Phvul.007G261100 | Phvul.007G261100 | PF08327,PF09 | PTHR13009,P | KOG2936 | | |
| 39 | 1 | Phvul.011G187600 | Phvul.011G187600 | PF11605,PF04 | PTHR13128,P | KOG2760 | | |
| 40 | 1 | Phvul.005G154600 | Phvul.005G154600 | PF04266 | PTHR34204,P | | 0 | |
| 41 | 1 | Phvul.008G273100 | Phvul.008G273100 | PF00149 | PTHR11668,P | | 0 | |
| 42 | 1 | Phvul.005G065300 | Phvul.005G065300 | PF11145 | PTHR33389,P | | 0 | |
| 43 | 2 | Phvul.006G206800 | Phvul.006G206800 | PF00806 | PTHR12537,P | | 0 | |
| 44 | 1 | Phvul.006G045600 | Phvul.006G045600 | PF00439 | PTHR22881,P | | 0 | |
| 45 | 3 | Phvul.008G216700 | Phvul.008G216700 | | 0 | 0 | 0 | |
| 46 | 1 | Phvul.011G111800 | Phvul.011G111800 | | 0 | 0 | 0 | |
| 47 | 1 | Phvul.010G144900 | Phvul.010G144900 | PF00349,PF03 | PTHR19443,P | | 0 | |

| | | | | | | | | |
|----|---|------------------|------------------|--------------|---------------|---------|--|---|
| 1 | | | | | | | | |
| 2 | 1 | Phvul.002G083800 | Phvul.002G083800 | PF00249 | PTHR10641,P | | | 0 |
| 3 | 1 | Phvul.007G270500 | Phvul.007G270500 | PF00400,PF08 | PTHR22840 | | | 0 |
| 4 | 1 | Phvul.001G067500 | Phvul.001G067500 | | 0 PTHR34194,P | | | 0 |
| 5 | 1 | Phvul.010G110700 | Phvul.010G110700 | PF08167 | PTHR34105 | | | 0 |
| 6 | 1 | Phvul.010G110700 | Phvul.010G110700 | PF08167 | PTHR34105 | | | 0 |
| 7 | 1 | Phvul.001G052300 | Phvul.001G052300 | | 0 PTHR35697,P | | | 0 |
| 8 | 1 | Phvul.008G279750 | Phvul.008G279750 | PF03552 | PTHR13301,P | | | 0 |
| 9 | 1 | Phvul.009G100000 | Phvul.009G100000 | PF00240,PF13 | PTHR24006 | KOG1863 | | |
| 10 | 1 | Phvul.009G100000 | Phvul.009G100000 | PF00240,PF13 | PTHR24006 | KOG1863 | | |
| 11 | 1 | Phvul.009G100000 | Phvul.009G100000 | PF00240,PF13 | PTHR24006 | KOG1863 | | |
| 12 | 1 | Phvul.009G100000 | Phvul.009G100000 | PF00240,PF13 | PTHR24006 | KOG1863 | | |
| 13 | 1 | Phvul.001G073300 | Phvul.001G073300 | | 0 PTHR35697,P | | | 0 |
| 14 | 1 | Phvul.010G152600 | Phvul.010G152600 | PF11145 | PTHR33389,P | | | 0 |
| 15 | 2 | Phvul.011G102400 | Phvul.011G102400 | | 0 | 0 | | 0 |
| 16 | 3 | Phvul.006G148800 | Phvul.006G148800 | | 0 | 0 | | 0 |
| 17 | 3 | Phvul.006G148800 | Phvul.006G148800 | | 0 | 0 | | 0 |
| 18 | 1 | Phvul.010G121200 | Phvul.010G121200 | PF03372 | PTHR12121,P | KOG2338 | | |
| 19 | 1 | Phvul.010G121200 | Phvul.010G121200 | PF03372 | PTHR12121,P | KOG2338 | | |
| 20 | 1 | Phvul.004G125900 | Phvul.004G125900 | PF00999 | PTHR16254,P | KOG1650 | | |
| 21 | 1 | Phvul.002G044500 | Phvul.002G044500 | PF14432,PF13 | PTHR24015,P | | | 0 |
| 22 | 1 | Phvul.007G113300 | Phvul.007G113300 | PF08031,PF01 | PTHR32448,P | | | 0 |
| 23 | 1 | Phvul.006G021500 | Phvul.006G021500 | PF14577,PF14 | PTHR33232,P | | | 0 |
| 24 | 1 | Phvul.009G177300 | Phvul.009G177300 | PF00787,PF13 | PTHR12326,P | | | 0 |
| 25 | 1 | Phvul.007G147400 | Phvul.007G147400 | PF00005,PF00 | PTHR24221,P | | | 0 |
| 26 | 1 | Phvul.003G178100 | Phvul.003G178100 | PF00226,PF01 | PTHR24078,P | KOG0714 | | |
| 27 | 1 | Phvul.005G154600 | Phvul.005G154600 | PF04266 | PTHR34204,P | | | 0 |
| 28 | 1 | Phvul.005G154600 | Phvul.005G154600 | PF04266 | PTHR34204,P | | | 0 |
| 29 | 1 | Phvul.001G106800 | Phvul.001G106800 | PF00249 | PTHR10641,P | KOG0048 | | |
| 30 | 1 | Phvul.007G261100 | Phvul.007G261100 | PF08327,PF09 | PTHR13009,P | KOG2936 | | |
| 31 | 1 | Phvul.007G261100 | Phvul.007G261100 | PF08327,PF09 | PTHR13009,P | KOG2936 | | |
| 32 | 1 | Phvul.011G187600 | Phvul.011G187600 | PF11605,PF04 | PTHR13128,P | KOG2760 | | |
| 33 | 1 | Phvul.005G154600 | Phvul.005G154600 | PF04266 | PTHR34204,P | | | 0 |
| 34 | 1 | Phvul.008G273100 | Phvul.008G273100 | PF00149 | PTHR11668,P | | | 0 |
| 35 | 1 | Phvul.005G065300 | Phvul.005G065300 | PF11145 | PTHR33389,P | | | 0 |
| 36 | 2 | Phvul.006G206800 | Phvul.006G206800 | PF00806 | PTHR12537,P | | | 0 |
| 37 | 1 | Phvul.006G045600 | Phvul.006G045600 | PF00439 | PTHR22881,P | | | 0 |
| 38 | 3 | Phvul.008G216700 | Phvul.008G216700 | | 0 | 0 | | 0 |
| 39 | 1 | Phvul.011G111800 | Phvul.011G111800 | | 0 | 0 | | 0 |
| 40 | 1 | Phvul.010G144900 | Phvul.010G144900 | PF00349,PF03 | PTHR19443,P | | | 0 |
| 41 | 1 | Phvul.002G083800 | Phvul.002G083800 | PF00249 | PTHR10641,P | | | 0 |
| 42 | 1 | Phvul.007G270500 | Phvul.007G270500 | PF00400,PF08 | PTHR22840 | | | 0 |
| 43 | 1 | Phvul.001G067500 | Phvul.001G067500 | | 0 PTHR34194,P | | | 0 |
| 44 | 1 | Phvul.001G067500 | Phvul.001G067500 | | 0 PTHR34194,P | | | 0 |
| 45 | 6 | Phvul.011G133575 | Phvul.011G133575 | | 0 | 0 | | 0 |
| 46 | 6 | Phvul.011G133575 | Phvul.011G133575 | | 0 | 0 | | 0 |
| 47 | 6 | Phvul.011G133575 | Phvul.011G133575 | | 0 | 0 | | 0 |

| | | | | | |
|----|--------------------|------------------|--------------------------------------|--------------------------|---------|
| 1 | | | | | |
| 2 | 6 Phvul.011G133575 | Phvul.011G133575 | 0 | 0 | 0 |
| 3 | 6 Phvul.011G133575 | Phvul.011G133575 | 0 | 0 | 0 |
| 4 | 6 Phvul.011G133575 | Phvul.011G133575 | 0 | 0 | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.004G019300 | Phvul.004G019300 | PF14416,PF13PTHR32285,P ⁻ | | 0 |
| 7 | 1 Phvul.004G019300 | Phvul.004G019300 | PF14416,PF13PTHR32285,P ⁻ | | 0 |
| 8 | 4 Phvul.009G104850 | Phvul.009G104850 | 0 | 0 | 0 |
| 9 | | | | | |
| 10 | 4 Phvul.009G104850 | Phvul.009G104850 | 0 | 0 | 0 |
| 11 | 4 Phvul.009G104850 | Phvul.009G104850 | 0 | 0 | 0 |
| 12 | 1 Phvul.003G158800 | Phvul.003G158800 | PF00704 | PTHR11177,P ⁻ | KOG2806 |
| 13 | 1 Phvul.006G173500 | Phvul.006G173500 | PF00847 | PTHR31194,P ⁻ | 0 |
| 14 | 1 Phvul.002G183700 | Phvul.002G183700 | 0 | 0 | 0 |
| 15 | 2 Phvul.011G102400 | Phvul.011G102400 | 0 | 0 | 0 |
| 16 | | | | | |
| 17 | 1 Phvul.007G027000 | Phvul.007G027000 | PF00847 | PTHR31194,P ⁻ | 0 |
| 18 | 1 Phvul.005G043000 | Phvul.005G043000 | PF06101 | PTHR17204,P ⁻ | 0 |
| 19 | | | | | |
| 20 | 4 Phvul.006G148800 | Phvul.006G148800 | 0 | 0 | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.011G069000 | Phvul.011G069000 | PF01535,PF13PTHR24015,P ⁻ | | 0 |
| 23 | 2 Phvul.006G206800 | Phvul.006G206800 | PF00806 | PTHR12537,P ⁻ | 0 |
| 24 | 1 Phvul.005G054600 | Phvul.005G054600 | PF01926,PF11PTHR23115,P ⁻ | | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.001G024200 | Phvul.001G024200 | PF00225 | PTHR24115,P ⁻ | 0 |
| 27 | 1 Phvul.008G060700 | Phvul.008G060700 | PF01554 | PTHR11206,P ⁻ | KOG1347 |
| 28 | 1 Phvul.004G147900 | Phvul.004G147900 | PF14531 | PTHR24361,P ⁻ | KOG0581 |
| 29 | 1 Phvul.001G057200 | Phvul.001G057200 | PF01269 | PTHR10335 | KOG1596 |
| 30 | | | | | |
| 31 | 1 Phvul.009G046200 | Phvul.009G046200 | PF07145,PF14PTHR24012 | | KOG0131 |
| 32 | 1 Phvul.011G133400 | Phvul.011G133400 | 0 | PTHR35420 | 0 |
| 33 | | | | | |
| 34 | 1 Phvul.008G111100 | Phvul.008G111100 | PF13639 | PTHR14155,P ⁻ | 0 |
| 35 | 1 Phvul.006G070000 | Phvul.006G070000 | PF13639 | PTHR14155,P ⁻ | KOG4172 |
| 36 | 1 Phvul.L001687 | Phvul.L001687 | PF02458 | PTHR31642,P ⁻ | 0 |
| 37 | 1 Phvul.008G033500 | Phvul.008G033500 | PF00076 | PTHR24012 | 0 |
| 38 | | | | | |
| 39 | 1 Phvul.008G036100 | Phvul.008G036100 | PF13445 | PTHR13139,P ⁻ | 0 |
| 40 | 1 Phvul.009G198900 | Phvul.009G198900 | PF05185 | PTHR11006,P ⁻ | KOG1499 |
| 41 | 1 Phvul.008G036100 | Phvul.008G036100 | PF13445 | PTHR13139,P ⁻ | 0 |
| 42 | | | | | |
| 43 | 1 Phvul.006G037000 | Phvul.006G037000 | PF02458 | PTHR31642,P ⁻ | 0 |
| 44 | 1 Phvul.001G205600 | Phvul.001G205600 | PF13414,PF11PTHR17130,P ⁻ | | 0 |
| 45 | 1 Phvul.011G159400 | Phvul.011G159400 | PF14259,PF00PTHR24012,P ⁻ | | KOG4205 |
| 46 | 1 Phvul.004G061900 | Phvul.004G061900 | PF07690 | PTHR23500,P ⁻ | KOG0254 |
| 47 | 1 Phvul.006G048000 | Phvul.006G048000 | PF00026 | PTHR13683,P ⁻ | KOG1339 |
| 48 | | | | | |
| 49 | 1 Phvul.009G007900 | Phvul.009G007900 | 0 | 0 | 0 |
| 50 | | | | | |
| 51 | 1 Phvul.005G067950 | Phvul.005G067950 | PF03634 | PTHR31072,P ⁻ | 0 |
| 52 | 6 Phvul.011G133575 | Phvul.011G133575 | 0 | 0 | 0 |
| 53 | 6 Phvul.011G133575 | Phvul.011G133575 | 0 | 0 | 0 |
| 54 | | | | | |
| 55 | 6 Phvul.011G133575 | Phvul.011G133575 | 0 | 0 | 0 |
| 56 | 6 Phvul.011G133575 | Phvul.011G133575 | 0 | 0 | 0 |
| 57 | 6 Phvul.011G133575 | Phvul.011G133575 | 0 | 0 | 0 |
| 58 | 6 Phvul.011G133575 | Phvul.011G133575 | 0 | 0 | 0 |
| 59 | 6 Phvul.011G133575 | Phvul.011G133575 | 0 | 0 | 0 |
| 60 | 1 Phvul.006G173500 | Phvul.006G173500 | PF00847 | PTHR31194,P ⁻ | 0 |
| | 1 Phvul.002G183700 | Phvul.002G183700 | 0 | 0 | 0 |

| | | | | | | |
|----|--------------------|------------------|-------------------------|---------------|---------|---|
| 1 | | | | | | |
| 2 | 1 Phvul.005G043000 | Phvul.005G043000 | PF06101 | PTHR17204,P | | 0 |
| 3 | 1 Phvul.004G019300 | Phvul.004G019300 | PF14416,PF13PTHR32285,P | | | 0 |
| 4 | 1 Phvul.004G019300 | Phvul.004G019300 | PF14416,PF13PTHR32285,P | | | 0 |
| 5 | 1 Phvul.011G069000 | Phvul.011G069000 | PF01535,PF13PTHR24015,P | | | 0 |
| 6 | 1 Phvul.002G231800 | Phvul.002G231800 | PF00011 | PTHR11527,P | KOG0710 | |
| 7 | 1 Phvul.L001687 | Phvul.L001687 | PF02458 | PTHR31642,P | | 0 |
| 8 | | | | | | |
| 9 | 2 Phvul.011G102400 | Phvul.011G102400 | | 0 | 0 | 0 |
| 10 | 1 Phvul.006G037000 | Phvul.006G037000 | PF02458 | PTHR31642,P | | 0 |
| 11 | 4 Phvul.009G104850 | Phvul.009G104850 | | 0 | 0 | 0 |
| 12 | 4 Phvul.009G104850 | Phvul.009G104850 | | 0 | 0 | 0 |
| 13 | 4 Phvul.009G104850 | Phvul.009G104850 | | 0 | 0 | 0 |
| 14 | 1 Phvul.003G158800 | Phvul.003G158800 | PF00704 | PTHR11177,P | KOG2806 | |
| 15 | 1 Phvul.001G057200 | Phvul.001G057200 | PF01269 | PTHR10335 | KOG1596 | |
| 16 | 1 Phvul.004G057900 | Phvul.004G057900 | PF01535,PF13PTHR24015,P | | | 0 |
| 17 | 1 Phvul.007G027000 | Phvul.007G027000 | PF00847 | PTHR31194,P | | 0 |
| 18 | 1 Phvul.009G063500 | Phvul.009G063500 | PF01734 | PTHR32176 | KOG0513 | |
| 19 | 1 Phvul.008G060700 | Phvul.008G060700 | PF01554 | PTHR11206,P | KOG1347 | |
| 20 | 1 Phvul.011G110000 | Phvul.011G110000 | PF02984,PF00PTHR10177,P | | KOG0656 | |
| 21 | 1 Phvul.010G003800 | Phvul.010G003800 | PF00854 | PTHR11654,P | KOG1237 | |
| 22 | 1 Phvul.009G063500 | Phvul.009G063500 | PF01734 | PTHR32176 | KOG0513 | |
| 23 | 2 Phvul.006G206800 | Phvul.006G206800 | PF00806 | PTHR12537,P | | 0 |
| 24 | 1 Phvul.005G054600 | Phvul.005G054600 | PF01926,PF11PTHR23115,P | | | 0 |
| 25 | 1 Phvul.001G024200 | Phvul.001G024200 | PF00225 | PTHR24115,P | | 0 |
| 26 | 2 Phvul.006G098000 | Phvul.006G098000 | PF13302 | PTHR13256,P | | 0 |
| 27 | 2 Phvul.006G098000 | Phvul.006G098000 | PF13302 | PTHR13256,P | | 0 |
| 28 | 1 Phvul.008G033500 | Phvul.008G033500 | PF00076 | PTHR24012 | | 0 |
| 29 | 1 Phvul.011G028900 | Phvul.011G028900 | PF01966 | PTHR33594,P | | 0 |
| 30 | 1 Phvul.008G036100 | Phvul.008G036100 | PF13445 | PTHR13139,P | | 0 |
| 31 | 1 Phvul.008G036100 | Phvul.008G036100 | PF13445 | PTHR13139,P | | 0 |
| 32 | 1 Phvul.004G061900 | Phvul.004G061900 | PF07690 | PTHR23500,P | KOG0254 | |
| 33 | 1 Phvul.006G048000 | Phvul.006G048000 | PF00026 | PTHR13683,P | KOG1339 | |
| 34 | 1 Phvul.007G156900 | Phvul.007G156900 | | 0 PTHR33981,P | | 0 |
| 35 | 6 Phvul.011G133575 | Phvul.011G133575 | | 0 | 0 | 0 |
| 36 | 6 Phvul.011G133575 | Phvul.011G133575 | | 0 | 0 | 0 |
| 37 | 6 Phvul.011G133575 | Phvul.011G133575 | | 0 | 0 | 0 |
| 38 | 6 Phvul.011G133575 | Phvul.011G133575 | | 0 | 0 | 0 |
| 39 | 6 Phvul.011G133575 | Phvul.011G133575 | | 0 | 0 | 0 |
| 40 | 6 Phvul.011G133575 | Phvul.011G133575 | | 0 | 0 | 0 |
| 41 | 1 Phvul.006G173500 | Phvul.006G173500 | PF00847 | PTHR31194,P | | 0 |
| 42 | 1 Phvul.002G183700 | Phvul.002G183700 | | 0 | 0 | 0 |
| 43 | 1 Phvul.005G043000 | Phvul.005G043000 | PF06101 | PTHR17204,P | | 0 |
| 44 | 1 Phvul.004G019300 | Phvul.004G019300 | PF14416,PF13PTHR32285,P | | | 0 |
| 45 | 1 Phvul.004G019300 | Phvul.004G019300 | PF14416,PF13PTHR32285,P | | | 0 |
| 46 | 1 Phvul.011G069000 | Phvul.011G069000 | PF01535,PF13PTHR24015,P | | | 0 |
| 47 | 1 Phvul.002G231800 | Phvul.002G231800 | PF00011 | PTHR11527,P | KOG0710 | |
| 48 | 1 Phvul.L001687 | Phvul.L001687 | PF02458 | PTHR31642,P | | 0 |

| | | | | | | |
|----|---|------------------|------------------|--------------|--------------------------|---------|
| 1 | | | | | | |
| 2 | 2 | Phvul.011G102400 | Phvul.011G102400 | 0 | 0 | 0 |
| 3 | 1 | Phvul.006G037000 | Phvul.006G037000 | PF02458 | PTHR31642,P ⁻ | 0 |
| 4 | 4 | Phvul.009G104850 | Phvul.009G104850 | 0 | 0 | 0 |
| 5 | 4 | Phvul.009G104850 | Phvul.009G104850 | 0 | 0 | 0 |
| 6 | 4 | Phvul.009G104850 | Phvul.009G104850 | 0 | 0 | 0 |
| 7 | 1 | Phvul.003G158800 | Phvul.003G158800 | PF00704 | PTHR11177,P ⁻ | KOG2806 |
| 8 | 1 | Phvul.001G057200 | Phvul.001G057200 | PF01269 | PTHR10335 | KOG1596 |
| 9 | 1 | Phvul.004G057900 | Phvul.004G057900 | PF01535,PF13 | PTHR24015,P ⁻ | 0 |
| 10 | 1 | Phvul.007G027000 | Phvul.007G027000 | PF00847 | PTHR31194,P ⁻ | 0 |
| 11 | 1 | Phvul.009G063500 | Phvul.009G063500 | PF01734 | PTHR32176 | KOG0513 |
| 12 | 1 | Phvul.008G060700 | Phvul.008G060700 | PF01554 | PTHR11206,P ⁻ | KOG1347 |
| 13 | 1 | Phvul.011G110000 | Phvul.011G110000 | PF02984,PF00 | PTHR10177,P ⁻ | KOG0656 |
| 14 | 1 | Phvul.010G003800 | Phvul.010G003800 | PF00854 | PTHR11654,P ⁻ | KOG1237 |
| 15 | 1 | Phvul.009G063500 | Phvul.009G063500 | PF01734 | PTHR32176 | KOG0513 |
| 16 | 2 | Phvul.006G206800 | Phvul.006G206800 | PF00806 | PTHR12537,P ⁻ | 0 |
| 17 | 1 | Phvul.005G054600 | Phvul.005G054600 | PF01926,PF11 | PTHR23115,P ⁻ | 0 |
| 18 | 1 | Phvul.001G024200 | Phvul.001G024200 | PF00225 | PTHR24115,P ⁻ | 0 |
| 19 | 2 | Phvul.006G098000 | Phvul.006G098000 | PF13302 | PTHR13256,P ⁻ | 0 |
| 20 | 2 | Phvul.006G098000 | Phvul.006G098000 | PF13302 | PTHR13256,P ⁻ | 0 |
| 21 | 1 | Phvul.008G033500 | Phvul.008G033500 | PF00076 | PTHR24012 | 0 |
| 22 | 1 | Phvul.011G028900 | Phvul.011G028900 | PF01966 | PTHR33594,P ⁻ | 0 |
| 23 | 1 | Phvul.008G036100 | Phvul.008G036100 | PF13445 | PTHR13139,P ⁻ | 0 |
| 24 | 1 | Phvul.008G036100 | Phvul.008G036100 | PF13445 | PTHR13139,P ⁻ | 0 |
| 25 | 1 | Phvul.004G061900 | Phvul.004G061900 | PF07690 | PTHR23500,P ⁻ | KOG0254 |
| 26 | 1 | Phvul.006G048000 | Phvul.006G048000 | PF00026 | PTHR13683,P ⁻ | KOG1339 |
| 27 | 1 | Phvul.007G156900 | Phvul.007G156900 | 0 | PTHR33981,P ⁻ | 0 |
| 28 | | | | | | |
| 29 | | | | | | |
| 30 | | | | | | |
| 31 | | | | | | |
| 32 | | | | | | |
| 33 | | | | | | |
| 34 | | | | | | |
| 35 | | | | | | |
| 36 | | | | | | |
| 37 | | | | | | |
| 38 | | | | | | |
| 39 | | | | | | |
| 40 | | | | | | |
| 41 | | | | | | |
| 42 | | | | | | |
| 43 | | | | | | |
| 44 | | | | | | |
| 45 | | | | | | |
| 46 | | | | | | |
| 47 | | | | | | |
| 48 | | | | | | |
| 49 | | | | | | |
| 50 | | | | | | |
| 51 | | | | | | |
| 52 | | | | | | |
| 53 | | | | | | |
| 54 | | | | | | |
| 55 | | | | | | |
| 56 | | | | | | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| 1 | KEGG | KOG | GO | Best-hit-arabi-arabi-symbol | |
|----|----------|--------|--------------|-------------------------------------|------------------|
| 2 | 3.1.27.1 | K01166 | GO:0033897,(| AT1G14220.1 | 0 |
| 3 | | 0 | 0 | 0 AT2G18660.1 PNP-A | |
| 4 | 2.5.1.55 | K01627 | GO:0009058,(| AT1G79500.4 AtkdsA1 | |
| 5 | 3.1.27.1 | K01166 | GO:0033897,(| AT1G14220.1 | 0 |
| 6 | | 0 | 0 | 0 AT2G18660.1 PNP-A | |
| 7 | 3.1.27.1 | K01166 | GO:0033897,(| AT1G14220.1 | 0 |
| 8 | | 0 | 0 | 0 AT2G18660.1 PNP-A | |
| 9 | 3.1.27.1 | K01166 | GO:0033897,(| AT1G14220.1 | 0 |
| 10 | | 0 | 0 | 0 AT2G18660.1 PNP-A | |
| 11 | | 0 | 0 | 0 AT2G24100.1 | 0 |
| 12 | | 0 | 0 | GO:0016021,(| AT1G34470.1 |
| 13 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 14 | | 0 | 0 | 0 0 | 0 |
| 15 | | 0 | 0 | 0 AT4G17430.1 | 0 |
| 16 | | 0 | 0 | GO:0006355,(| AT5G60450.1 ARF4 |
| 17 | | 0 | 0 | GO:0006355,(| AT5G60450.1 ARF4 |
| 18 | | 0 | 0 | 0 AT5G07890.1 | 0 |
| 19 | | 0 | 0 | 0 AT5G07890.1 | 0 |
| 20 | | 0 | 0 | 0 AT5G07890.1 | 0 |
| 21 | 2.7.6.2 | | 0 | GO:0016787 AT5G19460.1 atnudt20,NUC | |
| 22 | 2.7.11.1 | | 0 | GO:0048544,(| AT4G27290.1 |
| 23 | 2.7.11.1 | | 0 | GO:0048544,(| AT4G27290.1 |
| 24 | 2.7.11.1 | | 0 | GO:0048544,(| AT4G27290.1 |
| 25 | | 0 | 0 | 0 AT2G35360.1 | 0 |
| 26 | | 0 | 0 | 0 AT2G35360.1 | 0 |
| 27 | 1.3.1.78 | K15227 | GO:0055114,(| AT5G34930.1 | 0 |
| 28 | | 0 | 0 | 0 AT2G24100.1 | 0 |
| 29 | | 0 | 0 | GO:0016021,(| AT1G34470.1 |
| 30 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 31 | 2.7.6.2 | | 0 | GO:0016787 AT5G19460.1 atnudt20,NUC | |
| 32 | | 0 | 0 | 0 0 | 0 |
| 33 | | 0 | 0 | 0 AT5G07890.1 | 0 |
| 34 | | 0 | 0 | 0 AT5G07890.1 | 0 |
| 35 | | 0 | 0 | 0 AT5G07890.1 | 0 |
| 36 | | 0 | 0 | 0 AT5G07890.1 | 0 |
| 37 | | 0 | 0 | 0 AT4G17430.1 | 0 |
| 38 | | 0 | 0 | GO:0006355,(| AT5G60450.1 ARF4 |
| 39 | | 0 | 0 | GO:0006355,(| AT5G60450.1 ARF4 |
| 40 | | 0 | 0 | 0 AT2G24100.1 | 0 |
| 41 | | 0 | 0 | GO:0016021,(| AT1G34470.1 |
| 42 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 43 | 2.7.6.2 | | 0 | GO:0016787 AT5G19460.1 atnudt20,NUC | |
| 44 | | 0 | 0 | 0 0 | 0 |
| 45 | | 0 | 0 | 0 AT5G07890.1 | 0 |
| 46 | | 0 | 0 | 0 AT5G07890.1 | 0 |
| 47 | | 0 | 0 | 0 AT5G07890.1 | 0 |
| 48 | | 0 | 0 | 0 AT5G07890.1 | 0 |
| 49 | | 0 | 0 | 0 AT4G17430.1 | 0 |
| 50 | | 0 | 0 | GO:0006355,(| AT5G60450.1 ARF4 |
| 51 | | 0 | 0 | GO:0006355,(| AT5G60450.1 ARF4 |
| 52 | | 0 | 0 | 0 AT2G24100.1 | 0 |
| 53 | | 0 | 0 | GO:0016021,(| AT1G34470.1 |
| 54 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 55 | 2.7.6.2 | | 0 | GO:0016787 AT5G19460.1 atnudt20,NUC | |
| 56 | | 0 | 0 | 0 0 | 0 |
| 57 | | 0 | 0 | 0 AT5G07890.1 | 0 |
| 58 | | 0 | 0 | 0 AT5G07890.1 | 0 |
| 59 | | 0 | 0 | 0 AT5G07890.1 | 0 |
| 60 | | 0 | 0 | 0 AT4G17430.1 | 0 |
| | | 0 | 0 | GO:0006355,(| AT5G60450.1 ARF4 |

| | | | | | |
|----|----------|----------|---------------------------------------|--------------------------------------|---|
| 1 | | | | | |
| 2 | | 0 | 0 | GO:0006355,(CAT5G60450.1 ARF4 | |
| 3 | | 0 | 0 | 0 AT4G11440.1 | 0 |
| 4 | | 0 | 0 | 0 AT4G11440.1 | 0 |
| 5 | | 0 | 0 | 0 AT4G11440.1 | 0 |
| 6 | | 0 | 0 | 0 AT4G11440.1 | 0 |
| 7 | | 0 | 0 | 0 AT1G64980.1 | 0 |
| 8 | | 0 | 0 | 0 AT1G64980.1 | 0 |
| 9 | | 0 K03236 | GO:0006413,(CAT2G04520.1 | | 0 |
| 10 | | 0 | 0 | 0 | 0 |
| 11 | 2.7.1.68 | | 0 | GO:0046488,(CAT1G10900.1 | 0 |
| 12 | 2.7.1.68 | | 0 | GO:0046488,(CAT1G10900.1 | 0 |
| 13 | 2.7.1.68 | | 0 | GO:0046488,(CAT1G10900.1 | 0 |
| 14 | 2.7.1.68 | | 0 | GO:0046488,(CAT1G10900.1 | 0 |
| 15 | 2.7.1.68 | | 0 | GO:0046488,(CAT1G10900.1 | 0 |
| 16 | | 0 K13993 | 0 | AT1G07400.1 | 0 |
| 17 | | 0 | 0 | GO:0008270,(CAT5G60410.3 ATSIZ1,SIZ1 | |
| 18 | | 0 | 0 | GO:0008270,(CAT5G60410.3 ATSIZ1,SIZ1 | |
| 19 | | 0 | 0 | GO:0008270,(CAT5G60410.3 ATSIZ1,SIZ1 | |
| 20 | | 0 | 0 | GO:0008270,(CAT5G60410.3 ATSIZ1,SIZ1 | |
| 21 | | 0 | 0 | GO:0008270,(CAT5G60410.3 ATSIZ1,SIZ1 | |
| 22 | | 0 | 0 | GO:0008270,(CAT5G60410.3 ATSIZ1,SIZ1 | |
| 23 | 3.1.3.16 | K18998 | 0 | AT4G21670.1 ATCPL1,CPL1,I | |
| 24 | | 0 | 0 | GO:0008270,(CAT5G60410.3 ATSIZ1,SIZ1 | |
| 25 | | 0 | 0 | GO:0008270,(CAT5G60410.3 ATSIZ1,SIZ1 | |
| 26 | | 0 | 0 | GO:0008270,(CAT5G60410.3 ATSIZ1,SIZ1 | |
| 27 | | 0 | 0 | 0 | 0 |
| 28 | | 0 | 0 | 0 AT1G25370.1 | 0 |
| 29 | | 0 | 0 | 0 AT2G34070.1 TBL37 | |
| 30 | | 0 | 0 | 0 AT2G34070.1 TBL37 | |
| 31 | 2.7.1.68 | K00889 | GO:0046488,(CAT1G10900.1 | | 0 |
| 32 | 3.6.4.13 | K17675 | GO:0016817 AT5G39840.1 | | 0 |
| 33 | | 0 | 0 | 0 | 0 |
| 34 | | 0 | 0 | 0 | 0 |
| 35 | | 0 | 0 | 0 | 0 |
| 36 | | 0 K02901 | GO:0006412,(CAT4G15000.1 | | 0 |
| 37 | 1.10.3.2 | K05909 | GO:0055114,(CAT5G48100.1 ATLAC15,LAC1 | | |
| 38 | | 0 | 0 | 0 AT3G50700.1 AtIDD2,IDD2 | |
| 39 | | 0 | 0 | 0 AT3G50700.1 AtIDD2,IDD2 | |
| 40 | | 0 | 0 | GO:0008270,(CAT4G28370.1 | 0 |
| 41 | | 0 | 0 | GO:0008270,(CAT4G28370.1 | 0 |
| 42 | | 0 | 0 | GO:0008270,(CAT4G28370.1 | 0 |
| 43 | | 0 | 0 | 0 AT4G11440.1 | 0 |
| 44 | | 0 | 0 | 0 AT4G11440.1 | 0 |
| 45 | | 0 | 0 | 0 AT4G11440.1 | 0 |
| 46 | | 0 | 0 | 0 AT4G11440.1 | 0 |
| 47 | | 0 | 0 | 0 AT1G64980.1 | 0 |
| 48 | | 0 | 0 | 0 | 0 |
| 49 | | 0 K03236 | GO:0006413,(CAT2G04520.1 | | 0 |
| 50 | | 0 | 0 | 0 | 0 |
| 51 | 2.7.1.68 | | 0 | GO:0046488,(CAT1G10900.1 | 0 |
| 52 | 2.7.1.68 | | 0 | GO:0046488,(CAT1G10900.1 | 0 |
| 53 | 2.7.1.68 | | 0 | GO:0046488,(CAT1G10900.1 | 0 |
| 54 | 2.7.1.68 | | 0 | GO:0046488,(CAT1G10900.1 | 0 |
| 55 | 2.7.1.68 | | 0 | GO:0046488,(CAT1G10900.1 | 0 |
| 56 | | 0 | 0 | 0 | 0 |
| 57 | | 0 | 0 | 0 | 0 |
| 58 | | 0 | 0 | 0 AT3G50700.1 AtIDD2,IDD2 | |
| 59 | | 0 | 0 | 0 AT3G50700.1 AtIDD2,IDD2 | |
| 60 | | 0 | 0 | 0 AT4G11440.1 | 0 |
| | | 0 | 0 | 0 AT4G11440.1 | 0 |

| | | | | | |
|----|-----------|----------|---|--|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 AT4G11440.1 | 0 |
| 3 | | 0 | 0 | 0 AT1G64980.1 | 0 |
| 4 | | 0 | 0 | 0 0 | 0 |
| 5 | | | | | |
| 6 | | 0 K03236 | | GO:0006413,(AT2G04520.1 | 0 |
| 7 | 2.7.1.68 | | | 0 GO:0046488,(AT1G10900.1 | 0 |
| 8 | 2.7.1.68 | | | 0 GO:0046488,(AT1G10900.1 | 0 |
| 9 | 2.7.1.68 | | | 0 GO:0046488,(AT1G10900.1 | 0 |
| 10 | 2.7.1.68 | | | 0 GO:0046488,(AT1G10900.1 | 0 |
| 11 | 2.7.1.68 | | | 0 GO:0046488,(AT1G10900.1 | 0 |
| 12 | | 0 | 0 | 0 0 | 0 |
| 13 | | 0 | 0 | 0 0 | 0 |
| 14 | | 0 | 0 | 0 AT3G50700.1 AtIDD2,IDD2 | |
| 15 | | 0 | 0 | 0 AT5G48920.1 TED7 | |
| 16 | | 0 | 0 | 0 AT1G30240.2 | 0 |
| 17 | | 0 | 0 | 0 AT1G30240.2 | 0 |
| 18 | | 0 | 0 | 0 AT1G30240.2 | 0 |
| 19 | | 0 | 0 | 0 AT1G30240.2 | 0 |
| 20 | 3.4.19.12 | K11858 | | GO:0005515 AT3G49600.1 ATUBP26,SUP | |
| 21 | 3.4.19.12 | K11858 | | GO:0005515 AT3G49600.1 ATUBP26,SUP | |
| 22 | 3.4.19.12 | K11858 | | GO:0005515 AT3G49600.1 ATUBP26,SUP | |
| 23 | 3.4.19.12 | K11858 | | GO:0005515 AT3G49600.1 ATUBP26,SUP | |
| 24 | 3.4.19.12 | K11858 | | GO:0005515 AT3G49600.1 ATUBP26,SUP | |
| 25 | | 0 | 0 | 0 AT1G43790.1 TED6 | |
| 26 | 2.4.1.12 | | | 0 GO:0030244,(AT1G55850.1 ATCSLE1,CSLE | |
| 27 | | 0 | 0 | 0 AT1G52780.1 | 0 |
| 28 | | 0 | 0 | 0 AT3G01680.1 | 0 |
| 29 | | 0 | 0 | 0 GO:0035091 AT3G48195.1 | 0 |
| 30 | | 0 | 0 | 0 GO:0035091 AT3G48195.1 | 0 |
| 31 | 3.6.3.44 | K05658 | | GO:0016887,(AT2G36910.1 ABCB1,ATPGP | |
| 32 | | 0 K09510 | | 0 AT2G20560.1 | 0 |
| 33 | | 0 | 0 | 0 0 0 | 0 |
| 34 | | 0 K09422 | | 0 AT5G17800.1 AtMYB56,MYE | |
| 35 | | 0 | 0 | 0 GO:0006950,(AT3G12050.1 | 0 |
| 36 | | 0 | 0 | 0 GO:0006950,(AT3G12050.1 | 0 |
| 37 | | 0 K12190 | | GO:0043130,(AT5G04920.1 | 0 |
| 38 | | 0 | 0 | 0 0 0 | 0 |
| 39 | | 0 | 0 | 0 0 0 | 0 |
| 40 | | 0 | 0 | 0 AT4G14820.1 | 0 |
| 41 | | 0 | 0 | 0 GO:0055114,(AT5G44390.1 | 0 |
| 42 | | 0 | 0 | 0 GO:0003723 AT1G78160.1 APUM7,PUM7 | |
| 43 | 2.7.1.1 | K00844 | | GO:0016773,(AT2G19860.1 ATHXK2,HXK2 | |
| 44 | | 0 K09422 | | 0 AT1G69560.1 ATMYB105,LC | |
| 45 | | 0 | 0 | 0 AT4G01170.1 | 0 |
| 46 | | 0 | 0 | 0 AT4G01170.1 | 0 |
| 47 | | 0 | 0 | 0 AT4G01170.1 | 0 |
| 48 | | 0 K11723 | | GO:0005515 AT5G55040.1 | 0 |
| 49 | | 0 | 0 | 0 AT3G15810.1 | 0 |
| 50 | | 0 | 0 | 0 GO:0055085,(AT5G26340.1 ATSTP13,MSS | |
| 51 | | 0 | 0 | 0 GO:0055085,(AT5G26340.1 ATSTP13,MSS | |
| 52 | | 0 | 0 | 0 AT2G43465.1 | 0 |
| 53 | | 0 | 0 | 0 AT2G43465.1 | 0 |
| 54 | | 0 | 0 | 0 AT2G43465.1 | 0 |
| 55 | | 0 | 0 | 0 AT2G43465.1 | 0 |
| 56 | | 0 | 0 | 0 AT2G43465.1 | 0 |
| 57 | | 0 | 0 | 0 AT2G43465.1 | 0 |
| 58 | | 0 | 0 | 0 AT2G43465.1 | 0 |
| 59 | | 0 | 0 | 0 AT2G43465.1 | 0 |
| 60 | | 0 | 0 | 0 AT2G43465.1 | 0 |

| | | | | | |
|----|-----------|----------|--------------------------------------|---------------------------------------|---|
| 1 | | | | | |
| 2 | | 0 | 0 | GO:0055085,(CAT5G26340.1 ATSTP13,MSS | |
| 3 | | 0 | 0 | GO:0055085,(CAT5G26340.1 ATSTP13,MSS | |
| 4 | | 0 | 0 | 0 AT2G43465.1 | 0 |
| 5 | | | | | |
| 6 | 3.1.3.16 | K15423 | GO:0016787 | AT5G55260.1 PPX-2,PPX2 | |
| 7 | | 0 | 0 | 0 | 0 |
| 8 | | 0 | 0 | 0 AT5G54130.2 | 0 |
| 9 | | 0 | 0 | 0 AT5G54130.2 | 0 |
| 10 | | 0 | 0 | 0 AT5G54130.2 | 0 |
| 11 | | 0 K10599 | GO:0005515 | AT2G33340.1 MAC3B | |
| 12 | | 0 | 0 | GO:0055085,(CAT5G51710.2 ATKEA5,KEA5 | |
| 13 | | 0 | 0 | GO:0043531 AT3G14470.1 | 0 |
| 14 | | 0 | 0 | 0 AT1G30240.2 | 0 |
| 15 | | 0 | 0 | 0 AT1G30240.2 | 0 |
| 16 | | 0 | 0 | 0 AT1G30240.2 | 0 |
| 17 | | 0 | 0 | 0 AT5G48920.1 TED7 | |
| 18 | | | | | |
| 19 | 2.4.1.12 | | 0 | GO:0030244,(CAT1G55850.1 ATCSLE1,CSLE | |
| 20 | 3.4.19.12 | K11858 | GO:0005515 | AT3G49600.1 ATUBP26,SUP | |
| 21 | | | | | |
| 22 | 3.4.19.12 | K11858 | GO:0005515 | AT3G49600.1 ATUBP26,SUP | |
| 23 | 3.4.19.12 | K11858 | GO:0005515 | AT3G49600.1 ATUBP26,SUP | |
| 24 | 3.4.19.12 | K11858 | GO:0005515 | AT3G49600.1 ATUBP26,SUP | |
| 25 | | | | | |
| 26 | | 0 | 0 | 0 AT1G43790.1 TED6 | |
| 27 | | 0 | 0 | 0 AT1G52780.1 | 0 |
| 28 | | 0 | 0 | 0 | 0 |
| 29 | | 0 | 0 | 0 | 0 |
| 30 | | 0 | 0 | 0 | 0 |
| 31 | | 0 | 0 | 0 | 0 |
| 32 | | 0 | 0 | 0 AT5G54130.2 | 0 |
| 33 | | 0 | 0 | 0 AT5G54130.2 | 0 |
| 34 | | | | | |
| 35 | | 0 | 0 | GO:0055085,(CAT5G51710.2 ATKEA5,KEA5 | |
| 36 | | 0 | 0 | 0 AT4G14820.1 | 0 |
| 37 | | 0 | 0 | GO:0055114,(CAT5G44390.1 | 0 |
| 38 | | 0 | 0 | 0 AT3G01680.1 | 0 |
| 39 | | 0 | 0 | 0 AT3G01680.1 | 0 |
| 40 | | 0 | 0 | GO:0035091 AT3G48195.1 | 0 |
| 41 | | | | | |
| 42 | 3.6.3.44 | K05658 | GO:0016887,(CAT2G36910.1 ABCB1,ATPGP | | |
| 43 | | 0 K09510 | 0 | AT2G20560.1 | 0 |
| 44 | | 0 | 0 | 0 AT2G43465.1 | 0 |
| 45 | | 0 | 0 | 0 AT2G43465.1 | 0 |
| 46 | | 0 | 0 | 0 AT2G43465.1 | 0 |
| 47 | | 0 K09422 | 0 | AT5G17800.1 AtMYB56,MYE | |
| 48 | | 0 | 0 | GO:0006950,(CAT3G12050.1 | 0 |
| 49 | | 0 | 0 | GO:0006950,(CAT3G12050.1 | 0 |
| 50 | | 0 | 0 | GO:0043130,(CAT5G04920.1 | 0 |
| 51 | | 0 K12190 | GO:0043130,(CAT5G04920.1 | | 0 |
| 52 | | 0 | 0 | 0 AT2G43465.1 | 0 |
| 53 | | | | | |
| 54 | 3.1.3.16 | K15423 | GO:0016787 | AT5G55260.1 PPX-2,PPX2 | |
| 55 | | 0 | 0 | 0 AT4G21700.1 | 0 |
| 56 | | 0 | 0 | GO:0003723 AT1G78160.1 APUM7,PUM7 | |
| 57 | | 0 K11723 | GO:0005515 | AT5G55040.1 | 0 |
| 58 | | 0 | 0 | 0 | 0 |
| 59 | | 0 | 0 | 0 | 0 |
| 60 | | 0 | 0 | 0 AT4G28210.1 emb1923 | |
| | 2.7.1.1 | K00844 | GO:0016773,(CAT2G19860.1 ATHXK2,HXK2 | | |

| | | | | | |
|----|-----------|----------|----------------|---------------------------|-------------------------|
| 1 | | | | | |
| 2 | | 0 K09422 | | 0 AT1G69560.1 ATMYB105,LC | |
| 3 | | 0 K10599 | GO:0005515 | AT2G33340.1 MAC3B | |
| 4 | | 0 | 0 | 0 AT4G01170.1 | 0 |
| 5 | | 0 | 0 | 0 AT1G30240.2 | 0 |
| 6 | | 0 | 0 | 0 AT1G30240.2 | 0 |
| 7 | | 0 | 0 | 0 AT5G48920.1 TED7 | |
| 8 | | 0 | 0 | 0 AT5G48920.1 TED7 | |
| 9 | | | | | |
| 10 | 2.4.1.12 | | 0 GO:0030244,(| AT1G55850.1 ATCSLE1,CSLE | |
| 11 | 3.4.19.12 | K11858 | GO:0005515 | AT3G49600.1 ATUBP26,SUP | |
| 12 | 3.4.19.12 | K11858 | GO:0005515 | AT3G49600.1 ATUBP26,SUP | |
| 13 | 3.4.19.12 | K11858 | GO:0005515 | AT3G49600.1 ATUBP26,SUP | |
| 14 | 3.4.19.12 | K11858 | GO:0005515 | AT3G49600.1 ATUBP26,SUP | |
| 15 | 3.4.19.12 | K11858 | GO:0005515 | AT3G49600.1 ATUBP26,SUP | |
| 16 | | 0 | 0 | 0 AT1G43790.1 TED6 | |
| 17 | | 0 | 0 | 0 AT1G52780.1 | 0 |
| 18 | | 0 | 0 | 0 | 0 |
| 19 | | 0 | 0 | 0 | 0 |
| 20 | | 0 | 0 | 0 | 0 |
| 21 | | 0 | 0 | 0 | 0 |
| 22 | | 0 | 0 | 0 | 0 |
| 23 | | 0 | 0 | 0 AT5G54130.2 | 0 |
| 24 | | 0 | 0 | 0 AT5G54130.2 | 0 |
| 25 | | 0 | 0 | 0 GO:0055085,(| AT5G51710.2 ATKEA5,KEA5 |
| 26 | | 0 | 0 | 0 AT4G14820.1 | 0 |
| 27 | | 0 | 0 | 0 AT4G14820.1 | 0 |
| 28 | | 0 | 0 GO:0055114,(| AT5G44390.1 | 0 |
| 29 | | 0 | 0 | 0 AT3G01680.1 | 0 |
| 30 | | 0 | 0 | 0 AT3G01680.1 | 0 |
| 31 | | 0 | 0 GO:0035091 | AT3G48195.1 | 0 |
| 32 | 3.6.3.44 | K05658 | GO:0016887,(| AT2G36910.1 ABCB1,ATPGP | |
| 33 | | 0 K09510 | | 0 AT2G20560.1 | 0 |
| 34 | | 0 | 0 | 0 AT2G43465.1 | 0 |
| 35 | | 0 | 0 | 0 AT2G43465.1 | 0 |
| 36 | | 0 | 0 | 0 AT2G43465.1 | 0 |
| 37 | | 0 K09422 | | 0 AT5G17800.1 AtMYB56,MYE | |
| 38 | | 0 | 0 | 0 AT5G17800.1 AtMYB56,MYE | |
| 39 | | 0 | 0 GO:0006950,(| AT3G12050.1 | 0 |
| 40 | | 0 | 0 GO:0006950,(| AT3G12050.1 | 0 |
| 41 | | 0 K12190 | GO:0043130,(| AT5G04920.1 | 0 |
| 42 | | 0 | 0 | 0 AT2G43465.1 | 0 |
| 43 | | 0 | 0 | 0 AT2G43465.1 | 0 |
| 44 | 3.1.3.16 | K15423 | GO:0016787 | AT5G55260.1 PPX-2,PPX2 | |
| 45 | | 0 | 0 | 0 AT4G21700.1 | 0 |
| 46 | | 0 | 0 | 0 AT4G21700.1 | 0 |
| 47 | | 0 | 0 GO:0003723 | AT1G78160.1 APUM7,PUM7 | |
| 48 | | 0 K11723 | GO:0005515 | AT5G55040.1 | 0 |
| 49 | | 0 | 0 | 0 | 0 |
| 50 | | 0 | 0 | 0 | 0 |
| 51 | | 0 | 0 | 0 AT4G28210.1 emb1923 | |
| 52 | 2.7.1.1 | K00844 | GO:0016773,(| AT2G19860.1 ATHXK2,HXK2 | |
| 53 | | 0 K09422 | | 0 AT1G69560.1 ATMYB105,LC | |
| 54 | | 0 K10599 | GO:0005515 | AT2G33340.1 MAC3B | |
| 55 | | 0 | 0 | 0 AT4G01170.1 | 0 |
| 56 | | 0 | 0 | 0 AT4G01170.1 | 0 |
| 57 | | 0 | 0 | 0 AT4G01170.1 | 0 |
| 58 | | 0 | 0 | 0 | 0 |
| 59 | | 0 | 0 | 0 | 0 |
| 60 | | 0 | 0 | 0 | 0 |

| | | | | | |
|----|-----------|----------|---------------------------------------|--------------------------|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 | 0 |
| 3 | | 0 | 0 | 0 | 0 |
| 4 | | 0 | 0 | 0 | 0 |
| 5 | | 0 | 0 | 0 | 0 |
| 6 | | 0 | 0 | 0 AT3G28150.1 TBL22 | |
| 7 | | 0 | 0 | 0 AT3G28150.1 TBL22 | |
| 8 | | 0 | 0 | 0 | 0 |
| 9 | | 0 | 0 | 0 | 0 |
| 10 | | 0 | 0 | 0 | 0 |
| 11 | | 0 | 0 | 0 | 0 |
| 12 | | 0 K01183 | GO:0005975,(AT4G19810.1 | | 0 |
| 13 | | 0 | 0 GO:0006355,(AT5G19790.1 RAP2.11 | | |
| 14 | | 0 | 0 | 0 | 0 |
| 15 | | 0 | 0 | 0 | 0 |
| 16 | | 0 | 0 | 0 | 0 |
| 17 | | 0 | 0 | 0 | 0 |
| 18 | | 0 | 0 GO:0006355,(AT3G25890.1 | | 0 |
| 19 | | 0 | 0 | 0 AT2G44260.2 | 0 |
| 20 | | 0 | 0 | 0 | 0 |
| 21 | | 0 | 0 | 0 | 0 |
| 22 | | 0 | 0 | 0 AT1G02420.1 | 0 |
| 23 | | 0 | 0 GO:0003723 AT1G78160.1 APUM7,PUM7 | | |
| 24 | 3.6.5.3 | K02519 | GO:0005525 AT1G17220.1 FUG1 | | |
| 25 | 3.6.4.4 | K10395 | GO:0008017,(AT5G47820.1 FRA1 | | |
| 26 | | 0 K03327 | GO:0055085,(AT4G00350.1 | | 0 |
| 27 | | | | | |
| 28 | 2.7.12.2 | | 0 | 0 AT1G73500.1 ATMKK9,MKK | |
| 29 | 3.6.4.13 | K14563 | GO:0008168,(AT5G52470.1 ATFBR1,ATFIB | | |
| 30 | | 0 | 0 GO:0003676 AT4G10610.1 ATRBP37,CID1 | | |
| 31 | | 0 | 0 | 0 | 0 |
| 32 | | 0 | 0 | 0 | 0 |
| 33 | | 0 | 0 GO:0008270,(AT3G16720.1 ATL2,TL2 | | |
| 34 | | 0 | 0 GO:0008270,(AT5G58580.1 ATL63,TL63 | | |
| 35 | | 0 | 0 | 0 | 0 |
| 36 | 2.3.1.133 | | 0 GO:0016747 AT2G19070.1 SHT | | |
| 37 | | 0 K12741 | GO:0003676 AT5G61030.1 GR-RBP3 | | |
| 38 | | | | | |
| 39 | 2.7.11.1 | | 0 | 0 AT3G29270.2 | 0 |
| 40 | 2.1.1.125 | K11434 | GO:0008168,(AT1G04870.2 ATPRMT10,PR | | |
| 41 | 2.7.11.1 | | 0 | 0 AT3G29270.2 | 0 |
| 42 | | | | | |
| 43 | 2.3.1.133 | K13065 | GO:0016747 AT2G19070.1 SHT | | |
| 44 | | 0 | 0 | 0 AT1G02910.1 LPA1 | |
| 45 | | 0 K12741 | GO:0003676 AT3G15010.2 | | 0 |
| 46 | | 0 | 0 GO:0055085,(AT5G16150.3 GLT1,PGLCT | | |
| 47 | | | | | |
| 48 | 3.4.23.12 | | 0 GO:0006508,(AT5G10770.1 | | 0 |
| 49 | | 0 | 0 | 0 | 0 |
| 50 | | 0 | 0 | 0 AT3G15030.2 MEE35,TCP4 | |
| 51 | | 0 | 0 | 0 | 0 |
| 52 | | 0 | 0 | 0 | 0 |
| 53 | | 0 | 0 | 0 | 0 |
| 54 | | 0 | 0 | 0 | 0 |
| 55 | | 0 | 0 | 0 | 0 |
| 56 | | 0 | 0 | 0 | 0 |
| 57 | | 0 | 0 | 0 | 0 |
| 58 | | 0 | 0 | 0 | 0 |
| 59 | | 0 | 0 | 0 | 0 |
| 60 | | 0 | 0 GO:0006355,(AT5G19790.1 RAP2.11 | | |
| | | 0 | 0 | 0 | 0 |

| | | | | | |
|----|-----------|----------|----------------|---------------------------|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 AT2G44260.2 | 0 |
| 3 | | 0 | 0 | 0 AT3G28150.1 TBL22 | |
| 4 | | 0 | 0 | 0 AT3G28150.1 TBL22 | |
| 5 | | 0 | 0 | 0 AT1G02420.1 | 0 |
| 6 | | 0 | 0 | 0 AT1G07400.1 | 0 |
| 7 | | 0 K13993 | | 0 AT1G07400.1 | 0 |
| 8 | 2.3.1.133 | | 0 GO:0016747 | AT2G19070.1 SHT | |
| 9 | | 0 | 0 | 0 | 0 |
| 10 | | 0 | 0 | 0 | 0 |
| 11 | 2.3.1.133 | K13065 | GO:0016747 | AT2G19070.1 SHT | |
| 12 | | 0 | 0 | 0 | 0 |
| 13 | | 0 | 0 | 0 | 0 |
| 14 | | 0 | 0 | 0 | 0 |
| 15 | | 0 | 0 | 0 | 0 |
| 16 | | 0 K01183 | GO:0005975,(| AT4G19810.1 | 0 |
| 17 | 3.6.4.13 | K14563 | GO:0008168,(| AT5G52470.1 ATFBR1,ATFIB | |
| 18 | | 0 | 0 | 0 AT1G79490.1 EMB2217 | |
| 19 | | 0 | 0 GO:0006355,(| AT3G25890.1 | 0 |
| 20 | | 0 | 0 GO:0006629 | AT2G26560.1 PLA IIA,PLA2A | |
| 21 | | 0 | 0 GO:0006629 | AT2G26560.1 PLA IIA,PLA2A | |
| 22 | | 0 K03327 | GO:0055085,(| AT4G00350.1 | 0 |
| 23 | | 0 K18812 | GO:0005634,(| AT4G03270.1 CYCD6;1 | |
| 24 | | 0 | 0 GO:0016020,(| AT3G53960.1 | 0 |
| 25 | | 0 | 0 GO:0006629 | AT2G26560.1 PLA IIA,PLA2A | |
| 26 | | 0 | 0 GO:0003723 | AT1G78160.1 APUM7,PUM7 | |
| 27 | | 0 | 0 GO:0003723 | AT1G78160.1 APUM7,PUM7 | |
| 28 | 3.6.5.3 | K02519 | GO:0005525 | AT1G17220.1 FUG1 | |
| 29 | 3.6.4.4 | K10395 | GO:0008017,(| AT5G47820.1 FRA1 | |
| 30 | 2.3.1.1 | | 0 GO:0008080 | AT3G22560.1 | 0 |
| 31 | 2.3.1.1 | | 0 GO:0008080 | AT3G22560.1 | 0 |
| 32 | | 0 K12741 | GO:0003676 | AT5G61030.1 GR-RBP3 | |
| 33 | | 0 K06950 | | 0 AT1G17330.1 | 0 |
| 34 | 2.7.11.1 | | 0 | 0 AT3G29270.2 | 0 |
| 35 | 2.7.11.1 | | 0 | 0 AT3G29270.2 | 0 |
| 36 | | 0 | 0 GO:0055085,(| AT5G16150.3 GLT1,PGLCT | |
| 37 | 3.4.23.12 | | 0 GO:0006508,(| AT5G10770.1 | 0 |
| 38 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 39 | | 0 | 0 | 0 | 0 |
| 40 | | 0 | 0 | 0 | 0 |
| 41 | | 0 | 0 | 0 | 0 |
| 42 | | 0 | 0 | 0 | 0 |
| 43 | | 0 | 0 | 0 | 0 |
| 44 | | 0 | 0 | 0 | 0 |
| 45 | | 0 | 0 | 0 | 0 |
| 46 | | 0 | 0 | 0 | 0 |
| 47 | | 0 | 0 | 0 | 0 |
| 48 | | 0 | 0 | 0 | 0 |
| 49 | | 0 | 0 | 0 | 0 |
| 50 | | 0 | 0 | 0 | 0 |
| 51 | | 0 | 0 | 0 | 0 |
| 52 | | 0 | 0 GO:0006355,(| AT5G19790.1 RAP2.11 | |
| 53 | | 0 | 0 | 0 | 0 |
| 54 | | 0 | 0 | 0 AT2G44260.2 | 0 |
| 55 | | 0 | 0 | 0 AT3G28150.1 TBL22 | |
| 56 | | 0 | 0 | 0 AT3G28150.1 TBL22 | |
| 57 | | 0 | 0 | 0 AT1G02420.1 | 0 |
| 58 | | 0 | 0 | 0 AT1G07400.1 | 0 |
| 59 | | 0 K13993 | | 0 AT1G07400.1 | 0 |
| 60 | 2.3.1.133 | | 0 GO:0016747 | AT2G19070.1 SHT | |

| | | | | | |
|----|-----------|--------|--------------|--------------|--------------|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 | 0 |
| 3 | 2.3.1.133 | K13065 | GO:0016747 | AT2G19070.1 | SHT |
| 4 | | 0 | 0 | 0 | 0 |
| 5 | | 0 | 0 | 0 | 0 |
| 6 | | 0 | 0 | 0 | 0 |
| 7 | | 0 | 0 | 0 | 0 |
| 8 | | 0 | K01183 | GO:0005975,(| AT4G19810.1 |
| 9 | 3.6.4.13 | K14563 | GO:0008168,(| AT5G52470.1 | ATFBR1,ATFIB |
| 10 | | 0 | 0 | 0 | AT1G79490.1 |
| 11 | | 0 | 0 | GO:0006355,(| AT3G25890.1 |
| 12 | | 0 | 0 | GO:0006629 | AT2G26560.1 |
| 13 | | 0 | 0 | GO:0006629 | AT2G26560.1 |
| 14 | | 0 | K03327 | GO:0055085,(| AT4G00350.1 |
| 15 | | 0 | K18812 | GO:0005634,(| AT4G03270.1 |
| 16 | | 0 | 0 | GO:0016020,(| AT3G53960.1 |
| 17 | | 0 | 0 | GO:0006629 | AT2G26560.1 |
| 18 | | 0 | 0 | GO:0003723 | AT1G78160.1 |
| 19 | 3.6.5.3 | K02519 | GO:0005525 | AT1G17220.1 | FUG1 |
| 20 | 3.6.4.4 | K10395 | GO:0008017,(| AT5G47820.1 | FRA1 |
| 21 | 2.3.1.1 | | 0 | GO:0008080 | AT3G22560.1 |
| 22 | 2.3.1.1 | | 0 | GO:0008080 | AT3G22560.1 |
| 23 | | 0 | K12741 | GO:0003676 | AT5G61030.1 |
| 24 | | 0 | K06950 | 0 | AT1G17330.1 |
| 25 | 2.7.11.1 | | 0 | 0 | AT3G29270.2 |
| 26 | 2.7.11.1 | | 0 | 0 | AT3G29270.2 |
| 27 | | 0 | 0 | GO:0055085,(| AT5G16150.3 |
| 28 | 3.4.23.12 | | 0 | GO:0006508,(| AT5G10770.1 |
| 29 | | 0 | 0 | 0 | AT2G37570.1 |
| 30 | | | | | |
| 31 | | | | | |
| 32 | | | | | |
| 33 | | | | | |
| 34 | | | | | |
| 35 | | | | | |
| 36 | | | | | |
| 37 | | | | | |
| 38 | | | | | |
| 39 | | | | | |
| 40 | | | | | |
| 41 | | | | | |
| 42 | | | | | |
| 43 | | | | | |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| 1 | arabi-defline | ID | Annot_defline | IDENTIFIER |
|----|--|--------------|-----------------|----------------|
| 2 | | | | |
| 3 | Ribonuclease T2 family protein | Phvul.004G06 | PTHR11240:Si | Phvul.004G06 |
| 4 | plant natriuretic peptide A | Phvul.009G09 | PTHR22595://I | Phvul.009G09 |
| 5 | | | | |
| 6 | Aldolase-type TIM barrel family protein | Phvul.008G04 | 2.5.1.55 - 3-de | Phvul.008G04 |
| 7 | Ribonuclease T2 family protein | Phvul.004G06 | PTHR11240:Si | Phvul.004G06 |
| 8 | plant natriuretic peptide A | Phvul.009G09 | PTHR22595://I | Phvul.009G09 |
| 9 | | | | |
| 10 | Ribonuclease T2 family protein | Phvul.004G06 | PTHR11240:Si | Phvul.004G06 |
| 11 | plant natriuretic peptide A | Phvul.009G09 | PTHR22595://I | Phvul.009G09 |
| 12 | | 0 | 0 | 0 Phvul.009G19 |
| 13 | Protein of unknown function (DUF803) | Phvul.008G19 | KOG2922 - Un | Phvul.008G19 |
| 14 | HSP20-like chaperones superfamily protein | Phvul.007G15 | PTHR33981:Si | Phvul.007G15 |
| 15 | | 0 | 0 | 0 Phvul.009G10 |
| 16 | | | | |
| 17 | O-fucosyltransferase family protein | Phvul.004G03 | PF10250 - GD | Phvul.004G03 |
| 18 | auxin response factor 4 | Phvul.011G07 | PTHR31384:Si | Phvul.011G07 |
| 19 | auxin response factor 4 | Phvul.011G07 | PTHR31384:Si | Phvul.011G07 |
| 20 | | | | |
| 21 | myosin heavy chain-related | | 0 | 0 Phvul.L00160 |
| 22 | myosin heavy chain-related | | 0 | 0 Phvul.L00160 |
| 23 | myosin heavy chain-related | | 0 | 0 Phvul.L00160 |
| 24 | | | | |
| 25 | nudix hydrolase homolog 20 | Phvul.004G16 | 2.7.6.2 - Thian | Phvul.004G16 |
| 26 | S-locus lectin protein kinase family protein | Phvul.011G15 | PTHR27002:Si | Phvul.011G15 |
| 27 | S-locus lectin protein kinase family protein | Phvul.011G15 | PTHR27002:Si | Phvul.011G15 |
| 28 | S-locus lectin protein kinase family protein | Phvul.011G15 | PTHR27002:Si | Phvul.011G15 |
| 29 | ubiquitin family protein | Phvul.003G22 | PTHR13527:Si | Phvul.003G22 |
| 30 | ubiquitin family protein | Phvul.003G22 | PTHR13527:Si | Phvul.003G22 |
| 31 | arogenate dehydrogenase | Phvul.003G17 | 1.3.1.78 - Aro | Phvul.003G17 |
| 32 | | 0 | 0 | 0 Phvul.009G19 |
| 33 | Protein of unknown function (DUF803) | Phvul.008G19 | KOG2922 - Un | Phvul.008G19 |
| 34 | HSP20-like chaperones superfamily protein | Phvul.007G15 | PTHR33981:Si | Phvul.007G15 |
| 35 | nudix hydrolase homolog 20 | Phvul.004G16 | 2.7.6.2 - Thian | Phvul.004G16 |
| 36 | | 0 | 0 | 0 Phvul.009G10 |
| 37 | myosin heavy chain-related | | 0 | 0 Phvul.L00160 |
| 38 | myosin heavy chain-related | | 0 | 0 Phvul.L00160 |
| 39 | myosin heavy chain-related | | 0 | 0 Phvul.L00160 |
| 40 | | | | |
| 41 | O-fucosyltransferase family protein | Phvul.004G03 | PF10250 - GD | Phvul.004G03 |
| 42 | auxin response factor 4 | Phvul.011G07 | PTHR31384:Si | Phvul.011G07 |
| 43 | auxin response factor 4 | Phvul.011G07 | PTHR31384:Si | Phvul.011G07 |
| 44 | | 0 | 0 | 0 Phvul.009G19 |
| 45 | Protein of unknown function (DUF803) | Phvul.008G19 | KOG2922 - Un | Phvul.008G19 |
| 46 | HSP20-like chaperones superfamily protein | Phvul.007G15 | PTHR33981:Si | Phvul.007G15 |
| 47 | nudix hydrolase homolog 20 | Phvul.004G16 | 2.7.6.2 - Thian | Phvul.004G16 |
| 48 | | 0 | 0 | 0 Phvul.009G10 |
| 49 | myosin heavy chain-related | | 0 | 0 Phvul.L00160 |
| 50 | myosin heavy chain-related | | 0 | 0 Phvul.L00160 |
| 51 | myosin heavy chain-related | | 0 | 0 Phvul.L00160 |
| 52 | | | | |
| 53 | O-fucosyltransferase family protein | Phvul.004G03 | PF10250 - GD | Phvul.004G03 |
| 54 | auxin response factor 4 | Phvul.011G07 | PTHR31384:Si | Phvul.011G07 |

| | | | | |
|----|---|--------------|----------------|----------------|
| 1 | | | | |
| 2 | auxin response factor 4 | Phvul.011G07 | PTHR31384:Si | Phvul.011G07 |
| 3 | Mitochondrial substrate carrier family protein | Phvul.002G28 | PTHR24089:Si | Phvul.002G28 |
| 4 | Mitochondrial substrate carrier family protein | Phvul.002G28 | PTHR24089:Si | Phvul.002G28 |
| 5 | Mitochondrial substrate carrier family protein | Phvul.002G28 | PTHR24089:Si | Phvul.002G28 |
| 6 | Mitochondrial substrate carrier family protein | Phvul.002G28 | PTHR24089:Si | Phvul.002G28 |
| 7 | Nucleotide-diphospho-sugar transferases superf | 0 | 0 | Phvul.002G04 |
| 8 | Nucleic acid-binding, OB-fold-like protein | Phvul.010G10 | K03236 - tran: | Phvul.010G10 |
| 9 | | 0 | 0 | 0 Phvul.006G14 |
| 10 | | 0 | 0 | 0 Phvul.006G14 |
| 11 | Phosphatidylinositol-4-phosphate 5-kinase famil | Phvul.006G21 | PTHR23086:Si | Phvul.006G21 |
| 12 | Phosphatidylinositol-4-phosphate 5-kinase famil | Phvul.006G21 | PTHR23086:Si | Phvul.006G21 |
| 13 | Phosphatidylinositol-4-phosphate 5-kinase famil | Phvul.006G21 | PTHR23086:Si | Phvul.006G21 |
| 14 | Phosphatidylinositol-4-phosphate 5-kinase famil | Phvul.006G21 | PTHR23086:Si | Phvul.006G21 |
| 15 | Phosphatidylinositol-4-phosphate 5-kinase famil | Phvul.006G21 | PTHR23086:Si | Phvul.006G21 |
| 16 | HSP20-like chaperones superfamily protein | Phvul.002G23 | PTHR11527:Si | Phvul.002G23 |
| 17 | DNA-binding protein with MIZ/SP-RING zinc fing | Phvul.005G13 | PTHR10782:Si | Phvul.005G13 |
| 18 | DNA-binding protein with MIZ/SP-RING zinc fing | Phvul.005G13 | PTHR10782:Si | Phvul.005G13 |
| 19 | DNA-binding protein with MIZ/SP-RING zinc fing | Phvul.005G13 | PTHR10782:Si | Phvul.005G13 |
| 20 | DNA-binding protein with MIZ/SP-RING zinc fing | Phvul.005G13 | PTHR10782:Si | Phvul.005G13 |
| 21 | DNA-binding protein with MIZ/SP-RING zinc fing | Phvul.005G13 | PTHR10782:Si | Phvul.005G13 |
| 22 | DNA-binding protein with MIZ/SP-RING zinc fing | Phvul.005G13 | PTHR10782:Si | Phvul.005G13 |
| 23 | C-terminal domain phosphatase-like 1 | Phvul.002G22 | PTHR23081:Si | Phvul.002G22 |
| 24 | DNA-binding protein with MIZ/SP-RING zinc fing | Phvul.005G13 | PTHR10782:Si | Phvul.005G13 |
| 25 | DNA-binding protein with MIZ/SP-RING zinc fing | Phvul.005G13 | PTHR10782:Si | Phvul.005G13 |
| 26 | DNA-binding protein with MIZ/SP-RING zinc fing | Phvul.005G13 | PTHR10782:Si | Phvul.005G13 |
| 27 | | 0 | 0 | 0 Phvul.007G22 |
| 28 | Protein of unknown function (DUF1639) | Phvul.007G02 | PF07797 - Pro | Phvul.007G02 |
| 29 | TRICHOME BIREFRINGENCE-LIKE 37 | Phvul.003G05 | PTHR32285:Si | Phvul.003G05 |
| 30 | Phosphatidylinositol-4-phosphate 5-kinase famil | Phvul.002G25 | PTHR23086:Si | Phvul.002G25 |
| 31 | ATP-dependent RNA helicase, mitochondrial, pu | Phvul.004G02 | PTHR12131:Si | Phvul.004G02 |
| 32 | | 0 | 0 | 0 Phvul.008G21 |
| 33 | | 0 | 0 | 0 Phvul.008G21 |
| 34 | | 0 | 0 | 0 Phvul.008G21 |
| 35 | | 0 | 0 | 0 Phvul.008G21 |
| 36 | Ribosomal L27e protein family | Phvul.002G19 | K02901 - large | Phvul.002G19 |
| 37 | Laccase/Diphenol oxidase family protein | Phvul.004G08 | PTHR11709:Si | Phvul.004G08 |
| 38 | indeterminate(ID)-domain 2 | Phvul.001G03 | PTHR10593:Si | Phvul.001G03 |
| 39 | RING/U-box superfamily protein | Phvul.005G10 | PTHR22763:Si | Phvul.005G10 |
| 40 | RING/U-box superfamily protein | Phvul.005G10 | PTHR22763:Si | Phvul.005G10 |
| 41 | RING/U-box superfamily protein | Phvul.005G10 | PTHR22763:Si | Phvul.005G10 |
| 42 | RING/U-box superfamily protein | Phvul.005G10 | PTHR22763:Si | Phvul.005G10 |
| 43 | Mitochondrial substrate carrier family protein | Phvul.002G28 | PTHR24089:Si | Phvul.002G28 |
| 44 | Mitochondrial substrate carrier family protein | Phvul.002G28 | PTHR24089:Si | Phvul.002G28 |
| 45 | Mitochondrial substrate carrier family protein | Phvul.002G28 | PTHR24089:Si | Phvul.002G28 |
| 46 | Mitochondrial substrate carrier family protein | Phvul.002G28 | PTHR24089:Si | Phvul.002G28 |
| 47 | Nucleotide-diphospho-sugar transferases superf | 0 | 0 | Phvul.002G04 |
| 48 | | 0 | 0 | 0 Phvul.006G14 |
| 49 | Nucleic acid-binding, OB-fold-like protein | Phvul.010G10 | K03236 - tran: | Phvul.010G10 |
| 50 | Phosphatidylinositol-4-phosphate 5-kinase famil | Phvul.006G21 | PTHR23086:Si | Phvul.006G21 |
| 51 | Phosphatidylinositol-4-phosphate 5-kinase famil | Phvul.006G21 | PTHR23086:Si | Phvul.006G21 |
| 52 | Phosphatidylinositol-4-phosphate 5-kinase famil | Phvul.006G21 | PTHR23086:Si | Phvul.006G21 |
| 53 | Phosphatidylinositol-4-phosphate 5-kinase famil | Phvul.006G21 | PTHR23086:Si | Phvul.006G21 |
| 54 | Phosphatidylinositol-4-phosphate 5-kinase famil | Phvul.006G21 | PTHR23086:Si | Phvul.006G21 |
| 55 | Phosphatidylinositol-4-phosphate 5-kinase famil | Phvul.006G21 | PTHR23086:Si | Phvul.006G21 |
| 56 | | 0 | 0 | 0 Phvul.008G21 |
| 57 | | 0 | 0 | 0 Phvul.008G21 |
| 58 | | 0 | 0 | 0 Phvul.008G21 |
| 59 | indeterminate(ID)-domain 2 | Phvul.001G03 | PTHR10593:Si | Phvul.001G03 |
| 60 | Mitochondrial substrate carrier family protein | Phvul.002G28 | PTHR24089:Si | Phvul.002G28 |
| | Mitochondrial substrate carrier family protein | Phvul.002G28 | PTHR24089:Si | Phvul.002G28 |

| | | | | |
|----|---|----------------------------------|---------------------|---------------------------|
| 1 | | | | |
| 2 | Mitochondrial substrate carrier family protein | Phvul.002G28PTHR24089:Si | Phvul.002G28 | |
| 3 | Nucleotide-diphospho-sugar transferases superf | 0 | 0 | Phvul.002G04 |
| 4 | | 0 | 0 | Phvul.006G14 |
| 5 | | | | |
| 6 | Nucleic acid-binding, OB-fold-like protein | Phvul.010G10K03236 - tran: | Phvul.010G10 | |
| 7 | Phosphatidylinositol-4-phosphate 5-kinase famil | Phvul.006G21PTHR23086:Si | Phvul.006G21 | |
| 8 | Phosphatidylinositol-4-phosphate 5-kinase famil | Phvul.006G21PTHR23086:Si | Phvul.006G21 | |
| 9 | | | | |
| 10 | Phosphatidylinositol-4-phosphate 5-kinase famil | Phvul.006G21PTHR23086:Si | Phvul.006G21 | |
| 11 | Phosphatidylinositol-4-phosphate 5-kinase famil | Phvul.006G21PTHR23086:Si | Phvul.006G21 | |
| 12 | | 0 | 0 | Phvul.008G21 |
| 13 | | 0 | 0 | Phvul.008G21 |
| 14 | | | | |
| 15 | indeterminate(ID)-domain 2 | Phvul.001G03PTHR10593:Si | Phvul.001G03 | |
| 16 | tracheary element differentiation-related 7 | 0 | 0 | Phvul.001G05 |
| 17 | | | | |
| 18 | | 0 | 0 | Phvul.010G11PF08167 - rRN |
| 19 | | 0 | 0 | Phvul.010G11PF08167 - rRN |
| 20 | ubiquitin-specific protease 26 | Phvul.009G10K11858 - ubiq | Phvul.009G10 | |
| 21 | ubiquitin-specific protease 26 | Phvul.009G10K11858 - ubiq | Phvul.009G10 | |
| 22 | ubiquitin-specific protease 26 | Phvul.009G10K11858 - ubiq | Phvul.009G10 | |
| 23 | ubiquitin-specific protease 26 | Phvul.009G10K11858 - ubiq | Phvul.009G10 | |
| 24 | ubiquitin-specific protease 26 | Phvul.009G10K11858 - ubiq | Phvul.009G10 | |
| 25 | tracheary element differentiation-related 6 | 0 | 0 | Phvul.001G07 |
| 26 | cellulose synthase like E1 | Phvul.008G27PTHR13301//I | Phvul.008G27 | |
| 27 | Protein of unknown function (DUF2921) | Phvul.010G15PF11145 - Pro | Phvul.010G15 | |
| 28 | | 0 | 0 | Phvul.006G02PF14577 - Sie |
| 29 | | | | |
| 30 | | | | |
| 31 | Phox (PX) domain-containing protein | Phvul.009G17PTHR12326 - I | Phvul.009G17 | |
| 32 | ATP binding cassette subfamily B1 | Phvul.007G14PTHR24221:Si | Phvul.007G14 | |
| 33 | DNAJ heat shock family protein | Phvul.003G17PTHR24078:Si | Phvul.003G17 | |
| 34 | | 0 | 0 | Phvul.011G10 |
| 35 | myb domain protein 56 | Phvul.001G10PTHR10641:Si | Phvul.001G10 | |
| 36 | Aha1 domain-containing protein | Phvul.007G26PTHR13009 - I | Phvul.007G26 | |
| 37 | Aha1 domain-containing protein | Phvul.007G26PTHR13009 - I | Phvul.007G26 | |
| 38 | EAP30/Vps36 family protein | Phvul.011G18K12190 - ESCF | Phvul.011G18 | |
| 39 | | 0 | 0 | Phvul.006G14 |
| 40 | | 0 | 0 | Phvul.006G14 |
| 41 | | | | |
| 42 | Pentatricopeptide repeat (PPR) superfamily prot | Phvul.002G04PF01535//PF1 | Phvul.002G04 | |
| 43 | FAD-binding Berberine family protein | Phvul.007G11PF01565//PFC | Phvul.007G11 | |
| 44 | pumilio 7 | Phvul.006G20PTHR12537:Si | Phvul.006G20 | |
| 45 | hexokinase 2 | Phvul.010G14PTHR19443//I | Phvul.010G14 | |
| 46 | myb domain protein 105 | Phvul.002G08PTHR10641:Si | Phvul.002G08 | |
| 47 | | 0 | 0 | Phvul.001G06PTHR34194:Si |
| 48 | | 0 | 0 | Phvul.001G06PTHR34194:Si |
| 49 | | 0 | 0 | Phvul.001G06PTHR34194:Si |
| 50 | | | | |
| 51 | DNA-binding bromodomain-containing protein | Phvul.006G04PTHR22881:Si | Phvul.006G04 | |
| 52 | Protein of unknown function (DUF567) | Phvul.010G15PTHR31087:Si | Phvul.010G15 | |
| 53 | Major facilitator superfamily protein | Phvul.007G05PTHR23500:Si | Phvul.007G05 | |
| 54 | Major facilitator superfamily protein | Phvul.007G05PTHR23500:Si | Phvul.007G05 | |
| 55 | RNA-binding ASCH domain protein | Phvul.005G15PTHR34204:Si | Phvul.005G15 | |
| 56 | RNA-binding ASCH domain protein | Phvul.005G15PTHR34204:Si | Phvul.005G15 | |

| | | |
|----|---|--|
| 1 | Major facilitator superfamily protein | Phvul.007G05 PTHR23500:SiPhvul.007G05 |
| 2 | Major facilitator superfamily protein | Phvul.007G05 PTHR23500:SiPhvul.007G05 |
| 3 | Major facilitator superfamily protein | Phvul.007G05 PTHR23500:SiPhvul.007G05 |
| 4 | RNA-binding ASCH domain protein | Phvul.005G15 PTHR34204:SiPhvul.005G15 |
| 5 | RNA-binding ASCH domain protein | Phvul.005G15 PTHR34204:SiPhvul.005G15 |
| 6 | protein phosphatase X 2 | Phvul.008G27K15423 - serirPhvul.008G27 |
| 7 | | 0 0 0 Phvul.008G21 |
| 8 | Calcium-binding endonuclease/exonuclease/phc | Phvul.010G12 PTHR12121//IPhvul.010G12 |
| 9 | Calcium-binding endonuclease/exonuclease/phc | Phvul.010G12 PTHR12121//IPhvul.010G12 |
| 10 | Calcium-binding endonuclease/exonuclease/phc | Phvul.010G12 PTHR12121//IPhvul.010G12 |
| 11 | MOS4-associated complex 3B | Phvul.007G27K10599 - pre-iPhvul.007G27 |
| 12 | K ⁺ efflux antiporter 5 | Phvul.004G12 PTHR16254:SiPhvul.004G12 |
| 13 | K ⁺ efflux antiporter 5 | Phvul.004G12 PTHR16254:SiPhvul.004G12 |
| 14 | NB-ARC domain-containing disease resistance p | Phvul.005G02 PTHR23155//IPhvul.005G02 |
| 15 | | 0 Phvul.010G11 PF08167 - rRNPhvul.010G11 |
| 16 | | 0 Phvul.010G11 PF08167 - rRNPhvul.010G11 |
| 17 | | 0 Phvul.010G11 PF08167 - rRNPhvul.010G11 |
| 18 | tracheary element differentiation-related 7 | 0 0 Phvul.001G05 |
| 19 | cellulose synthase like E1 | Phvul.008G27 PTHR13301//IPhvul.008G27 |
| 20 | ubiquitin-specific protease 26 | Phvul.009G10K11858 - ubiq Phvul.009G10 |
| 21 | ubiquitin-specific protease 26 | Phvul.009G10K11858 - ubiq Phvul.009G10 |
| 22 | ubiquitin-specific protease 26 | Phvul.009G10K11858 - ubiq Phvul.009G10 |
| 23 | ubiquitin-specific protease 26 | Phvul.009G10K11858 - ubiq Phvul.009G10 |
| 24 | ubiquitin-specific protease 26 | Phvul.009G10K11858 - ubiq Phvul.009G10 |
| 25 | ubiquitin-specific protease 26 | Phvul.009G10K11858 - ubiq Phvul.009G10 |
| 26 | tracheary element differentiation-related 6 | 0 0 Phvul.001G07 |
| 27 | Protein of unknown function (DUF2921) | Phvul.010G15 PF11145 - ProPhvul.010G15 |
| 28 | | 0 0 0 Phvul.011G10 |
| 29 | | 0 0 0 Phvul.011G10 |
| 30 | | 0 0 0 Phvul.006G14 |
| 31 | | 0 0 0 Phvul.006G14 |
| 32 | Calcium-binding endonuclease/exonuclease/phc | Phvul.010G12 PTHR12121//IPhvul.010G12 |
| 33 | Calcium-binding endonuclease/exonuclease/phc | Phvul.010G12 PTHR12121//IPhvul.010G12 |
| 34 | Calcium-binding endonuclease/exonuclease/phc | Phvul.010G12 PTHR12121//IPhvul.010G12 |
| 35 | K ⁺ efflux antiporter 5 | Phvul.004G12 PTHR16254:SiPhvul.004G12 |
| 36 | Pentatricopeptide repeat (PPR) superfamily prot | Phvul.002G04 PF01535//PF1Phvul.002G04 |
| 37 | FAD-binding Berberine family protein | Phvul.007G11 PF01565//PFCPhvul.007G11 |
| 38 | FAD-binding Berberine family protein | Phvul.007G11 PF01565//PFCPhvul.007G11 |
| 39 | | 0 Phvul.006G02 PF14577 - SiePhvul.006G02 |
| 40 | Phox (PX) domain-containing protein | Phvul.009G17 PTHR12326 - IPhvul.009G17 |
| 41 | ATP binding cassette subfamily B1 | Phvul.007G14 PTHR24221:SiPhvul.007G14 |
| 42 | ATP binding cassette subfamily B1 | Phvul.007G14 PTHR24221:SiPhvul.007G14 |
| 43 | DNAJ heat shock family protein | Phvul.003G17 PTHR24078:SiPhvul.003G17 |
| 44 | RNA-binding ASCH domain protein | Phvul.005G15 PTHR34204:SiPhvul.005G15 |
| 45 | RNA-binding ASCH domain protein | Phvul.005G15 PTHR34204:SiPhvul.005G15 |
| 46 | RNA-binding ASCH domain protein | Phvul.005G15 PTHR34204:SiPhvul.005G15 |
| 47 | myb domain protein 56 | Phvul.001G10 PTHR10641:SiPhvul.001G10 |
| 48 | Aha1 domain-containing protein | Phvul.007G26 PTHR13009 - IPhvul.007G26 |
| 49 | Aha1 domain-containing protein | Phvul.007G26 PTHR13009 - IPhvul.007G26 |
| 50 | Aha1 domain-containing protein | Phvul.007G26 PTHR13009 - IPhvul.007G26 |
| 51 | EAP30/Vps36 family protein | Phvul.011G18K12190 - ESCFPhvul.011G18 |
| 52 | RNA-binding ASCH domain protein | Phvul.005G15 PTHR34204:SiPhvul.005G15 |
| 53 | RNA-binding ASCH domain protein | Phvul.005G15 PTHR34204:SiPhvul.005G15 |
| 54 | protein phosphatase X 2 | Phvul.008G27K15423 - serirPhvul.008G27 |
| 55 | Protein of unknown function (DUF2921) | Phvul.005G06 PF11145 - ProPhvul.005G06 |
| 56 | pumilio 7 | Phvul.006G20 PTHR12537:SiPhvul.006G20 |
| 57 | DNA-binding bromodomain-containing protein | Phvul.006G04 PTHR22881:SiPhvul.006G04 |
| 58 | | 0 0 0 Phvul.008G21 |
| 59 | embryo defective 1923 | 0 0 0 Phvul.011G11 |
| 60 | hexokinase 2 | Phvul.010G14 PTHR19443//IPhvul.010G14 |

| | | | | |
|----|---|---|---|--|
| 1 | | | | |
| 2 | myb domain protein 105 | | | Phvul.002G08PTHR10641:SiPhvul.002G08 |
| 3 | MOS4-associated complex 3B | | | Phvul.007G27K10599 - pre-iPhvul.007G27 |
| 4 | | | | 0 Phvul.001G06PTHR34194:SiPhvul.001G06 |
| 5 | | | | 0 Phvul.010G11PF08167 - rRNPhvul.010G11 |
| 6 | | | | 0 Phvul.010G11PF08167 - rRNPhvul.010G11 |
| 7 | | | | 0 Phvul.010G11PF08167 - rRNPhvul.010G11 |
| 8 | tracheary element differentiation-related 7 | 0 | 0 | Phvul.001G05 |
| 9 | cellulose synthase like E1 | | | Phvul.008G27PTHR13301//IPhvul.008G27 |
| 10 | ubiquitin-specific protease 26 | | | Phvul.009G10K11858 - ubiq Phvul.009G10 |
| 11 | ubiquitin-specific protease 26 | | | Phvul.009G10K11858 - ubiq Phvul.009G10 |
| 12 | ubiquitin-specific protease 26 | | | Phvul.009G10K11858 - ubiq Phvul.009G10 |
| 13 | ubiquitin-specific protease 26 | | | Phvul.009G10K11858 - ubiq Phvul.009G10 |
| 14 | ubiquitin-specific protease 26 | | | Phvul.009G10K11858 - ubiq Phvul.009G10 |
| 15 | ubiquitin-specific protease 26 | | | Phvul.009G10K11858 - ubiq Phvul.009G10 |
| 16 | tracheary element differentiation-related 6 | 0 | 0 | Phvul.001G07 |
| 17 | Protein of unknown function (DUF2921) | | | Phvul.010G15PF11145 - ProPhvul.010G15 |
| 18 | | 0 | 0 | 0 Phvul.011G10 |
| 19 | | 0 | 0 | 0 Phvul.006G14 |
| 20 | | 0 | 0 | 0 Phvul.006G14 |
| 21 | | 0 | 0 | 0 Phvul.006G14 |
| 22 | | | | |
| 23 | Calcium-binding endonuclease/exonuclease/phc | | | Phvul.010G12PTHR12121//IPhvul.010G12 |
| 24 | Calcium-binding endonuclease/exonuclease/phc | | | Phvul.010G12PTHR12121//IPhvul.010G12 |
| 25 | K ⁺ efflux antiporter 5 | | | Phvul.004G12PTHR16254:SiPhvul.004G12 |
| 26 | Pentatricopeptide repeat (PPR) superfamily prot | | | Phvul.002G04PF01535//PF1Phvul.002G04 |
| 27 | FAD-binding Berberine family protein | | | Phvul.007G11PF01565//PF0Phvul.007G11 |
| 28 | | | | 0 Phvul.006G02PF14577 - SievPhvul.006G02 |
| 29 | | | | |
| 30 | | | | |
| 31 | Phox (PX) domain-containing protein | | | Phvul.009G17PTHR12326 - IPhvul.009G17 |
| 32 | ATP binding cassette subfamily B1 | | | Phvul.007G14PTHR24221:SiPhvul.007G14 |
| 33 | DNAJ heat shock family protein | | | Phvul.003G17PTHR24078:SiPhvul.003G17 |
| 34 | RNA-binding ASCH domain protein | | | Phvul.005G15PTHR34204:SiPhvul.005G15 |
| 35 | RNA-binding ASCH domain protein | | | Phvul.005G15PTHR34204:SiPhvul.005G15 |
| 36 | myb domain protein 56 | | | Phvul.001G10PTHR10641:SiPhvul.001G10 |
| 37 | Aha1 domain-containing protein | | | Phvul.007G26PTHR13009 - IPhvul.007G26 |
| 38 | Aha1 domain-containing protein | | | Phvul.007G26PTHR13009 - IPhvul.007G26 |
| 39 | EAP30/Vps36 family protein | | | Phvul.011G18K12190 - ESCFPhvul.011G18 |
| 40 | RNA-binding ASCH domain protein | | | Phvul.005G15PTHR34204:SiPhvul.005G15 |
| 41 | protein phosphatase X 2 | | | Phvul.008G27K15423 - serirPhvul.008G27 |
| 42 | Protein of unknown function (DUF2921) | | | Phvul.005G06PF11145 - ProPhvul.005G06 |
| 43 | pumilio 7 | | | Phvul.006G20PTHR12537:SiPhvul.006G20 |
| 44 | DNA-binding bromodomain-containing protein | | | Phvul.006G04PTHR22881:SiPhvul.006G04 |
| 45 | | 0 | 0 | 0 Phvul.008G21 |
| 46 | | | | |
| 47 | embryo defective 1923 | | 0 | 0 Phvul.011G11 |
| 48 | hexokinase 2 | | | Phvul.010G14PTHR19443//IPhvul.010G14 |
| 49 | myb domain protein 105 | | | Phvul.002G08PTHR10641:SiPhvul.002G08 |
| 50 | MOS4-associated complex 3B | | | Phvul.007G27K10599 - pre-iPhvul.007G27 |
| 51 | | | | 0 Phvul.001G06PTHR34194:SiPhvul.001G06 |
| 52 | | | | 0 Phvul.001G06PTHR34194:SiPhvul.001G06 |
| 53 | | 0 | 0 | 0 Phvul.011G13 |
| 54 | | 0 | 0 | 0 Phvul.011G13 |
| 55 | | 0 | 0 | 0 Phvul.011G13 |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

| | | | | |
|----|--|--------------|----------------|----------------|
| 1 | | | | |
| 2 | | 0 | 0 | 0 Phvul.011G13 |
| 3 | | 0 | 0 | 0 Phvul.011G13 |
| 4 | | 0 | 0 | 0 Phvul.011G13 |
| 5 | | | | |
| 6 | TRICHOME BIREFRINGENCE-LIKE 22 | Phvul.004G01 | PTHR32285:Si | Phvul.004G01 |
| 7 | TRICHOME BIREFRINGENCE-LIKE 22 | Phvul.004G01 | PTHR32285:Si | Phvul.004G01 |
| 8 | | 0 | 0 | 0 Phvul.009G10 |
| 9 | | 0 | 0 | 0 Phvul.009G10 |
| 10 | | 0 | 0 | 0 Phvul.009G10 |
| 11 | | 0 | 0 | 0 Phvul.009G10 |
| 12 | Glycosyl hydrolase family protein with chitinase | Phvul.003G15 | PTHR11177://I | Phvul.003G15 |
| 13 | related to AP2 11 | Phvul.006G17 | PTHR31194://I | Phvul.006G17 |
| 14 | | 0 | 0 | 0 Phvul.002G18 |
| 15 | | 0 | 0 | 0 Phvul.011G10 |
| 16 | | | | |
| 17 | Integrase-type DNA-binding superfamily protein | Phvul.007G02 | PTHR31194://I | Phvul.007G02 |
| 18 | Plant protein of unknown function (DUF946) | Phvul.005G04 | PTHR17204:Si | Phvul.005G04 |
| 19 | | 0 | 0 | 0 Phvul.006G14 |
| 20 | | | | |
| 21 | Pentatricopeptide repeat (PPR) superfamily prot | Phvul.011G06 | PF01535://PF1 | Phvul.011G06 |
| 22 | pumilio 7 | Phvul.006G20 | PTHR12537:Si | Phvul.006G20 |
| 23 | Translation initiation factor 2, small GTP-binding | Phvul.005G05 | PTHR23115:Si | Phvul.005G05 |
| 24 | P-loop containing nucleoside triphosphate hydr | Phvul.001G02 | K10395 - kine | Phvul.001G02 |
| 25 | MATE efflux family protein | Phvul.008G06 | PTHR11206:Si | Phvul.008G06 |
| 26 | MAP kinase kinase 9 | Phvul.004G14 | PTHR24361:Si | Phvul.004G14 |
| 27 | fibrillarlin 1 | Phvul.001G05 | K14563 - rRN | Phvul.001G05 |
| 28 | CTC-interacting domain 12 | Phvul.009G04 | PF00076://PFC | Phvul.009G04 |
| 29 | | 0 | 0 | 0 Phvul.011G13 |
| 30 | | | | |
| 31 | TOXICOS EN LEVADURA 2 | Phvul.008G11 | PTHR14155:Si | Phvul.008G11 |
| 32 | TOXICOS EN LEVADURA 63 | Phvul.006G07 | PTHR14155:Si | Phvul.006G07 |
| 33 | spermidine hydroxycinnamoyl transferase | Phvul.L00168 | PTHR31642:Si | Phvul.L00168 |
| 34 | glycine-rich RNA-binding protein 3 | Phvul.008G03 | K12741 - hete | Phvul.008G03 |
| 35 | RING/U-box superfamily protein | Phvul.008G03 | PTHR13139 - I | Phvul.008G03 |
| 36 | protein arginine methyltransferase 10 | Phvul.009G19 | PTHR11006:Si | Phvul.009G19 |
| 37 | RING/U-box superfamily protein | Phvul.008G03 | PTHR13139 - I | Phvul.008G03 |
| 38 | spermidine hydroxycinnamoyl transferase | Phvul.006G03 | K13065 - shiki | Phvul.006G03 |
| 39 | tetratricopeptide repeat (TPR)-containing protei | Phvul.001G20 | PTHR17130:Si | Phvul.001G20 |
| 40 | RNA-binding (RRM/RBD/RNP motifs) family prot | Phvul.011G15 | PTHR24012:Si | Phvul.011G15 |
| 41 | plastidic GLC translocator | Phvul.004G06 | PTHR23500:Si | Phvul.004G06 |
| 42 | Eukaryotic aspartyl protease family protein | Phvul.006G04 | PTHR13683:Si | Phvul.006G04 |
| 43 | | 0 | 0 | 0 Phvul.009G00 |
| 44 | | | | |
| 45 | TCP family transcription factor 4 | Phvul.005G06 | PTHR31072:Si | Phvul.005G06 |
| 46 | | 0 | 0 | 0 Phvul.011G13 |
| 47 | | 0 | 0 | 0 Phvul.011G13 |
| 48 | | 0 | 0 | 0 Phvul.011G13 |
| 49 | | 0 | 0 | 0 Phvul.011G13 |
| 50 | | 0 | 0 | 0 Phvul.011G13 |
| 51 | | 0 | 0 | 0 Phvul.011G13 |
| 52 | | 0 | 0 | 0 Phvul.011G13 |
| 53 | | 0 | 0 | 0 Phvul.011G13 |
| 54 | | 0 | 0 | 0 Phvul.011G13 |
| 55 | | 0 | 0 | 0 Phvul.011G13 |
| 56 | | 0 | 0 | 0 Phvul.011G13 |
| 57 | | 0 | 0 | 0 Phvul.011G13 |
| 58 | | 0 | 0 | 0 Phvul.011G13 |
| 59 | | 0 | 0 | 0 Phvul.011G13 |
| 60 | related to AP2 11 | Phvul.006G17 | PTHR31194://I | Phvul.006G17 |
| | | 0 | 0 | 0 Phvul.002G18 |

| | | | |
|----|--|----------------------------|---------------|
| 1 | | | |
| 2 | Plant protein of unknown function (DUF946) | Phvul.005G04PTHR17204:Si | Phvul.005G04 |
| 3 | TRICHOME BIREFRINGENCE-LIKE 22 | Phvul.004G01PTHR32285:Si | Phvul.004G01 |
| 4 | TRICHOME BIREFRINGENCE-LIKE 22 | Phvul.004G01PTHR32285:Si | Phvul.004G01 |
| 5 | | | |
| 6 | Pentatricopeptide repeat (PPR) superfamily prot | Phvul.011G06PF01535//PF1 | Phvul.011G06 |
| 7 | HSP20-like chaperones superfamily protein | Phvul.002G23PTHR11527:Si | Phvul.002G23 |
| 8 | spermidine hydroxycinnamoyl transferase | Phvul.L00168:PTHR31642:Si | Phvul.L00168: |
| 9 | | | |
| 10 | | 0 | 0 |
| 11 | spermidine hydroxycinnamoyl transferase | Phvul.006G03K13065 - shiki | Phvul.006G03 |
| 12 | | 0 | 0 |
| 13 | | 0 | 0 |
| 14 | | 0 | 0 |
| 15 | | 0 | 0 |
| 16 | Glycosyl hydrolase family protein with chitinase | Phvul.003G15PTHR11177//I | Phvul.003G15 |
| 17 | fibrillarlin 1 | Phvul.001G05K14563 - rRN | Phvul.001G05 |
| 18 | | | |
| 19 | Pentatricopeptide repeat (PPR) superfamily prot | Phvul.004G05PF01535//PF1 | Phvul.004G05 |
| 20 | Integrase-type DNA-binding superfamily protein | Phvul.007G02PTHR31194//I | Phvul.007G02 |
| 21 | | | |
| 22 | phospholipase A 2A | Phvul.009G06KOG0513 - Ca | Phvul.009G06 |
| 23 | MATE efflux family protein | Phvul.008G06PTHR11206:Si | Phvul.008G06 |
| 24 | Cyclin D6;1 | Phvul.011G11K18812 - cycli | Phvul.011G11 |
| 25 | Major facilitator superfamily protein | Phvul.010G00PTHR11654//I | Phvul.010G00 |
| 26 | | | |
| 27 | phospholipase A 2A | Phvul.009G06KOG0513 - Ca | Phvul.009G06 |
| 28 | pumilio 7 | Phvul.006G20PTHR12537:Si | Phvul.006G20 |
| 29 | Translation initiation factor 2, small GTP-binding | Phvul.005G05PTHR23115:Si | Phvul.005G05 |
| 30 | | | |
| 31 | P-loop containing nucleoside triphosphate hydr | Phvul.001G02K10395 - kine | Phvul.001G02 |
| 32 | Acyl-CoA N-acyltransferases (NAT) superfamily p | Phvul.006G09PTHR13256:Si | Phvul.006G09 |
| 33 | Acyl-CoA N-acyltransferases (NAT) superfamily p | Phvul.006G09PTHR13256:Si | Phvul.006G09 |
| 34 | | | |
| 35 | glycine-rich RNA-binding protein 3 | Phvul.008G03K12741 - hete | Phvul.008G03 |
| 36 | Metal-dependent phosphohydrolase | Phvul.011G02K06950 - unch | Phvul.011G02 |
| 37 | | | |
| 38 | RING/U-box superfamily protein | Phvul.008G03PTHR13139 - I | Phvul.008G03 |
| 39 | RING/U-box superfamily protein | Phvul.008G03PTHR13139 - I | Phvul.008G03 |
| 40 | plastidic GLC translocator | Phvul.004G06PTHR23500:Si | Phvul.004G06 |
| 41 | Eukaryotic aspartyl protease family protein | Phvul.006G04PTHR13683:Si | Phvul.006G04 |
| 42 | | | |
| 43 | HSP20-like chaperones superfamily protein | Phvul.007G15PTHR33981:Si | Phvul.007G15 |
| 44 | | 0 | 0 |
| 45 | | 0 | 0 |
| 46 | | 0 | 0 |
| 47 | | 0 | 0 |
| 48 | | 0 | 0 |
| 49 | | 0 | 0 |
| 50 | | 0 | 0 |
| 51 | | 0 | 0 |
| 52 | related to AP2 11 | Phvul.006G17PTHR31194//I | Phvul.006G17 |
| 53 | | 0 | 0 |
| 54 | | | |
| 55 | Plant protein of unknown function (DUF946) | Phvul.005G04PTHR17204:Si | Phvul.005G04 |
| 56 | TRICHOME BIREFRINGENCE-LIKE 22 | Phvul.004G01PTHR32285:Si | Phvul.004G01 |
| 57 | TRICHOME BIREFRINGENCE-LIKE 22 | Phvul.004G01PTHR32285:Si | Phvul.004G01 |
| 58 | | | |
| 59 | Pentatricopeptide repeat (PPR) superfamily prot | Phvul.011G06PF01535//PF1 | Phvul.011G06 |
| 60 | HSP20-like chaperones superfamily protein | Phvul.002G23PTHR11527:Si | Phvul.002G23 |
| | spermidine hydroxycinnamoyl transferase | Phvul.L00168:PTHR31642:Si | Phvul.L00168: |

| | | | | |
|----|--|----------------------------|--------------|----------------|
| 1 | | | | |
| 2 | | 0 | 0 | 0 Phvul.011G10 |
| 3 | spermidine hydroxycinnamoyl transferase | Phvul.006G03K13065 - shiki | Phvul.006G03 | |
| 4 | | 0 | 0 | 0 Phvul.009G10 |
| 5 | | 0 | 0 | 0 Phvul.009G10 |
| 6 | | 0 | 0 | 0 Phvul.009G10 |
| 7 | | 0 | 0 | 0 Phvul.009G10 |
| 8 | Glycosyl hydrolase family protein with chitinase | Phvul.003G15PTHR11177//I | Phvul.003G15 | |
| 9 | fibrillarlin 1 | Phvul.001G05K14563 - rRN | Phvul.001G05 | |
| 10 | Pentatricopeptide repeat (PPR) superfamily prot | Phvul.004G05PF01535//PF1 | Phvul.004G05 | |
| 11 | Integrase-type DNA-binding superfamily protein | Phvul.007G02PTHR31194//I | Phvul.007G02 | |
| 12 | phospholipase A 2A | Phvul.009G06KOG0513 - Ca | Phvul.009G06 | |
| 13 | MATE efflux family protein | Phvul.008G06PTHR11206:Si | Phvul.008G06 | |
| 14 | Cyclin D6;1 | Phvul.011G11K18812 - cycli | Phvul.011G11 | |
| 15 | Major facilitator superfamily protein | Phvul.010G00PTHR11654//I | Phvul.010G00 | |
| 16 | phospholipase A 2A | Phvul.009G06KOG0513 - Ca | Phvul.009G06 | |
| 17 | pumilio 7 | Phvul.006G20PTHR12537:Si | Phvul.006G20 | |
| 18 | Translation initiation factor 2, small GTP-binding | Phvul.005G05PTHR23115:Si | Phvul.005G05 | |
| 19 | P-loop containing nucleoside triphosphate hydr | Phvul.001G02K10395 - kine | Phvul.001G02 | |
| 20 | Acyl-CoA N-acyltransferases (NAT) superfamily p | Phvul.006G09PTHR13256:Si | Phvul.006G09 | |
| 21 | Acyl-CoA N-acyltransferases (NAT) superfamily p | Phvul.006G09PTHR13256:Si | Phvul.006G09 | |
| 22 | glycine-rich RNA-binding protein 3 | Phvul.008G03K12741 - hete | Phvul.008G03 | |
| 23 | Metal-dependent phosphohydrolase | Phvul.011G02K06950 - unch | Phvul.011G02 | |
| 24 | RING/U-box superfamily protein | Phvul.008G03PTHR13139 - I | Phvul.008G03 | |
| 25 | RING/U-box superfamily protein | Phvul.008G03PTHR13139 - I | Phvul.008G03 | |
| 26 | plastidic GLC translocator | Phvul.004G06PTHR23500:Si | Phvul.004G06 | |
| 27 | Eukaryotic aspartyl protease family protein | Phvul.006G04PTHR13683:Si | Phvul.006G04 | |
| 28 | HSP20-like chaperones superfamily protein | Phvul.007G15PTHR33981:Si | Phvul.007G15 | |
| 29 | | | | |
| 30 | | | | |
| 31 | | | | |
| 32 | | | | |
| 33 | | | | |
| 34 | | | | |
| 35 | | | | |
| 36 | | | | |
| 37 | | | | |
| 38 | | | | |
| 39 | | | | |
| 40 | | | | |
| 41 | | | | |
| 42 | | | | |
| 43 | | | | |
| 44 | | | | |
| 45 | | | | |
| 46 | | | | |
| 47 | | | | |
| 48 | | | | |
| 49 | | | | |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

| 1 | NAME | DESCRIPTION |
|----|-----------------|---|
| 2 | not assigned.ε | (original description: pacid=37161909 transcript=Phvul.004G064100.1 locus=Phvul.C |
| 3 | not assigned.r | no hits & (original description: pacid=37150946 transcript=Phvul.009G096000.1 locu |
| 4 | Cell wall organ | KDO-8-phosphate synthase (original description: pacid=37161420 transcript=Phvul.0 |
| 5 | not assigned.ε | (original description: pacid=37161909 transcript=Phvul.004G064100.1 locus=Phvul.C |
| 6 | not assigned.r | no hits & (original description: pacid=37150946 transcript=Phvul.009G096000.1 locu |
| 7 | not assigned.ε | (original description: pacid=37161909 transcript=Phvul.004G064100.1 locus=Phvul.C |
| 8 | not assigned.r | no hits & (original description: pacid=37150946 transcript=Phvul.009G096000.1 locu |
| 9 | not assigned.ε | (original description: pacid=37161909 transcript=Phvul.004G064100.1 locus=Phvul.C |
| 10 | not assigned.r | no hits & (original description: pacid=37150946 transcript=Phvul.009G096000.1 locu |
| 11 | not assigned.r | no hits & (original description: pacid=37148987 transcript=Phvul.009G196100.1 locu |
| 12 | not assigned.ε | (original description: pacid=37159372 transcript=Phvul.008G199900.1 locus=Phvul.C |
| 13 | not assigned.r | no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu |
| 14 | not assigned.r | no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu |
| 15 | not assigned.ε | (original description: pacid=37163516 transcript=Phvul.004G038100.1 locus=Phvul.C |
| 16 | RNA biosynth | transcription factor (ARF) (original description: pacid=37155087 transcript=Phvul.011 |
| 17 | RNA biosynth | transcription factor (ARF) (original description: pacid=37155087 transcript=Phvul.011 |
| 18 | not assigned.r | no hits & (original description: pacid=37157501 transcript=Phvul.L001604.5 locus=Pl |
| 19 | not assigned.r | no hits & (original description: pacid=37157501 transcript=Phvul.L001604.5 locus=Pl |
| 20 | not assigned.r | no hits & (original description: pacid=37157501 transcript=Phvul.L001604.5 locus=Pl |
| 21 | not assigned.ε | (original description: pacid=37162066 transcript=Phvul.004G160700.1 locus=Phvul.C |
| 22 | Protein modif | protein kinase (SD-1) (original description: pacid=37155634 transcript=Phvul.011G15 |
| 23 | Protein modif | protein kinase (SD-1) (original description: pacid=37155634 transcript=Phvul.011G15 |
| 24 | Protein modif | protein kinase (SD-1) (original description: pacid=37155634 transcript=Phvul.011G15 |
| 25 | not assigned.r | no hits & (original description: pacid=37147055 transcript=Phvul.003G229300.2 locu |
| 26 | not assigned.r | no hits & (original description: pacid=37147055 transcript=Phvul.003G229300.2 locu |
| 27 | Amino acid m | arogenate dehydrogenase (ADH) (original description: pacid=37145367 transcript=Ph |
| 28 | not assigned.r | no hits & (original description: pacid=37148987 transcript=Phvul.009G196100.1 locu |
| 29 | not assigned.ε | (original description: pacid=37159372 transcript=Phvul.008G199900.1 locus=Phvul.C |
| 30 | not assigned.r | no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu |
| 31 | not assigned.ε | (original description: pacid=37162066 transcript=Phvul.004G160700.1 locus=Phvul.C |
| 32 | not assigned.r | no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu |
| 33 | not assigned.r | no hits & (original description: pacid=37157501 transcript=Phvul.L001604.5 locus=Pl |
| 34 | not assigned.r | no hits & (original description: pacid=37157501 transcript=Phvul.L001604.5 locus=Pl |
| 35 | not assigned.r | no hits & (original description: pacid=37157501 transcript=Phvul.L001604.5 locus=Pl |
| 36 | not assigned.ε | (original description: pacid=37163516 transcript=Phvul.004G038100.1 locus=Phvul.C |
| 37 | RNA biosynth | transcription factor (ARF) (original description: pacid=37155087 transcript=Phvul.011 |
| 38 | RNA biosynth | transcription factor (ARF) (original description: pacid=37155087 transcript=Phvul.011 |
| 39 | not assigned.r | no hits & (original description: pacid=37148987 transcript=Phvul.009G196100.1 locu |
| 40 | not assigned.ε | (original description: pacid=37159372 transcript=Phvul.008G199900.1 locus=Phvul.C |
| 41 | not assigned.r | no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu |
| 42 | not assigned.ε | (original description: pacid=37162066 transcript=Phvul.004G160700.1 locus=Phvul.C |
| 43 | not assigned.r | no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu |
| 44 | not assigned.r | no hits & (original description: pacid=37157501 transcript=Phvul.L001604.5 locus=Pl |
| 45 | not assigned.r | no hits & (original description: pacid=37157501 transcript=Phvul.L001604.5 locus=Pl |
| 46 | not assigned.ε | (original description: pacid=37163516 transcript=Phvul.004G038100.1 locus=Phvul.C |
| 47 | RNA biosynth | transcription factor (ARF) (original description: pacid=37155087 transcript=Phvul.011 |
| 48 | RNA biosynth | transcription factor (ARF) (original description: pacid=37155087 transcript=Phvul.011 |
| 49 | not assigned.r | no hits & (original description: pacid=37148987 transcript=Phvul.009G196100.1 locu |
| 50 | not assigned.ε | (original description: pacid=37159372 transcript=Phvul.008G199900.1 locus=Phvul.C |
| 51 | not assigned.r | no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu |
| 52 | not assigned.ε | (original description: pacid=37162066 transcript=Phvul.004G160700.1 locus=Phvul.C |
| 53 | not assigned.r | no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu |
| 54 | not assigned.r | no hits & (original description: pacid=37157501 transcript=Phvul.L001604.5 locus=Pl |
| 55 | not assigned.r | no hits & (original description: pacid=37157501 transcript=Phvul.L001604.5 locus=Pl |
| 56 | not assigned.r | no hits & (original description: pacid=37157501 transcript=Phvul.L001604.5 locus=Pl |
| 57 | not assigned.ε | (original description: pacid=37163516 transcript=Phvul.004G038100.1 locus=Phvul.C |
| 58 | RNA biosynth | transcription factor (ARF) (original description: pacid=37155087 transcript=Phvul.011 |
| 59 | not assigned.r | no hits & (original description: pacid=37157501 transcript=Phvul.L001604.5 locus=Pl |
| 60 | not assigned.ε | (original description: pacid=37163516 transcript=Phvul.004G038100.1 locus=Phvul.C |
| | RNA biosynth | transcription factor (ARF) (original description: pacid=37155087 transcript=Phvul.011 |

1 RNA biosynth transcription factor (ARF) (original description: pacid=37155087 transcript=Phvul.011
2 Solute transpc solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00
3 Solute transpc solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00
4 Solute transpc solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00
5 Solute transpc solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00
6 not assigned.ε (original description: pacid=37174808 transcript=Phvul.002G041900.1 locus=Phvul.C
7 Protein biosyr assembly factor (eIF1A) of eIF1 (original description: pacid=37144013 transcript=Phv
8 not assigned.r no hits & (original description: pacid=37172393 transcript=Phvul.006G148800.1 locu
9 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
10 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
11 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
12 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
13 Protein home class-C-I small heat-shock-responsive protein (original description: pacid=37177788 t
14 Protein home SUMO E3 ligase (SIZ1) (original description: pacid=37153775 transcript=Phvul.005G1
15 Protein home SUMO E3 ligase (SIZ1) (original description: pacid=37153775 transcript=Phvul.005G1
16 Protein home SUMO E3 ligase (SIZ1) (original description: pacid=37153775 transcript=Phvul.005G1
17 Protein home SUMO E3 ligase (SIZ1) (original description: pacid=37153775 transcript=Phvul.005G1
18 Protein modif CPL phosphatase (original description: pacid=37178354 transcript=Phvul.002G22690
19 Protein home SUMO E3 ligase (SIZ1) (original description: pacid=37153775 transcript=Phvul.005G1
20 Protein home SUMO E3 ligase (SIZ1) (original description: pacid=37153775 transcript=Phvul.005G1
21 not assigned.r no hits & (original description: pacid=37164826 transcript=Phvul.007G222000.1 locu
22 not assigned.r no hits & (original description: pacid=37165981 transcript=Phvul.007G029200.1 locu
23 not assigned.ε (original description: pacid=37146336 transcript=Phvul.003G058400.1 locus=Phvul.C
24 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37174
25 not assigned.ε (original description: pacid=37163186 transcript=Phvul.004G028100.1 locus=Phvul.C
26 not assigned.r no hits & (original description: pacid=37159849 transcript=Phvul.008G216700.1 locu
27 not assigned.r no hits & (original description: pacid=37159849 transcript=Phvul.008G216700.1 locu
28 Protein biosyr component RPL27 of LSU proteome component (original description: pacid=371773C
29 Enzyme classii Laccase-15 OS=Arabidopsis thaliana (sp|q84j37|lac15_arath : 554.0) & Enzyme classi
30 RNA biosynth C2H2 zinc finger transcription factor (original description: pacid=37170711 transcript
31 not assigned.ε (original description: pacid=37153077 transcript=Phvul.005G102100.2 locus=Phvul.C
32 not assigned.ε (original description: pacid=37153077 transcript=Phvul.005G102100.2 locus=Phvul.C
33 Solute transpc solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00
34 Solute transpc solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00
35 Solute transpc solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00
36 not assigned.ε (original description: pacid=37174808 transcript=Phvul.002G041900.1 locus=Phvul.C
37 not assigned.r no hits & (original description: pacid=37172393 transcript=Phvul.006G148800.1 locu
38 Protein biosyr assembly factor (eIF1A) of eIF1 (original description: pacid=37144013 transcript=Phv
39 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
40 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
41 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
42 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
43 not assigned.r no hits & (original description: pacid=37159849 transcript=Phvul.008G216700.1 locu
44 not assigned.r no hits & (original description: pacid=37159849 transcript=Phvul.008G216700.1 locu
45 RNA biosynth C2H2 zinc finger transcription factor (original description: pacid=37170711 transcript
46 Solute transpc solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00
47 Solute transpc solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00

1 Solute transp
2 solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00
3 not assigned.ε (original description: pacid=37174808 transcript=Phvul.002G041900.1 locus=Phvul.C
4 not assigned.r no hits & (original description: pacid=37172393 transcript=Phvul.006G148800.1 locu
5 Protein biosyr
6 assembly factor (eIF1A) of eIF1 (original description: pacid=37144013 transcript=Phv
7 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
8 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
9 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
10 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
11 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
12 not assigned.r no hits & (original description: pacid=37159849 transcript=Phvul.008G216700.1 locu
13 not assigned.r no hits & (original description: pacid=37159849 transcript=Phvul.008G216700.1 locu
14 RNA biosynth
15 C2H2 zinc finger transcription factor (original description: pacid=37170711 transcript
16 Cell wall orgar
17 TED-type cellulose synthase CSC-interactive protein (original description: pacid=3717
18 not assigned.r no hits & (original description: pacid=37142568 transcript=Phvul.010G110700.2 locu
19 not assigned.r no hits & (original description: pacid=37142568 transcript=Phvul.010G110700.2 locu
20 **Protein home**
21 **deubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G**
22 Protein home
23 deubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G
24 Protein home
25 deubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G
26 Cell wall orgar
27 TED-type cellulose synthase CSC-interactive protein (original description: pacid=3716
28 not assigned.ε (original description: pacid=37161159 transcript=Phvul.008G279750.1 locus=Phvul.C
29 not assigned.r no hits & (original description: pacid=37143128 transcript=Phvul.010G152600.2 locu
30 not assigned.ε (original description: pacid=37172660 transcript=Phvul.006G021500.1 locus=Phvul.C
31 not assigned.r no hits & (original description: pacid=37150183 transcript=Phvul.009G177300.1 locu
32 Solute transp
33 subfamily ABCB transporter (original description: pacid=37164519 transcript=Phvul.C
34 Protein home
35 co-chaperone (Hsp40) (original description: pacid=37145763 transcript=Phvul.003G1
36 not assigned.r no hits & (original description: pacid=37154896 transcript=Phvul.011G102400.1 locu
37 RNA biosynth
38 transcription factor (MYB) (original description: pacid=37169002 transcript=Phvul.00
39 not assigned.r no hits & (original description: pacid=37165440 transcript=Phvul.007G261100.2 locu
40 not assigned.r no hits & (original description: pacid=37165440 transcript=Phvul.007G261100.2 locu
41 Vesicle trafficl
42 component VPS36 of ESCRT-II complex (original description: pacid=37155231 transcr
43 not assigned.r no hits & (original description: pacid=37172393 transcript=Phvul.006G148800.1 locu
44 not assigned.r no hits & (original description: pacid=37172393 transcript=Phvul.006G148800.1 locu
45 not assigned.ε (original description: pacid=37176369 transcript=Phvul.002G044500.1 locus=Phvul.C
46 Enzyme classii
47 Enzyme classification.EC_1 oxidoreductases.EC_1.1 oxidoreductase acting on CH-OH
48 not assigned.ε (original description: pacid=37174127 transcript=Phvul.006G206800.1 locus=Phvul.C
49 Carbohydrate hexokinase (original description: pacid=37142381 transcript=Phvul.010G144900.1 lo
50 RNA biosynth
51 transcription factor (MYB) (original description: pacid=37177338 transcript=Phvul.00
52 not assigned.r no hits & (original description: pacid=37170216 transcript=Phvul.001G067500.3 locu
53 not assigned.r no hits & (original description: pacid=37170216 transcript=Phvul.001G067500.3 locu
54 not assigned.r no hits & (original description: pacid=37170216 transcript=Phvul.001G067500.3 locu
55 not assigned.r no hits & (original description: pacid=37171775 transcript=Phvul.006G045600.1 locu
56 not assigned.ε (original description: pacid=37143985 transcript=Phvul.010G156000.1 locus=Phvul.C
57 Solute transp
58 monosaccharide transporter (STP) (original description: pacid=37167067 transcript=f
59 Solute transp
60 monosaccharide transporter (STP) (original description: pacid=37167067 transcript=f
not assigned.r no hits & (original description: pacid=37154072 transcript=Phvul.005G154600.3 locu
not assigned.r no hits & (original description: pacid=37154072 transcript=Phvul.005G154600.3 locu

1 Solute transp:monosaccharide transporter (STP) (original description: pacid=37166808 transcript=f
2 Solute transp:monosaccharide transporter (STP) (original description: pacid=37166808 transcript=f
3 not assigned.r no hits & (original description: pacid=37154072 transcript=Phvul.005G154600.3 locu
4 Protein modif catalytic component PP4c of PP4 phosphatase complex (original description: pacid=3
5 not assigned.r no hits & (original description: pacid=37159849 transcript=Phvul.008G216700.1 locu
6 not assigned.ã (original description: pacid=37143248 transcript=Phvul.010G121200.2 locus=Phvul.C
7 not assigned.ã (original description: pacid=37143248 transcript=Phvul.010G121200.2 locus=Phvul.C
8 RNA processir component MAC3 of non-snRNP MOS4-associated complex (original description: pac
9 Solute transp:proton:potassium cation antiporter (KEA) (original description: pacid=37162662 tran
10 not assigned.ã (original description: pacid=37152789 transcript=Phvul.005G027200.1 locus=Phvul.C
11 not assigned.r no hits & (original description: pacid=37142568 transcript=Phvul.010G110700.2 locu
12 not assigned.r no hits & (original description: pacid=37142568 transcript=Phvul.010G110700.2 locu
13 Cell wall orgarTED-type cellulose synthase CSC-interactive protein (original description: pacid=3717
14 not assigned.ã (original description: pacid=37161159 transcript=Phvul.008G279750.1 locus=Phvul.C
15 Protein home:deubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G
16 Protein home:deubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G
17 Protein home:deubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G
18 Protein home:deubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G
19 Cell wall orgarTED-type cellulose synthase CSC-interactive protein (original description: pacid=3716
20 not assigned.r no hits & (original description: pacid=37143128 transcript=Phvul.010G152600.2 locu
21 not assigned.r no hits & (original description: pacid=37154896 transcript=Phvul.011G102400.1 locu
22 not assigned.r no hits & (original description: pacid=37172393 transcript=Phvul.006G148800.1 locu
23 not assigned.r no hits & (original description: pacid=37172393 transcript=Phvul.006G148800.1 locu
24 not assigned.ã (original description: pacid=37143248 transcript=Phvul.010G121200.2 locus=Phvul.C
25 not assigned.ã (original description: pacid=37143248 transcript=Phvul.010G121200.2 locus=Phvul.C
26 Solute transp:proton:potassium cation antiporter (KEA) (original description: pacid=37162662 tran
27 not assigned.ã (original description: pacid=37176369 transcript=Phvul.002G044500.1 locus=Phvul.C
28 Enzyme classiiEnzyme classification.EC_1 oxidoreductases.EC_1.1 oxidoreductase acting on CH-OH
29 not assigned.ã (original description: pacid=37172660 transcript=Phvul.006G021500.1 locus=Phvul.C
30 not assigned.r no hits & (original description: pacid=37150183 transcript=Phvul.009G177300.1 locu
31 Solute transp:subfamily ABCB transporter (original description: pacid=37164519 transcript=Phvul.C
32 Protein home:co-chaperone (Hsp40) (original description: pacid=37145763 transcript=Phvul.003G1
33 not assigned.r no hits & (original description: pacid=37154072 transcript=Phvul.005G154600.3 locu
34 not assigned.r no hits & (original description: pacid=37154072 transcript=Phvul.005G154600.3 locu
35 RNA biosynth:transcription factor (MYB) (original description: pacid=37169002 transcript=Phvul.00
36 not assigned.r no hits & (original description: pacid=37165440 transcript=Phvul.007G261100.2 locu
37 not assigned.r no hits & (original description: pacid=37165440 transcript=Phvul.007G261100.2 locu
38 Vesicle trafficl component VPS36 of ESCRT-II complex (original description: pacid=37155231 transcr
39 not assigned.r no hits & (original description: pacid=37154072 transcript=Phvul.005G154600.3 locu
40 Protein modif catalytic component PP4c of PP4 phosphatase complex (original description: pacid=3
41 not assigned.r no hits & (original description: pacid=37152330 transcript=Phvul.005G065300.1 locu
42 not assigned.ã (original description: pacid=37174127 transcript=Phvul.006G206800.1 locus=Phvul.C
43 not assigned.r no hits & (original description: pacid=37171775 transcript=Phvul.006G045600.1 locu
44 not assigned.r no hits & (original description: pacid=37159849 transcript=Phvul.008G216700.1 locu
45 not assigned.r no hits & (original description: pacid=37157005 transcript=Phvul.011G111800.1 locu
46 Carbohydrate hexokinase (original description: pacid=37142381 transcript=Phvul.010G144900.1 lo

1 RNA biosynthtranscription factor (MYB) (original description: pacid=37177338 transcript=Phvul.00
2 RNA processir component MAC3 of non-snRNP MOS4-associated complex (original description: pac
3 not assigned.r no hits & (original description: pacid=37170216 transcript=Phvul.001G067500.3 locu
4 not assigned.r no hits & (original description: pacid=37142568 transcript=Phvul.010G110700.2 locu
5 not assigned.r no hits & (original description: pacid=37142568 transcript=Phvul.010G110700.2 locu
6 Cell wall orgarTED-type cellulose synthase CSC-interactive protein (original description: pacid=3717
7 not assigned.ε (original description: pacid=37161159 transcript=Phvul.008G279750.1 locus=Phvul.C
8 Protein homeideubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G
9 Protein homeideubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G
10 Protein homeideubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G
11 Protein homeideubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G
12 Cell wall orgarTED-type cellulose synthase CSC-interactive protein (original description: pacid=3716
13 not assigned.r no hits & (original description: pacid=37143128 transcript=Phvul.010G152600.2 locu
14 not assigned.r no hits & (original description: pacid=37154896 transcript=Phvul.011G102400.1 locu
15 not assigned.r no hits & (original description: pacid=37172393 transcript=Phvul.006G148800.1 locu
16 not assigned.r no hits & (original description: pacid=37172393 transcript=Phvul.006G148800.1 locu
17 not assigned.ε (original description: pacid=37143248 transcript=Phvul.010G121200.2 locus=Phvul.C
18 not assigned.ε (original description: pacid=37143248 transcript=Phvul.010G121200.2 locus=Phvul.C
19 Solute transp proton:potassium cation antiporter (KEA) (original description: pacid=37162662 tran
20 not assigned.ε (original description: pacid=37176369 transcript=Phvul.002G044500.1 locus=Phvul.C
21 Enzyme classiiEnzyme classification.EC_1 oxidoreductases.EC_1.1 oxidoreductase acting on CH-OH
22 not assigned.ε (original description: pacid=37172660 transcript=Phvul.006G021500.1 locus=Phvul.C
23 not assigned.r no hits & (original description: pacid=37150183 transcript=Phvul.009G177300.1 locu
24 Solute transp subfamily ABCB transporter (original description: pacid=37164519 transcript=Phvul.C
25 Protein homeico-chaperone (Hsp40) (original description: pacid=37145763 transcript=Phvul.003G1
26 not assigned.r no hits & (original description: pacid=37154072 transcript=Phvul.005G154600.3 locu
27 not assigned.r no hits & (original description: pacid=37154072 transcript=Phvul.005G154600.3 locu
28 RNA biosynthtranscription factor (MYB) (original description: pacid=37169002 transcript=Phvul.00
29 not assigned.r no hits & (original description: pacid=37165440 transcript=Phvul.007G261100.2 locu
30 not assigned.r no hits & (original description: pacid=37165440 transcript=Phvul.007G261100.2 locu
31 Vesicle trafficl component VPS36 of ESCRT-II complex (original description: pacid=37155231 transcr
32 not assigned.r no hits & (original description: pacid=37154072 transcript=Phvul.005G154600.3 locu
33 Protein modif catalytic component PP4c of PP4 phosphatase complex (original description: pacid=3
34 not assigned.r no hits & (original description: pacid=37152330 transcript=Phvul.005G065300.1 locu
35 not assigned.ε (original description: pacid=37174127 transcript=Phvul.006G206800.1 locus=Phvul.C
36 not assigned.r no hits & (original description: pacid=37171775 transcript=Phvul.006G045600.1 locu
37 not assigned.r no hits & (original description: pacid=37159849 transcript=Phvul.008G216700.1 locu
38 not assigned.r no hits & (original description: pacid=37157005 transcript=Phvul.011G111800.1 locu
39 Carbohydrate hexokinase (original description: pacid=37142381 transcript=Phvul.010G144900.1 lo
40 RNA biosynthtranscription factor (MYB) (original description: pacid=37177338 transcript=Phvul.00
41 RNA processir component MAC3 of non-snRNP MOS4-associated complex (original description: pac
42 not assigned.r no hits & (original description: pacid=37170216 transcript=Phvul.001G067500.3 locu
43 not assigned.r no hits & (original description: pacid=37170216 transcript=Phvul.001G067500.3 locu
44 not assigned.r no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
45 not assigned.r no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
46 not assigned.r no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu

1 not assigned.r no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
2 not assigned.r no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
3 not assigned.r no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
4 not assigned.ã (original description: pacid=37162149 transcript=Phvul.004G019300.2 locus=Phvul.C
5 not assigned.ã (original description: pacid=37162149 transcript=Phvul.004G019300.2 locus=Phvul.C
6 not assigned.r no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu
7 not assigned.r no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu
8 not assigned.r no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu
9 Enzyme classii no description available(sp|a0a072ur65|cht5b_medtr : 395.0) & Enzyme classificati
10 External stimu transcription factor (ERN1) (original description: pacid=37171836 transcript=Phvul.00
11 not assigned.r no hits & (original description: pacid=37177963 transcript=Phvul.002G183700.1 locu
12 not assigned.r no hits & (original description: pacid=37154896 transcript=Phvul.011G102400.1 locu
13 RNA biosynthetranscription factor (ERF) (original description: pacid=37164213 transcript=Phvul.007
14 not assigned.r no hits & (original description: pacid=37153363 transcript=Phvul.005G043000.2 locu
15 not assigned.r no hits & (original description: pacid=37172393 transcript=Phvul.006G148800.1 locu
16 not assigned.ã (original description: pacid=37155075 transcript=Phvul.011G069000.1 locus=Phvul.C
17 not assigned.ã (original description: pacid=37174127 transcript=Phvul.006G206800.1 locus=Phvul.C
18 Protein biosyr IF-2 translation initiation factor (original description: pacid=37154471 transcript=Phv
19 Cytoskeleton imotor protein (Kinesin-4) (original description: pacid=37168025 transcript=Phvul.001
20 Solute transpmetabolite transporter (DXT) (original description: pacid=37157842 transcript=Phvul
21 Protein modif protein kinase (MAPKK) (original description: pacid=37161740 transcript=Phvul.004G
22 Protein biosyr methyltransferase component Nop1/fibrillarlin of snoRNP rRNA methylation complex
23 not assigned.ã (original description: pacid=37150174 transcript=Phvul.009G046200.1 locus=Phvul.C
24 not assigned.r no hits & (original description: pacid=37157319 transcript=Phvul.011G133400.1 locu
25 Protein homee RING-H2-class E3 ligase (original description: pacid=37158322 transcript=Phvul.008G
26 Protein homee RING-H2-class E3 ligase (original description: pacid=37173182 transcript=Phvul.006G
27 Enzyme classiiEnzyme classification.EC_2 transferases.EC_2.3 acyltransferase(50.2.3 : 24.7) (origina
28 RNA processir RNA editing factor (ORRM) (original description: pacid=37160922 transcript=Phvul.00
29 Protein homee RING-HC-class E3 ligase (original description: pacid=37160948 transcript=Phvul.008G
30 not assigned.ã (original description: pacid=37151221 transcript=Phvul.009G198900.1 locus=Phvul.C
31 Protein homee RING-HC-class E3 ligase (original description: pacid=37160948 transcript=Phvul.008G
32 Enzyme classiiSpermidine hydroxycinnamoyl transferase OS=Arabidopsis thaliana (sp|o64470|sht_
33 PhotosynthesiLPA1 protein involved in PS-II assembly (original description: pacid=37169924 transci
34 not assigned.ã (original description: pacid=37156262 transcript=Phvul.011G159400.1 locus=Phvul.C
35 Solute transpçhexose transporter (SGB/GlcT) (original description: pacid=37162603 transcript=Phv
36 Protein homee pepsin-type protease (original description: pacid=37173754 transcript=Phvul.006G04
37 not assigned.r no hits & (original description: pacid=37150915 transcript=Phvul.009G007900.1 locu
38 RNA biosynthetranscription factor (TCP) (original description: pacid=37152688 transcript=Phvul.005
39 not assigned.r no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
40 not assigned.r no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
41 not assigned.r no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
42 not assigned.r no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
43 not assigned.r no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
44 not assigned.r no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
45 not assigned.r no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
46 External stimu transcription factor (ERN1) (original description: pacid=37171836 transcript=Phvul.00
47 not assigned.r no hits & (original description: pacid=37177963 transcript=Phvul.002G183700.1 locu

1 not assigned.r no hits & (original description: pacid=37153363 transcript=Phvul.005G043000.2 locu
2 not assigned.ε (original description: pacid=37162149 transcript=Phvul.004G019300.2 locus=Phvul.C
3 not assigned.ε (original description: pacid=37162149 transcript=Phvul.004G019300.2 locus=Phvul.C
4 not assigned.ε (original description: pacid=37155075 transcript=Phvul.011G069000.1 locus=Phvul.C
5 Protein home class-C-I small heat-shock-responsive protein (original description: pacid=37177788 t
6 Enzyme classiiEnzyme classification.EC_2 transferases.EC_2.3 acyltransferase(50.2.3 : 24.7) (origina
7 not assigned.r no hits & (original description: pacid=37154896 transcript=Phvul.011G102400.1 locu
8 Enzyme classiiSpermidine hydroxycinnamoyl transferase OS=Arabidopsis thaliana (sp|o64470|sht_
9 not assigned.r no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu
10 not assigned.r no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu
11 not assigned.r no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu
12 Enzyme classii no description available(sp|a0a072ur65|cht5b_medtr : 395.0) & Enzyme classificat
13 Protein biosyr methyltransferase component Nop1/fibrillarlin of snoRNP rRNA methylation complex
14 not assigned.ε (original description: pacid=37162384 transcript=Phvul.004G057900.1 locus=Phvul.C
15 RNA biosynthtranscription factor (ERF) (original description: pacid=37164213 transcript=Phvul.007
16 Lipid metaboliphospholipase A2 (pPLA2-II) (original description: pacid=37149281 transcript=Phvul.(
17 Solute transpmetabolite transporter (DXT) (original description: pacid=37157842 transcript=Phvul
18 Cell cycle orgacyclin (CYCD) (original description: pacid=37157024 transcript=Phvul.011G110000.1 |
19 Solute transp anion transporter (NRT1/PTR) (original description: pacid=37143370 transcript=Phvu
20 Lipid metaboliphospholipase A2 (pPLA2-II) (original description: pacid=37149281 transcript=Phvul.(
21 not assigned.ε (original description: pacid=37174127 transcript=Phvul.006G206800.1 locus=Phvul.C
22 Protein biosyr IF-2 translation initiation factor (original description: pacid=37154471 transcript=Phv
23 Cytoskeleton motor protein (Kinesin-4) (original description: pacid=37168025 transcript=Phvul.001
24 not assigned.r no hits & (original description: pacid=37171812 transcript=Phvul.006G098000.1 locu
25 not assigned.r no hits & (original description: pacid=37171812 transcript=Phvul.006G098000.1 locu
26 RNA processir RNA editing factor (ORRM) (original description: pacid=37160922 transcript=Phvul.0(
27 not assigned.r no hits & (original description: pacid=37155232 transcript=Phvul.011G028900.1 locu
28 Protein home RING-HC-class E3 ligase (original description: pacid=37160948 transcript=Phvul.008G
29 Protein home RING-HC-class E3 ligase (original description: pacid=37160948 transcript=Phvul.008G
30 Solute transp hexose transporter (SGB/GlcT) (original description: pacid=37162603 transcript=Phvu
31 Protein home pepsin-type protease (original description: pacid=37173754 transcript=Phvul.006G04
32 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
33 not assigned.r no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
34 not assigned.r no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
35 not assigned.r no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
36 not assigned.r no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
37 not assigned.r no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
38 not assigned.r no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
39 External stimu transcription factor (ERN1) (original description: pacid=37171836 transcript=Phvul.0(
40 not assigned.r no hits & (original description: pacid=37177963 transcript=Phvul.002G183700.1 locu
41 not assigned.r no hits & (original description: pacid=37153363 transcript=Phvul.005G043000.2 locu
42 not assigned.ε (original description: pacid=37162149 transcript=Phvul.004G019300.2 locus=Phvul.C
43 not assigned.ε (original description: pacid=37162149 transcript=Phvul.004G019300.2 locus=Phvul.C
44 not assigned.ε (original description: pacid=37155075 transcript=Phvul.011G069000.1 locus=Phvul.C
45 Protein home class-C-I small heat-shock-responsive protein (original description: pacid=37177788 t
46 Enzyme classiiEnzyme classification.EC_2 transferases.EC_2.3 acyltransferase(50.2.3 : 24.7) (origina

1 not assigned.r no hits & (original description: pacid=37154896 transcript=Phvul.011G102400.1 locu
2 Enzyme classiiSpermidine hydroxycinnamoyl transferase OS=Arabidopsis thaliana (sp|o64470|sht_
3 not assigned.r no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu
4 not assigned.r no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu
5 not assigned.r no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu
6 Enzyme classii no description available(sp|a0a072ur65|cht5b_medtr : 395.0) & Enzyme classificac
7 Protein biosyr methyltransferase component Nop1/fibrillarlin of snoRNP rRNA methylation complex
8 not assigned.ε (original description: pacid=37162384 transcript=Phvul.004G057900.1 locus=Phvul.C
9 RNA biosynthtranscription factor (ERF) (original description: pacid=37164213 transcript=Phvul.007
10 Lipid metaboliphospholipase A2 (pPLA2-II) (original description: pacid=37149281 transcript=Phvul.(
11 Solute transpmetabolite transporter (DXT) (original description: pacid=37157842 transcript=Phvul
12 Cell cycle orgacyclin (CYCD) (original description: pacid=37157024 transcript=Phvul.011G110000.1 |
13 Solute transp anion transporter (NRT1/PTR) (original description: pacid=37143370 transcript=Phvu
14 Lipid metaboliphospholipase A2 (pPLA2-II) (original description: pacid=37149281 transcript=Phvul.(
15 not assigned.ε (original description: pacid=37174127 transcript=Phvul.006G206800.1 locus=Phvul.C
16 Protein biosyr IF-2 translation initiation factor (original description: pacid=37154471 transcript=Phv
17 Cytoskeleton motor protein (Kinesin-4) (original description: pacid=37168025 transcript=Phvul.001
18 not assigned.r no hits & (original description: pacid=37171812 transcript=Phvul.006G098000.1 locu
19 not assigned.r no hits & (original description: pacid=37171812 transcript=Phvul.006G098000.1 locu
20 RNA processir RNA editing factor (ORRM) (original description: pacid=37160922 transcript=Phvul.00
21 not assigned.r no hits & (original description: pacid=37155232 transcript=Phvul.011G028900.1 locu
22 Protein homee RING-HC-class E3 ligase (original description: pacid=37160948 transcript=Phvul.008G
23 Protein homee RING-HC-class E3 ligase (original description: pacid=37160948 transcript=Phvul.008G
24 Solute transp hexose transporter (SGB/GlcT) (original description: pacid=37162603 transcript=Phvu
25 Protein homee pepsin-type protease (original description: pacid=37173754 transcript=Phvul.006G04
26 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3 J04G064100 ID=Phvul.004G064100.1.v2.1 annot-version=v2.1) & Ribonuclease 2 OS=Arabidopsis th
4 us=Phvul.009G096000 ID=Phvul.009G096000.1.v2.1 annot-version=v2.1)
5 J08G049000.1 locus=Phvul.008G049000 ID=Phvul.008G049000.1.v2.1 annot-version=v2.1) &
6 J04G064100 ID=Phvul.004G064100.1.v2.1 annot-version=v2.1) & Ribonuclease 2 OS=Arabidopsis th
7 us=Phvul.009G096000 ID=Phvul.009G096000.1.v2.1 annot-version=v2.1)
8 J04G064100 ID=Phvul.004G064100.1.v2.1 annot-version=v2.1) & Ribonuclease 2 OS=Arabidopsis th
9 us=Phvul.009G096000 ID=Phvul.009G096000.1.v2.1 annot-version=v2.1)
10 J04G064100 ID=Phvul.004G064100.1.v2.1 annot-version=v2.1) & Ribonuclease 2 OS=Arabidopsis th
11 us=Phvul.009G096000 ID=Phvul.009G096000.1.v2.1 annot-version=v2.1)
12 us=Phvul.009G196100 ID=Phvul.009G196100.1.v2.1 annot-version=v2.1)
13 J08G199900 ID=Phvul.008G199900.1.v2.1 annot-version=v2.1) & Probable magnesium transporter
14 us=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
15 us=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)
16 J04G038100 ID=Phvul.004G038100.1.v2.1 annot-version=v2.1) & O-fucosyltransferase 30 OS=Arabi
17 1G073600.2 locus=Phvul.011G073600 ID=Phvul.011G073600.2.v2.1 annot-version=v2.1) &
18 1G073600.2 locus=Phvul.011G073600 ID=Phvul.011G073600.2.v2.1 annot-version=v2.1) &
19 hvul.L001604 ID=Phvul.L001604.5.v2.1 annot-version=v2.1)
20 hvul.L001604 ID=Phvul.L001604.5.v2.1 annot-version=v2.1)
21 hvul.L001604 ID=Phvul.L001604.5.v2.1 annot-version=v2.1)
22 J04G160700 ID=Phvul.004G160700.1.v2.1 annot-version=v2.1) & Nudix hydrolase 20, chloroplastic
23 i2300.3 locus=Phvul.011G152300 ID=Phvul.011G152300.3.v2.1 annot-version=v2.1) &
24 i2300.3 locus=Phvul.011G152300 ID=Phvul.011G152300.3.v2.1 annot-version=v2.1) &
25 i2300.3 locus=Phvul.011G152300 ID=Phvul.011G152300.3.v2.1 annot-version=v2.1) &
26 us=Phvul.003G229300 ID=Phvul.003G229300.2.v2.1 annot-version=v2.1)
27 us=Phvul.003G229300 ID=Phvul.003G229300.2.v2.1 annot-version=v2.1)
28 hvul.003G178200.1 locus=Phvul.003G178200 ID=Phvul.003G178200.1.v2.1 annot-version=v2.1) &
29 us=Phvul.009G196100 ID=Phvul.009G196100.1.v2.1 annot-version=v2.1)
30 J08G199900 ID=Phvul.008G199900.1.v2.1 annot-version=v2.1) & Probable magnesium transporter
31 us=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
32 J04G160700 ID=Phvul.004G160700.1.v2.1 annot-version=v2.1) & Nudix hydrolase 20, chloroplastic
33 us=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)
34 hvul.L001604 ID=Phvul.L001604.5.v2.1 annot-version=v2.1)
35 hvul.L001604 ID=Phvul.L001604.5.v2.1 annot-version=v2.1)
36 hvul.L001604 ID=Phvul.L001604.5.v2.1 annot-version=v2.1)
37 J04G038100 ID=Phvul.004G038100.1.v2.1 annot-version=v2.1) & O-fucosyltransferase 30 OS=Arabi
38 1G073600.2 locus=Phvul.011G073600 ID=Phvul.011G073600.2.v2.1 annot-version=v2.1) &
39 1G073600.2 locus=Phvul.011G073600 ID=Phvul.011G073600.2.v2.1 annot-version=v2.1) &
40 us=Phvul.009G196100 ID=Phvul.009G196100.1.v2.1 annot-version=v2.1)
41 J08G199900 ID=Phvul.008G199900.1.v2.1 annot-version=v2.1) & Probable magnesium transporter
42 us=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
43 J04G160700 ID=Phvul.004G160700.1.v2.1 annot-version=v2.1) & Nudix hydrolase 20, chloroplastic
44 us=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)
45 hvul.L001604 ID=Phvul.L001604.5.v2.1 annot-version=v2.1)
46 hvul.L001604 ID=Phvul.L001604.5.v2.1 annot-version=v2.1)
47 hvul.L001604 ID=Phvul.L001604.5.v2.1 annot-version=v2.1)
48 J04G038100 ID=Phvul.004G038100.1.v2.1 annot-version=v2.1) & O-fucosyltransferase 30 OS=Arabi
49 1G073600.2 locus=Phvul.011G073600 ID=Phvul.011G073600.2.v2.1 annot-version=v2.1) &
50 1G073600.2 locus=Phvul.011G073600 ID=Phvul.011G073600.2.v2.1 annot-version=v2.1) &
51 us=Phvul.009G196100 ID=Phvul.009G196100.1.v2.1 annot-version=v2.1)
52 J08G199900 ID=Phvul.008G199900.1.v2.1 annot-version=v2.1) & Probable magnesium transporter
53 us=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
54 J04G160700 ID=Phvul.004G160700.1.v2.1 annot-version=v2.1) & Nudix hydrolase 20, chloroplastic
55 us=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)
56 hvul.L001604 ID=Phvul.L001604.5.v2.1 annot-version=v2.1)
57 hvul.L001604 ID=Phvul.L001604.5.v2.1 annot-version=v2.1)
58 hvul.L001604 ID=Phvul.L001604.5.v2.1 annot-version=v2.1)
59 J04G038100 ID=Phvul.004G038100.1.v2.1 annot-version=v2.1) & O-fucosyltransferase 30 OS=Arabi
60 1G073600.2 locus=Phvul.011G073600 ID=Phvul.011G073600.2.v2.1 annot-version=v2.1) &

1 1G073600.2 locus=Phvul.011G073600 ID=Phvul.011G073600.2.v2.1 annot-version=v2.1) &
2)2G289600.3 locus=Phvul.002G289600 ID=Phvul.002G289600.3.v2.1 annot-version=v2.1) &
3)2G289600.3 locus=Phvul.002G289600 ID=Phvul.002G289600.3.v2.1 annot-version=v2.1) &
4)2G289600.3 locus=Phvul.002G289600 ID=Phvul.002G289600.3.v2.1 annot-version=v2.1) &
5)2G289600.3 locus=Phvul.002G289600 ID=Phvul.002G289600.3.v2.1 annot-version=v2.1) &
6)02G041900 ID=Phvul.002G041900.1.v2.1 annot-version=v2.1) & Protein CDI OS=Arabidopsis thalia
7 'ul.010G108300.1 locus=Phvul.010G108300 ID=Phvul.010G108300.1.v2.1 annot-version=v2.1) &
8 's=Phvul.006G148800 ID=Phvul.006G148800.1.v2.1 annot-version=v2.1)
9 2657 transcript=Phvul.006G214700.4 locus=Phvul.006G214700 ID=Phvul.006G214700.4.v2.1 annot-
10 2657 transcript=Phvul.006G214700.4 locus=Phvul.006G214700 ID=Phvul.006G214700.4.v2.1 annot-
11 2657 transcript=Phvul.006G214700.4 locus=Phvul.006G214700 ID=Phvul.006G214700.4.v2.1 annot-
12 2657 transcript=Phvul.006G214700.4 locus=Phvul.006G214700 ID=Phvul.006G214700.4.v2.1 annot-
13 2657 transcript=Phvul.006G214700.4 locus=Phvul.006G214700 ID=Phvul.006G214700.4.v2.1 annot-
14 2657 transcript=Phvul.006G214700.4 locus=Phvul.006G214700 ID=Phvul.006G214700.4.v2.1 annot-
15 2657 transcript=Phvul.006G214700.4 locus=Phvul.006G214700 ID=Phvul.006G214700.4.v2.1 annot-
16 transcript=Phvul.002G231800.1 locus=Phvul.002G231800 ID=Phvul.002G231800.1.v2.1 annot-versi
17 .37000.6 locus=Phvul.005G137000 ID=Phvul.005G137000.6.v2.1 annot-version=v2.1) &
18 .37000.6 locus=Phvul.005G137000 ID=Phvul.005G137000.6.v2.1 annot-version=v2.1) &
19 .37000.6 locus=Phvul.005G137000 ID=Phvul.005G137000.6.v2.1 annot-version=v2.1) &
20 .37000.6 locus=Phvul.005G137000 ID=Phvul.005G137000.6.v2.1 annot-version=v2.1) &
21 .37000.6 locus=Phvul.005G137000 ID=Phvul.005G137000.6.v2.1 annot-version=v2.1) &
22 .37000.6 locus=Phvul.005G137000 ID=Phvul.005G137000.6.v2.1 annot-version=v2.1) &
23)0.1 locus=Phvul.002G226900 ID=Phvul.002G226900.1.v2.1 annot-version=v2.1) &
24 .37000.6 locus=Phvul.005G137000 ID=Phvul.005G137000.6.v2.1 annot-version=v2.1) &
25 .37000.6 locus=Phvul.005G137000 ID=Phvul.005G137000.6.v2.1 annot-version=v2.1) &
26 .37000.6 locus=Phvul.005G137000 ID=Phvul.005G137000.6.v2.1 annot-version=v2.1) &
27 's=Phvul.007G222000 ID=Phvul.007G222000.1.v2.1 annot-version=v2.1)
28 's=Phvul.007G029200 ID=Phvul.007G029200.1.v2.1 annot-version=v2.1)
29)03G058400 ID=Phvul.003G058400.1.v2.1 annot-version=v2.1) & Protein trichome birefringence-lik
30 4602 transcript=Phvul.002G250000.1 locus=Phvul.002G250000 ID=Phvul.002G250000.1.v2.1 annot-
31)04G028100 ID=Phvul.004G028100.1.v2.1 annot-version=v2.1) & DExH-box ATP-dependent RNA he
32 's=Phvul.008G216700 ID=Phvul.008G216700.1.v2.1 annot-version=v2.1)
33 's=Phvul.008G216700 ID=Phvul.008G216700.1.v2.1 annot-version=v2.1)
34)3 transcript=Phvul.002G190100.1 locus=Phvul.002G190100 ID=Phvul.002G190100.1.v2.1 annot-ve
35 ification.EC_1 oxidoreductases.EC_1.10 oxidoreductase acting on diphenol or related substance as
36 t=Phvul.001G036500.1 locus=Phvul.001G036500 ID=Phvul.001G036500.1.v2.1 annot-version=v2.1)
37)05G102100 ID=Phvul.005G102100.2.v2.1 annot-version=v2.1) & no description available(sp|q5ppz
38)05G102100 ID=Phvul.005G102100.2.v2.1 annot-version=v2.1) & no description available(sp|q5ppz
39)2G289600.3 locus=Phvul.002G289600 ID=Phvul.002G289600.3.v2.1 annot-version=v2.1) &
40)2G289600.3 locus=Phvul.002G289600 ID=Phvul.002G289600.3.v2.1 annot-version=v2.1) &
41)2G289600.3 locus=Phvul.002G289600 ID=Phvul.002G289600.3.v2.1 annot-version=v2.1) &
42)2G289600.3 locus=Phvul.002G289600 ID=Phvul.002G289600.3.v2.1 annot-version=v2.1) &
43)02G041900 ID=Phvul.002G041900.1.v2.1 annot-version=v2.1) & Protein CDI OS=Arabidopsis thalia
44 's=Phvul.006G148800 ID=Phvul.006G148800.1.v2.1 annot-version=v2.1)
45 'ul.010G108300.1 locus=Phvul.010G108300 ID=Phvul.010G108300.1.v2.1 annot-version=v2.1) &
46 2657 transcript=Phvul.006G214700.4 locus=Phvul.006G214700 ID=Phvul.006G214700.4.v2.1 annot-
47 2657 transcript=Phvul.006G214700.4 locus=Phvul.006G214700 ID=Phvul.006G214700.4.v2.1 annot-
48 2657 transcript=Phvul.006G214700.4 locus=Phvul.006G214700 ID=Phvul.006G214700.4.v2.1 annot-
49 2657 transcript=Phvul.006G214700.4 locus=Phvul.006G214700 ID=Phvul.006G214700.4.v2.1 annot-
50 's=Phvul.008G216700 ID=Phvul.008G216700.1.v2.1 annot-version=v2.1)
51 's=Phvul.008G216700 ID=Phvul.008G216700.1.v2.1 annot-version=v2.1)
52 t=Phvul.001G036500.1 locus=Phvul.001G036500 ID=Phvul.001G036500.1.v2.1 annot-version=v2.1)
53)2G289600.3 locus=Phvul.002G289600 ID=Phvul.002G289600.3.v2.1 annot-version=v2.1) &
54)2G289600.3 locus=Phvul.002G289600 ID=Phvul.002G289600.3.v2.1 annot-version=v2.1) &

1)2G289600.3 locus=Phvul.002G289600 ID=Phvul.002G289600.3.v2.1 annot-version=v2.1) &
2)02G041900 ID=Phvul.002G041900.1.v2.1 annot-version=v2.1) & Protein CDI OS=Arabidopsis thalia
3 us=Phvul.006G148800 ID=Phvul.006G148800.1.v2.1 annot-version=v2.1)
4 ul.010G108300.1 locus=Phvul.010G108300 ID=Phvul.010G108300.1.v2.1 annot-version=v2.1) &
5 2657 transcript=Phvul.006G214700.4 locus=Phvul.006G214700 ID=Phvul.006G214700.4.v2.1 annot-
6 2657 transcript=Phvul.006G214700.4 locus=Phvul.006G214700 ID=Phvul.006G214700.4.v2.1 annot-
7 2657 transcript=Phvul.006G214700.4 locus=Phvul.006G214700 ID=Phvul.006G214700.4.v2.1 annot-
8 2657 transcript=Phvul.006G214700.4 locus=Phvul.006G214700 ID=Phvul.006G214700.4.v2.1 annot-
9 us=Phvul.008G216700 ID=Phvul.008G216700.1.v2.1 annot-version=v2.1)
10 us=Phvul.008G216700 ID=Phvul.008G216700.1.v2.1 annot-version=v2.1)
11 t=Phvul.001G036500.1 locus=Phvul.001G036500 ID=Phvul.001G036500.1.v2.1 annot-version=v2.1)
12 71276 transcript=Phvul.001G052300.1 locus=Phvul.001G052300 ID=Phvul.001G052300.1.v2.1 anno
13 us=Phvul.010G110700 ID=Phvul.010G110700.2.v2.1 annot-version=v2.1)
14 us=Phvul.010G110700 ID=Phvul.010G110700.2.v2.1 annot-version=v2.1)
15 **5100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &**
16 **5100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &**
17 **5100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &**
18 **5100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &**
19 57914 transcript=Phvul.001G073300.1 locus=Phvul.001G073300 ID=Phvul.001G073300.1.v2.1 anno
20)08G279750 ID=Phvul.008G279750.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein E6
21 us=Phvul.010G152600 ID=Phvul.010G152600.2.v2.1 annot-version=v2.1)
22)06G021500 ID=Phvul.006G021500.1.v2.1 annot-version=v2.1) & Protein SIEVE ELEMENT OCCLUSIC
23 us=Phvul.009G177300 ID=Phvul.009G177300.1.v2.1 annot-version=v2.1)
24)07G147400.1 locus=Phvul.007G147400 ID=Phvul.007G147400.1.v2.1 annot-version=v2.1) &
25)78100.1 locus=Phvul.003G178100 ID=Phvul.003G178100.1.v2.1 annot-version=v2.1) &
26 us=Phvul.011G102400 ID=Phvul.011G102400.1.v2.1 annot-version=v2.1)
27)1G106800.2 locus=Phvul.001G106800 ID=Phvul.001G106800.2.v2.1 annot-version=v2.1) &
28 us=Phvul.007G261100 ID=Phvul.007G261100.2.v2.1 annot-version=v2.1)
29 us=Phvul.007G261100 ID=Phvul.007G261100.2.v2.1 annot-version=v2.1)
30 ript=Phvul.011G187600.1 locus=Phvul.011G187600 ID=Phvul.011G187600.1.v2.1 annot-version=v2.
31 us=Phvul.006G148800 ID=Phvul.006G148800.1.v2.1 annot-version=v2.1)
32 us=Phvul.006G148800 ID=Phvul.006G148800.1.v2.1 annot-version=v2.1)
33)02G044500 ID=Phvul.002G044500.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
34 group of donor(50.1.1 : 747.9) & Reticuline oxidase OS=Papaver somniferum (sp|p93479|reto_pap
35)06G206800 ID=Phvul.006G206800.1.v2.1 annot-version=v2.1) & Putative pumilio homolog 7, chlor
36 us=Phvul.010G144900 ID=Phvul.010G144900.1.v2.1 annot-version=v2.1) &
37)2G083800.1 locus=Phvul.002G083800 ID=Phvul.002G083800.1.v2.1 annot-version=v2.1) &
38 us=Phvul.001G067500 ID=Phvul.001G067500.3.v2.1 annot-version=v2.1)
39 us=Phvul.001G067500 ID=Phvul.001G067500.3.v2.1 annot-version=v2.1)
40 us=Phvul.001G067500 ID=Phvul.001G067500.3.v2.1 annot-version=v2.1)
41 us=Phvul.006G045600 ID=Phvul.006G045600.1.v2.1 annot-version=v2.1)
42)10G156000 ID=Phvul.010G156000.1.v2.1 annot-version=v2.1) & Protein LURP-one-related 12 OS=
43 Phvul.007G055500.1 locus=Phvul.007G055500 ID=Phvul.007G055500.1.v2.1 annot-version=v2.1) &
44 Phvul.007G055500.1 locus=Phvul.007G055500 ID=Phvul.007G055500.1.v2.1 annot-version=v2.1) &
45 us=Phvul.005G154600 ID=Phvul.005G154600.3.v2.1 annot-version=v2.1)
46 us=Phvul.005G154600 ID=Phvul.005G154600.3.v2.1 annot-version=v2.1)

1 Phvul.007G055200.1 locus=Phvul.007G055200 ID=Phvul.007G055200.1.v2.1 annot-version=v2.1) &
2 Phvul.007G055200.1 locus=Phvul.007G055200 ID=Phvul.007G055200.1.v2.1 annot-version=v2.1) &
3 us=Phvul.005G154600 ID=Phvul.005G154600.3.v2.1 annot-version=v2.1)
4 }37160063 transcript=Phvul.008G273100.1 locus=Phvul.008G273100 ID=Phvul.008G273100.1.v2.1 a
5 us=Phvul.008G216700 ID=Phvul.008G216700.1.v2.1 annot-version=v2.1)
6 }10G121200 ID=Phvul.010G121200.2.v2.1 annot-version=v2.1) & Uncharacterized calcium-binding |
7 }10G121200 ID=Phvul.010G121200.2.v2.1 annot-version=v2.1) & Uncharacterized calcium-binding |
8 id=37164150 transcript=Phvul.007G270500.1 locus=Phvul.007G270500 ID=Phvul.007G270500.1.v2
9 ript=Phvul.004G125900.1 locus=Phvul.004G125900 ID=Phvul.004G125900.1.v2.1 annot-version=
10 }05G027200 ID=Phvul.005G027200.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
11 us=Phvul.010G110700 ID=Phvul.010G110700.2.v2.1 annot-version=v2.1)
12 us=Phvul.010G110700 ID=Phvul.010G110700.2.v2.1 annot-version=v2.1)
13 }71276 transcript=Phvul.001G052300.1 locus=Phvul.001G052300 ID=Phvul.001G052300.1.v2.1 anno
14 }08G279750 ID=Phvul.008G279750.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein E6
15 }100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &
16 }100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &
17 }100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &
18 }100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &
19 }57914 transcript=Phvul.001G073300.1 locus=Phvul.001G073300 ID=Phvul.001G073300.1.v2.1 anno
20 us=Phvul.010G152600 ID=Phvul.010G152600.2.v2.1 annot-version=v2.1)
21 us=Phvul.011G102400 ID=Phvul.011G102400.1.v2.1 annot-version=v2.1)
22 us=Phvul.006G148800 ID=Phvul.006G148800.1.v2.1 annot-version=v2.1)
23 us=Phvul.006G148800 ID=Phvul.006G148800.1.v2.1 annot-version=v2.1)
24 }10G121200 ID=Phvul.010G121200.2.v2.1 annot-version=v2.1) & Uncharacterized calcium-binding |
25 }10G121200 ID=Phvul.010G121200.2.v2.1 annot-version=v2.1) & Uncharacterized calcium-binding |
26 ript=Phvul.004G125900.1 locus=Phvul.004G125900 ID=Phvul.004G125900.1.v2.1 annot-version=
27 }02G044500 ID=Phvul.002G044500.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
28 ng group of donor(50.1.1 : 747.9) & Reticuline oxidase OS=Papaver somniferum (sp|p93479|reto_pag
29 }06G021500 ID=Phvul.006G021500.1.v2.1 annot-version=v2.1) & Protein SIEVE ELEMENT OCCLUSIC
30 us=Phvul.009G177300 ID=Phvul.009G177300.1.v2.1 annot-version=v2.1)
31 }07G147400.1 locus=Phvul.007G147400 ID=Phvul.007G147400.1.v2.1 annot-version=v2.1) &
32 }178100.1 locus=Phvul.003G178100 ID=Phvul.003G178100.1.v2.1 annot-version=v2.1) &
33 us=Phvul.005G154600 ID=Phvul.005G154600.3.v2.1 annot-version=v2.1)
34 us=Phvul.005G154600 ID=Phvul.005G154600.3.v2.1 annot-version=v2.1)
35 }1G106800.2 locus=Phvul.001G106800 ID=Phvul.001G106800.2.v2.1 annot-version=v2.1) &
36 us=Phvul.007G261100 ID=Phvul.007G261100.2.v2.1 annot-version=v2.1)
37 us=Phvul.007G261100 ID=Phvul.007G261100.2.v2.1 annot-version=v2.1)
38 ript=Phvul.011G187600.1 locus=Phvul.011G187600 ID=Phvul.011G187600.1.v2.1 annot-version=v2.
39 us=Phvul.005G154600 ID=Phvul.005G154600.3.v2.1 annot-version=v2.1)
40 }37160063 transcript=Phvul.008G273100.1 locus=Phvul.008G273100 ID=Phvul.008G273100.1.v2.1 a
41 us=Phvul.005G065300 ID=Phvul.005G065300.1.v2.1 annot-version=v2.1)
42 }06G206800 ID=Phvul.006G206800.1.v2.1 annot-version=v2.1) & Putative pumilio homolog 7, chlor
43 us=Phvul.006G045600 ID=Phvul.006G045600.1.v2.1 annot-version=v2.1)
44 us=Phvul.008G216700 ID=Phvul.008G216700.1.v2.1 annot-version=v2.1)
45 us=Phvul.011G111800 ID=Phvul.011G111800.1.v2.1 annot-version=v2.1)
46 us=Phvul.010G144900 ID=Phvul.010G144900.1.v2.1 annot-version=v2.1) &

1 02G083800.1 locus=Phvul.002G083800 ID=Phvul.002G083800.1.v2.1 annot-version=v2.1) &
2 cid=37164150 transcript=Phvul.007G270500.1 locus=Phvul.007G270500 ID=Phvul.007G270500.1.v2
3 us=Phvul.001G067500 ID=Phvul.001G067500.3.v2.1 annot-version=v2.1)
4 us=Phvul.010G110700 ID=Phvul.010G110700.2.v2.1 annot-version=v2.1)
5 us=Phvul.010G110700 ID=Phvul.010G110700.2.v2.1 annot-version=v2.1)
6 71276 transcript=Phvul.001G052300.1 locus=Phvul.001G052300 ID=Phvul.001G052300.1.v2.1 anno
7 008G279750 ID=Phvul.008G279750.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein E6
8 5100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &
9 5100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &
10 5100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &
11 5100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &
12 57914 transcript=Phvul.001G073300.1 locus=Phvul.001G073300 ID=Phvul.001G073300.1.v2.1 anno
13 us=Phvul.010G152600 ID=Phvul.010G152600.2.v2.1 annot-version=v2.1)
14 us=Phvul.011G102400 ID=Phvul.011G102400.1.v2.1 annot-version=v2.1)
15 us=Phvul.006G148800 ID=Phvul.006G148800.1.v2.1 annot-version=v2.1)
16 us=Phvul.006G148800 ID=Phvul.006G148800.1.v2.1 annot-version=v2.1)
17 010G121200 ID=Phvul.010G121200.2.v2.1 annot-version=v2.1) & Uncharacterized calcium-binding |
18 010G121200 ID=Phvul.010G121200.2.v2.1 annot-version=v2.1) & Uncharacterized calcium-binding |
19 ript=Phvul.004G125900.1 locus=Phvul.004G125900 ID=Phvul.004G125900.1.v2.1 annot-version=
20 002G044500 ID=Phvul.002G044500.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
21 group of donor(50.1.1 : 747.9) & Reticuline oxidase OS=Papaver somniferum (sp|p93479|reto_pap
22 006G021500 ID=Phvul.006G021500.1.v2.1 annot-version=v2.1) & Protein SIEVE ELEMENT OCCLUSIC
23 us=Phvul.009G177300 ID=Phvul.009G177300.1.v2.1 annot-version=v2.1)
24 007G147400.1 locus=Phvul.007G147400 ID=Phvul.007G147400.1.v2.1 annot-version=v2.1) &
25 178100.1 locus=Phvul.003G178100 ID=Phvul.003G178100.1.v2.1 annot-version=v2.1) &
26 us=Phvul.005G154600 ID=Phvul.005G154600.3.v2.1 annot-version=v2.1)
27 us=Phvul.005G154600 ID=Phvul.005G154600.3.v2.1 annot-version=v2.1)
28 01G106800.2 locus=Phvul.001G106800 ID=Phvul.001G106800.2.v2.1 annot-version=v2.1) &
29 us=Phvul.007G261100 ID=Phvul.007G261100.2.v2.1 annot-version=v2.1)
30 us=Phvul.007G261100 ID=Phvul.007G261100.2.v2.1 annot-version=v2.1)
31 ript=Phvul.011G187600.1 locus=Phvul.011G187600 ID=Phvul.011G187600.1.v2.1 annot-version=v2.
32 us=Phvul.005G154600 ID=Phvul.005G154600.3.v2.1 annot-version=v2.1)
33 37160063 transcript=Phvul.008G273100.1 locus=Phvul.008G273100 ID=Phvul.008G273100.1.v2.1 ai
34 us=Phvul.005G065300 ID=Phvul.005G065300.1.v2.1 annot-version=v2.1)
35 006G206800 ID=Phvul.006G206800.1.v2.1 annot-version=v2.1) & Putative pumilio homolog 7, chlor
36 us=Phvul.006G045600 ID=Phvul.006G045600.1.v2.1 annot-version=v2.1)
37 us=Phvul.008G216700 ID=Phvul.008G216700.1.v2.1 annot-version=v2.1)
38 us=Phvul.011G111800 ID=Phvul.011G111800.1.v2.1 annot-version=v2.1)
39 cus=Phvul.010G144900 ID=Phvul.010G144900.1.v2.1 annot-version=v2.1) &
40 02G083800.1 locus=Phvul.002G083800 ID=Phvul.002G083800.1.v2.1 annot-version=v2.1) &
41 cid=37164150 transcript=Phvul.007G270500.1 locus=Phvul.007G270500 ID=Phvul.007G270500.1.v2
42 us=Phvul.001G067500 ID=Phvul.001G067500.3.v2.1 annot-version=v2.1)
43 us=Phvul.001G067500 ID=Phvul.001G067500.3.v2.1 annot-version=v2.1)
44 us=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)
45 us=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)
46 us=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)

1 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)
2 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)
3 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)
4 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)
5 004G019300 ID=Phvul.004G019300.2.v2.1 annot-version=v2.1) & Protein ALTERED XYLOGLUCAN 4-
6 004G019300 ID=Phvul.004G019300.2.v2.1 annot-version=v2.1) & Protein ALTERED XYLOGLUCAN 4-
7 js=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)
8 js=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)
9 js=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)
10 on.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2 : 132.1) (original description: pacid=37146097 transcr
11 006G173500.1 locus=Phvul.006G173500 ID=Phvul.006G173500.1.v2.1 annot-version=v2.1) &
12 js=Phvul.002G183700 ID=Phvul.002G183700.1.v2.1 annot-version=v2.1)
13 js=Phvul.011G102400 ID=Phvul.011G102400.1.v2.1 annot-version=v2.1)
14 007G027000.1 locus=Phvul.007G027000 ID=Phvul.007G027000.1.v2.1 annot-version=v2.1) &
15 js=Phvul.005G043000 ID=Phvul.005G043000.2.v2.1 annot-version=v2.1)
16 js=Phvul.006G148800 ID=Phvul.006G148800.1.v2.1 annot-version=v2.1)
17 011G069000 ID=Phvul.011G069000.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat
18 006G206800 ID=Phvul.006G206800.1.v2.1 annot-version=v2.1) & Putative pumilio homolog 7, chlor
19 ul.005G054600.1 locus=Phvul.005G054600 ID=Phvul.005G054600.1.v2.1 annot-version=v2.1) &
20 001G024200.1 locus=Phvul.001G024200 ID=Phvul.001G024200.1.v2.1 annot-version=v2.1) &
21 008G060700.1 locus=Phvul.008G060700 ID=Phvul.008G060700.1.v2.1 annot-version=v2.1) &
22 004G147900.1 locus=Phvul.004G147900 ID=Phvul.004G147900.1.v2.1 annot-version=v2.1) &
23 < (original description: pacid=37170855 transcript=Phvul.001G057200.1 locus=Phvul.001G057200 ID
24 009G046200 ID=Phvul.009G046200.1.v2.1 annot-version=v2.1) & Polyadenylate-binding protein-int
25 js=Phvul.011G133400 ID=Phvul.011G133400.1.v2.1 annot-version=v2.1)
26 008G111100.1 locus=Phvul.008G111100 ID=Phvul.008G111100.1.v2.1 annot-version=v2.1) &
27 006G070000.2 locus=Phvul.006G070000 ID=Phvul.006G070000.2.v2.1 annot-version=v2.1) &
28 al description: pacid=37171282 transcript=Phvul.L001687.1 locus=Phvul.L001687 ID=Phvul.L001687
29 008G033500.1 locus=Phvul.008G033500 ID=Phvul.008G033500.1.v2.1 annot-version=v2.1) &
30 008G036100.2 locus=Phvul.008G036100 ID=Phvul.008G036100.2.v2.1 annot-version=v2.1) &
31 009G198900 ID=Phvul.009G198900.1.v2.1 annot-version=v2.1) & Protein arginine N-methyltransfer
32 008G036100.2 locus=Phvul.008G036100 ID=Phvul.008G036100.2.v2.1 annot-version=v2.1) &
33 _arath : 311.0) & Enzyme classification.EC_2 transferases.EC_2.3 acyltransferase(50.2.3 : 22.0) (origi
34 ript=Phvul.001G205600.1 locus=Phvul.001G205600 ID=Phvul.001G205600.1.v2.1 annot-version=v2
35 011G159400 ID=Phvul.011G159400.1.v2.1 annot-version=v2.1) & UBP1-associated protein 2C OS=A
36 ul.004G061900.1 locus=Phvul.004G061900 ID=Phvul.004G061900.1.v2.1 annot-version=v2.1) &
37 006G048000.1 locus=Phvul.006G048000 ID=Phvul.006G048000.1.v2.1 annot-version=v2.1) &
38 js=Phvul.009G007900 ID=Phvul.009G007900.1.v2.1 annot-version=v2.1)
39 005G067950.1 locus=Phvul.005G067950 ID=Phvul.005G067950.1.v2.1 annot-version=v2.1) &
40 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)
41 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)
42 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)
43 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)
44 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)
45 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)
46 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)
47 006G173500.1 locus=Phvul.006G173500 ID=Phvul.006G173500.1.v2.1 annot-version=v2.1) &
48 js=Phvul.002G183700 ID=Phvul.002G183700.1.v2.1 annot-version=v2.1)

1
2 js=Phvul.005G043000 ID=Phvul.005G043000.2.v2.1 annot-version=v2.1)
3 J04G019300 ID=Phvul.004G019300.2.v2.1 annot-version=v2.1) & Protein ALTERED XYLOGLUCAN 4-
4 J04G019300 ID=Phvul.004G019300.2.v2.1 annot-version=v2.1) & Protein ALTERED XYLOGLUCAN 4-
5 J11G069000 ID=Phvul.011G069000.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat
6 transcript=Phvul.002G231800.1 locus=Phvul.002G231800 ID=Phvul.002G231800.1.v2.1 annot-versi
7 al description: pacid=37171282 transcript=Phvul.L001687.1 locus=Phvul.L001687 ID=Phvul.L001687
8
9 js=Phvul.011G102400 ID=Phvul.011G102400.1.v2.1 annot-version=v2.1)
10
11 arath : 311.0) & Enzyme classification.EC_2 transferases.EC_2.3 acyltransferase(50.2.3 : 22.0) (origi
12 js=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)
13 js=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)
14 js=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)
15 on.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2 : 132.1) (original description: pacid=37146097 transcr
16 < (original description: pacid=37170855 transcript=Phvul.001G057200.1 locus=Phvul.001G057200 ID
17 J04G057900 ID=Phvul.004G057900.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
18 7G027000.1 locus=Phvul.007G027000 ID=Phvul.007G027000.1.v2.1 annot-version=v2.1) &
19 009G063500.2 locus=Phvul.009G063500 ID=Phvul.009G063500.2.v2.1 annot-version=v2.1) &
20 l.008G060700.1 locus=Phvul.008G060700 ID=Phvul.008G060700.1.v2.1 annot-version=v2.1) &
21 locus=Phvul.011G110000 ID=Phvul.011G110000.1.v2.1 annot-version=v2.1) &
22 il.010G003800.1 locus=Phvul.010G003800 ID=Phvul.010G003800.1.v2.1 annot-version=v2.1) &
23 009G063500.2 locus=Phvul.009G063500 ID=Phvul.009G063500.2.v2.1 annot-version=v2.1) &
24 J06G206800 ID=Phvul.006G206800.1.v2.1 annot-version=v2.1) & Putative pumilio homolog 7, chlor
25 ul.005G054600.1 locus=Phvul.005G054600 ID=Phvul.005G054600.1.v2.1 annot-version=v2.1) &
26 1G024200.1 locus=Phvul.001G024200 ID=Phvul.001G024200.1.v2.1 annot-version=v2.1) &
27 js=Phvul.006G098000 ID=Phvul.006G098000.1.v2.1 annot-version=v2.1)
28 js=Phvul.006G098000 ID=Phvul.006G098000.1.v2.1 annot-version=v2.1)
29 08G033500.1 locus=Phvul.008G033500 ID=Phvul.008G033500.1.v2.1 annot-version=v2.1) &
30 js=Phvul.011G028900 ID=Phvul.011G028900.1.v2.1 annot-version=v2.1)
31 i036100.2 locus=Phvul.008G036100 ID=Phvul.008G036100.2.v2.1 annot-version=v2.1) &
32 i036100.2 locus=Phvul.008G036100 ID=Phvul.008G036100.2.v2.1 annot-version=v2.1) &
33 ul.004G061900.1 locus=Phvul.004G061900 ID=Phvul.004G061900.1.v2.1 annot-version=v2.1) &
34 48000.1 locus=Phvul.006G048000 ID=Phvul.006G048000.1.v2.1 annot-version=v2.1) &
35 js=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)
36 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)
37 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)
38 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)
39 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)
40 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)
41 js=Phvul.011G133575 ID=Phvul.011G133575.1.v2.1 annot-version=v2.1)
42 06G173500.1 locus=Phvul.006G173500 ID=Phvul.006G173500.1.v2.1 annot-version=v2.1) &
43 js=Phvul.002G183700 ID=Phvul.002G183700.1.v2.1 annot-version=v2.1)
44 js=Phvul.005G043000 ID=Phvul.005G043000.2.v2.1 annot-version=v2.1)
45 J04G019300 ID=Phvul.004G019300.2.v2.1 annot-version=v2.1) & Protein ALTERED XYLOGLUCAN 4-
46 J04G019300 ID=Phvul.004G019300.2.v2.1 annot-version=v2.1) & Protein ALTERED XYLOGLUCAN 4-
47 J11G069000 ID=Phvul.011G069000.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat
48 transcript=Phvul.002G231800.1 locus=Phvul.002G231800 ID=Phvul.002G231800.1.v2.1 annot-versi
49 al description: pacid=37171282 transcript=Phvul.L001687.1 locus=Phvul.L001687 ID=Phvul.L001687

1
2 js=Phvul.011G102400 ID=Phvul.011G102400.1.v2.1 annot-version=v2.1)
3 _arath : 311.0) & Enzyme classification.EC_2 transferases.EC_2.3 acyltransferase(50.2.3 : 22.0) (origi
4 js=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)
5 js=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)
6 js=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)
7 on.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2 : 132.1) (original description: pacid=37146097 transcr
8 < (original description: pacid=37170855 transcript=Phvul.001G057200.1 locus=Phvul.001G057200 ID
9 004G057900 ID=Phvul.004G057900.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
10 7G027000.1 locus=Phvul.007G027000 ID=Phvul.007G027000.1.v2.1 annot-version=v2.1) &
11 009G063500.2 locus=Phvul.009G063500 ID=Phvul.009G063500.2.v2.1 annot-version=v2.1) &
12 l.008G060700.1 locus=Phvul.008G060700 ID=Phvul.008G060700.1.v2.1 annot-version=v2.1) &
13 locus=Phvul.011G110000 ID=Phvul.011G110000.1.v2.1 annot-version=v2.1) &
14 il.010G003800.1 locus=Phvul.010G003800 ID=Phvul.010G003800.1.v2.1 annot-version=v2.1) &
15 009G063500.2 locus=Phvul.009G063500 ID=Phvul.009G063500.2.v2.1 annot-version=v2.1) &
16 006G206800 ID=Phvul.006G206800.1.v2.1 annot-version=v2.1) & Putative pumilio homolog 7, chlor
17 ul.005G054600.1 locus=Phvul.005G054600 ID=Phvul.005G054600.1.v2.1 annot-version=v2.1) &
18 1G024200.1 locus=Phvul.001G024200 ID=Phvul.001G024200.1.v2.1 annot-version=v2.1) &
19 js=Phvul.006G098000 ID=Phvul.006G098000.1.v2.1 annot-version=v2.1)
20 js=Phvul.006G098000 ID=Phvul.006G098000.1.v2.1 annot-version=v2.1)
21 08G033500.1 locus=Phvul.008G033500 ID=Phvul.008G033500.1.v2.1 annot-version=v2.1) &
22 js=Phvul.011G028900 ID=Phvul.011G028900.1.v2.1 annot-version=v2.1)
23 i036100.2 locus=Phvul.008G036100 ID=Phvul.008G036100.2.v2.1 annot-version=v2.1) &
24 i036100.2 locus=Phvul.008G036100 ID=Phvul.008G036100.2.v2.1 annot-version=v2.1) &
25 ul.004G061900.1 locus=Phvul.004G061900 ID=Phvul.004G061900.1.v2.1 annot-version=v2.1) &
26 48000.1 locus=Phvul.006G048000 ID=Phvul.006G048000.1.v2.1 annot-version=v2.1) &
27 js=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3 thaliana (sp|p42814|rns2_arath : 111.0)
4
5
6

7 thaliana (sp|p42814|rns2_arath : 111.0)
8
9

10 thaliana (sp|p42814|rns2_arath : 111.0)
11
12

13
14 NIPA3 OS=Arabidopsis thaliana (sp|q9lnk7|nipa3_arath : 384.0)
15
16

17
18 idopsis thaliana (sp|q1jpm5|oft30_arath : 545.0)
19
20

21
22
23
24
25
26 OS=Arabidopsis thaliana (sp|q8vxz0|nud20_arath : 429.0)
27
28

29
30
31
32
33
34
35
36 NIPA3 OS=Arabidopsis thaliana (sp|q9lnk7|nipa3_arath : 384.0)
37
38

39 OS=Arabidopsis thaliana (sp|q8vxz0|nud20_arath : 429.0)
40
41

42
43
44
45 idopsis thaliana (sp|q1jpm5|oft30_arath : 545.0)
46
47

48
49
50
51 NIPA3 OS=Arabidopsis thaliana (sp|q9lnk7|nipa3_arath : 384.0)
52
53

54 OS=Arabidopsis thaliana (sp|q8vxz0|nud20_arath : 429.0)
55
56

57
58
59
60 idopsis thaliana (sp|q1jpm5|oft30_arath : 545.0)

1
2
3
4
5
6
7 ina (sp|q9xip8|cdi_arath : 441.0)

8
9
10
11 -version=v2.1) &

12 -version=v2.1) &

13 -version=v2.1) &

14 -version=v2.1) &

15 on=v2.1) &

16
17
18
19
20
21
22
23
24
25
26
27
28
29 ce 37 OS=Arabidopsis thaliana (sp|o22960|tbl37_arath : 515.0)

30 -version=v2.1) &

31 elicase DExH18, mitochondrial OS=Arabidopsis thaliana (sp|f4kfv7|suv3l_arath : 1000.0)

32
33
34
35
36 -version=v2.1) &

37 donor(50.1.10 : 222.3) (original description: pacid=37161921 transcript=Phvul.004G087000.1 locus:

38 &

39 23|fly1_arath : 853.0)

40 23|fly1_arath : 853.0)

41
42
43
44
45
46 ina (sp|q9xip8|cdi_arath : 441.0)

47
48
49
50
51 -version=v2.1) &

52 -version=v2.1) &

53 -version=v2.1) &

54 -version=v2.1) &

55
56
57
58 &

59
60

1
2
3 ina (sp|q9xip8|cdi_arath : 441.0)
4
5
6

7 -version=v2.1) &

8 -version=v2.1) &

9 -version=v2.1) &

10 -version=v2.1) &

11 -version=v2.1) &

12
13
14
15 &

16 it-version=v2.1) &

17
18
19
20
21
22
23
24
25 it-version=v2.1) &

26 i OS=*Oryza sativa* subsp. *japonica* (sp|q651x6|csle6_orysj : 667.0)

27
28
29 DN B OS=*Arabidopsis thaliana* (sp|q9ss87|seob_arath : 193.0)
30
31
32
33
34
35
36
37
38
39

40 .1) &

41
42
43
44 ing protein At4g14820 OS=*Arabidopsis thaliana* (sp|o23337|pp311_arath : 842.0)

45 oso : 452.0) (original description: pacid=37165503 transcript=Phvul.007G113300.1 locus=Phvul.007)

46 roplastic OS=*Arabidopsis thaliana* (sp|q9c9r6|pum7_arath : 433.0)
47
48
49
50
51
52
53
54
55

56 *Arabidopsis thaliana* (sp|q9lvz8|lor12_arath : 212.0)
57
58
59
60

1
2
3
4
5
6 nnot-version=v2.1) &

7
8 protein At1g02270 OS=Arabidopsis thaliana (sp|o81916|yc22_arath : 560.0)

9 protein At1g02270 OS=Arabidopsis thaliana (sp|o81916|yc22_arath : 560.0)

10
11 2.1 annot-version=v2.1) &

12 v2.1) &

13
14 in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1_solbu : 363.0)

15
16
17 it-version=v2.1) &

18 i OS=Oryza sativa subsp. japonica (sp|q651x6|csle6_orysj : 667.0)

19
20
21
22
23
24
25 it-version=v2.1) &

26
27
28
29
30
31
32 protein At1g02270 OS=Arabidopsis thaliana (sp|o81916|yc22_arath : 560.0)

33 protein At1g02270 OS=Arabidopsis thaliana (sp|o81916|yc22_arath : 560.0)

34
35 v2.1) &

36 ing protein At4g14820 OS=Arabidopsis thaliana (sp|o23337|pp311_arath : 842.0)

37 oso : 452.0) (original description: pacid=37165503 transcript=Phvul.007G113300.1 locus=Phvul.007G113300.1)

38
39 ON B OS=Arabidopsis thaliana (sp|q9ss87|seob_arath : 193.0)

40
41
42
43
44
45
46
47
48
49
50
51 .1) &

52
53 nnot-version=v2.1) &

54
55
56 roplastic OS=Arabidopsis thaliana (sp|q9c9r6|pum7_arath : 433.0)

57
58
59
60

1
2
3 2.1 annot-version=v2.1) &
4
5
6
7

8 t-version=v2.1) &
9

10 i OS=*Oryza sativa* subsp. *japonica* (sp|q651x6|csle6_orysj : 667.0)
11
12
13
14
15

16 t-version=v2.1) &
17
18
19
20
21
22

23 protein At1g02270 OS=*Arabidopsis thaliana* (sp|o81916|yc22_arath : 560.0)

24 protein At1g02270 OS=*Arabidopsis thaliana* (sp|o81916|yc22_arath : 560.0)

25 :v2.1) &
26

27 ing protein At4g14820 OS=*Arabidopsis thaliana* (sp|o23337|pp311_arath : 842.0)

28 o : 452.0) (original description: pacid=37165503 transcript=Phvul.007G113300.1 locus=Phvul.007G113300.1)

29 ON B OS=*Arabidopsis thaliana* (sp|q9ss87|seob_arath : 193.0)
30
31
32
33
34
35
36
37
38
39
40

41 .1) &
42
43

44 nnot-version=v2.1) &
45
46

47 roplastic OS=*Arabidopsis thaliana* (sp|q9c9r6|pum7_arath : 433.0)
48
49
50
51
52
53

54 2.1 annot-version=v2.1) &
55
56
57
58
59
60

1
2
3
4
5
6 like OS=Arabidopsis thaliana (sp|q9lrs2|tbl22_arath : 415.0)

7 like OS=Arabidopsis thaliana (sp|q9lrs2|tbl22_arath : 415.0)

8
9
10
11
12 ript=Phvul.003G158800.1 locus=Phvul.003G158800 ID=Phvul.003G158800.1.v2.1 annot-version=v2.
13
14
15
16
17
18
19
20

21 t-containing protein At1g02420 OS=Arabidopsis thaliana (sp|q9fz19|ppr5_arath : 632.0)

22 roplastic OS=Arabidopsis thaliana (sp|q9c9r6|pum7_arath : 433.0)

23
24
25
26
27
28
29 D=Phvul.001G057200.1.v2.1 annot-version=v2.1) &

30 teracting protein 12 OS=Arabidopsis thaliana (sp|q9s7n9|cid12_arath : 405.0)

31
32
33
34
35
36 '.1.v2.1 annot-version=v2.1) &

37
38
39
40 rase PRMT10 OS=Arabidopsis thaliana (sp|q9mat5|anm10_arath : 573.0)

41
42 inal description: pacid=37174189 transcript=Phvul.006G037000.1 locus=Phvul.006G037000 ID=Phvul.006G037000.1.v2.1) &

43
44 rabadopsis thaliana (sp|q9lka4|uba2c_arath : 315.0)

45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

like OS=Arabidopsis thaliana (sp|q9lrs2|tbl22_arath : 415.0)

like OS=Arabidopsis thaliana (sp|q9lrs2|tbl22_arath : 415.0)

t-containing protein At1g02420 OS=Arabidopsis thaliana (sp|q9fz19|ppr5_arath : 632.0)

on=v2.1) &

'.1.v2.1 annot-version=v2.1) &

inal description: pacid=37174189 transcript=Phvul.006G037000.1 locus=Phvul.006G037000 ID=Phvi

ript=Phvul.003G158800.1 locus=Phvul.003G158800 ID=Phvul.003G158800.1.v2.1 annot-version=v2.

D=Phvul.001G057200.1.v2.1 annot-version=v2.1) &

ing protein At1g79490, mitochondrial OS=Arabidopsis thaliana (sp|q9sak0|pp132_arath : 1241.0)

roplastic OS=Arabidopsis thaliana (sp|q9c9r6|pum7_arath : 433.0)

like OS=Arabidopsis thaliana (sp|q9lrs2|tbl22_arath : 415.0)

like OS=Arabidopsis thaliana (sp|q9lrs2|tbl22_arath : 415.0)

t-containing protein At1g02420 OS=Arabidopsis thaliana (sp|q9fz19|ppr5_arath : 632.0)

on=v2.1) &

'.1.v2.1 annot-version=v2.1) &

1
2
3 inal description: pacid=37174189 transcript=Phvul.006G037000.1 locus=Phvul.006G037000 ID=Phvul.006G037000.1
4
5
6
7

8 ript=Phvul.003G158800.1 locus=Phvul.003G158800 ID=Phvul.003G158800.1.v2.1 annot-version=v2.1
9

10 D=Phvul.001G057200.1.v2.1 annot-version=v2.1) &

11 ing protein At1g79490, mitochondrial OS=Arabidopsis thaliana (sp|q9sak0|pp132_arath : 1241.0)
12
13
14
15
16
17
18
19

20 roplastic OS=Arabidopsis thaliana (sp|q9c9r6|pum7_arath : 433.0)
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

=Phvul.004G087000 ID=Phvul.004G087000.1.v2.1 annot-version=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

G113300 ID=Phvul.007G113300.1.v2.1 annot-version=v2.1) &

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

G113300 ID=Phvul.007G113300.1.v2.1 annot-version=v2.1) &

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

G113300 ID=Phvul.007G113300.1.v2.1 annot-version=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

.1) &

ul.006G037000.1.v2.1 annot-version=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

ul.006G037000.1.v2.1 annot-version=v2.1) &

.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

ul.006G037000.1.v2.1 annot-version=v2.1) &

.1) &

Do not distribute

| | miRNA_Acc. | Target_Acc. | Expectation | UPE\$ | miRNA_start | miRNA_end |
|----|--------------|--------------------|-------------|-------|-------------|-----------|
| 1 | | | | | | |
| 2 | | | | | | |
| 3 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 5 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 6 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 9 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 10 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 13 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 14 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 17 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 18 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 21 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 22 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 25 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 26 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 29 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 30 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 33 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 34 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 37 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 38 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 39 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 41 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 42 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 43 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 45 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 46 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 21 |
| 47 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 22 |
| 49 | uggagaagcagg | Phvul.003G189000.1 | 0.5 | -1 | 1 | 22 |
| 50 | uggagaagcagg | Phvul.009G186000.1 | 0.5 | -1 | 1 | 22 |
| 51 | uggagaagcagg | Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 52 | uggagaagcagg | Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 53 | uggagaagcagg | Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 54 | uggagaagcagg | Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 55 | uggagaagcagg | Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 56 | uggagaagcagg | Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 57 | uggagaagcagg | Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 58 | uggagaagcagg | Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 59 | uggagaagcagg | Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 60 | uggagaagcagg | Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| | uggagaagcagg | Phvul.005G055400.1 | 1 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 13 | uggagaagcagg Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 14 | uggagaagcagg Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 17 | uggagaagcagg Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 18 | uggagaagcagg Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 21 | uggagaagcagg Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 22 | uggagaagcagg Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 25 | uggagaagcagg Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 26 | uggagaagcagg Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 29 | uggagaagcagg Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 30 | uggagaagcagg Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 33 | uggagaagcagg Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 34 | uggagaagcagg Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 38 | uggagaagcagg Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 42 | uggagaagcagg Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 46 | uggagaagcagg Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 50 | uggagaagcagg Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 51 | uggagaagcagg Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 54 | uggagaagcagg Phvul.005G074500.1 | 1 | -1 | 1 | 21 |
| 55 | uggagaagcagg Phvul.011G160400.1 | 1 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.005G055400.1 | 1 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.005G074500.1 | 1 | -1 | 1 | 22 |
| 58 | uggagaagcagg Phvul.011G160400.1 | 1 | -1 | 1 | 22 |
| 59 | uggagaagcagg Phvul.005G055400.1 | 1 | -1 | 1 | 22 |
| 60 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.007G164800.1 | 2.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.011G065700.1 | 2.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.011G065700.3 | 2.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.011G065700.2 | 2.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.007G164800.1 | 2.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.011G065700.1 | 2.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.011G065700.3 | 2.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.011G065700.2 | 2.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.007G164800.1 | 2.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.011G065700.1 | 2.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.011G065700.3 | 2.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.011G065700.2 | 2.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.007G164800.1 | 2.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.011G065700.1 | 2.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.011G065700.3 | 2.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.011G065700.2 | 2.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.007G164800.1 | 2.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.011G065700.1 | 2.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.011G065700.3 | 2.5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.011G065700.2 | 2.5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.007G164800.1 | 2.5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.011G065700.1 | 2.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.011G065700.3 | 2.5 | -1 | 1 | 21 |
| 45 | | | | | |
| 46 | uggagaagcagg Phvul.011G065700.2 | 2.5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 21 |
| 49 | | | | | |
| 50 | uggagaagcagg Phvul.007G164800.1 | 2.5 | -1 | 1 | 21 |
| 51 | uggagaagcagg Phvul.011G065700.1 | 2.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.011G065700.3 | 2.5 | -1 | 1 | 21 |
| 53 | | | | | |
| 54 | uggagaagcagg Phvul.011G065700.2 | 2.5 | -1 | 1 | 21 |
| 55 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 21 |
| 57 | | | | | |
| 58 | uggagaagcagg Phvul.007G164800.1 | 2.5 | -1 | 1 | 21 |
| 59 | uggagaagcagg Phvul.011G065700.1 | 2.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.011G065700.3 | 2.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.011G065700.2 | 2.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.007G164800.1 | 2.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.011G065700.1 | 2.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.011G065700.3 | 2.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.011G065700.2 | 2.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.007G164800.1 | 2.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.011G065700.1 | 2.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.011G065700.3 | 2.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.011G065700.2 | 2.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.007G164800.1 | 2.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.011G065700.1 | 2.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.011G065700.3 | 2.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.011G065700.2 | 2.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.007G164800.1 | 2.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.011G065700.1 | 2.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.011G065700.3 | 2.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.011G065700.2 | 2.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.007G164800.1 | 2.5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.011G065700.1 | 2.5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.011G065700.3 | 2.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.011G065700.2 | 2.5 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.007G164800.1 | 2.5 | -1 | 1 | 21 |
| 45 | | | | | |
| 46 | uggagaagcagg Phvul.011G065700.1 | 2.5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.011G065700.3 | 2.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.011G065700.2 | 2.5 | -1 | 1 | 21 |
| 49 | | | | | |
| 50 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 21 |
| 51 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.007G164800.1 | 2.5 | -1 | 1 | 21 |
| 53 | | | | | |
| 54 | uggagaagcagg Phvul.011G065700.1 | 2.5 | -1 | 1 | 21 |
| 55 | uggagaagcagg Phvul.011G065700.3 | 2.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.011G065700.2 | 2.5 | -1 | 1 | 21 |
| 57 | | | | | |
| 58 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 21 |
| 59 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.007G164800.1 | 2.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.011G065700.1 | 2.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.011G065700.3 | 2.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.011G065700.2 | 2.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 21 |
| 5 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 21 |
| 6 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.007G164800.1 | 2.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.011G065700.1 | 2.5 | -1 | 1 | 21 |
| 9 | uggagaagcagg Phvul.011G065700.1 | 2.5 | -1 | 1 | 21 |
| 10 | uggagaagcagg Phvul.011G065700.3 | 2.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.011G065700.2 | 2.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 21 |
| 13 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 21 |
| 14 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 22 |
| 15 | uggagaagcagg Phvul.006G169300.1 | 2.5 | -1 | 1 | 22 |
| 16 | uggagaagcagg Phvul.007G164800.1 | 2.5 | -1 | 1 | 22 |
| 17 | uggagaagcagg Phvul.011G065700.1 | 2.5 | -1 | 1 | 22 |
| 18 | uggagaagcagg Phvul.011G065700.3 | 2.5 | -1 | 1 | 22 |
| 19 | uggagaagcagg Phvul.011G065700.2 | 2.5 | -1 | 1 | 22 |
| 20 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 22 |
| 21 | uggagaagcagg Phvul.004G172600.1 | 2.5 | -1 | 1 | 22 |
| 22 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 25 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 26 | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 29 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 30 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.006G086200.1 | 3 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 33 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 34 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 38 | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 42 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.006G086200.1 | 3 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 46 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 50 | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 21 |
| 51 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 54 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 55 | uggagaagcagg Phvul.006G086200.1 | 3 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 58 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 59 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 5 | uggagaagcagg Phvul.006G086200.1 | 3 | -1 | 1 | 21 |
| 6 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| 9 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 10 | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 13 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 14 | uggagaagcagg Phvul.006G086200.1 | 3 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 17 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| 18 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |
| 21 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 22 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.006G086200.1 | 3 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 25 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 26 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 21 |
| 29 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |
| 30 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.006G086200.1 | 3 | -1 | 1 | 21 |
| 33 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 34 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 21 |
| 38 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.006G086200.1 | 3 | -1 | 1 | 21 |
| 42 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 46 | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 50 | uggagaagcagg Phvul.006G086200.1 | 3 | -1 | 1 | 21 |
| 51 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| 54 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 55 | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 58 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 59 | uggagaagcagg Phvul.006G086200.1 | 3 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.006G086200.1 | 3 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.006G086200.1 | 3 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.006G086200.1 | 3 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.006G086200.1 | 3 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.006G086200.1 | 3 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.006G086200.1 | 3 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 13 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 14 | uggagaagcagg Phvul.006G086200.1 | 3 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 17 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 18 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 21 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 22 | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 25 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 26 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.006G086200.1 | 3 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 29 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 30 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 33 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 21 |
| 34 | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 38 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.006G086200.1 | 3 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.010G128500.1 | 3 | -1 | 1 | 21 |
| 42 | uggagaagcagg Phvul.010G089100.2 | 3 | -1 | 1 | 22 |
| 43 | uggagaagcagg Phvul.002G325300.2 | 3 | -1 | 1 | 22 |
| 44 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 22 |
| 45 | uggagaagcagg Phvul.004G139200.1 | 3 | -1 | 1 | 22 |
| 46 | uggagaagcagg Phvul.005G001200.1 | 3 | -1 | 1 | 22 |
| 47 | uggagaagcagg Phvul.008G147100.2 | 3 | -1 | 1 | 22 |
| 48 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 22 |
| 49 | uggagaagcagg Phvul.008G147100.4 | 3 | -1 | 1 | 22 |
| 50 | uggagaagcagg Phvul.008G147100.3 | 3 | -1 | 1 | 22 |
| 51 | uggagaagcagg Phvul.007G083500.1 | 3.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 54 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 55 | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.011G110300.1 | 3.5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |
| 58 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |
| 59 | uggagaagcagg Phvul.005G005200.1 | 3.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.008G277800.1 | 3.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.003G067000.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.005G087600.1 | 3.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.009G130000.1 | 3.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.011G108000.1 | 3.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.007G083500.1 | 3.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.011G110300.1 | 3.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.005G005200.1 | 3.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.008G277800.1 | 3.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.003G067000.1 | 3.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.005G087600.1 | 3.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.009G130000.1 | 3.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.011G108000.1 | 3.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.007G083500.1 | 3.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.011G110300.1 | 3.5 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.005G005200.1 | 3.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.008G277800.1 | 3.5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.003G067000.1 | 3.5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.005G087600.1 | 3.5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.009G130000.1 | 3.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.011G108000.1 | 3.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.007G083500.1 | 3.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.011G110300.1 | 3.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.005G005200.1 | 3.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.008G277800.1 | 3.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.003G067000.1 | 3.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |
| 13 | uggagaagcagg Phvul.005G087600.1 | 3.5 | -1 | 1 | 21 |
| 14 | uggagaagcagg Phvul.009G130000.1 | 3.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.011G108000.1 | 3.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| 17 | uggagaagcagg Phvul.007G083500.1 | 3.5 | -1 | 1 | 21 |
| 18 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 21 |
| 21 | uggagaagcagg Phvul.011G110300.1 | 3.5 | -1 | 1 | 21 |
| 22 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.005G005200.1 | 3.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.008G277800.1 | 3.5 | -1 | 1 | 21 |
| 25 | uggagaagcagg Phvul.003G067000.1 | 3.5 | -1 | 1 | 21 |
| 26 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 21 |
| 29 | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |
| 30 | uggagaagcagg Phvul.005G087600.1 | 3.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.009G130000.1 | 3.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.011G108000.1 | 3.5 | -1 | 1 | 21 |
| 33 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| 34 | uggagaagcagg Phvul.007G083500.1 | 3.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 21 |
| 38 | uggagaagcagg Phvul.011G110300.1 | 3.5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.005G005200.1 | 3.5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.008G277800.1 | 3.5 | -1 | 1 | 21 |
| 42 | uggagaagcagg Phvul.003G067000.1 | 3.5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 21 |
| 46 | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.005G087600.1 | 3.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.009G130000.1 | 3.5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.011G108000.1 | 3.5 | -1 | 1 | 21 |
| 50 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| 51 | uggagaagcagg Phvul.007G083500.1 | 3.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 54 | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 21 |
| 55 | uggagaagcagg Phvul.011G110300.1 | 3.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.005G005200.1 | 3.5 | -1 | 1 | 21 |
| 58 | uggagaagcagg Phvul.008G277800.1 | 3.5 | -1 | 1 | 21 |
| 59 | uggagaagcagg Phvul.003G067000.1 | 3.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.005G087600.1 | 3.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.009G130000.1 | 3.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.011G108000.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.007G083500.1 | 3.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.011G110300.1 | 3.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.005G005200.1 | 3.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.008G277800.1 | 3.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.003G067000.1 | 3.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.005G087600.1 | 3.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.009G130000.1 | 3.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.011G108000.1 | 3.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.007G083500.1 | 3.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.011G110300.1 | 3.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.005G005200.1 | 3.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.008G277800.1 | 3.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.003G067000.1 | 3.5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.005G087600.1 | 3.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.009G130000.1 | 3.5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.011G108000.1 | 3.5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.007G083500.1 | 3.5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.011G110300.1 | 3.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.005G005200.1 | 3.5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.008G277800.1 | 3.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.003G067000.1 | 3.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.005G087600.1 | 3.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.009G130000.1 | 3.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.011G108000.1 | 3.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.007G083500.1 | 3.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.011G110300.1 | 3.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.005G005200.1 | 3.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.008G277800.1 | 3.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.003G067000.1 | 3.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.005G087600.1 | 3.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.009G130000.1 | 3.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.011G108000.1 | 3.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.007G083500.1 | 3.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.011G110300.1 | 3.5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.005G005200.1 | 3.5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.008G277800.1 | 3.5 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.003G067000.1 | 3.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.005G087600.1 | 3.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.009G130000.1 | 3.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.011G108000.1 | 3.5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.007G083500.1 | 3.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.011G110300.1 | 3.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.005G005200.1 | 3.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.008G277800.1 | 3.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.003G067000.1 | 3.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.005G087600.1 | 3.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.009G130000.1 | 3.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.011G108000.1 | 3.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.007G083500.1 | 3.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.011G110300.1 | 3.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.005G005200.1 | 3.5 | -1 | 1 | 21 |
| 25 | uggagaagcagg Phvul.008G277800.1 | 3.5 | -1 | 1 | 21 |
| 26 | | | | | |
| 27 | uggagaagcagg Phvul.003G067000.1 | 3.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.005G087600.1 | 3.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.009G130000.1 | 3.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.011G108000.1 | 3.5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.007G083500.1 | 3.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.011G110300.1 | 3.5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.005G005200.1 | 3.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.008G277800.1 | 3.5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.003G067000.1 | 3.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.005G087600.1 | 3.5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.009G130000.1 | 3.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.011G108000.1 | 3.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.007G083500.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.011G110300.1 | 3.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.005G005200.1 | 3.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.008G277800.1 | 3.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.003G067000.1 | 3.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 21 |
| 13 | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 21 |
| 14 | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |
| 17 | uggagaagcagg Phvul.005G087600.1 | 3.5 | -1 | 1 | 21 |
| 18 | uggagaagcagg Phvul.009G130000.1 | 3.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.011G108000.1 | 3.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| 21 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| 22 | uggagaagcagg Phvul.007G083500.1 | 3.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 25 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 26 | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.011G110300.1 | 3.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |
| 29 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |
| 30 | uggagaagcagg Phvul.005G005200.1 | 3.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.008G277800.1 | 3.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.003G067000.1 | 3.5 | -1 | 1 | 21 |
| 33 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 21 |
| 34 | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |
| 38 | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.005G087600.1 | 3.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.009G130000.1 | 3.5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.011G108000.1 | 3.5 | -1 | 1 | 21 |
| 42 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.007G083500.1 | 3.5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 21 |
| 46 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 21 |
| 50 | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 21 |
| 51 | uggagaagcagg Phvul.011G110300.1 | 3.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.005G005200.1 | 3.5 | -1 | 1 | 21 |
| 54 | uggagaagcagg Phvul.008G277800.1 | 3.5 | -1 | 1 | 21 |
| 55 | uggagaagcagg Phvul.003G067000.1 | 3.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 21 |
| 58 | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 21 |
| 59 | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.005G087600.1 | 3.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.009G130000.1 | 3.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.011G108000.1 | 3.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.007G083500.1 | 3.5 | -1 | 1 | 22 |
| 8 | uggagaagcagg Phvul.007G083500.2 | 3.5 | -1 | 1 | 22 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.011G079800.1 | 3.5 | -1 | 1 | 22 |
| 11 | uggagaagcagg Phvul.011G054900.1 | 3.5 | -1 | 1 | 22 |
| 12 | uggagaagcagg Phvul.008G077800.1 | 3.5 | -1 | 1 | 22 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.011G110300.1 | 3.5 | -1 | 1 | 22 |
| 15 | uggagaagcagg Phvul.008G077700.1 | 3.5 | -1 | 1 | 22 |
| 16 | uggagaagcagg Phvul.005G005200.1 | 3.5 | -1 | 1 | 22 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.002G073200.1 | 3.5 | -1 | 1 | 22 |
| 19 | uggagaagcagg Phvul.002G073100.2 | 3.5 | -1 | 1 | 22 |
| 20 | uggagaagcagg Phvul.002G073100.1 | 3.5 | -1 | 1 | 22 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.008G277800.1 | 3.5 | -1 | 1 | 22 |
| 23 | uggagaagcagg Phvul.003G067000.1 | 3.5 | -1 | 1 | 22 |
| 24 | uggagaagcagg Phvul.001G240500.1 | 3.5 | -1 | 1 | 22 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.008G061000.1 | 3.5 | -1 | 1 | 22 |
| 27 | uggagaagcagg Phvul.003G246400.1 | 3.5 | -1 | 1 | 22 |
| 28 | uggagaagcagg Phvul.009G132000.1 | 3.5 | -1 | 1 | 22 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.004G099100.1 | 4 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.002G157300.1 | 4 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.011G046800.1 | 4 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.006G023000.2 | 4 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.001G151600.1 | 4 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | uggagaagcagg Phvul.007G231200.1 | 4 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.004G037600.2 | 4 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.004G037600.3 | 4 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.007G156900.1 | 4 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.007G157000.1 | 4 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.007G105700.1 | 4 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.008G159000.1 | 4 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.005G114000.1 | 4 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.001G031000.1 | 4 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.004G041500.1 | 4 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.004G041500.2 | 4 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.007G084000.1 | 4 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.009G119100.1 | 4 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.006G102900.2 | 4 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.006G102900.1 | 4 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.010G079200.1 | 4 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.010G079200.2 | 4 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.008G127800.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.001G038000.1 | 4 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.002G105200.1 | 4 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.008G032900.1 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.009G244600.1 | 4 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.004G099100.1 | 4 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.002G157300.1 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.011G046800.1 | 4 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.006G023000.2 | 4 | -1 | 1 | 21 |
| 13 | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 21 |
| 14 | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.001G151600.1 | 4 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.007G231200.1 | 4 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.004G037600.2 | 4 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.004G037600.3 | 4 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.007G156900.1 | 4 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.007G157000.1 | 4 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.007G105700.1 | 4 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.008G159000.1 | 4 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.005G114000.1 | 4 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.001G031000.1 | 4 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.004G041500.1 | 4 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.004G041500.2 | 4 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.007G084000.1 | 4 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.009G119100.1 | 4 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.006G102900.2 | 4 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.006G102900.1 | 4 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.010G079200.1 | 4 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.010G079200.2 | 4 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.008G127800.1 | 4 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.001G038000.1 | 4 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.002G105200.1 | 4 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.008G032900.1 | 4 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.009G244600.1 | 4 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.004G099100.1 | 4 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.002G157300.1 | 4 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.011G046800.1 | 4 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.006G023000.2 | 4 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.001G151600.1 | 4 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.007G231200.1 | 4 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.004G037600.2 | 4 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.004G037600.3 | 4 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.007G156900.1 | 4 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.007G157000.1 | 4 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.007G105700.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.008G159000.1 | 4 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.005G114000.1 | 4 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.001G031000.1 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.004G041500.1 | 4 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.004G041500.2 | 4 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.007G084000.1 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.009G119100.1 | 4 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.006G102900.2 | 4 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.006G102900.1 | 4 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.010G079200.1 | 4 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.010G079200.2 | 4 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.008G127800.1 | 4 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.001G038000.1 | 4 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.002G105200.1 | 4 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.008G032900.1 | 4 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.009G244600.1 | 4 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.004G099100.1 | 4 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.002G157300.1 | 4 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.011G046800.1 | 4 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.006G023000.2 | 4 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.001G151600.1 | 4 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.007G231200.1 | 4 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.004G037600.2 | 4 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.004G037600.3 | 4 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.007G156900.1 | 4 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.007G157000.1 | 4 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | uggagaagcagg Phvul.007G105700.1 | 4 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.008G159000.1 | 4 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.005G114000.1 | 4 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.001G031000.1 | 4 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.004G041500.1 | 4 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.004G041500.2 | 4 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.007G084000.1 | 4 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.009G119100.1 | 4 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.006G102900.2 | 4 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.006G102900.1 | 4 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.010G079200.1 | 4 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.010G079200.2 | 4 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.008G127800.1 | 4 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.001G038000.1 | 4 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.002G105200.1 | 4 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.008G032900.1 | 4 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.009G244600.1 | 4 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.004G099100.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.002G157300.1 | 4 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.011G046800.1 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.006G023000.2 | 4 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.001G151600.1 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.007G231200.1 | 4 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.004G037600.2 | 4 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.004G037600.3 | 4 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.007G156900.1 | 4 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.007G157000.1 | 4 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.007G105700.1 | 4 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.008G159000.1 | 4 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.005G114000.1 | 4 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.001G031000.1 | 4 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.004G041500.1 | 4 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.004G041500.2 | 4 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.007G084000.1 | 4 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.009G119100.1 | 4 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.006G102900.2 | 4 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.006G102900.1 | 4 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.010G079200.1 | 4 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.010G079200.2 | 4 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.008G127800.1 | 4 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.001G038000.1 | 4 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.002G105200.1 | 4 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.008G032900.1 | 4 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.009G244600.1 | 4 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.004G099100.1 | 4 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.002G157300.1 | 4 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.011G046800.1 | 4 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.006G023000.2 | 4 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.001G151600.1 | 4 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.007G231200.1 | 4 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.004G037600.2 | 4 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.004G037600.3 | 4 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.007G156900.1 | 4 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.007G157000.1 | 4 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.007G105700.1 | 4 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.008G159000.1 | 4 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.005G114000.1 | 4 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.001G031000.1 | 4 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.004G041500.1 | 4 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.004G041500.2 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.007G084000.1 | 4 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.009G119100.1 | 4 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.006G102900.2 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.006G102900.1 | 4 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.010G079200.1 | 4 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.010G079200.2 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.008G127800.1 | 4 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.001G038000.1 | 4 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.002G105200.1 | 4 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.008G032900.1 | 4 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.009G244600.1 | 4 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.004G099100.1 | 4 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.002G157300.1 | 4 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.011G046800.1 | 4 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.006G023000.2 | 4 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.001G151600.1 | 4 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.007G231200.1 | 4 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.004G037600.2 | 4 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.004G037600.3 | 4 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.007G156900.1 | 4 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.007G157000.1 | 4 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.007G105700.1 | 4 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.008G159000.1 | 4 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.005G114000.1 | 4 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.001G031000.1 | 4 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.004G041500.1 | 4 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.004G041500.2 | 4 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.007G084000.1 | 4 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.009G119100.1 | 4 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.006G102900.2 | 4 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.006G102900.1 | 4 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.010G079200.1 | 4 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.010G079200.2 | 4 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.008G127800.1 | 4 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.001G038000.1 | 4 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.002G105200.1 | 4 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.008G032900.1 | 4 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.009G244600.1 | 4 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.004G099100.1 | 4 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.002G157300.1 | 4 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.011G046800.1 | 4 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.006G023000.2 | 4 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.001G151600.1 | 4 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.007G231200.1 | 4 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.004G037600.2 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.004G037600.3 | 4 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.007G156900.1 | 4 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.007G157000.1 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.007G105700.1 | 4 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.008G159000.1 | 4 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.005G114000.1 | 4 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.001G031000.1 | 4 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.004G041500.1 | 4 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.004G041500.2 | 4 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.007G084000.1 | 4 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.009G119100.1 | 4 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.006G102900.2 | 4 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.006G102900.1 | 4 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.010G079200.1 | 4 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.010G079200.2 | 4 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.008G127800.1 | 4 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.001G038000.1 | 4 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.002G105200.1 | 4 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.008G032900.1 | 4 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.009G244600.1 | 4 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.004G099100.1 | 4 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.002G157300.1 | 4 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.011G046800.1 | 4 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.006G023000.2 | 4 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.001G151600.1 | 4 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.007G231200.1 | 4 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.004G037600.2 | 4 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.004G037600.3 | 4 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.007G156900.1 | 4 | -1 | 1 | 21 |
| 46 | uggagaagcagg Phvul.007G157000.1 | 4 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.007G105700.1 | 4 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.008G159000.1 | 4 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.005G114000.1 | 4 | -1 | 1 | 21 |
| 50 | uggagaagcagg Phvul.001G031000.1 | 4 | -1 | 1 | 21 |
| 51 | uggagaagcagg Phvul.004G041500.1 | 4 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.004G041500.2 | 4 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.007G084000.1 | 4 | -1 | 1 | 21 |
| 54 | uggagaagcagg Phvul.009G119100.1 | 4 | -1 | 1 | 21 |
| 55 | uggagaagcagg Phvul.006G102900.2 | 4 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.006G102900.1 | 4 | -1 | 1 | 21 |
| 57 | | | | | |
| 58 | uggagaagcagg Phvul.010G079200.1 | 4 | -1 | 1 | 21 |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.010G079200.2 | 4 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.008G127800.1 | 4 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.001G038000.1 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.002G105200.1 | 4 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.008G032900.1 | 4 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.009G244600.1 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.004G099100.1 | 4 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.002G157300.1 | 4 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.011G046800.1 | 4 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.006G023000.2 | 4 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.001G151600.1 | 4 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.007G231200.1 | 4 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.004G037600.2 | 4 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.004G037600.3 | 4 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.007G156900.1 | 4 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.007G157000.1 | 4 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.007G105700.1 | 4 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.008G159000.1 | 4 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.005G114000.1 | 4 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.001G031000.1 | 4 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.004G041500.1 | 4 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.004G041500.2 | 4 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.007G084000.1 | 4 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.009G119100.1 | 4 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.006G102900.2 | 4 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.006G102900.1 | 4 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | uggagaagcagg Phvul.010G079200.1 | 4 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.010G079200.2 | 4 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.008G127800.1 | 4 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.001G038000.1 | 4 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.002G105200.1 | 4 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.008G032900.1 | 4 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.009G244600.1 | 4 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.004G099100.1 | 4 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.002G157300.1 | 4 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.011G046800.1 | 4 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.006G023000.2 | 4 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.001G151600.1 | 4 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.007G231200.1 | 4 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.004G037600.2 | 4 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.004G037600.3 | 4 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.007G156900.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.007G157000.1 | 4 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.007G105700.1 | 4 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.008G159000.1 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.005G114000.1 | 4 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.001G031000.1 | 4 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.004G041500.1 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.004G041500.2 | 4 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.007G084000.1 | 4 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.009G119100.1 | 4 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.006G102900.2 | 4 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.006G102900.1 | 4 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.010G079200.1 | 4 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.010G079200.2 | 4 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.008G127800.1 | 4 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.001G038000.1 | 4 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.002G105200.1 | 4 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.008G032900.1 | 4 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.009G244600.1 | 4 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.004G099100.1 | 4 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.002G157300.1 | 4 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.011G046800.1 | 4 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.006G023000.2 | 4 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.001G151600.1 | 4 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.007G231200.1 | 4 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.004G037600.2 | 4 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.004G037600.3 | 4 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.007G156900.1 | 4 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.007G157000.1 | 4 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.007G105700.1 | 4 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.008G159000.1 | 4 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.005G114000.1 | 4 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.001G031000.1 | 4 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.004G041500.1 | 4 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.004G041500.2 | 4 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.007G084000.1 | 4 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.009G119100.1 | 4 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.006G102900.2 | 4 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.006G102900.1 | 4 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.010G079200.1 | 4 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.010G079200.2 | 4 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.008G127800.1 | 4 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.001G038000.1 | 4 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.002G105200.1 | 4 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.008G032900.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.009G244600.1 | 4 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.004G099100.1 | 4 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.002G157300.1 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.011G046800.1 | 4 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.006G023000.2 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.001G151600.1 | 4 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.007G231200.1 | 4 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.004G037600.2 | 4 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.004G037600.3 | 4 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.007G156900.1 | 4 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.007G157000.1 | 4 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.007G105700.1 | 4 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.008G159000.1 | 4 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.005G114000.1 | 4 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.001G031000.1 | 4 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.004G041500.1 | 4 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.004G041500.2 | 4 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.007G084000.1 | 4 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.009G119100.1 | 4 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.006G102900.2 | 4 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.006G102900.1 | 4 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.010G079200.1 | 4 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.010G079200.2 | 4 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.008G127800.1 | 4 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.001G038000.1 | 4 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.002G105200.1 | 4 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.008G032900.1 | 4 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.009G244600.1 | 4 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.004G099100.1 | 4 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.002G157300.1 | 4 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.011G046800.1 | 4 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.006G023000.2 | 4 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.001G151600.1 | 4 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.007G231200.1 | 4 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.004G037600.2 | 4 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.004G037600.3 | 4 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.007G156900.1 | 4 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.007G157000.1 | 4 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.007G105700.1 | 4 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.008G159000.1 | 4 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.005G114000.1 | 4 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.001G031000.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.004G041500.1 | 4 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.004G041500.2 | 4 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.007G084000.1 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.009G119100.1 | 4 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.006G102900.2 | 4 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.006G102900.1 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.010G079200.1 | 4 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.010G079200.2 | 4 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.008G127800.1 | 4 | -1 | 1 | 21 |
| 13 | uggagaagcagg Phvul.001G038000.1 | 4 | -1 | 1 | 21 |
| 14 | uggagaagcagg Phvul.002G105200.1 | 4 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.008G032900.1 | 4 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.008G032900.1 | 4 | -1 | 1 | 21 |
| 17 | uggagaagcagg Phvul.009G244600.1 | 4 | -1 | 1 | 21 |
| 18 | uggagaagcagg Phvul.009G244600.1 | 4 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.004G099100.1 | 4 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.002G157300.1 | 4 | -1 | 1 | 21 |
| 21 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 21 |
| 22 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.011G046800.1 | 4 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.006G023000.2 | 4 | -1 | 1 | 21 |
| 25 | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 21 |
| 26 | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.001G151600.1 | 4 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.007G231200.1 | 4 | -1 | 1 | 21 |
| 29 | uggagaagcagg Phvul.007G231200.1 | 4 | -1 | 1 | 21 |
| 30 | uggagaagcagg Phvul.004G037600.2 | 4 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.004G037600.3 | 4 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.007G156900.1 | 4 | -1 | 1 | 21 |
| 33 | uggagaagcagg Phvul.007G157000.1 | 4 | -1 | 1 | 21 |
| 34 | uggagaagcagg Phvul.007G157000.1 | 4 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.007G105700.1 | 4 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.008G159000.1 | 4 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.005G114000.1 | 4 | -1 | 1 | 21 |
| 38 | uggagaagcagg Phvul.005G114000.1 | 4 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.001G031000.1 | 4 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.004G041500.1 | 4 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.004G041500.2 | 4 | -1 | 1 | 21 |
| 42 | uggagaagcagg Phvul.004G041500.2 | 4 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.007G084000.1 | 4 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.009G119100.1 | 4 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.009G119100.1 | 4 | -1 | 1 | 21 |
| 46 | uggagaagcagg Phvul.006G102900.2 | 4 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.006G102900.1 | 4 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.010G079200.1 | 4 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.010G079200.2 | 4 | -1 | 1 | 21 |
| 50 | uggagaagcagg Phvul.010G079200.2 | 4 | -1 | 1 | 21 |
| 51 | uggagaagcagg Phvul.008G127800.1 | 4 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.008G127800.1 | 4 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.001G038000.1 | 4 | -1 | 1 | 21 |
| 54 | uggagaagcagg Phvul.002G105200.1 | 4 | -1 | 1 | 21 |
| 55 | uggagaagcagg Phvul.008G032900.1 | 4 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.008G032900.1 | 4 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.009G244600.1 | 4 | -1 | 1 | 21 |
| 58 | uggagaagcagg Phvul.004G099100.1 | 4 | -1 | 1 | 21 |
| 59 | uggagaagcagg Phvul.002G157300.1 | 4 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.011G046800.1 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.006G023000.2 | 4 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.001G151600.1 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.007G231200.1 | 4 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.004G037600.2 | 4 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.004G037600.3 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.007G156900.1 | 4 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.007G157000.1 | 4 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.007G105700.1 | 4 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.008G159000.1 | 4 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.005G114000.1 | 4 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.001G031000.1 | 4 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.004G041500.1 | 4 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.004G041500.2 | 4 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.007G084000.1 | 4 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.009G119100.1 | 4 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.006G102900.2 | 4 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.006G102900.1 | 4 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.010G079200.1 | 4 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.010G079200.2 | 4 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.008G127800.1 | 4 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.001G038000.1 | 4 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.002G105200.1 | 4 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.008G032900.1 | 4 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.009G244600.1 | 4 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.004G099100.1 | 4 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.002G157300.1 | 4 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.011G046800.1 | 4 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.006G023000.2 | 4 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.001G151600.1 | 4 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.007G231200.1 | 4 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.004G037600.2 | 4 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.004G037600.3 | 4 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.007G156900.1 | 4 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.007G157000.1 | 4 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.007G105700.1 | 4 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.008G159000.1 | 4 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.005G114000.1 | 4 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.001G031000.1 | 4 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.004G041500.1 | 4 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.004G041500.2 | 4 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.007G084000.1 | 4 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.009G119100.1 | 4 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.006G102900.2 | 4 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.006G102900.1 | 4 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.010G079200.1 | 4 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.010G079200.2 | 4 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.008G127800.1 | 4 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.001G038000.1 | 4 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.002G105200.1 | 4 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.008G032900.1 | 4 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.009G244600.1 | 4 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.007G105700.1 | 4 | -1 | 1 | 22 |
| 13 | uggagaagcagg Phvul.011G046800.1 | 4 | -1 | 1 | 22 |
| 14 | uggagaagcagg Phvul.006G102900.2 | 4 | -1 | 1 | 22 |
| 15 | uggagaagcagg Phvul.006G102900.1 | 4 | -1 | 1 | 22 |
| 16 | uggagaagcagg Phvul.006G102900.1 | 4 | -1 | 1 | 22 |
| 17 | uggagaagcagg Phvul.006G023000.2 | 4 | -1 | 1 | 22 |
| 18 | uggagaagcagg Phvul.004G099100.1 | 4 | -1 | 1 | 22 |
| 19 | uggagaagcagg Phvul.002G157300.1 | 4 | -1 | 1 | 22 |
| 20 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 22 |
| 21 | uggagaagcagg Phvul.009G146400.1 | 4 | -1 | 1 | 22 |
| 22 | uggagaagcagg Phvul.006G093600.1 | 4 | -1 | 1 | 22 |
| 23 | uggagaagcagg Phvul.001G151600.1 | 4 | -1 | 1 | 22 |
| 24 | uggagaagcagg Phvul.009G244600.1 | 4 | -1 | 1 | 22 |
| 25 | uggagaagcagg Phvul.009G121200.1 | 4 | -1 | 1 | 22 |
| 26 | uggagaagcagg Phvul.009G121200.2 | 4 | -1 | 1 | 22 |
| 27 | uggagaagcagg Phvul.007G156900.1 | 4 | -1 | 1 | 22 |
| 28 | uggagaagcagg Phvul.007G157000.1 | 4 | -1 | 1 | 22 |
| 29 | uggagaagcagg Phvul.008G159000.1 | 4 | -1 | 1 | 22 |
| 30 | uggagaagcagg Phvul.007G231200.1 | 4 | -1 | 1 | 22 |
| 31 | uggagaagcagg Phvul.004G037600.2 | 4 | -1 | 1 | 22 |
| 32 | uggagaagcagg Phvul.004G037600.3 | 4 | -1 | 1 | 22 |
| 33 | uggagaagcagg Phvul.005G114000.1 | 4 | -1 | 1 | 22 |
| 34 | uggagaagcagg Phvul.001G031000.1 | 4 | -1 | 1 | 22 |
| 35 | uggagaagcagg Phvul.004G041500.1 | 4 | -1 | 1 | 22 |
| 36 | uggagaagcagg Phvul.004G041500.2 | 4 | -1 | 1 | 22 |
| 37 | uggagaagcagg Phvul.002G105200.1 | 4 | -1 | 1 | 22 |
| 38 | uggagaagcagg Phvul.007G084000.1 | 4 | -1 | 1 | 22 |
| 39 | uggagaagcagg Phvul.009G119100.1 | 4 | -1 | 1 | 22 |
| 40 | uggagaagcagg Phvul.010G079200.1 | 4 | -1 | 1 | 22 |
| 41 | uggagaagcagg Phvul.010G079200.2 | 4 | -1 | 1 | 22 |
| 42 | uggagaagcagg Phvul.008G127800.1 | 4 | -1 | 1 | 22 |
| 43 | uggagaagcagg Phvul.007G029900.1 | 4 | -1 | 1 | 22 |
| 44 | uggagaagcagg Phvul.010G156200.1 | 4.5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.009G217000.1 | 4.5 | -1 | 1 | 21 |
| 46 | uggagaagcagg Phvul.008G043500.1 | 4.5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.009G079400.3 | 4.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.001G193000.3 | 4.5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.001G193000.4 | 4.5 | -1 | 1 | 21 |
| 50 | uggagaagcagg Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 51 | uggagaagcagg Phvul.009G030200.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.004G166100.1 | 4.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.009G160200.1 | 4.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.002G119600.1 | 4.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.002G150800.1 | 4.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.002G271400.1 | 4.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.011G166200.1 | 4.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.001G110100.1 | 4.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.002G037500.1 | 4.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.002G017700.2 | 4.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.002G017700.1 | 4.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.007G022500.3 | 4.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.010G115000.1 | 4.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.010G115000.2 | 4.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.006G154900.1 | 4.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.006G047000.1 | 4.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.005G001000.1 | 4.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.003G056900.1 | 4.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.003G056900.2 | 4.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.008G017200.1 | 4.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.008G017200.2 | 4.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.003G056900.3 | 4.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.007G106300.1 | 4.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.009G034400.1 | 4.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.L002444.2 | 4.5 | -1 | 1 | 21 |
| 33 | uggagaagcagg Phvul.L002444.1 | 4.5 | -1 | 1 | 21 |
| 34 | | | | | |
| 35 | uggagaagcagg Phvul.008G070000.1 | 4.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.010G156200.1 | 4.5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.009G217000.1 | 4.5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.008G043500.1 | 4.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.009G079400.3 | 4.5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.001G193000.3 | 4.5 | -1 | 1 | 21 |
| 42 | uggagaagcagg Phvul.001G193000.4 | 4.5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.009G030200.1 | 4.5 | -1 | 1 | 21 |
| 45 | | | | | |
| 46 | uggagaagcagg Phvul.004G166100.1 | 4.5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.009G160200.1 | 4.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.002G119600.1 | 4.5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.002G150800.1 | 4.5 | -1 | 1 | 21 |
| 50 | uggagaagcagg Phvul.002G271400.1 | 4.5 | -1 | 1 | 21 |
| 51 | uggagaagcagg Phvul.011G166200.1 | 4.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.001G110100.1 | 4.5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.002G037500.1 | 4.5 | -1 | 1 | 21 |
| 54 | uggagaagcagg Phvul.002G017700.2 | 4.5 | -1 | 1 | 21 |
| 55 | uggagaagcagg Phvul.002G017700.1 | 4.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.007G022500.3 | 4.5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.010G115000.1 | 4.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.007G022500.3 | 4.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.010G115000.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.010G115000.2 | 4.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.006G154900.1 | 4.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.006G047000.1 | 4.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.005G001000.1 | 4.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.003G056900.1 | 4.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.003G056900.2 | 4.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.008G017200.1 | 4.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.008G017200.2 | 4.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.003G056900.3 | 4.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.007G106300.1 | 4.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.009G034400.1 | 4.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.L002444.2 | 4.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.L002444.1 | 4.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.008G070000.1 | 4.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.010G156200.1 | 4.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.009G217000.1 | 4.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.008G043500.1 | 4.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.009G079400.3 | 4.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.001G193000.3 | 4.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.001G193000.4 | 4.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.009G030200.1 | 4.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.004G166100.1 | 4.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.009G160200.1 | 4.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.002G119600.1 | 4.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.002G150800.1 | 4.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.002G271400.1 | 4.5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.011G166200.1 | 4.5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.001G110100.1 | 4.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.002G037500.1 | 4.5 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.002G017700.2 | 4.5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.002G017700.1 | 4.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.007G022500.3 | 4.5 | -1 | 1 | 21 |
| 45 | | | | | |
| 46 | uggagaagcagg Phvul.010G115000.1 | 4.5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.010G115000.2 | 4.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.006G154900.1 | 4.5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.006G047000.1 | 4.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.005G001000.1 | 4.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.003G056900.1 | 4.5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.003G056900.2 | 4.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.008G017200.1 | 4.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.008G017200.2 | 4.5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.003G056900.3 | 4.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.007G106300.1 | 4.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.009G034400.1 | 4.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.L002444.2 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.L002444.1 | 4.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.008G070000.1 | 4.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.010G156200.1 | 4.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.009G217000.1 | 4.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.008G043500.1 | 4.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.009G079400.3 | 4.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.001G193000.3 | 4.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.001G193000.4 | 4.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.009G030200.1 | 4.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.004G166100.1 | 4.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.009G160200.1 | 4.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.002G119600.1 | 4.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.002G150800.1 | 4.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.002G271400.1 | 4.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.011G166200.1 | 4.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.001G110100.1 | 4.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.002G037500.1 | 4.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.002G017700.2 | 4.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.002G017700.1 | 4.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.007G022500.3 | 4.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.010G115000.1 | 4.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.010G115000.2 | 4.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.006G154900.1 | 4.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.006G047000.1 | 4.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.005G001000.1 | 4.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.003G056900.1 | 4.5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.003G056900.2 | 4.5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.008G017200.1 | 4.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.008G017200.2 | 4.5 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.003G056900.3 | 4.5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.007G106300.1 | 4.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.009G034400.1 | 4.5 | -1 | 1 | 21 |
| 45 | | | | | |
| 46 | uggagaagcagg Phvul.L002444.2 | 4.5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.L002444.1 | 4.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.008G070000.1 | 4.5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.010G156200.1 | 4.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.009G217000.1 | 4.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.008G043500.1 | 4.5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.009G079400.3 | 4.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.001G193000.3 | 4.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.001G193000.4 | 4.5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.009G030200.1 | 4.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.004G166100.1 | 4.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.009G160200.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.002G119600.1 | 4.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.002G150800.1 | 4.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.002G271400.1 | 4.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.011G166200.1 | 4.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.001G110100.1 | 4.5 | -1 | 1 | 21 |
| 8 | | | | | |
| 9 | uggagaagcagg Phvul.002G037500.1 | 4.5 | -1 | 1 | 21 |
| 10 | uggagaagcagg Phvul.002G017700.2 | 4.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.002G017700.1 | 4.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.007G022500.3 | 4.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.010G115000.1 | 4.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.010G115000.2 | 4.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.006G154900.1 | 4.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.006G047000.1 | 4.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.005G001000.1 | 4.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.003G056900.1 | 4.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.003G056900.2 | 4.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.008G017200.1 | 4.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.008G017200.2 | 4.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.003G056900.3 | 4.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.007G106300.1 | 4.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.009G034400.1 | 4.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.L002444.2 | 4.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.L002444.1 | 4.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.008G070000.1 | 4.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.010G156200.1 | 4.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.009G217000.1 | 4.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.008G043500.1 | 4.5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.009G079400.3 | 4.5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.001G193000.3 | 4.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.001G193000.4 | 4.5 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.009G030200.1 | 4.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.004G166100.1 | 4.5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.009G160200.1 | 4.5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.002G119600.1 | 4.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.002G150800.1 | 4.5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.002G271400.1 | 4.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.011G166200.1 | 4.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.001G110100.1 | 4.5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.002G037500.1 | 4.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.002G017700.2 | 4.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.002G017700.1 | 4.5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.007G022500.3 | 4.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.010G115000.1 | 4.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.010G115000.2 | 4.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.006G154900.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.006G047000.1 | 4.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.005G001000.1 | 4.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.003G056900.1 | 4.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.003G056900.2 | 4.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.008G017200.1 | 4.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.008G017200.2 | 4.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.003G056900.3 | 4.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.007G106300.1 | 4.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.009G034400.1 | 4.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.L002444.2 | 4.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.L002444.1 | 4.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.008G070000.1 | 4.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.010G156200.1 | 4.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.009G217000.1 | 4.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.008G043500.1 | 4.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.009G079400.3 | 4.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.001G193000.3 | 4.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.001G193000.4 | 4.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.009G030200.1 | 4.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.004G166100.1 | 4.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.009G160200.1 | 4.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.002G119600.1 | 4.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.002G150800.1 | 4.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.002G271400.1 | 4.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.011G166200.1 | 4.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.001G110100.1 | 4.5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.002G037500.1 | 4.5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.002G017700.2 | 4.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.002G017700.1 | 4.5 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.007G022500.3 | 4.5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.010G115000.1 | 4.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.010G115000.2 | 4.5 | -1 | 1 | 21 |
| 45 | | | | | |
| 46 | uggagaagcagg Phvul.006G154900.1 | 4.5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.006G047000.1 | 4.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.005G001000.1 | 4.5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.003G056900.1 | 4.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.003G056900.2 | 4.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.008G017200.1 | 4.5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.008G017200.2 | 4.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.003G056900.3 | 4.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.007G106300.1 | 4.5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.009G034400.1 | 4.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.L002444.2 | 4.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.L002444.1 | 4.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.008G070000.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.010G156200.1 | 4.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.009G217000.1 | 4.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.008G043500.1 | 4.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.009G079400.3 | 4.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.001G193000.3 | 4.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.001G193000.4 | 4.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.009G030200.1 | 4.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.004G166100.1 | 4.5 | -1 | 1 | 21 |
| 13 | uggagaagcagg Phvul.009G160200.1 | 4.5 | -1 | 1 | 21 |
| 14 | uggagaagcagg Phvul.002G119600.1 | 4.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.002G150800.1 | 4.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.002G150800.1 | 4.5 | -1 | 1 | 21 |
| 17 | uggagaagcagg Phvul.002G271400.1 | 4.5 | -1 | 1 | 21 |
| 18 | uggagaagcagg Phvul.011G166200.1 | 4.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.001G110100.1 | 4.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.002G037500.1 | 4.5 | -1 | 1 | 21 |
| 21 | uggagaagcagg Phvul.002G037500.1 | 4.5 | -1 | 1 | 21 |
| 22 | uggagaagcagg Phvul.002G017700.2 | 4.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.002G017700.1 | 4.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.007G022500.3 | 4.5 | -1 | 1 | 21 |
| 25 | uggagaagcagg Phvul.010G115000.1 | 4.5 | -1 | 1 | 21 |
| 26 | uggagaagcagg Phvul.010G115000.2 | 4.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.010G115000.2 | 4.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.006G154900.1 | 4.5 | -1 | 1 | 21 |
| 29 | uggagaagcagg Phvul.006G047000.1 | 4.5 | -1 | 1 | 21 |
| 30 | uggagaagcagg Phvul.006G047000.1 | 4.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.005G001000.1 | 4.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.003G056900.1 | 4.5 | -1 | 1 | 21 |
| 33 | uggagaagcagg Phvul.003G056900.1 | 4.5 | -1 | 1 | 21 |
| 34 | uggagaagcagg Phvul.003G056900.2 | 4.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.008G017200.1 | 4.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.008G017200.1 | 4.5 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.008G017200.2 | 4.5 | -1 | 1 | 21 |
| 38 | uggagaagcagg Phvul.008G017200.2 | 4.5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.003G056900.3 | 4.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.007G106300.1 | 4.5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.009G034400.1 | 4.5 | -1 | 1 | 21 |
| 42 | uggagaagcagg Phvul.009G034400.1 | 4.5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.L002444.2 | 4.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.L002444.1 | 4.5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.008G070000.1 | 4.5 | -1 | 1 | 21 |
| 46 | uggagaagcagg Phvul.010G156200.1 | 4.5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.010G156200.1 | 4.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.009G217000.1 | 4.5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.008G043500.1 | 4.5 | -1 | 1 | 21 |
| 50 | uggagaagcagg Phvul.008G043500.1 | 4.5 | -1 | 1 | 21 |
| 51 | uggagaagcagg Phvul.009G079400.3 | 4.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.001G193000.3 | 4.5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.001G193000.4 | 4.5 | -1 | 1 | 21 |
| 54 | uggagaagcagg Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 55 | uggagaagcagg Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.009G030200.1 | 4.5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.004G166100.1 | 4.5 | -1 | 1 | 21 |
| 58 | uggagaagcagg Phvul.004G166100.1 | 4.5 | -1 | 1 | 21 |
| 59 | uggagaagcagg Phvul.009G160200.1 | 4.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.002G119600.1 | 4.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.002G150800.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.002G271400.1 | 4.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.011G166200.1 | 4.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.001G110100.1 | 4.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.002G037500.1 | 4.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.002G017700.2 | 4.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.002G017700.1 | 4.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.007G022500.3 | 4.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.010G115000.1 | 4.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.010G115000.2 | 4.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.006G154900.1 | 4.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.006G047000.1 | 4.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.005G001000.1 | 4.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.003G056900.1 | 4.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.003G056900.2 | 4.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.008G017200.1 | 4.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.008G017200.2 | 4.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.003G056900.3 | 4.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.007G106300.1 | 4.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.009G034400.1 | 4.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.L002444.2 | 4.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.L002444.1 | 4.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.008G070000.1 | 4.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.010G156200.1 | 4.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.009G217000.1 | 4.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.008G043500.1 | 4.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.009G079400.3 | 4.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.001G193000.3 | 4.5 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.001G193000.4 | 4.5 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | uggagaagcagg Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.009G030200.1 | 4.5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.004G166100.1 | 4.5 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.009G160200.1 | 4.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.002G119600.1 | 4.5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.002G150800.1 | 4.5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.002G271400.1 | 4.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.011G166200.1 | 4.5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.001G110100.1 | 4.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.002G037500.1 | 4.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.002G017700.2 | 4.5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.002G017700.1 | 4.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.007G022500.3 | 4.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.010G115000.1 | 4.5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.010G115000.2 | 4.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.006G154900.1 | 4.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.006G047000.1 | 4.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.005G001000.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.003G056900.1 | 4.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.003G056900.2 | 4.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.008G017200.1 | 4.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.008G017200.2 | 4.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.003G056900.3 | 4.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.007G106300.1 | 4.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.009G034400.1 | 4.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.L002444.2 | 4.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.L002444.1 | 4.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.008G070000.1 | 4.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.010G156200.1 | 4.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.009G217000.1 | 4.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.008G043500.1 | 4.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.009G079400.3 | 4.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.001G193000.3 | 4.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.001G193000.4 | 4.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.009G030200.1 | 4.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.004G166100.1 | 4.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.009G160200.1 | 4.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.002G119600.1 | 4.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.002G150800.1 | 4.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.002G271400.1 | 4.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.011G166200.1 | 4.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.001G110100.1 | 4.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.002G037500.1 | 4.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.002G017700.2 | 4.5 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.002G017700.1 | 4.5 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | uggagaagcagg Phvul.007G022500.3 | 4.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.010G115000.1 | 4.5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.010G115000.2 | 4.5 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.006G154900.1 | 4.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.006G047000.1 | 4.5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.005G001000.1 | 4.5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.003G056900.1 | 4.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.003G056900.2 | 4.5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.008G017200.1 | 4.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.008G017200.2 | 4.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.003G056900.3 | 4.5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.007G106300.1 | 4.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.009G034400.1 | 4.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.L002444.2 | 4.5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.L002444.1 | 4.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.008G070000.1 | 4.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.010G156200.1 | 4.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.009G217000.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.008G043500.1 | 4.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.009G079400.3 | 4.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.001G193000.3 | 4.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.001G193000.4 | 4.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 8 | | | | | |
| 9 | uggagaagcagg Phvul.009G030200.1 | 4.5 | -1 | 1 | 21 |
| 10 | uggagaagcagg Phvul.004G166100.1 | 4.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.009G160200.1 | 4.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.002G119600.1 | 4.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.002G150800.1 | 4.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.002G271400.1 | 4.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.011G166200.1 | 4.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.001G110100.1 | 4.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.002G037500.1 | 4.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.002G017700.2 | 4.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.002G017700.1 | 4.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.007G022500.3 | 4.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.010G115000.1 | 4.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.010G115000.2 | 4.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.006G154900.1 | 4.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.006G047000.1 | 4.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.005G001000.1 | 4.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.003G056900.1 | 4.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.003G056900.2 | 4.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.008G017200.1 | 4.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.008G017200.2 | 4.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.003G056900.3 | 4.5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.007G106300.1 | 4.5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.009G034400.1 | 4.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.L002444.2 | 4.5 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.L002444.1 | 4.5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.008G070000.1 | 4.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.010G156200.1 | 4.5 | -1 | 1 | 21 |
| 45 | | | | | |
| 46 | uggagaagcagg Phvul.009G217000.1 | 4.5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.008G043500.1 | 4.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.009G079400.3 | 4.5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.001G193000.3 | 4.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.001G193000.4 | 4.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.009G030200.1 | 4.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.004G166100.1 | 4.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.009G160200.1 | 4.5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.002G119600.1 | 4.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.002G150800.1 | 4.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.002G271400.1 | 4.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.011G166200.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.001G110100.1 | 4.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.002G037500.1 | 4.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.002G017700.2 | 4.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.002G017700.1 | 4.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.007G022500.3 | 4.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.010G115000.1 | 4.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.010G115000.2 | 4.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.006G154900.1 | 4.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.006G047000.1 | 4.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.005G001000.1 | 4.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.003G056900.1 | 4.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.003G056900.2 | 4.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.008G017200.1 | 4.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.008G017200.2 | 4.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.003G056900.3 | 4.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.007G106300.1 | 4.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.009G034400.1 | 4.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.L002444.2 | 4.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.L002444.1 | 4.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.008G070000.1 | 4.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.010G156200.1 | 4.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.009G217000.1 | 4.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.008G043500.1 | 4.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.009G079400.3 | 4.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.001G193000.3 | 4.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.001G193000.4 | 4.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.009G030200.1 | 4.5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.004G166100.1 | 4.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.009G160200.1 | 4.5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.002G119600.1 | 4.5 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.002G150800.1 | 4.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.002G271400.1 | 4.5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.011G166200.1 | 4.5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.001G110100.1 | 4.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.002G037500.1 | 4.5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.002G017700.2 | 4.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.002G017700.1 | 4.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.007G022500.3 | 4.5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.010G115000.1 | 4.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.010G115000.2 | 4.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.006G154900.1 | 4.5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.006G047000.1 | 4.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.005G001000.1 | 4.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.003G056900.1 | 4.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.003G056900.2 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.008G017200.1 | 4.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.008G017200.2 | 4.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.003G056900.3 | 4.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.007G106300.1 | 4.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.009G034400.1 | 4.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.L002444.2 | 4.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.L002444.1 | 4.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.008G070000.1 | 4.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.010G156200.1 | 4.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.009G217000.1 | 4.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.008G043500.1 | 4.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.009G079400.3 | 4.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.001G193000.3 | 4.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.001G193000.4 | 4.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.009G030200.1 | 4.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.004G166100.1 | 4.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.009G160200.1 | 4.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.002G119600.1 | 4.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.002G150800.1 | 4.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.002G271400.1 | 4.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.011G166200.1 | 4.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.001G110100.1 | 4.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.002G037500.1 | 4.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.002G017700.2 | 4.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.002G017700.1 | 4.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.007G022500.3 | 4.5 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.010G115000.1 | 4.5 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | uggagaagcagg Phvul.010G115000.2 | 4.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.006G154900.1 | 4.5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.006G047000.1 | 4.5 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.005G001000.1 | 4.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.003G056900.1 | 4.5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.003G056900.2 | 4.5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.008G017200.1 | 4.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.008G017200.2 | 4.5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.003G056900.3 | 4.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.007G106300.1 | 4.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.009G034400.1 | 4.5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.L002444.2 | 4.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.L002444.1 | 4.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.008G070000.1 | 4.5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.010G156200.1 | 4.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.009G217000.1 | 4.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.008G043500.1 | 4.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.009G079400.3 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.001G193000.3 | 4.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.001G193000.4 | 4.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.009G030200.1 | 4.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.004G166100.1 | 4.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.009G160200.1 | 4.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.002G119600.1 | 4.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.002G150800.1 | 4.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.002G271400.1 | 4.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.011G166200.1 | 4.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.001G110100.1 | 4.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.002G037500.1 | 4.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.002G017700.2 | 4.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.002G017700.1 | 4.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.007G022500.3 | 4.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.010G115000.1 | 4.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.010G115000.2 | 4.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.006G154900.1 | 4.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.006G047000.1 | 4.5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.005G001000.1 | 4.5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.003G056900.1 | 4.5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.003G056900.2 | 4.5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.008G017200.1 | 4.5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.008G017200.2 | 4.5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.003G056900.3 | 4.5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.007G106300.1 | 4.5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.009G034400.1 | 4.5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.L002444.2 | 4.5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.L002444.1 | 4.5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.008G070000.1 | 4.5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.010G156200.1 | 4.5 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.009G217000.1 | 4.5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.008G043500.1 | 4.5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.009G079400.3 | 4.5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.001G193000.3 | 4.5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.001G193000.4 | 4.5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.003G154400.1 | 4.5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.009G030200.1 | 4.5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.004G166100.1 | 4.5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.009G160200.1 | 4.5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.002G119600.1 | 4.5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.002G150800.1 | 4.5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.002G271400.1 | 4.5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.011G166200.1 | 4.5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.001G110100.1 | 4.5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.002G037500.1 | 4.5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|-----|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.002G017700.2 | 4.5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.002G017700.1 | 4.5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.007G022500.3 | 4.5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.010G115000.1 | 4.5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.010G115000.2 | 4.5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.006G154900.1 | 4.5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.006G047000.1 | 4.5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.005G001000.1 | 4.5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.003G056900.1 | 4.5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.003G056900.2 | 4.5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.008G017200.1 | 4.5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.008G017200.2 | 4.5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.003G056900.3 | 4.5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.007G106300.1 | 4.5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.009G034400.1 | 4.5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.L002444.2 | 4.5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.L002444.1 | 4.5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.008G070000.1 | 4.5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.010G156200.1 | 4.5 | -1 | 1 | 22 |
| 27 | uggagaagcagg Phvul.009G160200.1 | 4.5 | -1 | 1 | 22 |
| 28 | uggagaagcagg Phvul.009G217000.1 | 4.5 | -1 | 1 | 22 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.007G022500.3 | 4.5 | -1 | 1 | 22 |
| 31 | uggagaagcagg Phvul.008G043500.1 | 4.5 | -1 | 1 | 22 |
| 32 | uggagaagcagg Phvul.009G079400.3 | 4.5 | -1 | 1 | 22 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.001G193000.3 | 4.5 | -1 | 1 | 22 |
| 35 | uggagaagcagg Phvul.001G193000.4 | 4.5 | -1 | 1 | 22 |
| 36 | uggagaagcagg Phvul.009G167700.2 | 4.5 | -1 | 1 | 22 |
| 37 | uggagaagcagg Phvul.003G154400.1 | 4.5 | -1 | 1 | 22 |
| 38 | | | | | |
| 39 | uggagaagcagg Phvul.L003746.2 | 4.5 | -1 | 1 | 22 |
| 40 | uggagaagcagg Phvul.L003746.1 | 4.5 | -1 | 1 | 22 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.009G030200.1 | 4.5 | -1 | 1 | 22 |
| 43 | uggagaagcagg Phvul.004G166100.1 | 4.5 | -1 | 1 | 22 |
| 44 | uggagaagcagg Phvul.002G119600.1 | 4.5 | -1 | 1 | 22 |
| 45 | uggagaagcagg Phvul.002G150800.1 | 4.5 | -1 | 1 | 22 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.002G271400.1 | 4.5 | -1 | 1 | 22 |
| 48 | uggagaagcagg Phvul.011G166200.1 | 4.5 | -1 | 1 | 22 |
| 49 | uggagaagcagg Phvul.006G067900.1 | 4.5 | -1 | 1 | 22 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.001G110100.1 | 4.5 | -1 | 1 | 22 |
| 52 | uggagaagcagg Phvul.002G037500.1 | 4.5 | -1 | 1 | 22 |
| 53 | uggagaagcagg Phvul.010G115000.1 | 4.5 | -1 | 1 | 22 |
| 54 | uggagaagcagg Phvul.010G115000.2 | 4.5 | -1 | 1 | 22 |
| 55 | uggagaagcagg Phvul.002G157000.1 | 4.5 | -1 | 1 | 22 |
| 56 | | | | | |
| 57 | uggagaagcagg Phvul.009G222600.1 | 5 | -1 | 1 | 21 |
| 58 | uggagaagcagg Phvul.002G106900.1 | 5 | -1 | 1 | 21 |
| 59 | uggagaagcagg Phvul.005G099500.1 | 5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.003G181900.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.003G181900.2 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.003G121200.1 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.003G121200.2 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.006G075600.1 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.008G284900.1 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.007G163400.1 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.001G266600.1 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.006G091100.2 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.006G091100.1 | 5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.003G037500.1 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.009G007300.1 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.003G100200.1 | 5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.003G100200.2 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.002G262600.1 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.002G262600.2 | 5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.002G299004.1 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.002G299004.3 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.007G156200.1 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.005G001000.1 | 5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.008G243700.1 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.007G201400.1 | 5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.003G181600.1 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.006G164800.1 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.005G059700.1 | 5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.005G059500.1 | 5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.002G116800.1 | 5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.008G103100.1 | 5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.008G075300.1 | 5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.003G262800.1 | 5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.008G072300.1 | 5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.008G072300.2 | 5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.004G088300.1 | 5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.004G088300.3 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.004G088300.2 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.009G201600.1 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.005G155100.1 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.005G155100.3 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.009G201600.2 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.004G088300.4 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.009G222600.1 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.002G106900.1 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.005G099500.1 | 5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.003G181900.1 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.003G181900.2 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.003G121200.1 | 5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.003G121200.2 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.006G075600.1 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.008G284900.1 | 5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.007G163400.1 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.001G266600.1 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.006G091100.2 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.006G091100.1 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.003G037500.1 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.009G007300.1 | 5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.003G100200.1 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.003G100200.2 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.002G262600.1 | 5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.002G262600.2 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.002G299004.1 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.002G299004.3 | 5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.007G156200.1 | 5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.005G001000.1 | 5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.008G243700.1 | 5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.007G201400.1 | 5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.003G181600.1 | 5 | -1 | 1 | 21 |
| 53 | | | | | |
| 54 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 55 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.006G164800.1 | 5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.005G059700.1 | 5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.005G059500.1 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.002G116800.1 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.008G103100.1 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.008G075300.1 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.003G262800.1 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.008G072300.1 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.008G072300.2 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.004G088300.1 | 5 | -1 | 1 | 21 |
| 13 | uggagaagcagg Phvul.004G088300.3 | 5 | -1 | 1 | 21 |
| 14 | uggagaagcagg Phvul.004G088300.2 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.009G201600.1 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.005G155100.1 | 5 | -1 | 1 | 21 |
| 17 | uggagaagcagg Phvul.005G155100.3 | 5 | -1 | 1 | 21 |
| 18 | uggagaagcagg Phvul.009G201600.2 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.004G088300.4 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.009G222600.1 | 5 | -1 | 1 | 21 |
| 21 | uggagaagcagg Phvul.002G106900.1 | 5 | -1 | 1 | 21 |
| 22 | uggagaagcagg Phvul.005G099500.1 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.003G181900.1 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.003G181900.2 | 5 | -1 | 1 | 21 |
| 25 | uggagaagcagg Phvul.003G121200.1 | 5 | -1 | 1 | 21 |
| 26 | uggagaagcagg Phvul.003G121200.2 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.006G075600.1 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.008G284900.1 | 5 | -1 | 1 | 21 |
| 29 | uggagaagcagg Phvul.007G163400.1 | 5 | -1 | 1 | 21 |
| 30 | uggagaagcagg Phvul.001G266600.1 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.006G091100.2 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.006G091100.1 | 5 | -1 | 1 | 21 |
| 33 | uggagaagcagg Phvul.003G037500.1 | 5 | -1 | 1 | 21 |
| 34 | uggagaagcagg Phvul.009G007300.1 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.003G100200.1 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.003G100200.2 | 5 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.002G262600.1 | 5 | -1 | 1 | 21 |
| 38 | uggagaagcagg Phvul.002G262600.2 | 5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.002G299004.1 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.002G299004.3 | 5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.007G156200.1 | 5 | -1 | 1 | 21 |
| 42 | uggagaagcagg Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.005G001000.1 | 5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 46 | uggagaagcagg Phvul.008G243700.1 | 5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.007G201400.1 | 5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.003G181600.1 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.006G164800.1 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.005G059700.1 | 5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.005G059500.1 | 5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.002G116800.1 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.008G103100.1 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.008G075300.1 | 5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.003G262800.1 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.008G072300.1 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.008G072300.2 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.004G088300.1 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.004G088300.3 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.004G088300.2 | 5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.009G201600.1 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.005G155100.1 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.005G155100.3 | 5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.009G201600.2 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.004G088300.4 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.009G222600.1 | 5 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.002G106900.1 | 5 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | uggagaagcagg Phvul.005G099500.1 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.003G181900.1 | 5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.003G181900.2 | 5 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.003G121200.1 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.003G121200.2 | 5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.006G075600.1 | 5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.008G284900.1 | 5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.007G163400.1 | 5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.001G266600.1 | 5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.006G091100.2 | 5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.006G091100.1 | 5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.003G037500.1 | 5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.009G007300.1 | 5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.003G100200.1 | 5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.003G100200.2 | 5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.002G262600.1 | 5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.002G262600.2 | 5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.002G299004.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.002G299004.3 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.007G156200.1 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.005G001000.1 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.008G243700.1 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.007G201400.1 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 13 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 14 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.003G181600.1 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.006G164800.1 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.005G059700.1 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.005G059500.1 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.002G116800.1 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.008G103100.1 | 5 | -1 | 1 | 21 |
| 33 | uggagaagcagg Phvul.008G075300.1 | 5 | -1 | 1 | 21 |
| 34 | uggagaagcagg Phvul.003G262800.1 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.008G072300.1 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.008G072300.2 | 5 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.008G072300.2 | 5 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | uggagaagcagg Phvul.004G088300.1 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.004G088300.3 | 5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.004G088300.2 | 5 | -1 | 1 | 21 |
| 42 | uggagaagcagg Phvul.009G201600.1 | 5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.005G155100.1 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.005G155100.3 | 5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.009G201600.2 | 5 | -1 | 1 | 21 |
| 46 | uggagaagcagg Phvul.004G088300.4 | 5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.009G222600.1 | 5 | -1 | 1 | 21 |
| 48 | | | | | |
| 49 | uggagaagcagg Phvul.002G106900.1 | 5 | -1 | 1 | 21 |
| 50 | uggagaagcagg Phvul.005G099500.1 | 5 | -1 | 1 | 21 |
| 51 | uggagaagcagg Phvul.003G181900.1 | 5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.003G181900.2 | 5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.003G121200.1 | 5 | -1 | 1 | 21 |
| 54 | uggagaagcagg Phvul.003G121200.2 | 5 | -1 | 1 | 21 |
| 55 | uggagaagcagg Phvul.006G075600.1 | 5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.008G284900.1 | 5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.007G163400.1 | 5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.001G266600.1 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.006G091100.2 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.006G091100.1 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.003G037500.1 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.009G007300.1 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.003G100200.1 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.003G100200.2 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.002G262600.1 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.002G262600.2 | 5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.002G299004.1 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.002G299004.3 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.007G156200.1 | 5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.005G001000.1 | 5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.008G243700.1 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.007G201400.1 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.003G181600.1 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 33 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 34 | | | | | |
| 35 | uggagaagcagg Phvul.006G164800.1 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | uggagaagcagg Phvul.005G059700.1 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.005G059500.1 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.002G116800.1 | 5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.008G103100.1 | 5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.008G075300.1 | 5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.003G262800.1 | 5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.008G072300.1 | 5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.008G072300.2 | 5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.004G088300.1 | 5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.004G088300.3 | 5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.004G088300.2 | 5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.009G201600.1 | 5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.005G155100.1 | 5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.005G155100.3 | 5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.009G201600.2 | 5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.004G088300.4 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.009G222600.1 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.002G106900.1 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.005G099500.1 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.003G181900.1 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.003G181900.2 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.003G121200.1 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.003G121200.2 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.006G075600.1 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.008G284900.1 | 5 | -1 | 1 | 21 |
| 13 | uggagaagcagg Phvul.007G163400.1 | 5 | -1 | 1 | 21 |
| 14 | uggagaagcagg Phvul.001G266600.1 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.006G091100.2 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.006G091100.1 | 5 | -1 | 1 | 21 |
| 17 | uggagaagcagg Phvul.006G091100.1 | 5 | -1 | 1 | 21 |
| 18 | uggagaagcagg Phvul.003G037500.1 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.009G007300.1 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.003G100200.1 | 5 | -1 | 1 | 21 |
| 21 | uggagaagcagg Phvul.003G100200.2 | 5 | -1 | 1 | 21 |
| 22 | uggagaagcagg Phvul.003G100200.2 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.002G262600.1 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.002G262600.2 | 5 | -1 | 1 | 21 |
| 25 | uggagaagcagg Phvul.002G299004.1 | 5 | -1 | 1 | 21 |
| 26 | uggagaagcagg Phvul.002G299004.3 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.002G299004.3 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.007G156200.1 | 5 | -1 | 1 | 21 |
| 29 | uggagaagcagg Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 30 | uggagaagcagg Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.005G001000.1 | 5 | -1 | 1 | 21 |
| 33 | uggagaagcagg Phvul.005G001000.1 | 5 | -1 | 1 | 21 |
| 34 | uggagaagcagg Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.008G243700.1 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.007G201400.1 | 5 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.007G201400.1 | 5 | -1 | 1 | 21 |
| 38 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 42 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.003G181600.1 | 5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 46 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.006G164800.1 | 5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 50 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 51 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.005G059700.1 | 5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 54 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 55 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.005G059500.1 | 5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.002G116800.1 | 5 | -1 | 1 | 21 |
| 58 | uggagaagcagg Phvul.002G116800.1 | 5 | -1 | 1 | 21 |
| 59 | uggagaagcagg Phvul.008G103100.1 | 5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.008G075300.1 | 5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.003G262800.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.008G072300.1 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.008G072300.2 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.004G088300.1 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.004G088300.3 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.004G088300.2 | 5 | -1 | 1 | 21 |
| 8 | | | | | |
| 9 | uggagaagcagg Phvul.009G201600.1 | 5 | -1 | 1 | 21 |
| 10 | uggagaagcagg Phvul.005G155100.1 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.005G155100.3 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.009G201600.2 | 5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.004G088300.4 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.009G222600.1 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.002G106900.1 | 5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.005G099500.1 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.003G181900.1 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.003G181900.2 | 5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.003G121200.1 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.003G121200.2 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.006G075600.1 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.008G284900.1 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.007G163400.1 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.001G266600.1 | 5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.006G091100.2 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.006G091100.1 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.003G037500.1 | 5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.009G007300.1 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.003G100200.1 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.003G100200.2 | 5 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.002G262600.1 | 5 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | uggagaagcagg Phvul.002G262600.2 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.002G299004.1 | 5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.002G299004.3 | 5 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.007G156200.1 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.005G001000.1 | 5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.008G243700.1 | 5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.007G201400.1 | 5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.003G181600.1 | 5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.006G164800.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.005G059700.1 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.005G059500.1 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.002G116800.1 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.008G103100.1 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.008G075300.1 | 5 | -1 | 1 | 21 |
| 13 | uggagaagcagg Phvul.003G262800.1 | 5 | -1 | 1 | 21 |
| 14 | uggagaagcagg Phvul.003G262800.1 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.008G072300.1 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.008G072300.2 | 5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.004G088300.1 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.004G088300.3 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.004G088300.2 | 5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.009G201600.1 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.005G155100.1 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.005G155100.3 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.009G201600.2 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.004G088300.4 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.009G222600.1 | 5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.002G106900.1 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.005G099500.1 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.003G181900.1 | 5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.003G181900.2 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.003G121200.1 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.003G121200.2 | 5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.006G075600.1 | 5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.008G284900.1 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.007G163400.1 | 5 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.001G266600.1 | 5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.006G091100.2 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.006G091100.1 | 5 | -1 | 1 | 21 |
| 45 | | | | | |
| 46 | uggagaagcagg Phvul.003G037500.1 | 5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.009G007300.1 | 5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.003G100200.1 | 5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.003G100200.2 | 5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.002G262600.1 | 5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.002G262600.2 | 5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.002G299004.1 | 5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.002G299004.3 | 5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.007G156200.1 | 5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.005G001000.1 | 5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.002G006400.2 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.008G243700.1 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.007G201400.1 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.003G181600.1 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.006G164800.1 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.005G059700.1 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.005G059500.1 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.002G116800.1 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.008G103100.1 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.008G075300.1 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.003G262800.1 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.008G072300.1 | 5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.008G072300.2 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.004G088300.1 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.004G088300.3 | 5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.004G088300.2 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.009G201600.1 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.005G155100.1 | 5 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.005G155100.3 | 5 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | uggagaagcagg Phvul.009G201600.2 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.004G088300.4 | 5 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.009G222600.1 | 5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.002G106900.1 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.005G099500.1 | 5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.003G181900.1 | 5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.003G181900.2 | 5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.003G121200.1 | 5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.003G121200.2 | 5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.006G075600.1 | 5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.008G284900.1 | 5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.007G163400.1 | 5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.001G266600.1 | 5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.006G091100.2 | 5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.006G091100.1 | 5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.003G037500.1 | 5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.009G007300.1 | 5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.003G100200.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.003G100200.2 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.002G262600.1 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.002G262600.2 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.002G299004.1 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.002G299004.3 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.007G156200.1 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.005G001000.1 | 5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.008G243700.1 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.007G201400.1 | 5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.003G181600.1 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.006G164800.1 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.005G059700.1 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.005G059500.1 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.002G116800.1 | 5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.008G103100.1 | 5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.008G075300.1 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.003G262800.1 | 5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.008G072300.1 | 5 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.008G072300.2 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.004G088300.1 | 5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.004G088300.3 | 5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.004G088300.2 | 5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.009G201600.1 | 5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.005G155100.1 | 5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.005G155100.3 | 5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.009G201600.2 | 5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.004G088300.4 | 5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.009G222600.1 | 5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.002G106900.1 | 5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.005G099500.1 | 5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.003G181900.1 | 5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.003G181900.2 | 5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.003G121200.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.003G121200.2 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.006G075600.1 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.008G284900.1 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.007G163400.1 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.001G266600.1 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.006G091100.2 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.006G091100.1 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.003G037500.1 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.009G007300.1 | 5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.003G100200.1 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.003G100200.2 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.002G262600.1 | 5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.002G262600.2 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.002G299004.1 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.002G299004.3 | 5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.007G156200.1 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.005G001000.1 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.008G243700.1 | 5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.007G201400.1 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.003G181600.1 | 5 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.006G164800.1 | 5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 42 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.005G059700.1 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 45 | | | | | |
| 46 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.005G059500.1 | 5 | -1 | 1 | 21 |
| 48 | | | | | |
| 49 | uggagaagcagg Phvul.002G116800.1 | 5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.008G103100.1 | 5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.008G075300.1 | 5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.003G262800.1 | 5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.008G072300.1 | 5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.008G072300.2 | 5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.004G088300.1 | 5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.004G088300.3 | 5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.004G088300.2 | 5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.009G201600.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.005G155100.1 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.005G155100.3 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.009G201600.2 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.004G088300.4 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.009G222600.1 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.002G106900.1 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.005G099500.1 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.003G181900.1 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.003G181900.2 | 5 | -1 | 1 | 21 |
| 13 | uggagaagcagg Phvul.003G121200.1 | 5 | -1 | 1 | 21 |
| 14 | uggagaagcagg Phvul.003G121200.2 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.006G075600.1 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.008G284900.1 | 5 | -1 | 1 | 21 |
| 17 | uggagaagcagg Phvul.007G163400.1 | 5 | -1 | 1 | 21 |
| 18 | uggagaagcagg Phvul.001G266600.1 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.006G091100.2 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.006G091100.1 | 5 | -1 | 1 | 21 |
| 21 | uggagaagcagg Phvul.003G037500.1 | 5 | -1 | 1 | 21 |
| 22 | uggagaagcagg Phvul.009G007300.1 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.003G100200.1 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.003G100200.2 | 5 | -1 | 1 | 21 |
| 25 | uggagaagcagg Phvul.002G262600.1 | 5 | -1 | 1 | 21 |
| 26 | uggagaagcagg Phvul.002G262600.2 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.002G299004.1 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.002G299004.3 | 5 | -1 | 1 | 21 |
| 29 | uggagaagcagg Phvul.007G156200.1 | 5 | -1 | 1 | 21 |
| 30 | uggagaagcagg Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.005G001000.1 | 5 | -1 | 1 | 21 |
| 33 | uggagaagcagg Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 34 | uggagaagcagg Phvul.008G243700.1 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.007G201400.1 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 38 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.003G181600.1 | 5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 42 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.006G164800.1 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 46 | uggagaagcagg Phvul.005G059700.1 | 5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.005G059500.1 | 5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.002G116800.1 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.008G103100.1 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.008G075300.1 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.003G262800.1 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.008G072300.1 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.008G072300.2 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.004G088300.1 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.004G088300.3 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.004G088300.2 | 5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.009G201600.1 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.005G155100.1 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.005G155100.3 | 5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.009G201600.2 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.004G088300.4 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.009G222600.1 | 5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.002G106900.1 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.005G099500.1 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.003G181900.1 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.003G181900.2 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.003G121200.1 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.003G121200.2 | 5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.006G075600.1 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.008G284900.1 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.007G163400.1 | 5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.001G266600.1 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.006G091100.2 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.006G091100.1 | 5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.003G037500.1 | 5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.009G007300.1 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.003G100200.1 | 5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.003G100200.2 | 5 | -1 | 1 | 21 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.002G262600.1 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.002G262600.2 | 5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.002G299004.1 | 5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.002G299004.3 | 5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.007G156200.1 | 5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.005G001000.1 | 5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.008G243700.1 | 5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.007G201400.1 | 5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.003G181600.1 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.006G164800.1 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.005G059700.1 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.005G059500.1 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.002G116800.1 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.008G103100.1 | 5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.008G075300.1 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.003G262800.1 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.008G072300.1 | 5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.008G072300.2 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.004G088300.1 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.004G088300.3 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.004G088300.2 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.009G201600.1 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.005G155100.1 | 5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.005G155100.3 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.009G201600.2 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.004G088300.4 | 5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.009G222600.1 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.002G106900.1 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.005G099500.1 | 5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.003G181900.1 | 5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.003G181900.2 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.003G121200.1 | 5 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.003G121200.2 | 5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.006G075600.1 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.008G284900.1 | 5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.007G163400.1 | 5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.001G266600.1 | 5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.006G091100.2 | 5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.006G091100.1 | 5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.003G037500.1 | 5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.009G007300.1 | 5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.003G100200.1 | 5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.003G100200.2 | 5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.002G262600.1 | 5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.002G262600.2 | 5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.002G299004.1 | 5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.002G299004.3 | 5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.007G156200.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.005G001000.1 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.008G243700.1 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.007G201400.1 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.003G181600.1 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.006G164800.1 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.005G059700.1 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.005G059500.1 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.002G116800.1 | 5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.008G103100.1 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.008G075300.1 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.003G262800.1 | 5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.008G072300.1 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.008G072300.2 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.004G088300.1 | 5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.004G088300.3 | 5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.004G088300.2 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.009G201600.1 | 5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.005G155100.1 | 5 | -1 | 1 | 21 |
| 42 | uggagaagcagg Phvul.005G155100.3 | 5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.009G201600.2 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.004G088300.4 | 5 | -1 | 1 | 21 |
| 45 | | | | | |
| 46 | uggagaagcagg Phvul.009G222600.1 | 5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.002G106900.1 | 5 | -1 | 1 | 21 |
| 48 | | | | | |
| 49 | uggagaagcagg Phvul.005G099500.1 | 5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.003G181900.1 | 5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.003G181900.2 | 5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.003G121200.1 | 5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.003G121200.2 | 5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.006G075600.1 | 5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.008G284900.1 | 5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.007G163400.1 | 5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.001G266600.1 | 5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.006G091100.2 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.006G091100.1 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.003G037500.1 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.009G007300.1 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.003G100200.1 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.003G100200.2 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.002G262600.1 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.002G262600.2 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.002G299004.1 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.002G299004.3 | 5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.007G156200.1 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.005G001000.1 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.008G243700.1 | 5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.007G201400.1 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.003G181600.1 | 5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.006G164800.1 | 5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.005G059700.1 | 5 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 38 | | | | | |
| 39 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.005G059500.1 | 5 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.002G116800.1 | 5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.008G103100.1 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.008G075300.1 | 5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.003G262800.1 | 5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.008G072300.1 | 5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.008G072300.2 | 5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.004G088300.1 | 5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.004G088300.3 | 5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.004G088300.2 | 5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.009G201600.1 | 5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.005G155100.1 | 5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.005G155100.3 | 5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.009G201600.2 | 5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.004G088300.4 | 5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.009G222600.1 | 5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.002G106900.1 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.005G099500.1 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.003G181900.1 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.003G181900.2 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.003G121200.1 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.003G121200.2 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.006G075600.1 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.008G284900.1 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.007G163400.1 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.001G266600.1 | 5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.006G091100.2 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.006G091100.1 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.003G037500.1 | 5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.009G007300.1 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.003G100200.1 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.003G100200.2 | 5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.002G262600.1 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.002G262600.2 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.002G299004.1 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.002G299004.3 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.007G156200.1 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.005G001000.1 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.008G243700.1 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.007G201400.1 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 41 | | | | | |
| 42 | uggagaagcagg Phvul.003G181600.1 | 5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.006G164800.1 | 5 | -1 | 1 | 21 |
| 46 | | | | | |
| 47 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.005G059700.1 | 5 | -1 | 1 | 21 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 52 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 53 | uggagaagcagg Phvul.005G059500.1 | 5 | -1 | 1 | 21 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.002G116800.1 | 5 | -1 | 1 | 21 |
| 56 | uggagaagcagg Phvul.008G103100.1 | 5 | -1 | 1 | 21 |
| 57 | uggagaagcagg Phvul.008G075300.1 | 5 | -1 | 1 | 21 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.003G262800.1 | 5 | -1 | 1 | 21 |
| 60 | uggagaagcagg Phvul.008G072300.1 | 5 | -1 | 1 | 21 |
| | uggagaagcagg Phvul.008G072300.2 | 5 | -1 | 1 | 21 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.004G088300.1 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.004G088300.3 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.004G088300.2 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.009G201600.1 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.005G155100.1 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.005G155100.3 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.009G201600.2 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.004G088300.4 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.009G222600.1 | 5 | -1 | 1 | 21 |
| 13 | uggagaagcagg Phvul.002G106900.1 | 5 | -1 | 1 | 21 |
| 14 | uggagaagcagg Phvul.005G099500.1 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.003G181900.1 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.003G181900.2 | 5 | -1 | 1 | 21 |
| 17 | uggagaagcagg Phvul.003G121200.1 | 5 | -1 | 1 | 21 |
| 18 | uggagaagcagg Phvul.003G121200.2 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.006G075600.1 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.008G284900.1 | 5 | -1 | 1 | 21 |
| 21 | uggagaagcagg Phvul.007G163400.1 | 5 | -1 | 1 | 21 |
| 22 | uggagaagcagg Phvul.001G266600.1 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.006G091100.2 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.006G091100.1 | 5 | -1 | 1 | 21 |
| 25 | uggagaagcagg Phvul.003G037500.1 | 5 | -1 | 1 | 21 |
| 26 | uggagaagcagg Phvul.009G007300.1 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.003G100200.1 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.003G100200.2 | 5 | -1 | 1 | 21 |
| 29 | uggagaagcagg Phvul.002G262600.1 | 5 | -1 | 1 | 21 |
| 30 | uggagaagcagg Phvul.002G262600.2 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.002G299004.1 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.002G299004.3 | 5 | -1 | 1 | 21 |
| 33 | uggagaagcagg Phvul.007G156200.1 | 5 | -1 | 1 | 21 |
| 34 | uggagaagcagg Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.005G001000.1 | 5 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 38 | uggagaagcagg Phvul.008G243700.1 | 5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.007G201400.1 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 42 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.003G181600.1 | 5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 46 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.006G164800.1 | 5 | -1 | 1 | 21 |
| 48 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 49 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 50 | | | | | |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.005G059700.1 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 5 | uggagaagcagg Phvul.005G059500.1 | 5 | -1 | 1 | 21 |
| 6 | uggagaagcagg Phvul.002G116800.1 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.008G103100.1 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.008G075300.1 | 5 | -1 | 1 | 21 |
| 9 | uggagaagcagg Phvul.003G262800.1 | 5 | -1 | 1 | 21 |
| 10 | uggagaagcagg Phvul.008G072300.1 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.008G072300.2 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.004G088300.1 | 5 | -1 | 1 | 21 |
| 13 | uggagaagcagg Phvul.004G088300.3 | 5 | -1 | 1 | 21 |
| 14 | uggagaagcagg Phvul.004G088300.2 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.009G201600.1 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.005G155100.1 | 5 | -1 | 1 | 21 |
| 17 | uggagaagcagg Phvul.005G155100.3 | 5 | -1 | 1 | 21 |
| 18 | uggagaagcagg Phvul.009G201600.2 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.004G088300.4 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.009G222600.1 | 5 | -1 | 1 | 21 |
| 21 | uggagaagcagg Phvul.002G106900.1 | 5 | -1 | 1 | 21 |
| 22 | uggagaagcagg Phvul.005G099500.1 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.003G181900.1 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.003G181900.2 | 5 | -1 | 1 | 21 |
| 25 | uggagaagcagg Phvul.003G121200.1 | 5 | -1 | 1 | 21 |
| 26 | uggagaagcagg Phvul.003G121200.2 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.006G075600.1 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.008G284900.1 | 5 | -1 | 1 | 21 |
| 29 | uggagaagcagg Phvul.007G163400.1 | 5 | -1 | 1 | 21 |
| 30 | uggagaagcagg Phvul.001G266600.1 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.006G091100.2 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.006G091100.1 | 5 | -1 | 1 | 21 |
| 33 | uggagaagcagg Phvul.003G037500.1 | 5 | -1 | 1 | 21 |
| 34 | uggagaagcagg Phvul.009G007300.1 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.003G100200.1 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.003G100200.2 | 5 | -1 | 1 | 21 |
| 37 | uggagaagcagg Phvul.002G262600.1 | 5 | -1 | 1 | 21 |
| 38 | uggagaagcagg Phvul.002G262600.2 | 5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.002G299004.1 | 5 | -1 | 1 | 21 |
| 40 | uggagaagcagg Phvul.002G299004.3 | 5 | -1 | 1 | 21 |
| 41 | uggagaagcagg Phvul.007G156200.1 | 5 | -1 | 1 | 21 |
| 42 | uggagaagcagg Phvul.002G006400.1 | 5 | -1 | 1 | 21 |
| 43 | uggagaagcagg Phvul.002G006400.3 | 5 | -1 | 1 | 21 |
| 44 | uggagaagcagg Phvul.005G001000.1 | 5 | -1 | 1 | 21 |
| 45 | uggagaagcagg Phvul.002G006400.2 | 5 | -1 | 1 | 21 |
| 46 | uggagaagcagg Phvul.008G243700.1 | 5 | -1 | 1 | 21 |
| 47 | uggagaagcagg Phvul.007G201400.1 | 5 | -1 | 1 | 21 |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 3 | uggagaagcagg Phvul.007G157500.2 | 5 | -1 | 1 | 21 |
| 4 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.007G157500.1 | 5 | -1 | 1 | 21 |
| 7 | uggagaagcagg Phvul.003G181600.1 | 5 | -1 | 1 | 21 |
| 8 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.007G157500.5 | 5 | -1 | 1 | 21 |
| 11 | uggagaagcagg Phvul.006G164800.1 | 5 | -1 | 1 | 21 |
| 12 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.007G157500.3 | 5 | -1 | 1 | 21 |
| 15 | uggagaagcagg Phvul.005G059700.1 | 5 | -1 | 1 | 21 |
| 16 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.007G157500.4 | 5 | -1 | 1 | 21 |
| 19 | uggagaagcagg Phvul.005G059500.1 | 5 | -1 | 1 | 21 |
| 20 | uggagaagcagg Phvul.002G116800.1 | 5 | -1 | 1 | 21 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.008G103100.1 | 5 | -1 | 1 | 21 |
| 23 | uggagaagcagg Phvul.008G075300.1 | 5 | -1 | 1 | 21 |
| 24 | uggagaagcagg Phvul.003G262800.1 | 5 | -1 | 1 | 21 |
| 25 | | | | | |
| 26 | uggagaagcagg Phvul.008G072300.1 | 5 | -1 | 1 | 21 |
| 27 | uggagaagcagg Phvul.008G072300.2 | 5 | -1 | 1 | 21 |
| 28 | uggagaagcagg Phvul.004G088300.1 | 5 | -1 | 1 | 21 |
| 29 | | | | | |
| 30 | uggagaagcagg Phvul.004G088300.3 | 5 | -1 | 1 | 21 |
| 31 | uggagaagcagg Phvul.004G088300.2 | 5 | -1 | 1 | 21 |
| 32 | uggagaagcagg Phvul.009G201600.1 | 5 | -1 | 1 | 21 |
| 33 | | | | | |
| 34 | uggagaagcagg Phvul.005G155100.1 | 5 | -1 | 1 | 21 |
| 35 | uggagaagcagg Phvul.005G155100.3 | 5 | -1 | 1 | 21 |
| 36 | uggagaagcagg Phvul.009G201600.2 | 5 | -1 | 1 | 21 |
| 37 | | | | | |
| 38 | uggagaagcagg Phvul.004G088300.4 | 5 | -1 | 1 | 21 |
| 39 | uggagaagcagg Phvul.006G075600.1 | 5 | -1 | 1 | 22 |
| 40 | uggagaagcagg Phvul.008G284900.1 | 5 | -1 | 1 | 22 |
| 41 | uggagaagcagg Phvul.006G091100.2 | 5 | -1 | 1 | 22 |
| 42 | | | | | |
| 43 | uggagaagcagg Phvul.009G222600.1 | 5 | -1 | 1 | 22 |
| 44 | uggagaagcagg Phvul.006G091100.1 | 5 | -1 | 1 | 22 |
| 45 | | | | | |
| 46 | uggagaagcagg Phvul.002G106900.1 | 5 | -1 | 1 | 22 |
| 47 | uggagaagcagg Phvul.005G099500.1 | 5 | -1 | 1 | 22 |
| 48 | uggagaagcagg Phvul.003G181900.1 | 5 | -1 | 1 | 22 |
| 49 | uggagaagcagg Phvul.003G181900.2 | 5 | -1 | 1 | 22 |
| 50 | | | | | |
| 51 | uggagaagcagg Phvul.003G121200.1 | 5 | -1 | 1 | 22 |
| 52 | uggagaagcagg Phvul.003G121200.2 | 5 | -1 | 1 | 22 |
| 53 | uggagaagcagg Phvul.005G059700.1 | 5 | -1 | 1 | 22 |
| 54 | | | | | |
| 55 | uggagaagcagg Phvul.005G059500.1 | 5 | -1 | 1 | 22 |
| 56 | uggagaagcagg Phvul.008G072300.1 | 5 | -1 | 1 | 22 |
| 57 | uggagaagcagg Phvul.008G072300.2 | 5 | -1 | 1 | 22 |
| 58 | | | | | |
| 59 | uggagaagcagg Phvul.009G201600.1 | 5 | -1 | 1 | 22 |
| 60 | uggagaagcagg Phvul.005G155100.1 | 5 | -1 | 1 | 22 |
| | uggagaagcagg Phvul.005G155100.3 | 5 | -1 | 1 | 22 |

| | | | | | |
|----|---------------------------------|---|----|---|----|
| 1 | | | | | |
| 2 | uggagaagcagg Phvul.009G201600.2 | 5 | -1 | 1 | 22 |
| 3 | uggagaagcagg Phvul.005G155100.2 | 5 | -1 | 1 | 22 |
| 4 | uggagaagcagg Phvul.009G114400.1 | 5 | -1 | 1 | 22 |
| 5 | | | | | |
| 6 | uggagaagcagg Phvul.003G240100.1 | 5 | -1 | 1 | 22 |
| 7 | uggagaagcagg Phvul.002G283000.3 | 5 | -1 | 1 | 22 |
| 8 | uggagaagcagg Phvul.002G283000.1 | 5 | -1 | 1 | 22 |
| 9 | | | | | |
| 10 | uggagaagcagg Phvul.002G283000.2 | 5 | -1 | 1 | 22 |
| 11 | uggagaagcagg Phvul.003G170100.1 | 5 | -1 | 1 | 22 |
| 12 | uggagaagcagg Phvul.011G173600.1 | 5 | -1 | 1 | 22 |
| 13 | | | | | |
| 14 | uggagaagcagg Phvul.003G283500.1 | 5 | -1 | 1 | 22 |
| 15 | uggagaagcagg Phvul.007G163400.1 | 5 | -1 | 1 | 22 |
| 16 | uggagaagcagg Phvul.003G037500.1 | 5 | -1 | 1 | 22 |
| 17 | | | | | |
| 18 | uggagaagcagg Phvul.001G266600.1 | 5 | -1 | 1 | 22 |
| 19 | uggagaagcagg Phvul.001G243500.2 | 5 | -1 | 1 | 22 |
| 20 | uggagaagcagg Phvul.006G067900.1 | 5 | -1 | 1 | 22 |
| 21 | | | | | |
| 22 | uggagaagcagg Phvul.008G140600.1 | 5 | -1 | 1 | 22 |
| 23 | | | | | |
| 24 | | | | | |
| 25 | | | | | |
| 26 | | | | | |
| 27 | | | | | |
| 28 | | | | | |
| 29 | | | | | |
| 30 | | | | | |
| 31 | | | | | |
| 32 | | | | | |
| 33 | | | | | |
| 34 | | | | | |
| 35 | | | | | |
| 36 | | | | | |
| 37 | | | | | |
| 38 | | | | | |
| 39 | | | | | |
| 40 | | | | | |
| 41 | | | | | |
| 42 | | | | | |
| 43 | | | | | |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

not distribute

| | | | | |
|----|------|-----------------|----------------------|--------------|
| 1 | | | | |
| 2 | 1273 | 1293 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371528 |
| 3 | 973 | 993 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371560 |
| 4 | 727 | 747 UGGAGAAGC/ | AGCAAGUGCC(Cleavage | pacid=371538 |
| 5 | | | | |
| 6 | 1273 | 1293 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371528 |
| 7 | 973 | 993 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371560 |
| 8 | 727 | 747 UGGAGAAGC/ | AGCAAGUGCC(Cleavage | pacid=371538 |
| 9 | | | | |
| 10 | 1273 | 1293 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371528 |
| 11 | 973 | 993 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371560 |
| 12 | 727 | 747 UGGAGAAGC/ | AGCAAGUGCC(Cleavage | pacid=371538 |
| 13 | | | | |
| 14 | 1273 | 1293 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371528 |
| 15 | 973 | 993 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371560 |
| 16 | 727 | 747 UGGAGAAGC/ | AGCAAGUGCC(Cleavage | pacid=371538 |
| 17 | | | | |
| 18 | 1273 | 1293 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371528 |
| 19 | 973 | 993 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371560 |
| 20 | 727 | 747 UGGAGAAGC/ | AGCAAGUGCC(Cleavage | pacid=371538 |
| 21 | | | | |
| 22 | 1273 | 1293 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371528 |
| 23 | 973 | 993 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371560 |
| 24 | 727 | 747 UGGAGAAGC/ | AGCAAGUGCC(Cleavage | pacid=371538 |
| 25 | | | | |
| 26 | 1273 | 1293 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371528 |
| 27 | 973 | 993 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371560 |
| 28 | 727 | 747 UGGAGAAGC/ | AGCAAGUGCC(Cleavage | pacid=371538 |
| 29 | | | | |
| 30 | 1273 | 1293 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371528 |
| 31 | 973 | 993 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371560 |
| 32 | 727 | 747 UGGAGAAGC/ | AGCAAGUGCC(Cleavage | pacid=371538 |
| 33 | | | | |
| 34 | 1273 | 1293 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371528 |
| 35 | 973 | 993 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371560 |
| 36 | 727 | 747 UGGAGAAGC/ | AGCAAGUGCC(Cleavage | pacid=371538 |
| 37 | | | | |
| 38 | 1273 | 1293 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371528 |
| 39 | 973 | 993 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371560 |
| 40 | 727 | 747 UGGAGAAGC/ | AGCAAGUGCC(Cleavage | pacid=371538 |
| 41 | | | | |
| 42 | 1273 | 1293 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371528 |
| 43 | 973 | 993 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371560 |
| 44 | 727 | 747 UGGAGAAGC/ | AGCAAGUGCC(Cleavage | pacid=371538 |
| 45 | | | | |
| 46 | 1273 | 1293 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371528 |
| 47 | 973 | 993 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371560 |
| 48 | 727 | 747 UGGAGAAGC/ | AGCAAGUGCC(Cleavage | pacid=371538 |
| 49 | | | | |
| 50 | 1273 | 1293 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371528 |
| 51 | 973 | 993 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371560 |
| 52 | 727 | 747 UGGAGAAGC/ | AGCAAGUGCC(Cleavage | pacid=371538 |
| 53 | | | | |
| 54 | 1273 | 1293 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371528 |
| 55 | 973 | 993 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371560 |
| 56 | 727 | 747 UGGAGAAGC/ | AGCAAGUGCC(Cleavage | pacid=371538 |
| 57 | | | | |
| 58 | 1272 | 1293 UGGAGAAGC/ | GAGCACGUGI(Cleavage | pacid=371528 |
| 59 | 972 | 993 UGGAGAAGC/ | GAGCACGUGI(Cleavage | pacid=371560 |
| 60 | 726 | 747 UGGAGAAGC/ | GAGCAAGUG(Cleavage | pacid=371538 |
| | 191 | 211 UGGAGAAGC/ | AGCAAGUGCC(Cleavage | pacid=371718 |

| | | | | |
|----|-----|----------------|--------------------------------------|--------------|
| 1 | | | | |
| 2 | 213 | 233 UGGAGAAGC/ | :: : ::::::::::: CACACUUCCC Cleavage | pacid=371629 |
| 3 | 191 | 211 UGGAGAAGC/ | :: ::::::::::: AGCAAGUGCC Cleavage | pacid=371718 |
| 4 | 496 | 516 UGGAGAAGC/ | ::::::::::: : CCCGCGUGCC Cleavage | pacid=371641 |
| 5 | 876 | 896 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 6 | 351 | 371 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 7 | 349 | 369 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 8 | | | | |
| 9 | | | | |
| 10 | 213 | 233 UGGAGAAGC/ | :: : ::::::::::: CACACUUCCC Cleavage | pacid=371629 |
| 11 | 191 | 211 UGGAGAAGC/ | :: ::::::::::: AGCAAGUGCC Cleavage | pacid=371718 |
| 12 | 496 | 516 UGGAGAAGC/ | ::::::::::: : CCCGCGUGCC Cleavage | pacid=371641 |
| 13 | 876 | 896 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 14 | 351 | 371 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 15 | 349 | 369 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 16 | | | | |
| 17 | | | | |
| 18 | 213 | 233 UGGAGAAGC/ | :: : ::::::::::: CACACUUCCC Cleavage | pacid=371629 |
| 19 | 191 | 211 UGGAGAAGC/ | :: ::::::::::: AGCAAGUGCC Cleavage | pacid=371718 |
| 20 | 496 | 516 UGGAGAAGC/ | ::::::::::: : CCCGCGUGCC Cleavage | pacid=371641 |
| 21 | 876 | 896 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 22 | 351 | 371 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 23 | 349 | 369 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 24 | | | | |
| 25 | | | | |
| 26 | 213 | 233 UGGAGAAGC/ | :: : ::::::::::: CACACUUCCC Cleavage | pacid=371629 |
| 27 | 191 | 211 UGGAGAAGC/ | :: ::::::::::: AGCAAGUGCC Cleavage | pacid=371718 |
| 28 | 496 | 516 UGGAGAAGC/ | ::::::::::: : CCCGCGUGCC Cleavage | pacid=371641 |
| 29 | 876 | 896 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 30 | 351 | 371 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 31 | 349 | 369 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 32 | | | | |
| 33 | | | | |
| 34 | 213 | 233 UGGAGAAGC/ | :: : ::::::::::: CACACUUCCC Cleavage | pacid=371629 |
| 35 | 191 | 211 UGGAGAAGC/ | :: ::::::::::: AGCAAGUGCC Cleavage | pacid=371718 |
| 36 | 496 | 516 UGGAGAAGC/ | ::::::::::: : CCCGCGUGCC Cleavage | pacid=371641 |
| 37 | 876 | 896 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 38 | 351 | 371 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 39 | 349 | 369 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 40 | | | | |
| 41 | | | | |
| 42 | 213 | 233 UGGAGAAGC/ | :: : ::::::::::: CACACUUCCC Cleavage | pacid=371629 |
| 43 | 191 | 211 UGGAGAAGC/ | :: ::::::::::: AGCAAGUGCC Cleavage | pacid=371718 |
| 44 | 496 | 516 UGGAGAAGC/ | ::::::::::: : CCCGCGUGCC Cleavage | pacid=371641 |
| 45 | 876 | 896 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 46 | 351 | 371 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 47 | 349 | 369 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 48 | | | | |
| 49 | | | | |
| 50 | 213 | 233 UGGAGAAGC/ | :: : ::::::::::: CACACUUCCC Cleavage | pacid=371629 |
| 51 | 191 | 211 UGGAGAAGC/ | :: ::::::::::: AGCAAGUGCC Cleavage | pacid=371718 |
| 52 | 496 | 516 UGGAGAAGC/ | ::::::::::: : CCCGCGUGCC Cleavage | pacid=371641 |
| 53 | 876 | 896 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 54 | 351 | 371 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 55 | 349 | 369 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |
| 56 | | | | |
| 57 | | | | |
| 58 | 213 | 233 UGGAGAAGC/ | :: : ::::::::::: CACACUUCCC Cleavage | pacid=371629 |
| 59 | 191 | 211 UGGAGAAGC/ | :: ::::::::::: AGCAAGUGCC Cleavage | pacid=371718 |
| 60 | 496 | 516 UGGAGAAGC/ | ::::::::::: : CCCGCGUGCC Cleavage | pacid=371641 |
| | 876 | 896 UGGAGAAGC/ | .. ::::::::::: CUUGCUUGU Cleavage | pacid=371574 |

| | | | | |
|----|-----|----------------|---------------------------------|--------------|
| 1 | | | | |
| 2 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 3 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 4 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 5 | 286 | 306 UGGAGAAGC/ | :: ::::: ACCAUUGGCL Cleavage | pacid=371732 |
| 6 | 79 | 98 UGGAGAAGC/ | :: ::::: CACAC-UGCU Cleavage | pacid=371439 |
| 7 | 180 | 200 UGGAGAAGC/ | :: ::::: UGCACGUGCC Cleavage | pacid=371438 |
| 8 | 508 | 528 UGGAGAAGC/ | :: ::::: ACUCCGUCCC Cleavage | pacid=371767 |
| 9 | 186 | 206 UGGAGAAGC/ | :: ::::: CUCACGUUUL Cleavage | pacid=371619 |
| 10 | 340 | 360 UGGAGAAGC/ | :: ::::: AACAGGUGCC Translation | pacid=371542 |
| 11 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 12 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 13 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 14 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 15 | 286 | 306 UGGAGAAGC/ | :: ::::: ACCAUUGGCL Cleavage | pacid=371732 |
| 16 | 79 | 98 UGGAGAAGC/ | :: ::::: CACAC-UGCU Cleavage | pacid=371439 |
| 17 | 180 | 200 UGGAGAAGC/ | :: ::::: UGCACGUGCC Cleavage | pacid=371438 |
| 18 | 508 | 528 UGGAGAAGC/ | :: ::::: ACUCCGUCCC Cleavage | pacid=371767 |
| 19 | 186 | 206 UGGAGAAGC/ | :: ::::: CUCACGUUUL Cleavage | pacid=371619 |
| 20 | 340 | 360 UGGAGAAGC/ | :: ::::: AACAGGUGCC Translation | pacid=371542 |
| 21 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 22 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 23 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 24 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 25 | 286 | 306 UGGAGAAGC/ | :: ::::: ACCAUUGGCL Cleavage | pacid=371732 |
| 26 | 79 | 98 UGGAGAAGC/ | :: ::::: CACAC-UGCU Cleavage | pacid=371439 |
| 27 | 180 | 200 UGGAGAAGC/ | :: ::::: UGCACGUGCC Cleavage | pacid=371438 |
| 28 | 508 | 528 UGGAGAAGC/ | :: ::::: ACUCCGUCCC Cleavage | pacid=371767 |
| 29 | 186 | 206 UGGAGAAGC/ | :: ::::: CUCACGUUUL Cleavage | pacid=371619 |
| 30 | 340 | 360 UGGAGAAGC/ | :: ::::: AACAGGUGCC Translation | pacid=371542 |
| 31 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 32 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 33 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 34 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 35 | 286 | 306 UGGAGAAGC/ | :: ::::: ACCAUUGGCL Cleavage | pacid=371732 |
| 36 | 79 | 98 UGGAGAAGC/ | :: ::::: CACAC-UGCU Cleavage | pacid=371439 |
| 37 | 180 | 200 UGGAGAAGC/ | :: ::::: UGCACGUGCC Cleavage | pacid=371438 |
| 38 | 508 | 528 UGGAGAAGC/ | :: ::::: ACUCCGUCCC Cleavage | pacid=371767 |
| 39 | 186 | 206 UGGAGAAGC/ | :: ::::: CUCACGUUUL Cleavage | pacid=371619 |
| 40 | 340 | 360 UGGAGAAGC/ | :: ::::: AACAGGUGCC Translation | pacid=371542 |
| 41 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 42 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 43 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 44 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 45 | 286 | 306 UGGAGAAGC/ | :: ::::: ACCAUUGGCL Cleavage | pacid=371732 |
| 46 | 79 | 98 UGGAGAAGC/ | :: ::::: CACAC-UGCU Cleavage | pacid=371439 |
| 47 | 180 | 200 UGGAGAAGC/ | :: ::::: UGCACGUGCC Cleavage | pacid=371438 |
| 48 | 508 | 528 UGGAGAAGC/ | :: ::::: ACUCCGUCCC Cleavage | pacid=371767 |
| 49 | 186 | 206 UGGAGAAGC/ | :: ::::: CUCACGUUUL Cleavage | pacid=371619 |
| 50 | 340 | 360 UGGAGAAGC/ | :: ::::: AACAGGUGCC Translation | pacid=371542 |
| 51 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 52 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 53 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 54 | 286 | 306 UGGAGAAGC/ | :: ::::: ACCAUUGGCL Cleavage | pacid=371732 |
| 55 | 79 | 98 UGGAGAAGC/ | :: ::::: CACAC-UGCU Cleavage | pacid=371439 |
| 56 | 180 | 200 UGGAGAAGC/ | :: ::::: UGCACGUGCC Cleavage | pacid=371438 |
| 57 | 508 | 528 UGGAGAAGC/ | :: ::::: ACUCCGUCCC Cleavage | pacid=371767 |
| 58 | 186 | 206 UGGAGAAGC/ | :: ::::: CUCACGUUUL Cleavage | pacid=371619 |
| 59 | 340 | 360 UGGAGAAGC/ | :: ::::: AACAGGUGCC Translation | pacid=371542 |
| 60 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |

| | | | | |
|----|-----|----------------|---------------------------------|--------------|
| 1 | | | | |
| 2 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 3 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 4 | 286 | 306 UGGAGAAGC/ | :: ::::: ACCAUUGGCL Cleavage | pacid=371732 |
| 5 | 79 | 98 UGGAGAAGC/ | :: ::::: CACAC-UGCU Cleavage | pacid=371439 |
| 6 | 180 | 200 UGGAGAAGC/ | :: ::::: UGCACGUGCC Cleavage | pacid=371438 |
| 7 | 508 | 528 UGGAGAAGC/ | :: ::::: ACUCCGUCCC Cleavage | pacid=371767 |
| 8 | 186 | 206 UGGAGAAGC/ | :: ::::: CUCACGUUUI Cleavage | pacid=371619 |
| 9 | 340 | 360 UGGAGAAGC/ | :: ::::: AACAGGUGCC Translation | pacid=371542 |
| 10 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 11 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 12 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 13 | 286 | 306 UGGAGAAGC/ | :: ::::: ACCAUUGGCL Cleavage | pacid=371732 |
| 14 | 79 | 98 UGGAGAAGC/ | :: ::::: CACAC-UGCU Cleavage | pacid=371439 |
| 15 | 180 | 200 UGGAGAAGC/ | :: ::::: UGCACGUGCC Cleavage | pacid=371438 |
| 16 | 508 | 528 UGGAGAAGC/ | :: ::::: ACUCCGUCCC Cleavage | pacid=371767 |
| 17 | 186 | 206 UGGAGAAGC/ | :: ::::: CUCACGUUUI Cleavage | pacid=371619 |
| 18 | 340 | 360 UGGAGAAGC/ | :: ::::: AACAGGUGCC Translation | pacid=371542 |
| 19 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 20 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 21 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 22 | 286 | 306 UGGAGAAGC/ | :: ::::: ACCAUUGGCL Cleavage | pacid=371732 |
| 23 | 79 | 98 UGGAGAAGC/ | :: ::::: CACAC-UGCU Cleavage | pacid=371439 |
| 24 | 180 | 200 UGGAGAAGC/ | :: ::::: UGCACGUGCC Cleavage | pacid=371438 |
| 25 | 508 | 528 UGGAGAAGC/ | :: ::::: ACUCCGUCCC Cleavage | pacid=371767 |
| 26 | 186 | 206 UGGAGAAGC/ | :: ::::: CUCACGUUUI Cleavage | pacid=371619 |
| 27 | 340 | 360 UGGAGAAGC/ | :: ::::: AACAGGUGCC Translation | pacid=371542 |
| 28 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 29 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 30 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 31 | 286 | 306 UGGAGAAGC/ | :: ::::: ACCAUUGGCL Cleavage | pacid=371732 |
| 32 | 79 | 98 UGGAGAAGC/ | :: ::::: CACAC-UGCU Cleavage | pacid=371439 |
| 33 | 180 | 200 UGGAGAAGC/ | :: ::::: UGCACGUGCC Cleavage | pacid=371438 |
| 34 | 508 | 528 UGGAGAAGC/ | :: ::::: ACUCCGUCCC Cleavage | pacid=371767 |
| 35 | 186 | 206 UGGAGAAGC/ | :: ::::: CUCACGUUUI Cleavage | pacid=371619 |
| 36 | 340 | 360 UGGAGAAGC/ | :: ::::: AACAGGUGCC Translation | pacid=371542 |
| 37 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 38 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 39 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 40 | 286 | 306 UGGAGAAGC/ | :: ::::: ACCAUUGGCL Cleavage | pacid=371732 |
| 41 | 79 | 98 UGGAGAAGC/ | :: ::::: CACAC-UGCU Cleavage | pacid=371439 |
| 42 | 180 | 200 UGGAGAAGC/ | :: ::::: UGCACGUGCC Cleavage | pacid=371438 |
| 43 | 508 | 528 UGGAGAAGC/ | :: ::::: ACUCCGUCCC Cleavage | pacid=371767 |
| 44 | 186 | 206 UGGAGAAGC/ | :: ::::: CUCACGUUUI Cleavage | pacid=371619 |
| 45 | 340 | 360 UGGAGAAGC/ | :: ::::: AACAGGUGCC Translation | pacid=371542 |
| 46 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 47 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 48 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 49 | 286 | 306 UGGAGAAGC/ | :: ::::: ACCAUUGGCL Cleavage | pacid=371732 |
| 50 | 79 | 98 UGGAGAAGC/ | :: ::::: CACAC-UGCU Cleavage | pacid=371439 |
| 51 | 180 | 200 UGGAGAAGC/ | :: ::::: UGCACGUGCC Cleavage | pacid=371438 |
| 52 | 508 | 528 UGGAGAAGC/ | :: ::::: ACUCCGUCCC Cleavage | pacid=371767 |
| 53 | 186 | 206 UGGAGAAGC/ | :: ::::: CUCACGUUUI Cleavage | pacid=371619 |
| 54 | 340 | 360 UGGAGAAGC/ | :: ::::: AACAGGUGCC Translation | pacid=371542 |
| 55 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 56 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 57 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 58 | 286 | 306 UGGAGAAGC/ | :: ::::: ACCAUUGGCL Cleavage | pacid=371732 |
| 59 | 79 | 98 UGGAGAAGC/ | :: ::::: CACAC-UGCU Cleavage | pacid=371439 |
| 60 | 180 | 200 UGGAGAAGC/ | :: ::::: UGCACGUGCC Cleavage | pacid=371438 |
| | 508 | 528 UGGAGAAGC/ | :: ::::: ACUCCGUCCC Cleavage | pacid=371767 |
| | 186 | 206 UGGAGAAGC/ | :: ::::: CUCACGUUUI Cleavage | pacid=371619 |
| | 340 | 360 UGGAGAAGC/ | :: ::::: AACAGGUGCC Translation | pacid=371542 |
| | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |

| | | | | |
|----|------|-----------------|---------------------------------|--------------|
| 1 | | | | |
| 2 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 3 | 286 | 306 UGGAGAAGC/ | :: ::::: ACCAUUGGCL Cleavage | pacid=371732 |
| 4 | 79 | 98 UGGAGAAGC/ | :: ::::: CACAC-UGCU Cleavage | pacid=371439 |
| 5 | 180 | 200 UGGAGAAGC/ | :: ::::: UGCACGUGCC Cleavage | pacid=371438 |
| 6 | 508 | 528 UGGAGAAGC/ | :: ::::: ACUCCGUCCC Cleavage | pacid=371767 |
| 7 | 186 | 206 UGGAGAAGC/ | :: ::::: CUCACGUUUL Cleavage | pacid=371619 |
| 8 | | | | |
| 9 | 340 | 360 UGGAGAAGC/ | :: ::::: AACAGGUGCC Translation | pacid=371542 |
| 10 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 11 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 12 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 13 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 14 | 286 | 306 UGGAGAAGC/ | :: ::::: ACCAUUGGCL Cleavage | pacid=371732 |
| 15 | 79 | 98 UGGAGAAGC/ | :: ::::: CACAC-UGCU Cleavage | pacid=371439 |
| 16 | 180 | 200 UGGAGAAGC/ | :: ::::: UGCACGUGCC Cleavage | pacid=371438 |
| 17 | 508 | 528 UGGAGAAGC/ | :: ::::: ACUCCGUCCC Cleavage | pacid=371767 |
| 18 | 186 | 206 UGGAGAAGC/ | :: ::::: CUCACGUUUL Cleavage | pacid=371619 |
| 19 | 340 | 360 UGGAGAAGC/ | :: ::::: AACAGGUGCC Translation | pacid=371542 |
| 20 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 21 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 22 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 23 | 286 | 306 UGGAGAAGC/ | :: ::::: ACCAUUGGCL Cleavage | pacid=371732 |
| 24 | 79 | 98 UGGAGAAGC/ | :: ::::: CACAC-UGCU Cleavage | pacid=371439 |
| 25 | 180 | 200 UGGAGAAGC/ | :: ::::: UGCACGUGCC Cleavage | pacid=371438 |
| 26 | 508 | 528 UGGAGAAGC/ | :: ::::: ACUCCGUCCC Cleavage | pacid=371767 |
| 27 | 186 | 206 UGGAGAAGC/ | :: ::::: CUCACGUUUL Cleavage | pacid=371619 |
| 28 | 340 | 360 UGGAGAAGC/ | :: ::::: AACAGGUGCC Translation | pacid=371542 |
| 29 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 30 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 31 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 32 | 286 | 306 UGGAGAAGC/ | :: ::::: ACCAUUGGCL Cleavage | pacid=371732 |
| 33 | 79 | 98 UGGAGAAGC/ | :: ::::: CACAC-UGCU Cleavage | pacid=371439 |
| 34 | 180 | 200 UGGAGAAGC/ | :: ::::: UGCACGUGCC Cleavage | pacid=371438 |
| 35 | 508 | 528 UGGAGAAGC/ | :: ::::: ACUCCGUCCC Cleavage | pacid=371767 |
| 36 | 186 | 206 UGGAGAAGC/ | :: ::::: CUCACGUUUL Cleavage | pacid=371619 |
| 37 | 340 | 360 UGGAGAAGC/ | :: ::::: AACAGGUGCC Translation | pacid=371542 |
| 38 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 39 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 40 | 182 | 202 UGGAGAAGC/ | :: ::::: GACACUUGCL Cleavage | pacid=371578 |
| 41 | 286 | 306 UGGAGAAGC/ | :: ::::: ACCAUUGGCL Cleavage | pacid=371732 |
| 42 | 79 | 98 UGGAGAAGC/ | :: ::::: CACAC-UGCU Cleavage | pacid=371439 |
| 43 | 179 | 200 UGGAGAAGC/ | :: ::::: GUGCACGUG Cleavage | pacid=371438 |
| 44 | 507 | 528 UGGAGAAGC/ | :: ::::: AACUCCGUCC Cleavage | pacid=371767 |
| 45 | 185 | 206 UGGAGAAGC/ | :: ::::: UCUCACGUUL Cleavage | pacid=371619 |
| 46 | 339 | 360 UGGAGAAGC/ | :: ::::: CAACAGGUG Translation | pacid=371542 |
| 47 | 181 | 202 UGGAGAAGC/ | :: ::::: GGACACUUG Cleavage | pacid=371578 |
| 48 | 181 | 202 UGGAGAAGC/ | :: ::::: GGACACUUG Cleavage | pacid=371578 |
| 49 | 181 | 202 UGGAGAAGC/ | :: ::::: GGACACUUG Cleavage | pacid=371578 |
| 50 | 1540 | 1560 UGGAGAAGC/ | :: ::::: UGCAGCUGCL Cleavage | pacid=371672 |
| 51 | 1459 | 1479 UGGAGAAGC/ | :: ::::: UGCAGCUGCL Cleavage | pacid=371672 |
| 52 | 3334 | 3354 UGGAGAAGC/ | :: ::::: UUA AUGUGC Cleavage | pacid=371569 |
| 53 | 395 | 415 UGGAGAAGC/ | :: ::::: CCAACGUGUC Cleavage | pacid=371597 |
| 54 | 349 | 369 UGGAGAAGC/ | :: ::::: CUCGCGUGCC Cleavage | pacid=371564 |
| 55 | 398 | 418 UGGAGAAGC/ | :: ::::: CCAACGUGCL Cleavage | pacid=371609 |
| 56 | 2339 | 2359 UGGAGAAGC/ | :: ::::: AACACGUGCC Cleavage | pacid=371543 |
| 57 | 512 | 532 UGGAGAAGC/ | :: ::::: GCCACGUGCA Cleavage | pacid=371586 |
| 58 | 749 | 769 UGGAGAAGC/ | :: ::::: CACAUGUGU Cleavage | pacid=371470 |
| 59 | | | | |
| 60 | | | | |

| | | | | |
|----|------|-----------------|--------------------------------|--------------|
| 1 | | | | |
| 2 | 134 | 154 UGGAGAAGC/ | ... : ::::: GGUGCAUUC(Cleavage | pacid=371704 |
| 3 | 6862 | 6882 UGGAGAAGC/ | . : ::::: UCAGCAUGU(Cleavage | pacid=371594 |
| 4 | 1550 | 1570 UGGAGAAGC/ | :: ::::: CUCACUUGCC Cleavage | pacid=371472 |
| 5 | 1368 | 1388 UGGAGAAGC/ | :: ::::: ACCACUUGUC Cleavage | pacid=371488 |
| 6 | 609 | 629 UGGAGAAGC/ | ::: : : GUCACGUUU(Translation | pacid=371524 |
| 7 | 904 | 924 UGGAGAAGC/ | . : : : ACUAUGUUU(Cleavage | pacid=371508 |
| 8 | | | | |
| 9 | 335 | 355 UGGAGAAGC/ | ::: : : CCCACGUCCU Cleavage | pacid=371552 |
| 10 | | | | |
| 11 | 3330 | 3350 UGGAGAAGC/ | : : : : UCUACAUUC Cleavage | pacid=371560 |
| 12 | 1540 | 1560 UGGAGAAGC/ | ::: : : UGCAGCUGCl Cleavage | pacid=371672 |
| 13 | | | | |
| 14 | 1459 | 1479 UGGAGAAGC/ | ::: : : UGCAGCUGCl Cleavage | pacid=371672 |
| 15 | 3334 | 3354 UGGAGAAGC/ | : : : : UUAUGUGCl Cleavage | pacid=371569 |
| 16 | 395 | 415 UGGAGAAGC/ | : : : : CCAACGUGUC Cleavage | pacid=371597 |
| 17 | 349 | 369 UGGAGAAGC/ | : : : : CUCGCGUGCC Cleavage | pacid=371564 |
| 18 | 398 | 418 UGGAGAAGC/ | : : : : CCAACGUGCl Cleavage | pacid=371609 |
| 19 | | | | |
| 20 | 2339 | 2359 UGGAGAAGC/ | : : : : AACACGUGCC Cleavage | pacid=371543 |
| 21 | | | | |
| 22 | 512 | 532 UGGAGAAGC/ | : : : : GCCACGUGCA Cleavage | pacid=371586 |
| 23 | 749 | 769 UGGAGAAGC/ | : : : : CACAUGUGU(Cleavage | pacid=371470 |
| 24 | 134 | 154 UGGAGAAGC/ | ... : ::::: GGUGCAUUC(Cleavage | pacid=371704 |
| 25 | | | | |
| 26 | 6862 | 6882 UGGAGAAGC/ | . : ::::: UCAGCAUGU(Cleavage | pacid=371594 |
| 27 | 1550 | 1570 UGGAGAAGC/ | :: ::::: CUCACUUGCC Cleavage | pacid=371472 |
| 28 | 1368 | 1388 UGGAGAAGC/ | :: ::::: ACCACUUGUC Cleavage | pacid=371488 |
| 29 | 609 | 629 UGGAGAAGC/ | ::: : : GUCACGUUU(Translation | pacid=371524 |
| 30 | 904 | 924 UGGAGAAGC/ | . : : : ACUAUGUUU(Cleavage | pacid=371508 |
| 31 | 335 | 355 UGGAGAAGC/ | ::: : : CCCACGUCCU Cleavage | pacid=371552 |
| 32 | | | | |
| 33 | 3330 | 3350 UGGAGAAGC/ | : : : : UCUACAUUC Cleavage | pacid=371560 |
| 34 | | | | |
| 35 | 1540 | 1560 UGGAGAAGC/ | ::: : : UGCAGCUGCl Cleavage | pacid=371672 |
| 36 | 1459 | 1479 UGGAGAAGC/ | ::: : : UGCAGCUGCl Cleavage | pacid=371672 |
| 37 | | | | |
| 38 | 3334 | 3354 UGGAGAAGC/ | : : : : UUAUGUGCl Cleavage | pacid=371569 |
| 39 | 395 | 415 UGGAGAAGC/ | : : : : CCAACGUGUC Cleavage | pacid=371597 |
| 40 | 349 | 369 UGGAGAAGC/ | : : : : CUCGCGUGCC Cleavage | pacid=371564 |
| 41 | 398 | 418 UGGAGAAGC/ | : : : : CCAACGUGCl Cleavage | pacid=371609 |
| 42 | | | | |
| 43 | 2339 | 2359 UGGAGAAGC/ | : : : : AACACGUGCC Cleavage | pacid=371543 |
| 44 | 512 | 532 UGGAGAAGC/ | : : : : GCCACGUGCA Cleavage | pacid=371586 |
| 45 | 749 | 769 UGGAGAAGC/ | : : : : CACAUGUGU(Cleavage | pacid=371470 |
| 46 | | | | |
| 47 | 134 | 154 UGGAGAAGC/ | ... : ::::: GGUGCAUUC(Cleavage | pacid=371704 |
| 48 | 6862 | 6882 UGGAGAAGC/ | . : ::::: UCAGCAUGU(Cleavage | pacid=371594 |
| 49 | 1550 | 1570 UGGAGAAGC/ | :: ::::: CUCACUUGCC Cleavage | pacid=371472 |
| 50 | 1368 | 1388 UGGAGAAGC/ | :: ::::: ACCACUUGUC Cleavage | pacid=371488 |
| 51 | 609 | 629 UGGAGAAGC/ | ::: : : GUCACGUUU(Translation | pacid=371524 |
| 52 | 904 | 924 UGGAGAAGC/ | . : : : ACUAUGUUU(Cleavage | pacid=371508 |
| 53 | 335 | 355 UGGAGAAGC/ | ::: : : CCCACGUCCU Cleavage | pacid=371552 |
| 54 | | | | |
| 55 | 3330 | 3350 UGGAGAAGC/ | : : : : UCUACAUUC Cleavage | pacid=371560 |
| 56 | 1540 | 1560 UGGAGAAGC/ | ::: : : UGCAGCUGCl Cleavage | pacid=371672 |
| 57 | | | | |
| 58 | 1459 | 1479 UGGAGAAGC/ | ::: : : UGCAGCUGCl Cleavage | pacid=371672 |
| 59 | 3334 | 3354 UGGAGAAGC/ | : : : : UUAUGUGCl Cleavage | pacid=371569 |
| 60 | 395 | 415 UGGAGAAGC/ | : : : : CCAACGUGUC Cleavage | pacid=371597 |

| | | | | | | |
|----|------|------|------------|--------------|-----------------------|--------------|
| 1 | | | | | | |
| 2 | 349 | 369 | UGGAGAAGC/ | :::.....:.. | CUCGCGUGCC Cleavage | pacid=371564 |
| 3 | 398 | 418 | UGGAGAAGC/ | :::.....: .. | CCAACGUGCL Cleavage | pacid=371609 |
| 4 | 2339 | 2359 | UGGAGAAGC/ | :::.....: :. | AACACGUGCC Cleavage | pacid=371543 |
| 5 | 512 | 532 | UGGAGAAGC/ | :::.....: . | GCCACGUGCA Cleavage | pacid=371586 |
| 6 | 749 | 769 | UGGAGAAGC/ | :::.....: : | CACAUGUGU(Cleavage | pacid=371470 |
| 7 | 134 | 154 | UGGAGAAGC/ | :::.....: : | GGUGCAUUC(Cleavage | pacid=371704 |
| 8 | 6862 | 6882 | UGGAGAAGC/ | :::.....: . | UCAGCAUGU(Cleavage | pacid=371594 |
| 9 | 1550 | 1570 | UGGAGAAGC/ | :::.....: . | CUCACUUGCC Cleavage | pacid=371472 |
| 10 | 1368 | 1388 | UGGAGAAGC/ | :::.....: .. | ACCACUUGUC Cleavage | pacid=371488 |
| 11 | 609 | 629 | UGGAGAAGC/ | :::.....: : | GUCACGUUU(Translation | pacid=371524 |
| 12 | 904 | 924 | UGGAGAAGC/ | :::.....: . | ACUAUGUUU(Cleavage | pacid=371508 |
| 13 | 335 | 355 | UGGAGAAGC/ | :::.....: . | CCCACGUCCU Cleavage | pacid=371552 |
| 14 | 3330 | 3350 | UGGAGAAGC/ | :::.....: . | UCUACAUUC Cleavage | pacid=371560 |
| 15 | 1540 | 1560 | UGGAGAAGC/ | :::.....: . | UGCAGCUGCL Cleavage | pacid=371672 |
| 16 | 1459 | 1479 | UGGAGAAGC/ | :::.....: . | UGCAGCUGCL Cleavage | pacid=371672 |
| 17 | 3334 | 3354 | UGGAGAAGC/ | :::.....: . | UUAUGUGC(Cleavage | pacid=371569 |
| 18 | 395 | 415 | UGGAGAAGC/ | :::.....: .. | CCAACGUGUC Cleavage | pacid=371597 |
| 19 | 349 | 369 | UGGAGAAGC/ | :::.....: .. | CUCGCGUGCC Cleavage | pacid=371564 |
| 20 | 398 | 418 | UGGAGAAGC/ | :::.....: .. | CCAACGUGCL Cleavage | pacid=371609 |
| 21 | 2339 | 2359 | UGGAGAAGC/ | :::.....: :. | AACACGUGCC Cleavage | pacid=371543 |
| 22 | 512 | 532 | UGGAGAAGC/ | :::.....: . | GCCACGUGCA Cleavage | pacid=371586 |
| 23 | 749 | 769 | UGGAGAAGC/ | :::.....: : | CACAUGUGU(Cleavage | pacid=371470 |
| 24 | 134 | 154 | UGGAGAAGC/ | :::.....: : | GGUGCAUUC(Cleavage | pacid=371704 |
| 25 | 6862 | 6882 | UGGAGAAGC/ | :::.....: . | UCAGCAUGU(Cleavage | pacid=371594 |
| 26 | 1550 | 1570 | UGGAGAAGC/ | :::.....: . | CUCACUUGCC Cleavage | pacid=371472 |
| 27 | 1368 | 1388 | UGGAGAAGC/ | :::.....: .. | ACCACUUGUC Cleavage | pacid=371488 |
| 28 | 609 | 629 | UGGAGAAGC/ | :::.....: : | GUCACGUUU(Translation | pacid=371524 |
| 29 | 904 | 924 | UGGAGAAGC/ | :::.....: . | ACUAUGUUU(Cleavage | pacid=371508 |
| 30 | 335 | 355 | UGGAGAAGC/ | :::.....: . | CCCACGUCCU Cleavage | pacid=371552 |
| 31 | 3330 | 3350 | UGGAGAAGC/ | :::.....: . | UCUACAUUC Cleavage | pacid=371560 |
| 32 | 1540 | 1560 | UGGAGAAGC/ | :::.....: . | UGCAGCUGCL Cleavage | pacid=371672 |
| 33 | 1459 | 1479 | UGGAGAAGC/ | :::.....: . | UGCAGCUGCL Cleavage | pacid=371672 |
| 34 | 3334 | 3354 | UGGAGAAGC/ | :::.....: . | UUAUGUGC(Cleavage | pacid=371569 |
| 35 | 395 | 415 | UGGAGAAGC/ | :::.....: .. | CCAACGUGUC Cleavage | pacid=371597 |
| 36 | 349 | 369 | UGGAGAAGC/ | :::.....: .. | CUCGCGUGCC Cleavage | pacid=371564 |
| 37 | 398 | 418 | UGGAGAAGC/ | :::.....: .. | CCAACGUGCL Cleavage | pacid=371609 |
| 38 | 2339 | 2359 | UGGAGAAGC/ | :::.....: :. | AACACGUGCC Cleavage | pacid=371543 |
| 39 | 512 | 532 | UGGAGAAGC/ | :::.....: . | GCCACGUGCA Cleavage | pacid=371586 |
| 40 | 749 | 769 | UGGAGAAGC/ | :::.....: : | CACAUGUGU(Cleavage | pacid=371470 |
| 41 | 134 | 154 | UGGAGAAGC/ | :::.....: : | GGUGCAUUC(Cleavage | pacid=371704 |
| 42 | 6862 | 6882 | UGGAGAAGC/ | :::.....: . | UCAGCAUGU(Cleavage | pacid=371594 |
| 43 | 1550 | 1570 | UGGAGAAGC/ | :::.....: . | CUCACUUGCC Cleavage | pacid=371472 |
| 44 | 1368 | 1388 | UGGAGAAGC/ | :::.....: .. | ACCACUUGUC Cleavage | pacid=371488 |
| 45 | 609 | 629 | UGGAGAAGC/ | :::.....: : | GUCACGUUU(Translation | pacid=371524 |
| 46 | 904 | 924 | UGGAGAAGC/ | :::.....: . | ACUAUGUUU(Cleavage | pacid=371508 |
| 47 | 335 | 355 | UGGAGAAGC/ | :::.....: . | CCCACGUCCU Cleavage | pacid=371552 |
| 48 | 3330 | 3350 | UGGAGAAGC/ | :::.....: . | UCUACAUUC Cleavage | pacid=371560 |
| 49 | 1540 | 1560 | UGGAGAAGC/ | :::.....: . | UGCAGCUGCL Cleavage | pacid=371672 |
| 50 | 1459 | 1479 | UGGAGAAGC/ | :::.....: . | UGCAGCUGCL Cleavage | pacid=371672 |
| 51 | 3334 | 3354 | UGGAGAAGC/ | :::.....: . | UUAUGUGC(Cleavage | pacid=371569 |
| 52 | 395 | 415 | UGGAGAAGC/ | :::.....: .. | CCAACGUGUC Cleavage | pacid=371597 |
| 53 | 349 | 369 | UGGAGAAGC/ | :::.....: .. | CUCGCGUGCC Cleavage | pacid=371564 |
| 54 | 398 | 418 | UGGAGAAGC/ | :::.....: .. | CCAACGUGCL Cleavage | pacid=371609 |
| 55 | 2339 | 2359 | UGGAGAAGC/ | :::.....: :. | AACACGUGCC Cleavage | pacid=371543 |
| 56 | 512 | 532 | UGGAGAAGC/ | :::.....: . | GCCACGUGCA Cleavage | pacid=371586 |
| 57 | 749 | 769 | UGGAGAAGC/ | :::.....: : | CACAUGUGU(Cleavage | pacid=371470 |
| 58 | 134 | 154 | UGGAGAAGC/ | :::.....: : | GGUGCAUUC(Cleavage | pacid=371704 |
| 59 | 6862 | 6882 | UGGAGAAGC/ | :::.....: . | UCAGCAUGU(Cleavage | pacid=371594 |
| 60 | 1550 | 1570 | UGGAGAAGC/ | :::.....: . | CUCACUUGCC Cleavage | pacid=371472 |
| 61 | 1368 | 1388 | UGGAGAAGC/ | :::.....: .. | ACCACUUGUC Cleavage | pacid=371488 |
| 62 | 609 | 629 | UGGAGAAGC/ | :::.....: : | GUCACGUUU(Translation | pacid=371524 |
| 63 | 904 | 924 | UGGAGAAGC/ | :::.....: . | ACUAUGUUU(Cleavage | pacid=371508 |
| 64 | 335 | 355 | UGGAGAAGC/ | :::.....: . | CCCACGUCCU Cleavage | pacid=371552 |

| | | | | |
|----|------|-----------------|-------------------------------|--------------|
| 1 | | | | |
| 2 | 1550 | 1570 UGGAGAAGC/ | ::: ::::: CUCACUUGCC Cleavage | pacid=371472 |
| 3 | 1368 | 1388 UGGAGAAGC/ | ::: ::::: ACCACUUGUC Cleavage | pacid=371488 |
| 4 | 609 | 629 UGGAGAAGC/ | ::: ::: GUCACGUUU(Translation | pacid=371524 |
| 5 | 904 | 924 UGGAGAAGC/ | ::: ::::: ACUAUGUUU Cleavage | pacid=371508 |
| 6 | 335 | 355 UGGAGAAGC/ | ::: ::: CCCACGUCCU Cleavage | pacid=371552 |
| 7 | 3330 | 3350 UGGAGAAGC/ | ::: ::: UCUACAUUC Cleavage | pacid=371560 |
| 8 | 1540 | 1560 UGGAGAAGC/ | ::: ::::: UGCAGCUGC Cleavage | pacid=371672 |
| 9 | 1459 | 1479 UGGAGAAGC/ | ::: ::::: UGCAGCUGC Cleavage | pacid=371672 |
| 10 | 3334 | 3354 UGGAGAAGC/ | ::: ::::: UUAUGUGC Cleavage | pacid=371569 |
| 11 | 395 | 415 UGGAGAAGC/ | ::: ::: CCAACGUGUC Cleavage | pacid=371597 |
| 12 | 349 | 369 UGGAGAAGC/ | ::: ::: CUCGCGUGCC Cleavage | pacid=371564 |
| 13 | 398 | 418 UGGAGAAGC/ | ::: ::: CCAACGUGC Cleavage | pacid=371609 |
| 14 | 2339 | 2359 UGGAGAAGC/ | ::: ::: AACACGUGCC Cleavage | pacid=371543 |
| 15 | 512 | 532 UGGAGAAGC/ | ::: ::: GCCACGUGC Cleavage | pacid=371586 |
| 16 | 749 | 769 UGGAGAAGC/ | ::: ::: CACAUGUGU(Cleavage | pacid=371470 |
| 17 | 134 | 154 UGGAGAAGC/ | ::: ::: GGUGCAUUC(Cleavage | pacid=371704 |
| 18 | 6862 | 6882 UGGAGAAGC/ | ::: ::: UCAGCAUGU(Cleavage | pacid=371594 |
| 19 | 1550 | 1570 UGGAGAAGC/ | ::: ::::: CUCACUUGCC Cleavage | pacid=371472 |
| 20 | 1368 | 1388 UGGAGAAGC/ | ::: ::::: ACCACUUGUC Cleavage | pacid=371488 |
| 21 | 609 | 629 UGGAGAAGC/ | ::: ::: GUCACGUUU(Translation | pacid=371524 |
| 22 | 904 | 924 UGGAGAAGC/ | ::: ::::: ACUAUGUUU Cleavage | pacid=371508 |
| 23 | 335 | 355 UGGAGAAGC/ | ::: ::: CCCACGUCCU Cleavage | pacid=371552 |
| 24 | 3330 | 3350 UGGAGAAGC/ | ::: ::: UCUACAUUC Cleavage | pacid=371560 |
| 25 | 1540 | 1560 UGGAGAAGC/ | ::: ::::: UGCAGCUGC Cleavage | pacid=371672 |
| 26 | 1459 | 1479 UGGAGAAGC/ | ::: ::::: UGCAGCUGC Cleavage | pacid=371672 |
| 27 | 3334 | 3354 UGGAGAAGC/ | ::: ::::: UUAUGUGC Cleavage | pacid=371569 |
| 28 | 395 | 415 UGGAGAAGC/ | ::: ::: CCAACGUGUC Cleavage | pacid=371597 |
| 29 | 349 | 369 UGGAGAAGC/ | ::: ::: CUCGCGUGCC Cleavage | pacid=371564 |
| 30 | 398 | 418 UGGAGAAGC/ | ::: ::: CCAACGUGC Cleavage | pacid=371609 |
| 31 | 2339 | 2359 UGGAGAAGC/ | ::: ::: AACACGUGCC Cleavage | pacid=371543 |
| 32 | 512 | 532 UGGAGAAGC/ | ::: ::: GCCACGUGC Cleavage | pacid=371586 |
| 33 | 749 | 769 UGGAGAAGC/ | ::: ::: CACAUGUGU(Cleavage | pacid=371470 |
| 34 | 134 | 154 UGGAGAAGC/ | ::: ::: GGUGCAUUC(Cleavage | pacid=371704 |
| 35 | 6862 | 6882 UGGAGAAGC/ | ::: ::: UCAGCAUGU(Cleavage | pacid=371594 |
| 36 | 1550 | 1570 UGGAGAAGC/ | ::: ::::: CUCACUUGCC Cleavage | pacid=371472 |
| 37 | 1368 | 1388 UGGAGAAGC/ | ::: ::::: ACCACUUGUC Cleavage | pacid=371488 |
| 38 | 609 | 629 UGGAGAAGC/ | ::: ::: GUCACGUUU(Translation | pacid=371524 |
| 39 | 904 | 924 UGGAGAAGC/ | ::: ::::: ACUAUGUUU Cleavage | pacid=371508 |
| 40 | 335 | 355 UGGAGAAGC/ | ::: ::: CCCACGUCCU Cleavage | pacid=371552 |
| 41 | 3330 | 3350 UGGAGAAGC/ | ::: ::: UCUACAUUC Cleavage | pacid=371560 |
| 42 | 1540 | 1560 UGGAGAAGC/ | ::: ::::: UGCAGCUGC Cleavage | pacid=371672 |
| 43 | 1459 | 1479 UGGAGAAGC/ | ::: ::::: UGCAGCUGC Cleavage | pacid=371672 |
| 44 | 3334 | 3354 UGGAGAAGC/ | ::: ::::: UUAUGUGC Cleavage | pacid=371569 |
| 45 | 395 | 415 UGGAGAAGC/ | ::: ::: CCAACGUGUC Cleavage | pacid=371597 |
| 46 | 349 | 369 UGGAGAAGC/ | ::: ::: CUCGCGUGCC Cleavage | pacid=371564 |
| 47 | 398 | 418 UGGAGAAGC/ | ::: ::: CCAACGUGC Cleavage | pacid=371609 |
| 48 | 2339 | 2359 UGGAGAAGC/ | ::: ::: AACACGUGCC Cleavage | pacid=371543 |
| 49 | 512 | 532 UGGAGAAGC/ | ::: ::: GCCACGUGC Cleavage | pacid=371586 |
| 50 | 749 | 769 UGGAGAAGC/ | ::: ::: CACAUGUGU(Cleavage | pacid=371470 |
| 51 | 134 | 154 UGGAGAAGC/ | ::: ::: GGUGCAUUC(Cleavage | pacid=371704 |
| 52 | 6862 | 6882 UGGAGAAGC/ | ::: ::: UCAGCAUGU(Cleavage | pacid=371594 |
| 53 | 1550 | 1570 UGGAGAAGC/ | ::: ::::: CUCACUUGCC Cleavage | pacid=371472 |
| 54 | 1368 | 1388 UGGAGAAGC/ | ::: ::::: ACCACUUGUC Cleavage | pacid=371488 |
| 55 | 609 | 629 UGGAGAAGC/ | ::: ::: GUCACGUUU(Translation | pacid=371524 |
| 56 | 904 | 924 UGGAGAAGC/ | ::: ::::: ACUAUGUUU Cleavage | pacid=371508 |
| 57 | 335 | 355 UGGAGAAGC/ | ::: ::: CCCACGUCCU Cleavage | pacid=371552 |
| 58 | 3330 | 3350 UGGAGAAGC/ | ::: ::: UCUACAUUC Cleavage | pacid=371560 |
| 59 | 1540 | 1560 UGGAGAAGC/ | ::: ::::: UGCAGCUGC Cleavage | pacid=371672 |
| 60 | 1459 | 1479 UGGAGAAGC/ | ::: ::::: UGCAGCUGC Cleavage | pacid=371672 |
| 61 | 3334 | 3354 UGGAGAAGC/ | ::: ::::: UUAUGUGC Cleavage | pacid=371569 |
| 62 | 395 | 415 UGGAGAAGC/ | ::: ::: CCAACGUGUC Cleavage | pacid=371597 |
| 63 | 349 | 369 UGGAGAAGC/ | ::: ::: CUCGCGUGCC Cleavage | pacid=371564 |
| 64 | 398 | 418 UGGAGAAGC/ | ::: ::: CCAACGUGC Cleavage | pacid=371609 |

| | | | | |
|----|------|-----------------|-------------------------------|--------------|
| 1 | | | | |
| 2 | 2339 | 2359 UGGAGAAGC/ | ::: ::: : AACACGUGCC Cleavage | pacid=371543 |
| 3 | 512 | 532 UGGAGAAGC/ | ::: : : GCCACGUGCA Cleavage | pacid=371586 |
| 4 | 749 | 769 UGGAGAAGC/ | ::: : : CACAUGUGU(Cleavage | pacid=371470 |
| 5 | 134 | 154 UGGAGAAGC/ | ::: : : GGUGCAUUC(Cleavage | pacid=371704 |
| 6 | 6862 | 6882 UGGAGAAGC/ | ::: : : UCAGCAUGU(Cleavage | pacid=371594 |
| 7 | 1550 | 1570 UGGAGAAGC/ | ::: : : CUCACUUGCC Cleavage | pacid=371472 |
| 8 | 1368 | 1388 UGGAGAAGC/ | ::: : : ACCACUUGUC Cleavage | pacid=371488 |
| 9 | 609 | 629 UGGAGAAGC/ | ::: : : GUCACGUUU(Translation | pacid=371524 |
| 10 | 904 | 924 UGGAGAAGC/ | ::: : : ACUAUGUUU(Cleavage | pacid=371508 |
| 11 | 335 | 355 UGGAGAAGC/ | ::: : : CCCACGUCCU Cleavage | pacid=371552 |
| 12 | 3330 | 3350 UGGAGAAGC/ | ::: : : UCUACAUUC(Cleavage | pacid=371560 |
| 13 | 1540 | 1560 UGGAGAAGC/ | ::: : : UGCAGCUGC(Cleavage | pacid=371672 |
| 14 | 1459 | 1479 UGGAGAAGC/ | ::: : : UGCAGCUGC(Cleavage | pacid=371672 |
| 15 | 3334 | 3354 UGGAGAAGC/ | ::: : : UUAUGUGC(Cleavage | pacid=371569 |
| 16 | 395 | 415 UGGAGAAGC/ | ::: : : CCAACGUGUC Cleavage | pacid=371597 |
| 17 | 349 | 369 UGGAGAAGC/ | ::: : : CUCGCGUGCC Cleavage | pacid=371564 |
| 18 | 398 | 418 UGGAGAAGC/ | ::: : : CCAACGUGC(Cleavage | pacid=371609 |
| 19 | 2339 | 2359 UGGAGAAGC/ | ::: ::: : AACACGUGCC Cleavage | pacid=371543 |
| 20 | 512 | 532 UGGAGAAGC/ | ::: : : GCCACGUGCA Cleavage | pacid=371586 |
| 21 | 749 | 769 UGGAGAAGC/ | ::: : : CACAUGUGU(Cleavage | pacid=371470 |
| 22 | 134 | 154 UGGAGAAGC/ | ::: : : GGUGCAUUC(Cleavage | pacid=371704 |
| 23 | 6862 | 6882 UGGAGAAGC/ | ::: : : UCAGCAUGU(Cleavage | pacid=371594 |
| 24 | 1550 | 1570 UGGAGAAGC/ | ::: : : CUCACUUGCC Cleavage | pacid=371472 |
| 25 | 1368 | 1388 UGGAGAAGC/ | ::: : : ACCACUUGUC Cleavage | pacid=371488 |
| 26 | 609 | 629 UGGAGAAGC/ | ::: : : GUCACGUUU(Translation | pacid=371524 |
| 27 | 904 | 924 UGGAGAAGC/ | ::: : : ACUAUGUUU(Cleavage | pacid=371508 |
| 28 | 335 | 355 UGGAGAAGC/ | ::: : : CCCACGUCCU Cleavage | pacid=371552 |
| 29 | 3330 | 3350 UGGAGAAGC/ | ::: : : UCUACAUUC(Cleavage | pacid=371560 |
| 30 | 1540 | 1560 UGGAGAAGC/ | ::: : : UGCAGCUGC(Cleavage | pacid=371672 |
| 31 | 1459 | 1479 UGGAGAAGC/ | ::: : : UGCAGCUGC(Cleavage | pacid=371672 |
| 32 | 3334 | 3354 UGGAGAAGC/ | ::: : : UUAUGUGC(Cleavage | pacid=371569 |
| 33 | 395 | 415 UGGAGAAGC/ | ::: : : CCAACGUGUC Cleavage | pacid=371597 |
| 34 | 349 | 369 UGGAGAAGC/ | ::: : : CUCGCGUGCC Cleavage | pacid=371564 |
| 35 | 398 | 418 UGGAGAAGC/ | ::: : : CCAACGUGC(Cleavage | pacid=371609 |
| 36 | 2339 | 2359 UGGAGAAGC/ | ::: ::: : AACACGUGCC Cleavage | pacid=371543 |
| 37 | 512 | 532 UGGAGAAGC/ | ::: : : GCCACGUGCA Cleavage | pacid=371586 |
| 38 | 749 | 769 UGGAGAAGC/ | ::: : : CACAUGUGU(Cleavage | pacid=371470 |
| 39 | 134 | 154 UGGAGAAGC/ | ::: : : GGUGCAUUC(Cleavage | pacid=371704 |
| 40 | 6862 | 6882 UGGAGAAGC/ | ::: : : UCAGCAUGU(Cleavage | pacid=371594 |
| 41 | 1550 | 1570 UGGAGAAGC/ | ::: : : CUCACUUGCC Cleavage | pacid=371472 |
| 42 | 1368 | 1388 UGGAGAAGC/ | ::: : : ACCACUUGUC Cleavage | pacid=371488 |
| 43 | 609 | 629 UGGAGAAGC/ | ::: : : GUCACGUUU(Translation | pacid=371524 |
| 44 | 904 | 924 UGGAGAAGC/ | ::: : : ACUAUGUUU(Cleavage | pacid=371508 |
| 45 | 335 | 355 UGGAGAAGC/ | ::: : : CCCACGUCCU Cleavage | pacid=371552 |
| 46 | 3330 | 3350 UGGAGAAGC/ | ::: : : UCUACAUUC(Cleavage | pacid=371560 |
| 47 | 1540 | 1560 UGGAGAAGC/ | ::: : : UGCAGCUGC(Cleavage | pacid=371672 |
| 48 | 1459 | 1479 UGGAGAAGC/ | ::: : : UGCAGCUGC(Cleavage | pacid=371672 |
| 49 | 3334 | 3354 UGGAGAAGC/ | ::: : : UUAUGUGC(Cleavage | pacid=371569 |
| 50 | 395 | 415 UGGAGAAGC/ | ::: : : CCAACGUGUC Cleavage | pacid=371597 |
| 51 | 349 | 369 UGGAGAAGC/ | ::: : : CUCGCGUGCC Cleavage | pacid=371564 |
| 52 | 398 | 418 UGGAGAAGC/ | ::: : : CCAACGUGC(Cleavage | pacid=371609 |
| 53 | 2339 | 2359 UGGAGAAGC/ | ::: ::: : AACACGUGCC Cleavage | pacid=371543 |
| 54 | 512 | 532 UGGAGAAGC/ | ::: : : GCCACGUGCA Cleavage | pacid=371586 |
| 55 | 749 | 769 UGGAGAAGC/ | ::: : : CACAUGUGU(Cleavage | pacid=371470 |
| 56 | 134 | 154 UGGAGAAGC/ | ::: : : GGUGCAUUC(Cleavage | pacid=371704 |
| 57 | 6862 | 6882 UGGAGAAGC/ | ::: : : UCAGCAUGU(Cleavage | pacid=371594 |
| 58 | 1550 | 1570 UGGAGAAGC/ | ::: : : CUCACUUGCC Cleavage | pacid=371472 |
| 59 | 1368 | 1388 UGGAGAAGC/ | ::: : : ACCACUUGUC Cleavage | pacid=371488 |
| 60 | 609 | 629 UGGAGAAGC/ | ::: : : GUCACGUUU(Translation | pacid=371524 |
| 61 | 904 | 924 UGGAGAAGC/ | ::: : : ACUAUGUUU(Cleavage | pacid=371508 |
| 62 | 335 | 355 UGGAGAAGC/ | ::: : : CCCACGUCCU Cleavage | pacid=371552 |
| 63 | 3330 | 3350 UGGAGAAGC/ | ::: : : UCUACAUUC(Cleavage | pacid=371560 |
| 64 | 1540 | 1560 UGGAGAAGC/ | ::: : : UGCAGCUGC(Cleavage | pacid=371672 |

| | | | | |
|----|------|-----------------|------------------------|---------------------------|
| 1 | | | | |
| 2 | 1459 | 1479 UGGAGAAGC/ | ::: : ::::: UGCAGCUGCl | Cleavage pacid=371672 |
| 3 | 3334 | 3354 UGGAGAAGC/ | : : : : : UUA AUGUGCl | Cleavage pacid=371569 |
| 4 | 395 | 415 UGGAGAAGC/ | : : : : : CCAACGUGUC | Cleavage pacid=371597 |
| 5 | 349 | 369 UGGAGAAGC/ | : : : : : CUCGCGUGCC | Cleavage pacid=371564 |
| 6 | 398 | 418 UGGAGAAGC/ | : : : : : CCAACGUGCl | Cleavage pacid=371609 |
| 7 | 2339 | 2359 UGGAGAAGC/ | : : : : : AACACGUGCC | Cleavage pacid=371543 |
| 8 | 512 | 532 UGGAGAAGC/ | : : : : : GCCACGUGCA | Cleavage pacid=371586 |
| 9 | 749 | 769 UGGAGAAGC/ | : : : : : CACAUGUGU | Cleavage pacid=371470 |
| 10 | 134 | 154 UGGAGAAGC/ | : : : : : GGUGCAUUC | Cleavage pacid=371704 |
| 11 | 6862 | 6882 UGGAGAAGC/ | : : : : : UCAGCAUGU | Cleavage pacid=371594 |
| 12 | 1550 | 1570 UGGAGAAGC/ | : : : : : CUCACUUGCC | Cleavage pacid=371472 |
| 13 | 1368 | 1388 UGGAGAAGC/ | : : : : : ACCACUUGUC | Cleavage pacid=371488 |
| 14 | 609 | 629 UGGAGAAGC/ | : : : : : GUCACGUUU | (Translation pacid=371524 |
| 15 | 904 | 924 UGGAGAAGC/ | : : : : : ACUAUGUUU | Cleavage pacid=371508 |
| 16 | 335 | 355 UGGAGAAGC/ | : : : : : CCCACGUCCU | Cleavage pacid=371552 |
| 17 | 3330 | 3350 UGGAGAAGC/ | : : : : : UCUACAUUC | Cleavage pacid=371560 |
| 18 | 1540 | 1560 UGGAGAAGC/ | : : : : : UGCAGCUGCl | Cleavage pacid=371672 |
| 19 | 1459 | 1479 UGGAGAAGC/ | : : : : : UGCAGCUGCl | Cleavage pacid=371672 |
| 20 | 3334 | 3354 UGGAGAAGC/ | : : : : : UUA AUGUGCl | Cleavage pacid=371569 |
| 21 | 395 | 415 UGGAGAAGC/ | : : : : : CCAACGUGUC | Cleavage pacid=371597 |
| 22 | 349 | 369 UGGAGAAGC/ | : : : : : CUCGCGUGCC | Cleavage pacid=371564 |
| 23 | 398 | 418 UGGAGAAGC/ | : : : : : CCAACGUGCl | Cleavage pacid=371609 |
| 24 | 2339 | 2359 UGGAGAAGC/ | : : : : : AACACGUGCC | Cleavage pacid=371543 |
| 25 | 512 | 532 UGGAGAAGC/ | : : : : : GCCACGUGCA | Cleavage pacid=371586 |
| 26 | 749 | 769 UGGAGAAGC/ | : : : : : CACAUGUGU | Cleavage pacid=371470 |
| 27 | 134 | 154 UGGAGAAGC/ | : : : : : GGUGCAUUC | Cleavage pacid=371704 |
| 28 | 6862 | 6882 UGGAGAAGC/ | : : : : : UCAGCAUGU | Cleavage pacid=371594 |
| 29 | 1550 | 1570 UGGAGAAGC/ | : : : : : CUCACUUGCC | Cleavage pacid=371472 |
| 30 | 1368 | 1388 UGGAGAAGC/ | : : : : : ACCACUUGUC | Cleavage pacid=371488 |
| 31 | 609 | 629 UGGAGAAGC/ | : : : : : GUCACGUUU | (Translation pacid=371524 |
| 32 | 904 | 924 UGGAGAAGC/ | : : : : : ACUAUGUUU | Cleavage pacid=371508 |
| 33 | 335 | 355 UGGAGAAGC/ | : : : : : CCCACGUCCU | Cleavage pacid=371552 |
| 34 | 3330 | 3350 UGGAGAAGC/ | : : : : : UCUACAUUC | Cleavage pacid=371560 |
| 35 | 1540 | 1560 UGGAGAAGC/ | : : : : : UGCAGCUGCl | Cleavage pacid=371672 |
| 36 | 1459 | 1479 UGGAGAAGC/ | : : : : : UGCAGCUGCl | Cleavage pacid=371672 |
| 37 | 3334 | 3354 UGGAGAAGC/ | : : : : : UUA AUGUGCl | Cleavage pacid=371569 |
| 38 | 395 | 415 UGGAGAAGC/ | : : : : : CCAACGUGUC | Cleavage pacid=371597 |
| 39 | 349 | 369 UGGAGAAGC/ | : : : : : CUCGCGUGCC | Cleavage pacid=371564 |
| 40 | 398 | 418 UGGAGAAGC/ | : : : : : CCAACGUGCl | Cleavage pacid=371609 |
| 41 | 2339 | 2359 UGGAGAAGC/ | : : : : : AACACGUGCC | Cleavage pacid=371543 |
| 42 | 512 | 532 UGGAGAAGC/ | : : : : : GCCACGUGCA | Cleavage pacid=371586 |
| 43 | 749 | 769 UGGAGAAGC/ | : : : : : CACAUGUGU | Cleavage pacid=371470 |
| 44 | 134 | 154 UGGAGAAGC/ | : : : : : GGUGCAUUC | Cleavage pacid=371704 |
| 45 | 6862 | 6882 UGGAGAAGC/ | : : : : : UCAGCAUGU | Cleavage pacid=371594 |
| 46 | 1550 | 1570 UGGAGAAGC/ | : : : : : CUCACUUGCC | Cleavage pacid=371472 |
| 47 | 1368 | 1388 UGGAGAAGC/ | : : : : : ACCACUUGUC | Cleavage pacid=371488 |
| 48 | 609 | 629 UGGAGAAGC/ | : : : : : GUCACGUUU | (Translation pacid=371524 |
| 49 | 904 | 924 UGGAGAAGC/ | : : : : : ACUAUGUUU | Cleavage pacid=371508 |
| 50 | 335 | 355 UGGAGAAGC/ | : : : : : CCCACGUCCU | Cleavage pacid=371552 |
| 51 | 3330 | 3350 UGGAGAAGC/ | : : : : : UCUACAUUC | Cleavage pacid=371560 |
| 52 | 1540 | 1560 UGGAGAAGC/ | : : : : : UGCAGCUGCl | Cleavage pacid=371672 |
| 53 | 1459 | 1479 UGGAGAAGC/ | : : : : : UGCAGCUGCl | Cleavage pacid=371672 |
| 54 | 3334 | 3354 UGGAGAAGC/ | : : : : : UUA AUGUGCl | Cleavage pacid=371569 |
| 55 | 395 | 415 UGGAGAAGC/ | : : : : : CCAACGUGUC | Cleavage pacid=371597 |
| 56 | 349 | 369 UGGAGAAGC/ | : : : : : CUCGCGUGCC | Cleavage pacid=371564 |
| 57 | 398 | 418 UGGAGAAGC/ | : : : : : CCAACGUGCl | Cleavage pacid=371609 |
| 58 | 2339 | 2359 UGGAGAAGC/ | : : : : : AACACGUGCC | Cleavage pacid=371543 |
| 59 | 512 | 532 UGGAGAAGC/ | : : : : : GCCACGUGCA | Cleavage pacid=371586 |
| 60 | 749 | 769 UGGAGAAGC/ | : : : : : CACAUGUGU | Cleavage pacid=371470 |
| 61 | 134 | 154 UGGAGAAGC/ | : : : : : GGUGCAUUC | Cleavage pacid=371704 |
| 62 | 6862 | 6882 UGGAGAAGC/ | : : : : : UCAGCAUGU | Cleavage pacid=371594 |
| 63 | 1550 | 1570 UGGAGAAGC/ | : : : : : CUCACUUGCC | Cleavage pacid=371472 |
| 64 | 1368 | 1388 UGGAGAAGC/ | : : : : : ACCACUUGUC | Cleavage pacid=371488 |

| | | | | |
|----|------|-----------------|-------------------------------------|--------------|
| 1 | | | | |
| 2 | 609 | 629 UGGAGAAGC/ | ::: : : ::::: GUCACGUUU(Translation | pacid=371524 |
| 3 | 904 | 924 UGGAGAAGC/ | ::: : ::::: ACUAUGUUU Cleavage | pacid=371508 |
| 4 | 335 | 355 UGGAGAAGC/ | ::: : ::::: CCCACGUCCU Cleavage | pacid=371552 |
| 5 | | | | |
| 6 | 3330 | 3350 UGGAGAAGC/ | ::: : ::::: UCUACAUUC Cleavage | pacid=371560 |
| 7 | 1539 | 1560 UGGAGAAGC/ | ::: : ::::: CUGCAGCUG Cleavage | pacid=371672 |
| 8 | 1458 | 1479 UGGAGAAGC/ | ::: : ::::: CUGCAGCUG Cleavage | pacid=371672 |
| 9 | | | | |
| 10 | 3333 | 3354 UGGAGAAGC/ | ::: : ::::: GUUAAUGUG Cleavage | pacid=371569 |
| 11 | 3329 | 3350 UGGAGAAGC/ | ::: : ::::: UUCUACAUU Cleavage | pacid=371560 |
| 12 | 394 | 415 UGGAGAAGC/ | ::: : ::::: UCCAACGUG Cleavage | pacid=371597 |
| 13 | | | | |
| 14 | 348 | 369 UGGAGAAGC/ | ::: : ::::: UCUCGCGUG Cleavage | pacid=371564 |
| 15 | 397 | 418 UGGAGAAGC/ | ::: : ::::: UCCAACGUG Cleavage | pacid=371609 |
| 16 | 2338 | 2359 UGGAGAAGC/ | ::: : ::::: GAACACGUG Cleavage | pacid=371543 |
| 17 | | | | |
| 18 | 440 | 461 UGGAGAAGC/ | ::: : ::::: UUCCCUAUG Cleavage | pacid=371782 |
| 19 | 412 | 433 UGGAGAAGC/ | ::: : ::::: UUCCCUUUG Cleavage | pacid=371745 |
| 20 | 354 | 375 UGGAGAAGC/ | ::: : ::::: UUCCCUUUG Cleavage | pacid=371745 |
| 21 | | | | |
| 22 | 511 | 532 UGGAGAAGC/ | ::: : ::::: AGCCACGUG Cleavage | pacid=371586 |
| 23 | 748 | 769 UGGAGAAGC/ | ::: : ::::: CCACAUGUG Cleavage | pacid=371470 |
| 24 | 133 | 154 UGGAGAAGC/ | ::: : ::::: GGGUGCAUU Cleavage | pacid=371704 |
| 25 | | | | |
| 26 | 6861 | 6882 UGGAGAAGC/ | ::: : ::::: AUCAGCAUG Cleavage | pacid=371594 |
| 27 | 1549 | 1570 UGGAGAAGC/ | ::: : ::::: ACUCACUUG Cleavage | pacid=371472 |
| 28 | 1367 | 1388 UGGAGAAGC/ | ::: : ::::: UACCACUUG Cleavage | pacid=371488 |
| 29 | | | | |
| 30 | 21 | 41 UGGAGAAGC/ | ::: : ::::: UGCACUUCU Cleavage | pacid=371620 |
| 31 | 1501 | 1521 UGGAGAAGC/ | ::: : ::::: GGCAUGUGG Cleavage | pacid=371757 |
| 32 | 432 | 452 UGGAGAAGC/ | ::: : ::::: GGUGCGUGC Translation | pacid=371502 |
| 33 | | | | |
| 34 | 1178 | 1198 UGGAGAAGC/ | ::: : ::::: CGUACGUGG Cleavage | pacid=371566 |
| 35 | 406 | 426 UGGAGAAGC/ | ::: : ::::: GGUGUGUGC Cleavage | pacid=371737 |
| 36 | 525 | 545 UGGAGAAGC/ | ::: : ::::: UGCACCUUCC Cleavage | pacid=371721 |
| 37 | | | | |
| 38 | 1996 | 2015 UGGAGAAGC/ | ::: : ::::: UGCAUG-GUC Cleavage | pacid=371696 |
| 39 | 898 | 918 UGGAGAAGC/ | ::: : ::::: AGCAAGUGC Cleavage | pacid=371646 |
| 40 | 129 | 149 UGGAGAAGC/ | ::: : ::::: GAGAUGUGU Cleavage | pacid=371632 |
| 41 | 129 | 149 UGGAGAAGC/ | ::: : ::::: GAGAUGUGU Cleavage | pacid=371632 |
| 42 | | | | |
| 43 | 431 | 451 UGGAGAAGC/ | ::: : ::::: AGCAUGGGU Cleavage | pacid=371640 |
| 44 | 322 | 342 UGGAGAAGC/ | ::: : ::::: AGCAUGGGU Cleavage | pacid=371664 |
| 45 | 1774 | 1794 UGGAGAAGC/ | ::: : ::::: UUCACGUGU Cleavage | pacid=371661 |
| 46 | | | | |
| 47 | 1651 | 1671 UGGAGAAGC/ | ::: : ::::: AGCAUGGGU Cleavage | pacid=371610 |
| 48 | 1516 | 1536 UGGAGAAGC/ | ::: : ::::: UUUUCGUGU Cleavage | pacid=371543 |
| 49 | 66 | 86 UGGAGAAGC/ | ::: : ::::: GAGAUGUGC Cleavage | pacid=371692 |
| 50 | | | | |
| 51 | 2150 | 2170 UGGAGAAGC/ | ::: : ::::: AAAAUGUGC Cleavage | pacid=371627 |
| 52 | 2011 | 2031 UGGAGAAGC/ | ::: : ::::: AAAAUGUGC Cleavage | pacid=371627 |
| 53 | 1437 | 1457 UGGAGAAGC/ | ::: : ::::: CUCACGUGCC Cleavage | pacid=371647 |
| 54 | | | | |
| 55 | 96 | 116 UGGAGAAGC/ | ::: : ::::: GUUGUGUGC Cleavage | pacid=371508 |
| 56 | 1414 | 1434 UGGAGAAGC/ | ::: : ::::: UUUUUGUGC Cleavage | pacid=371727 |
| 57 | 1417 | 1437 UGGAGAAGC/ | ::: : ::::: UUUUUGUGC Cleavage | pacid=371727 |
| 58 | | | | |
| 59 | 391 | 411 UGGAGAAGC/ | ::: : ::::: CAUGCGUGG Cleavage | pacid=371424 |
| 60 | 391 | 411 UGGAGAAGC/ | ::: : ::::: CAUGCGUGG Cleavage | pacid=371424 |
| | 238 | 258 UGGAGAAGC/ | ::: : ::::: UUCAUGUGU Cleavage | pacid=371581 |

| | | | | |
|----|------|-----------------|--|--------------|
| 1 | | | | |
| 2 | 1651 | 1671 UGGAGAAGC/ | ::: : ..:::..... AGCAUGGGUICleavage | pacid=371610 |
| 3 | 1516 | 1536 UGGAGAAGC/ | ::: : ..:::..... UUUUCGUGU Cleavage | pacid=371543 |
| 4 | 66 | 86 UGGAGAAGC/ | ::: : ..:::..... GAGAUGUGC(Cleavage | pacid=371692 |
| 5 | 2150 | 2170 UGGAGAAGC/ | ::: : ..:::..... : AAAAUGUGC(Cleavage | pacid=371627 |
| 6 | 2011 | 2031 UGGAGAAGC/ | ::: : ..:::..... : AAAAUGUGC(Cleavage | pacid=371627 |
| 7 | 1437 | 1457 UGGAGAAGC/ | ::: : ..:::..... : CUCACGUGCC Cleavage | pacid=371647 |
| 8 | 96 | 116 UGGAGAAGC/ | ::: : ..:::..... GUUGUGUGC Cleavage | pacid=371508 |
| 9 | 1414 | 1434 UGGAGAAGC/ | ::: : ..:::..... UUUUAUGUGC Cleavage | pacid=371727 |
| 10 | 1417 | 1437 UGGAGAAGC/ | ::: : ..:::..... UUUUAUGUGC Cleavage | pacid=371727 |
| 11 | 391 | 411 UGGAGAAGC/ | ::: : ..:::..... CAUGCGUGG(Cleavage | pacid=371424 |
| 12 | 391 | 411 UGGAGAAGC/ | ::: : ..:::..... CAUGCGUGG(Cleavage | pacid=371424 |
| 13 | 238 | 258 UGGAGAAGC/ | ::: : ..:::..... : UUCAUGUGU Cleavage | pacid=371581 |
| 14 | 360 | 380 UGGAGAAGC/ | ::: : ..:::..... : AUCAUGUGC(Translation | pacid=371680 |
| 15 | 112 | 132 UGGAGAAGC/ | ::: : ..:::..... UUGACGUAU(Cleavage | pacid=371766 |
| 16 | 1338 | 1358 UGGAGAAGC/ | ::: : ..:::..... : AGGACAUGCC Cleavage | pacid=371602 |
| 17 | 622 | 642 UGGAGAAGC/ | ::: : ..:::..... : UUCUUGUGC(Cleavage | pacid=371502 |
| 18 | 21 | 41 UGGAGAAGC/ | ::: : ..:::..... UGCACUUCU(Cleavage | pacid=371620 |
| 19 | 1501 | 1521 UGGAGAAGC/ | ::: : ..:::..... : GGCAUGUGG(Cleavage | pacid=371757 |
| 20 | 432 | 452 UGGAGAAGC/ | ::: : ..:::..... GGUGCGUGC(Translation | pacid=371502 |
| 21 | 1178 | 1198 UGGAGAAGC/ | ::: : ..:::..... CGUACGUGG(Cleavage | pacid=371566 |
| 22 | 406 | 426 UGGAGAAGC/ | ::: : ..:::..... : GGUGUGUGC Cleavage | pacid=371737 |
| 23 | 525 | 545 UGGAGAAGC/ | ::: : ..:::..... UGCACCUUCC Cleavage | pacid=371721 |
| 24 | 1996 | 2015 UGGAGAAGC/ | ::: : ..:::..... : UGCAUG-GUC Cleavage | pacid=371696 |
| 25 | 898 | 918 UGGAGAAGC/ | ::: : ..:::..... AGCAAGUGCC Cleavage | pacid=371646 |
| 26 | 129 | 149 UGGAGAAGC/ | ::: : ..:::..... GAGAUGUGU Cleavage | pacid=371632 |
| 27 | 129 | 149 UGGAGAAGC/ | ::: : ..:::..... GAGAUGUGU Cleavage | pacid=371632 |
| 28 | 431 | 451 UGGAGAAGC/ | ::: : ..:::..... AGCAUGGGU(Cleavage | pacid=371640 |
| 29 | 322 | 342 UGGAGAAGC/ | ::: : ..:::..... AGCAUGGGU(Cleavage | pacid=371664 |
| 30 | 1774 | 1794 UGGAGAAGC/ | ::: : ..:::..... UUCACGUGUICleavage | pacid=371661 |
| 31 | 1651 | 1671 UGGAGAAGC/ | ::: : ..:::..... AGCAUGGGUICleavage | pacid=371610 |
| 32 | 1516 | 1536 UGGAGAAGC/ | ::: : ..:::..... UUUUCGUGU Cleavage | pacid=371543 |
| 33 | 66 | 86 UGGAGAAGC/ | ::: : ..:::..... GAGAUGUGC(Cleavage | pacid=371692 |
| 34 | 2150 | 2170 UGGAGAAGC/ | ::: : ..:::..... : AAAAUGUGC(Cleavage | pacid=371627 |
| 35 | 2011 | 2031 UGGAGAAGC/ | ::: : ..:::..... : AAAAUGUGC(Cleavage | pacid=371627 |
| 36 | 1437 | 1457 UGGAGAAGC/ | ::: : ..:::..... : CUCACGUGCC Cleavage | pacid=371647 |
| 37 | 96 | 116 UGGAGAAGC/ | ::: : ..:::..... GUUGUGUGC Cleavage | pacid=371508 |
| 38 | 1414 | 1434 UGGAGAAGC/ | ::: : ..:::..... UUUUAUGUGC Cleavage | pacid=371727 |
| 39 | 1417 | 1437 UGGAGAAGC/ | ::: : ..:::..... UUUUAUGUGC Cleavage | pacid=371727 |
| 40 | 391 | 411 UGGAGAAGC/ | ::: : ..:::..... CAUGCGUGG(Cleavage | pacid=371424 |
| 41 | 391 | 411 UGGAGAAGC/ | ::: : ..:::..... CAUGCGUGG(Cleavage | pacid=371424 |
| 42 | 238 | 258 UGGAGAAGC/ | ::: : ..:::..... : UUCAUGUGU Cleavage | pacid=371581 |
| 43 | 360 | 380 UGGAGAAGC/ | ::: : ..:::..... : AUCAUGUGC(Translation | pacid=371680 |
| 44 | 112 | 132 UGGAGAAGC/ | ::: : ..:::..... UUGACGUAU(Cleavage | pacid=371766 |
| 45 | 1338 | 1358 UGGAGAAGC/ | ::: : ..:::..... : AGGACAUGCC Cleavage | pacid=371602 |
| 46 | 622 | 642 UGGAGAAGC/ | ::: : ..:::..... : UUCUUGUGC(Cleavage | pacid=371502 |
| 47 | 21 | 41 UGGAGAAGC/ | ::: : ..:::..... UGCACUUCU(Cleavage | pacid=371620 |

| | | | | |
|----|------|-----------------|------------------------------|--------------|
| 1 | | | | |
| 2 | 1501 | 1521 UGGAGAAGC/ | ::: :: GGCAUGUGG(Cleavage | pacid=371757 |
| 3 | 432 | 452 UGGAGAAGC/ | ::: :: GGUGCGUGC(Translation | pacid=371502 |
| 4 | 1178 | 1198 UGGAGAAGC/ | ::: :: CGUACGUGG(Cleavage | pacid=371566 |
| 5 | 406 | 426 UGGAGAAGC/ | ::: :: GGUGUGUGC Cleavage | pacid=371737 |
| 6 | 406 | 426 UGGAGAAGC/ | ::: :: GGUGUGUGC Cleavage | pacid=371737 |
| 7 | 525 | 545 UGGAGAAGC/ | ::: :: UGCACCUUCC Cleavage | pacid=371721 |
| 8 | 1996 | 2015 UGGAGAAGC/ | ::: :: UGCAUG-GUC Cleavage | pacid=371696 |
| 9 | 898 | 918 UGGAGAAGC/ | ::: :: AGCAAGUGCC Cleavage | pacid=371646 |
| 10 | 898 | 918 UGGAGAAGC/ | ::: :: AGCAAGUGCC Cleavage | pacid=371646 |
| 11 | 129 | 149 UGGAGAAGC/ | ::: :: GAGAUGUGU Cleavage | pacid=371632 |
| 12 | 129 | 149 UGGAGAAGC/ | ::: :: GAGAUGUGU Cleavage | pacid=371632 |
| 13 | 129 | 149 UGGAGAAGC/ | ::: :: GAGAUGUGU Cleavage | pacid=371632 |
| 14 | 431 | 451 UGGAGAAGC/ | ::: :: AGCAUGGGU(Cleavage | pacid=371640 |
| 15 | 322 | 342 UGGAGAAGC/ | ::: :: AGCAUGGGU(Cleavage | pacid=371664 |
| 16 | 322 | 342 UGGAGAAGC/ | ::: :: AGCAUGGGU(Cleavage | pacid=371664 |
| 17 | 1774 | 1794 UGGAGAAGC/ | ::: :: UUCACGUGU(Cleavage | pacid=371661 |
| 18 | 1651 | 1671 UGGAGAAGC/ | ::: :: AGCAUGGGU(Cleavage | pacid=371610 |
| 19 | 1516 | 1536 UGGAGAAGC/ | ::: :: UUUUCGUGU Cleavage | pacid=371543 |
| 20 | 66 | 86 UGGAGAAGC/ | ::: :: GAGAUGUGC(Cleavage | pacid=371692 |
| 21 | 66 | 86 UGGAGAAGC/ | ::: :: GAGAUGUGC(Cleavage | pacid=371692 |
| 22 | 2150 | 2170 UGGAGAAGC/ | ::: :: AAAAUGUGC(Cleavage | pacid=371627 |
| 23 | 2011 | 2031 UGGAGAAGC/ | ::: :: AAAAUGUGC(Cleavage | pacid=371627 |
| 24 | 1437 | 1457 UGGAGAAGC/ | ::: :: CUCACGUGCC Cleavage | pacid=371647 |
| 25 | 1437 | 1457 UGGAGAAGC/ | ::: :: CUCACGUGCC Cleavage | pacid=371647 |
| 26 | 96 | 116 UGGAGAAGC/ | ::: :: GUUGUGUGC Cleavage | pacid=371508 |
| 27 | 1414 | 1434 UGGAGAAGC/ | ::: :: UUUUUGUGC Cleavage | pacid=371727 |
| 28 | 1417 | 1437 UGGAGAAGC/ | ::: :: UUUUUGUGC Cleavage | pacid=371727 |
| 29 | 1417 | 1437 UGGAGAAGC/ | ::: :: UUUUUGUGC Cleavage | pacid=371727 |
| 30 | 391 | 411 UGGAGAAGC/ | ::: :: CAUGCGUGG(Cleavage | pacid=371424 |
| 31 | 391 | 411 UGGAGAAGC/ | ::: :: CAUGCGUGG(Cleavage | pacid=371424 |
| 32 | 391 | 411 UGGAGAAGC/ | ::: :: CAUGCGUGG(Cleavage | pacid=371424 |
| 33 | 238 | 258 UGGAGAAGC/ | ::: :: UUCAUGUGU Cleavage | pacid=371581 |
| 34 | 360 | 380 UGGAGAAGC/ | ::: :: AUCAUGUGC(Translation | pacid=371680 |
| 35 | 112 | 132 UGGAGAAGC/ | ::: :: UUGACGUAU(Cleavage | pacid=371766 |
| 36 | 1338 | 1358 UGGAGAAGC/ | ::: :: AGGACAUGCC Cleavage | pacid=371602 |
| 37 | 622 | 642 UGGAGAAGC/ | ::: :: UUCUUGUGC(Cleavage | pacid=371502 |
| 38 | 622 | 642 UGGAGAAGC/ | ::: :: UUCUUGUGC(Cleavage | pacid=371502 |
| 39 | 21 | 41 UGGAGAAGC/ | ::: :: UGCACUUCU(Cleavage | pacid=371620 |
| 40 | 1501 | 1521 UGGAGAAGC/ | ::: :: GGCAUGUGG(Cleavage | pacid=371757 |
| 41 | 1501 | 1521 UGGAGAAGC/ | ::: :: GGCAUGUGG(Cleavage | pacid=371757 |
| 42 | 432 | 452 UGGAGAAGC/ | ::: :: GGUGCGUGC(Translation | pacid=371502 |
| 43 | 1178 | 1198 UGGAGAAGC/ | ::: :: CGUACGUGG(Cleavage | pacid=371566 |
| 44 | 406 | 426 UGGAGAAGC/ | ::: :: GGUGUGUGC Cleavage | pacid=371737 |
| 45 | 406 | 426 UGGAGAAGC/ | ::: :: GGUGUGUGC Cleavage | pacid=371737 |
| 46 | 525 | 545 UGGAGAAGC/ | ::: :: UGCACCUUCC Cleavage | pacid=371721 |
| 47 | 1996 | 2015 UGGAGAAGC/ | ::: :: UGCAUG-GUC Cleavage | pacid=371696 |
| 48 | 898 | 918 UGGAGAAGC/ | ::: :: AGCAAGUGCC Cleavage | pacid=371646 |
| 49 | 898 | 918 UGGAGAAGC/ | ::: :: AGCAAGUGCC Cleavage | pacid=371646 |
| 50 | 129 | 149 UGGAGAAGC/ | ::: :: GAGAUGUGU Cleavage | pacid=371632 |
| 51 | 129 | 149 UGGAGAAGC/ | ::: :: GAGAUGUGU Cleavage | pacid=371632 |
| 52 | 129 | 149 UGGAGAAGC/ | ::: :: GAGAUGUGU Cleavage | pacid=371632 |
| 53 | 431 | 451 UGGAGAAGC/ | ::: :: AGCAUGGGU(Cleavage | pacid=371640 |
| 54 | 322 | 342 UGGAGAAGC/ | ::: :: AGCAUGGGU(Cleavage | pacid=371664 |
| 55 | 1774 | 1794 UGGAGAAGC/ | ::: :: UUCACGUGU(Cleavage | pacid=371661 |
| 56 | 1651 | 1671 UGGAGAAGC/ | ::: :: AGCAUGGGU(Cleavage | pacid=371610 |
| 57 | 1516 | 1536 UGGAGAAGC/ | ::: :: UUUUCGUGU Cleavage | pacid=371543 |
| 58 | 1516 | 1536 UGGAGAAGC/ | ::: :: UUUUCGUGU Cleavage | pacid=371543 |
| 59 | 66 | 86 UGGAGAAGC/ | ::: :: GAGAUGUGC(Cleavage | pacid=371692 |
| 60 | 2150 | 2170 UGGAGAAGC/ | ::: :: AAAAUGUGC(Cleavage | pacid=371627 |
| 60 | 2011 | 2031 UGGAGAAGC/ | ::: :: AAAAUGUGC(Cleavage | pacid=371627 |

| | | | | |
|----|------|-----------------|---------------------------------|--------------|
| 1 | | | | |
| 2 | 1437 | 1457 UGGAGAAGC/ | :::~::~: :: CUCACGUGCC Cleavage | pacid=371647 |
| 3 | 96 | 116 UGGAGAAGC/ |: GUUGUGUGC Cleavage | pacid=371508 |
| 4 | 1414 | 1434 UGGAGAAGC/ | :.....: UUU AUGUGC Cleavage | pacid=371727 |
| 5 | 1417 | 1437 UGGAGAAGC/ | :.....: UUU AUGUGC Cleavage | pacid=371727 |
| 6 | 391 | 411 UGGAGAAGC/ |: CAUGCUGG(Cleavage | pacid=371424 |
| 7 | 391 | 411 UGGAGAAGC/ |: CAUGCUGG(Cleavage | pacid=371424 |
| 8 | 238 | 258 UGGAGAAGC/ | :.....: UUCAUGUGU Cleavage | pacid=371581 |
| 9 | 360 | 380 UGGAGAAGC/ | :.....: AUCAUGUGC(Translation | pacid=371680 |
| 10 | 112 | 132 UGGAGAAGC/ | :.....: UUGACGUAU(Cleavage | pacid=371766 |
| 11 | 1338 | 1358 UGGAGAAGC/ | :.....: AGGACAUGCC Cleavage | pacid=371602 |
| 12 | 622 | 642 UGGAGAAGC/ | :.....: UUCUUGUGC(Cleavage | pacid=371502 |
| 13 | 21 | 41 UGGAGAAGC/ | :.....: UGCACUUCU(Cleavage | pacid=371620 |
| 14 | 1501 | 1521 UGGAGAAGC/ | :.....: GGCAUGUGG(Cleavage | pacid=371757 |
| 15 | 432 | 452 UGGAGAAGC/ |: GGUGCGUGC(Translation | pacid=371502 |
| 16 | 1178 | 1198 UGGAGAAGC/ | :.....: CGUACGUGG(Cleavage | pacid=371566 |
| 17 | 406 | 426 UGGAGAAGC/ | :.....: GGUGUGUGC Cleavage | pacid=371737 |
| 18 | 525 | 545 UGGAGAAGC/ | :.....: UGCACCUUCC Cleavage | pacid=371721 |
| 19 | 1996 | 2015 UGGAGAAGC/ | :.....: UGCAUG-GUC Cleavage | pacid=371696 |
| 20 | 898 | 918 UGGAGAAGC/ | :.....: AGCAAGUGCC Cleavage | pacid=371646 |
| 21 | 129 | 149 UGGAGAAGC/ | :.....: GAGAUGUGU Cleavage | pacid=371632 |
| 22 | 129 | 149 UGGAGAAGC/ | :.....: GAGAUGUGU Cleavage | pacid=371632 |
| 23 | 431 | 451 UGGAGAAGC/ | :.....: AGCAUGGGU(Cleavage | pacid=371640 |
| 24 | 322 | 342 UGGAGAAGC/ | :.....: AGCAUGGGU(Cleavage | pacid=371664 |
| 25 | 1774 | 1794 UGGAGAAGC/ | :.....: UUCACGUGU(Cleavage | pacid=371661 |
| 26 | 1651 | 1671 UGGAGAAGC/ | :.....: AGCAUGGGU(Cleavage | pacid=371610 |
| 27 | 1516 | 1536 UGGAGAAGC/ | :.....: UUUUCGUGU Cleavage | pacid=371543 |
| 28 | 66 | 86 UGGAGAAGC/ | :.....: GAGAUGUGC(Cleavage | pacid=371692 |
| 29 | 2150 | 2170 UGGAGAAGC/ | :.....: AAAAUGUGC(Cleavage | pacid=371627 |
| 30 | 2011 | 2031 UGGAGAAGC/ | :.....: AAAAUGUGC(Cleavage | pacid=371627 |
| 31 | 1437 | 1457 UGGAGAAGC/ | :::~::~: :: CUCACGUGCC Cleavage | pacid=371647 |
| 32 | 96 | 116 UGGAGAAGC/ |: GUUGUGUGC Cleavage | pacid=371508 |
| 33 | 1414 | 1434 UGGAGAAGC/ | :.....: UUU AUGUGC Cleavage | pacid=371727 |
| 34 | 1417 | 1437 UGGAGAAGC/ | :.....: UUU AUGUGC Cleavage | pacid=371727 |
| 35 | 391 | 411 UGGAGAAGC/ |: CAUGCUGG(Cleavage | pacid=371424 |
| 36 | 391 | 411 UGGAGAAGC/ |: CAUGCUGG(Cleavage | pacid=371424 |
| 37 | 238 | 258 UGGAGAAGC/ | :.....: UUCAUGUGU Cleavage | pacid=371581 |
| 38 | 360 | 380 UGGAGAAGC/ | :.....: AUCAUGUGC(Translation | pacid=371680 |
| 39 | 112 | 132 UGGAGAAGC/ | :.....: UUGACGUAU(Cleavage | pacid=371766 |
| 40 | 1338 | 1358 UGGAGAAGC/ | :.....: AGGACAUGCC Cleavage | pacid=371602 |
| 41 | 622 | 642 UGGAGAAGC/ | :.....: UUCUUGUGC(Cleavage | pacid=371502 |
| 42 | 21 | 41 UGGAGAAGC/ | :.....: UGCACUUCU(Cleavage | pacid=371620 |
| 43 | 1501 | 1521 UGGAGAAGC/ | :.....: GGCAUGUGG(Cleavage | pacid=371757 |
| 44 | 432 | 452 UGGAGAAGC/ |: GGUGCGUGC(Translation | pacid=371502 |
| 45 | 1178 | 1198 UGGAGAAGC/ | :.....: CGUACGUGG(Cleavage | pacid=371566 |
| 46 | 406 | 426 UGGAGAAGC/ | :.....: GGUGUGUGC Cleavage | pacid=371737 |
| 47 | 525 | 545 UGGAGAAGC/ | :.....: UGCACCUUCC Cleavage | pacid=371721 |
| 48 | | | | |
| 49 | | | | |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

| | | | | |
|----|------|-----------------|------------------------|--------------|
| 1 | | | | |
| 2 | 1996 | 2015 UGGAGAAGC/ | UGCAUG-GUC Cleavage | pacid=371696 |
| 3 | 898 | 918 UGGAGAAGC/ | AGCAAGUGCC Cleavage | pacid=371646 |
| 4 | 129 | 149 UGGAGAAGC/ | GAGAUUGUGU Cleavage | pacid=371632 |
| 5 | 129 | 149 UGGAGAAGC/ | GAGAUUGUGU Cleavage | pacid=371632 |
| 6 | 431 | 451 UGGAGAAGC/ | AGCAUGGGU(Cleavage | pacid=371640 |
| 7 | 322 | 342 UGGAGAAGC/ | AGCAUGGGU(Cleavage | pacid=371664 |
| 8 | | | | |
| 9 | 1774 | 1794 UGGAGAAGC/ | UUCACGUGUI Cleavage | pacid=371661 |
| 10 | 1651 | 1671 UGGAGAAGC/ | AGCAUGGGU(Cleavage | pacid=371610 |
| 11 | 1516 | 1536 UGGAGAAGC/ | UUUUCGUGU Cleavage | pacid=371543 |
| 12 | | | | |
| 13 | 66 | 86 UGGAGAAGC/ | GAGAUUGUC(Cleavage | pacid=371692 |
| 14 | 2150 | 2170 UGGAGAAGC/ | AAAAUGUGCC Cleavage | pacid=371627 |
| 15 | 2011 | 2031 UGGAGAAGC/ | AAAAUGUGCC Cleavage | pacid=371627 |
| 16 | 1437 | 1457 UGGAGAAGC/ | CUCACGUGCC Cleavage | pacid=371647 |
| 17 | 96 | 116 UGGAGAAGC/ | GUUGUGUGC Cleavage | pacid=371508 |
| 18 | 1414 | 1434 UGGAGAAGC/ | UUUAUGUGC Cleavage | pacid=371727 |
| 19 | 1417 | 1437 UGGAGAAGC/ | UUUAUGUGC Cleavage | pacid=371727 |
| 20 | 391 | 411 UGGAGAAGC/ | CAUGCUGGC(Cleavage | pacid=371424 |
| 21 | 391 | 411 UGGAGAAGC/ | CAUGCUGGC(Cleavage | pacid=371424 |
| 22 | 238 | 258 UGGAGAAGC/ | UUCAUGUGU Cleavage | pacid=371581 |
| 23 | 360 | 380 UGGAGAAGC/ | AUCAUGUGCC(Translation | pacid=371680 |
| 24 | 112 | 132 UGGAGAAGC/ | UUGACGUAU(Cleavage | pacid=371766 |
| 25 | 1338 | 1358 UGGAGAAGC/ | AGGACAUGCC Cleavage | pacid=371602 |
| 26 | 622 | 642 UGGAGAAGC/ | UUCUUGUGC(Cleavage | pacid=371502 |
| 27 | 21 | 41 UGGAGAAGC/ | UGCACUUCU(Cleavage | pacid=371620 |
| 28 | 1501 | 1521 UGGAGAAGC/ | GGCAUGUGGC Cleavage | pacid=371757 |
| 29 | 432 | 452 UGGAGAAGC/ | GGUGCGUGC(Translation | pacid=371502 |
| 30 | 1178 | 1198 UGGAGAAGC/ | CGUACGUGGC(Cleavage | pacid=371566 |
| 31 | 406 | 426 UGGAGAAGC/ | GGUGUGUGC Cleavage | pacid=371737 |
| 32 | 525 | 545 UGGAGAAGC/ | UGCACCUUCC Cleavage | pacid=371721 |
| 33 | 1996 | 2015 UGGAGAAGC/ | UGCAUG-GUC Cleavage | pacid=371696 |
| 34 | 898 | 918 UGGAGAAGC/ | AGCAAGUGCC Cleavage | pacid=371646 |
| 35 | 129 | 149 UGGAGAAGC/ | GAGAUUGUGU Cleavage | pacid=371632 |
| 36 | 129 | 149 UGGAGAAGC/ | GAGAUUGUGU Cleavage | pacid=371632 |
| 37 | 431 | 451 UGGAGAAGC/ | AGCAUGGGU(Cleavage | pacid=371640 |
| 38 | 322 | 342 UGGAGAAGC/ | AGCAUGGGU(Cleavage | pacid=371664 |
| 39 | 1774 | 1794 UGGAGAAGC/ | UUCACGUGUI Cleavage | pacid=371661 |
| 40 | 1651 | 1671 UGGAGAAGC/ | AGCAUGGGU(Cleavage | pacid=371610 |
| 41 | 1516 | 1536 UGGAGAAGC/ | UUUUCGUGU Cleavage | pacid=371543 |
| 42 | 66 | 86 UGGAGAAGC/ | GAGAUUGUC(Cleavage | pacid=371692 |
| 43 | 2150 | 2170 UGGAGAAGC/ | AAAAUGUGCC Cleavage | pacid=371627 |
| 44 | 2011 | 2031 UGGAGAAGC/ | AAAAUGUGCC Cleavage | pacid=371627 |
| 45 | 1437 | 1457 UGGAGAAGC/ | CUCACGUGCC Cleavage | pacid=371647 |
| 46 | 96 | 116 UGGAGAAGC/ | GUUGUGUGC Cleavage | pacid=371508 |
| 47 | 1414 | 1434 UGGAGAAGC/ | UUUAUGUGC Cleavage | pacid=371727 |
| 48 | 1417 | 1437 UGGAGAAGC/ | UUUAUGUGC Cleavage | pacid=371727 |
| 49 | 391 | 411 UGGAGAAGC/ | CAUGCUGGC(Cleavage | pacid=371424 |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

| | | | | |
|----|------|-----------------|------------------------------|--------------|
| 1 | | | | |
| 2 | 391 | 411 UGGAGAAGC/ |: CAUGCUGUGG(Cleavage | pacid=371424 |
| 3 | 238 | 258 UGGAGAAGC/ |: UUCAUGUGU Cleavage | pacid=371581 |
| 4 | 360 | 380 UGGAGAAGC/ |: AUCAUGUGC(Translation | pacid=371680 |
| 5 | 112 | 132 UGGAGAAGC/ |: UUGACGUAU(Cleavage | pacid=371766 |
| 6 | 1338 | 1358 UGGAGAAGC/ |: AGGACAUGCC Cleavage | pacid=371602 |
| 7 | 622 | 642 UGGAGAAGC/ |: UUCUUGUGC(Cleavage | pacid=371502 |
| 8 | 21 | 41 UGGAGAAGC/ |: UGCACUUCU(Cleavage | pacid=371620 |
| 9 | 1501 | 1521 UGGAGAAGC/ |: GGCAUGUGG(Cleavage | pacid=371757 |
| 10 | 432 | 452 UGGAGAAGC/ |: GGUGCGUGC(Translation | pacid=371502 |
| 11 | 1178 | 1198 UGGAGAAGC/ |: CGUACGUGG(Cleavage | pacid=371566 |
| 12 | 406 | 426 UGGAGAAGC/ |: GGUGUGUGC Cleavage | pacid=371737 |
| 13 | 525 | 545 UGGAGAAGC/ |: UGCACCUUCC Cleavage | pacid=371721 |
| 14 | 1996 | 2015 UGGAGAAGC/ |: UGCAUG-GUC Cleavage | pacid=371696 |
| 15 | 898 | 918 UGGAGAAGC/ |: AGCAAGUGCC Cleavage | pacid=371646 |
| 16 | 129 | 149 UGGAGAAGC/ |: GAGAUGUGU Cleavage | pacid=371632 |
| 17 | 129 | 149 UGGAGAAGC/ |: GAGAUGUGU Cleavage | pacid=371632 |
| 18 | 431 | 451 UGGAGAAGC/ |: AGCAUGGGU(Cleavage | pacid=371640 |
| 19 | 322 | 342 UGGAGAAGC/ |: AGCAUGGGU(Cleavage | pacid=371664 |
| 20 | 1774 | 1794 UGGAGAAGC/ |: UUCACGUGU(Cleavage | pacid=371661 |
| 21 | 1651 | 1671 UGGAGAAGC/ |: AGCAUGGGU(Cleavage | pacid=371610 |
| 22 | 1516 | 1536 UGGAGAAGC/ |: UUUUCGUGU Cleavage | pacid=371543 |
| 23 | 66 | 86 UGGAGAAGC/ |: GAGAUGUGC(Cleavage | pacid=371692 |
| 24 | 2150 | 2170 UGGAGAAGC/ |: AAAAUGUGC(Cleavage | pacid=371627 |
| 25 | 2011 | 2031 UGGAGAAGC/ |: AAAAUGUGC(Cleavage | pacid=371627 |
| 26 | 1437 | 1457 UGGAGAAGC/ |: CUCACGUGCC Cleavage | pacid=371647 |
| 27 | 96 | 116 UGGAGAAGC/ |: GUUGUGUGC Cleavage | pacid=371508 |
| 28 | 1414 | 1434 UGGAGAAGC/ |: UUUUAUGUGC Cleavage | pacid=371727 |
| 29 | 1417 | 1437 UGGAGAAGC/ |: UUUUAUGUGC Cleavage | pacid=371727 |
| 30 | 391 | 411 UGGAGAAGC/ |: CAUGCUGUGG(Cleavage | pacid=371424 |
| 31 | 391 | 411 UGGAGAAGC/ |: CAUGCUGUGG(Cleavage | pacid=371424 |
| 32 | 238 | 258 UGGAGAAGC/ |: UUCAUGUGU Cleavage | pacid=371581 |
| 33 | 360 | 380 UGGAGAAGC/ |: AUCAUGUGC(Translation | pacid=371680 |
| 34 | 112 | 132 UGGAGAAGC/ |: UUGACGUAU(Cleavage | pacid=371766 |
| 35 | 1338 | 1358 UGGAGAAGC/ |: AGGACAUGCC Cleavage | pacid=371602 |
| 36 | 622 | 642 UGGAGAAGC/ |: UUCUUGUGC(Cleavage | pacid=371502 |
| 37 | 21 | 41 UGGAGAAGC/ |: UGCACUUCU(Cleavage | pacid=371620 |
| 38 | 1501 | 1521 UGGAGAAGC/ |: GGCAUGUGG(Cleavage | pacid=371757 |
| 39 | 432 | 452 UGGAGAAGC/ |: GGUGCGUGC(Translation | pacid=371502 |
| 40 | 1178 | 1198 UGGAGAAGC/ |: CGUACGUGG(Cleavage | pacid=371566 |
| 41 | 406 | 426 UGGAGAAGC/ |: GGUGUGUGC Cleavage | pacid=371737 |
| 42 | 525 | 545 UGGAGAAGC/ |: UGCACCUUCC Cleavage | pacid=371721 |
| 43 | 1996 | 2015 UGGAGAAGC/ |: UGCAUG-GUC Cleavage | pacid=371696 |
| 44 | 898 | 918 UGGAGAAGC/ |: AGCAAGUGCC Cleavage | pacid=371646 |
| 45 | 129 | 149 UGGAGAAGC/ |: GAGAUGUGU Cleavage | pacid=371632 |
| 46 | 129 | 149 UGGAGAAGC/ |: GAGAUGUGU Cleavage | pacid=371632 |
| 47 | 431 | 451 UGGAGAAGC/ |: AGCAUGGGU(Cleavage | pacid=371640 |

| | | | | |
|----|------|-----------------|---|--------------|
| 1 | | | | |
| 2 | 322 | 342 UGGAGAAGC/ | ::: : :::::..... AGCAUGGGU(Cleavage | pacid=371664 |
| 3 | 1774 | 1794 UGGAGAAGC/ | : :::::.....: UUCACGUGU(Cleavage | pacid=371661 |
| 4 | 1651 | 1671 UGGAGAAGC/ | ::: : :::::..... AGCAUGGGU(Cleavage | pacid=371610 |
| 5 | 1516 | 1536 UGGAGAAGC/ | : ::::: : ::::: UUUUCGUGU Cleavage | pacid=371543 |
| 6 | 66 | 86 UGGAGAAGC/ | : ::::: : ::::: GAGAUGUGC(Cleavage | pacid=371692 |
| 7 | 2150 | 2170 UGGAGAAGC/ | : :::::.....: AAAAUGUGC(Cleavage | pacid=371627 |
| 8 | 2011 | 2031 UGGAGAAGC/ | : :::::.....: AAAAUGUGC(Cleavage | pacid=371627 |
| 9 | 1437 | 1457 UGGAGAAGC/ | : :::::.....: CUCACGUGCC Cleavage | pacid=371647 |
| 10 | 96 | 116 UGGAGAAGC/ | : :::::.....: GUUGUGUGC Cleavage | pacid=371508 |
| 11 | 1414 | 1434 UGGAGAAGC/ | : :::::.....: UUUUUGUGC Cleavage | pacid=371727 |
| 12 | 1417 | 1437 UGGAGAAGC/ | : :::::.....: UUUUUGUGC Cleavage | pacid=371727 |
| 13 | 391 | 411 UGGAGAAGC/ | : ::::: : ::::: CAUGCGUGG(Cleavage | pacid=371424 |
| 14 | 391 | 411 UGGAGAAGC/ | : ::::: : ::::: CAUGCGUGG(Cleavage | pacid=371424 |
| 15 | 238 | 258 UGGAGAAGC/ | : :::::.....: UUCAUGUGU Cleavage | pacid=371581 |
| 16 | 360 | 380 UGGAGAAGC/ | : ::::: : ::::: AUCAUGUGC(Translation | pacid=371680 |
| 17 | 112 | 132 UGGAGAAGC/ | : ::: : ::::: UUGACGUAU(Cleavage | pacid=371766 |
| 18 | 1338 | 1358 UGGAGAAGC/ | : : ::::: : ::::: AGGACAUGCC Cleavage | pacid=371602 |
| 19 | 622 | 642 UGGAGAAGC/ | : : ::::: : ::::: UUCUUGUGC(Cleavage | pacid=371502 |
| 20 | 21 | 41 UGGAGAAGC/ | : ::::: : ::::: UGCACUUCU(Cleavage | pacid=371620 |
| 21 | 1501 | 1521 UGGAGAAGC/ | : ::::: : ::::: : GGCAUGUGG(Cleavage | pacid=371757 |
| 22 | 432 | 452 UGGAGAAGC/ | : ::::: : ::::: : GGUGCGUGC(Translation | pacid=371502 |
| 23 | 1178 | 1198 UGGAGAAGC/ | : ::::: : : ::::: CGUACGUGG(Cleavage | pacid=371566 |
| 24 | 406 | 426 UGGAGAAGC/ | : :::::.....: GGUGUGUGC Cleavage | pacid=371737 |
| 25 | 525 | 545 UGGAGAAGC/ | : ::::: : : ::::: UGCACCUUCC Cleavage | pacid=371721 |
| 26 | 1996 | 2015 UGGAGAAGC/ | : ::::: : ::::: : UGCAUG-GUC Cleavage | pacid=371696 |
| 27 | 898 | 918 UGGAGAAGC/ | : : :::::.....: AGCAAGUGC(Cleavage | pacid=371646 |
| 28 | 129 | 149 UGGAGAAGC/ | : :::::.....: GAGAUGUGU Cleavage | pacid=371632 |
| 29 | 129 | 149 UGGAGAAGC/ | : :::::.....: GAGAUGUGU Cleavage | pacid=371632 |
| 30 | 431 | 451 UGGAGAAGC/ | : ::: : :::::..... AGCAUGGGU(Cleavage | pacid=371640 |
| 31 | 322 | 342 UGGAGAAGC/ | : ::: : :::::..... AGCAUGGGU(Cleavage | pacid=371664 |
| 32 | 1774 | 1794 UGGAGAAGC/ | : :::::.....: UUCACGUGU(Cleavage | pacid=371661 |
| 33 | 1651 | 1671 UGGAGAAGC/ | : ::: : :::::..... AGCAUGGGU(Cleavage | pacid=371610 |
| 34 | 1516 | 1536 UGGAGAAGC/ | : ::::: : ::::: UUUUCGUGU Cleavage | pacid=371543 |
| 35 | 66 | 86 UGGAGAAGC/ | : ::::: : ::::: GAGAUGUGC(Cleavage | pacid=371692 |
| 36 | 2150 | 2170 UGGAGAAGC/ | : :::::.....: AAAAUGUGC(Cleavage | pacid=371627 |
| 37 | 2011 | 2031 UGGAGAAGC/ | : :::::.....: AAAAUGUGC(Cleavage | pacid=371627 |
| 38 | 1437 | 1457 UGGAGAAGC/ | : :::::.....: CUCACGUGCC Cleavage | pacid=371647 |
| 39 | 96 | 116 UGGAGAAGC/ | : :::::.....: GUUGUGUGC Cleavage | pacid=371508 |
| 40 | 1414 | 1434 UGGAGAAGC/ | : :::::.....: UUUUUGUGC Cleavage | pacid=371727 |
| 41 | 1417 | 1437 UGGAGAAGC/ | : :::::.....: UUUUUGUGC Cleavage | pacid=371727 |
| 42 | 391 | 411 UGGAGAAGC/ | : ::::: : ::::: CAUGCGUGG(Cleavage | pacid=371424 |
| 43 | 391 | 411 UGGAGAAGC/ | : ::::: : ::::: CAUGCGUGG(Cleavage | pacid=371424 |
| 44 | 238 | 258 UGGAGAAGC/ | : :::::.....: UUCAUGUGU Cleavage | pacid=371581 |
| 45 | 360 | 380 UGGAGAAGC/ | : ::::: : ::::: AUCAUGUGC(Translation | pacid=371680 |
| 46 | 112 | 132 UGGAGAAGC/ | : ::: : ::::: UUGACGUAU(Cleavage | pacid=371766 |
| 47 | 1338 | 1358 UGGAGAAGC/ | : : ::::: : ::::: AGGACAUGCC Cleavage | pacid=371602 |

| | | | |
|----|------|--|--------------|
| 1 | | | |
| 2 | 406 | 426 UGGAGAAGC/ :.....: :: GGUGUGUGC Cleavage | pacid=371737 |
| 3 | 525 | 545 UGGAGAAGC/ :... : ... : UGCACCUUCC Cleavage | pacid=371721 |
| 4 | 1996 | 2015 UGGAGAAGC/ :... : : UGCAUG-GUC Cleavage | pacid=371696 |
| 5 | 898 | 918 UGGAGAAGC/ :: : AGCAAGUGCC Cleavage | pacid=371646 |
| 6 | 129 | 149 UGGAGAAGC/ :.....: : GAGAUGUGU Cleavage | pacid=371632 |
| 7 | 129 | 149 UGGAGAAGC/ :.....: : GAGAUGUGU Cleavage | pacid=371632 |
| 8 | | | |
| 9 | 431 | 451 UGGAGAAGC/ :... : : AGCAUGGGU(Cleavage | pacid=371640 |
| 10 | 322 | 342 UGGAGAAGC/ :... : : AGCAUGGGU(Cleavage | pacid=371664 |
| 11 | 1774 | 1794 UGGAGAAGC/ :.....: : UUCACGUGU(Cleavage | pacid=371661 |
| 12 | 1651 | 1671 UGGAGAAGC/ :... : : AGCAUGGGU(Cleavage | pacid=371610 |
| 13 | 1516 | 1536 UGGAGAAGC/ :.....: : UUUUCGUGU Cleavage | pacid=371543 |
| 14 | 66 | 86 UGGAGAAGC/ :.....: : GAGAUGUGC(Cleavage | pacid=371692 |
| 15 | 2150 | 2170 UGGAGAAGC/ :.....: : AAAAUGUGC(Cleavage | pacid=371627 |
| 16 | 2011 | 2031 UGGAGAAGC/ :.....: : AAAAUGUGC(Cleavage | pacid=371627 |
| 17 | 1437 | 1457 UGGAGAAGC/ :.....: : CUCACGUGCC Cleavage | pacid=371647 |
| 18 | 96 | 116 UGGAGAAGC/ :.....: : GUUGUGUGC Cleavage | pacid=371508 |
| 19 | 1414 | 1434 UGGAGAAGC/ :.....: : UUUUUGUGC Cleavage | pacid=371727 |
| 20 | 1417 | 1437 UGGAGAAGC/ :.....: : UUUUUGUGC Cleavage | pacid=371727 |
| 21 | 391 | 411 UGGAGAAGC/ :... : : CAUGCGUGG(Cleavage | pacid=371424 |
| 22 | 391 | 411 UGGAGAAGC/ :... : : CAUGCGUGG(Cleavage | pacid=371424 |
| 23 | 238 | 258 UGGAGAAGC/ :.....: : UUCAUGUGU Cleavage | pacid=371581 |
| 24 | 360 | 380 UGGAGAAGC/ :.....: : AUCAUGUGC(Translation | pacid=371680 |
| 25 | 112 | 132 UGGAGAAGC/ :... : : UUGACGUAU(Cleavage | pacid=371766 |
| 26 | 1338 | 1358 UGGAGAAGC/ :... : : AGGACAUGCC Cleavage | pacid=371602 |
| 27 | 622 | 642 UGGAGAAGC/ :... : : UUCUUGUGC(Cleavage | pacid=371502 |
| 28 | 21 | 41 UGGAGAAGC/ :... : : UGCACUUCU(Cleavage | pacid=371620 |
| 29 | 1501 | 1521 UGGAGAAGC/ :.....: : GGCAUGUGG(Cleavage | pacid=371757 |
| 30 | 432 | 452 UGGAGAAGC/ :.....: : GGUGCGUGC(Translation | pacid=371502 |
| 31 | 1178 | 1198 UGGAGAAGC/ :.....: : CGUACGUGG(Cleavage | pacid=371566 |
| 32 | 406 | 426 UGGAGAAGC/ :.....: : GGUGUGUGC Cleavage | pacid=371737 |
| 33 | 525 | 545 UGGAGAAGC/ :... : ... : UGCACCUUCC Cleavage | pacid=371721 |
| 34 | 1996 | 2015 UGGAGAAGC/ :... : : UGCAUG-GUC Cleavage | pacid=371696 |
| 35 | 898 | 918 UGGAGAAGC/ :: : AGCAAGUGCC Cleavage | pacid=371646 |
| 36 | 129 | 149 UGGAGAAGC/ :.....: : GAGAUGUGU Cleavage | pacid=371632 |
| 37 | 129 | 149 UGGAGAAGC/ :.....: : GAGAUGUGU Cleavage | pacid=371632 |
| 38 | 431 | 451 UGGAGAAGC/ :... : : AGCAUGGGU(Cleavage | pacid=371640 |
| 39 | 322 | 342 UGGAGAAGC/ :... : : AGCAUGGGU(Cleavage | pacid=371664 |
| 40 | 1774 | 1794 UGGAGAAGC/ :.....: : UUCACGUGU(Cleavage | pacid=371661 |
| 41 | 1651 | 1671 UGGAGAAGC/ :... : : AGCAUGGGU(Cleavage | pacid=371610 |
| 42 | 1516 | 1536 UGGAGAAGC/ :.....: : UUUUCGUGU Cleavage | pacid=371543 |
| 43 | 66 | 86 UGGAGAAGC/ :.....: : GAGAUGUGC(Cleavage | pacid=371692 |
| 44 | 2150 | 2170 UGGAGAAGC/ :.....: : AAAAUGUGC(Cleavage | pacid=371627 |
| 45 | 2011 | 2031 UGGAGAAGC/ :.....: : AAAAUGUGC(Cleavage | pacid=371627 |
| 46 | 1437 | 1457 UGGAGAAGC/ :.....: : CUCACGUGCC Cleavage | pacid=371647 |
| 47 | 96 | 116 UGGAGAAGC/ :.....: : GUUGUGUGC Cleavage | pacid=371508 |
| 48 | 1414 | 1434 UGGAGAAGC/ :.....: : UUUUUGUGC Cleavage | pacid=371727 |
| 49 | | | |
| 50 | | | |
| 51 | | | |
| 52 | | | |
| 53 | | | |
| 54 | | | |
| 55 | | | |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

| | | | |
|----|------|--|--------------|
| 1 | | | |
| 2 | 210 | 230 UGGAGAAGC/ :::::::::: :::: ... AGCACGUGCC Translation | pacid=371623 |
| 3 | 676 | 696 UGGAGAAGC/ :::: : ::::: UGCGAGGGU Cleavage | pacid=371516 |
| 4 | 1409 | 1429 UGGAGAAGC/ :::: : ::::: UGCUGGUGC Cleavage | pacid=371770 |
| 5 | 480 | 500 UGGAGAAGC/ :::: : ::::: UGCAAGUUU Cleavage | pacid=371764 |
| 6 | 876 | 896 UGGAGAAGC/ :::: : ::::: UGCAGUUGC Translation | pacid=371754 |
| 7 | 1302 | 1321 UGGAGAAGC/ :::::::::: ::::: AGCAUGUGC Cleavage | pacid=371566 |
| 8 | 1139 | 1159 UGGAGAAGC/ :::: : ::::: UGCACUGGCC Cleavage | pacid=371699 |
| 9 | 998 | 1018 UGGAGAAGC/ :::: : ::::: UGUAGGAGC Cleavage | pacid=371749 |
| 10 | 564 | 584 UGGAGAAGC/ : :::::::::: ::::: CGAACGUGCC Cleavage | pacid=371759 |
| 11 | 564 | 584 UGGAGAAGC/ : :::::::::: ::::: CGAACGUGCC Cleavage | pacid=371759 |
| 12 | 78 | 97 UGGAGAAGC/ ::::: : ::::: UGCAUGU-UC Cleavage | pacid=371675 |
| 13 | 49 | 69 UGGAGAAGC/ ::: : ::::: GGUACAUGU Cleavage | pacid=371422 |
| 14 | 49 | 69 UGGAGAAGC/ ::: : ::::: GGUACAUGU Cleavage | pacid=371422 |
| 15 | 3477 | 3497 UGGAGAAGC/ ::::: GGGCUGUGC Cleavage | pacid=371724 |
| 16 | 372 | 392 UGGAGAAGC/ :::: : ::::: AGCGUUUGC Cleavage | pacid=371721 |
| 17 | 304 | 324 UGGAGAAGC/ ::::: : ::::: UCUCGUGC Cleavage | pacid=371530 |
| 18 | 2017 | 2037 UGGAGAAGC/ ::::: : ::::: GGCAUGUCU Cleavage | pacid=371461 |
| 19 | 1749 | 1769 UGGAGAAGC/ ::::: : ::::: GGCAUGUCU Cleavage | pacid=371461 |
| 20 | 151 | 171 UGGAGAAGC/ ::: : ::::: GCCGCUUGC Cleavage | pacid=371589 |
| 21 | 151 | 171 UGGAGAAGC/ ::: : ::::: GCCGCUUGC Cleavage | pacid=371589 |
| 22 | 1700 | 1720 UGGAGAAGC/ ::::: : ::::: GGCAUGUCU Cleavage | pacid=371461 |
| 23 | 1369 | 1389 UGGAGAAGC/ :::: : ::::: CGCAUCUGCC Cleavage | pacid=371646 |
| 24 | 775 | 795 UGGAGAAGC/ : ::::: AGUUCGUGU Translation | pacid=371518 |
| 25 | 1011 | 1031 UGGAGAAGC/ :::: : ::::: AGUACGGGC Cleavage | pacid=371742 |
| 26 | 879 | 899 UGGAGAAGC/ :::: : ::::: AGUACGGGC Cleavage | pacid=371742 |
| 27 | 772 | 792 UGGAGAAGC/ ::: : ::::: AGUGCAUGC Cleavage | pacid=371577 |
| 28 | 526 | 546 UGGAGAAGC/ :::::::::: ::::: UGCAUGUGC Cleavage | pacid=371422 |
| 29 | 220 | 240 UGGAGAAGC/ :::::::::: ::::: ACCACGUGC Cleavage | pacid=371515 |
| 30 | 1359 | 1379 UGGAGAAGC/ :::: : ::::: UGCACUUGG Cleavage | pacid=371586 |
| 31 | 1415 | 1435 UGGAGAAGC/ ::: ::::: UGUUUGUGU Cleavage | pacid=371487 |
| 32 | 1237 | 1257 UGGAGAAGC/ ::: ::::: UGUUCGUGC Translation | pacid=371708 |
| 33 | 1208 | 1228 UGGAGAAGC/ ::: ::::: UGUUCGUGC Translation | pacid=371708 |
| 34 | 238 | 257 UGGAGAAGC/ :::::::::: ::::: CGCACGUGCC Cleavage | pacid=371484 |
| 35 | 182 | 202 UGGAGAAGC/ :::::: : ::::: GGU AUGUGC Cleavage | pacid=371500 |
| 36 | 210 | 230 UGGAGAAGC/ :::::::::: ::::: ... AGCACGUGCC Translation | pacid=371623 |
| 37 | 676 | 696 UGGAGAAGC/ :::: : ::::: UGCGAGGGU Cleavage | pacid=371516 |
| 38 | 1409 | 1429 UGGAGAAGC/ :::: : ::::: UGCUGGUGC Cleavage | pacid=371770 |
| 39 | 480 | 500 UGGAGAAGC/ :::: : ::::: UGCAAGUUU Cleavage | pacid=371764 |
| 40 | 876 | 896 UGGAGAAGC/ :::: : ::::: UGCAGUUGC Translation | pacid=371754 |
| 41 | 1302 | 1321 UGGAGAAGC/ :::::::::: ::::: AGCAUGUGC Cleavage | pacid=371566 |
| 42 | 1139 | 1159 UGGAGAAGC/ :::: : ::::: UGCACUGGCC Cleavage | pacid=371699 |
| 43 | 998 | 1018 UGGAGAAGC/ :::: : ::::: UGUAGGAGC Cleavage | pacid=371749 |
| 44 | 564 | 584 UGGAGAAGC/ : :::::::::: ::::: CGAACGUGCC Cleavage | pacid=371759 |
| 45 | 564 | 584 UGGAGAAGC/ : :::::::::: ::::: CGAACGUGCC Cleavage | pacid=371759 |
| 46 | 78 | 97 UGGAGAAGC/ ::::: : ::::: UGCAUGU-UC Cleavage | pacid=371675 |
| 47 | 49 | 69 UGGAGAAGC/ ::: : ::::: GGUACAUGU Cleavage | pacid=371422 |
| 48 | | | |
| 49 | | | |
| 50 | | | |
| 51 | | | |
| 52 | | | |
| 53 | | | |
| 54 | | | |
| 55 | | | |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

| | | | | |
|----|------|-----------------|--|--------------|
| 1 | | | | |
| 2 | 49 | 69 UGGAGAAGC/ | ::: ::::: ::::: GGUACAUGUICleavage | pacid=371422 |
| 3 | 3477 | 3497 UGGAGAAGC/ | ::: ::::: ::::: GGGCUGUGCICleavage | pacid=371724 |
| 4 | 372 | 392 UGGAGAAGC/ | ::: ::::: ::::: AGCGUUUGCICleavage | pacid=371721 |
| 5 | 304 | 324 UGGAGAAGC/ | ::: ::::: ::::: UCUCGUGCICleavage | pacid=371530 |
| 6 | 2017 | 2037 UGGAGAAGC/ | ::: ::::: ::::: GGCAUGUCUICleavage | pacid=371461 |
| 7 | 1749 | 1769 UGGAGAAGC/ | ::: ::::: ::::: GGCAUGUCUICleavage | pacid=371461 |
| 8 | 151 | 171 UGGAGAAGC/ | ::: ::::: ::::: GCCGCUUGCICleavage | pacid=371589 |
| 9 | 151 | 171 UGGAGAAGC/ | ::: ::::: ::::: GCCGCUUGCICleavage | pacid=371589 |
| 10 | 1700 | 1720 UGGAGAAGC/ | ::: ::::: ::::: GGCAUGUCUICleavage | pacid=371461 |
| 11 | 1369 | 1389 UGGAGAAGC/ | ::: ::::: ::::: CGCAUCUGCCCleavage | pacid=371646 |
| 12 | 775 | 795 UGGAGAAGC/ | ::: ::::: ::::: AGUUCGUGU Translation | pacid=371518 |
| 13 | 1011 | 1031 UGGAGAAGC/ | ::: ::::: ::::: AGUACGGGC/Cleavage | pacid=371742 |
| 14 | 879 | 899 UGGAGAAGC/ | ::: ::::: ::::: AGUACGGGC/Cleavage | pacid=371742 |
| 15 | 772 | 792 UGGAGAAGC/ | ::: ::::: ::::: AGUGCAUGCCCleavage | pacid=371577 |
| 16 | 526 | 546 UGGAGAAGC/ | ::: ::::: ::::: UGCAUGUGCICleavage | pacid=371422 |
| 17 | 220 | 240 UGGAGAAGC/ | ::: ::::: ::::: ACCACGUGCICleavage | pacid=371515 |
| 18 | 1359 | 1379 UGGAGAAGC/ | ::: ::::: ::::: UGCACUUGGICleavage | pacid=371586 |
| 19 | 1415 | 1435 UGGAGAAGC/ | ::: ::::: ::::: UGUUUGUGUCleavage | pacid=371487 |
| 20 | 1237 | 1257 UGGAGAAGC/ | ::: ::::: ::::: UGUUCGUGCITranslation | pacid=371708 |
| 21 | 1208 | 1228 UGGAGAAGC/ | ::: ::::: ::::: UGUUCGUGCITranslation | pacid=371708 |
| 22 | 238 | 257 UGGAGAAGC/ | ::: ::::: ::::: CGCACGUGCCCleavage | pacid=371484 |
| 23 | 182 | 202 UGGAGAAGC/ | ::: ::::: ::::: GGU AUGUGC.Cleavage | pacid=371500 |
| 24 | 210 | 230 UGGAGAAGC/ | ::: ::::: ::::: ... AGCACGUGCC Translation | pacid=371623 |
| 25 | 676 | 696 UGGAGAAGC/ | ::: ::::: ::::: UGCGAGGGUICleavage | pacid=371516 |
| 26 | 1409 | 1429 UGGAGAAGC/ | ::: ::::: ::::: UGCUGGUGCICleavage | pacid=371770 |
| 27 | 480 | 500 UGGAGAAGC/ | ::: ::::: ::::: UGCAAGUUUICleavage | pacid=371764 |
| 28 | 876 | 896 UGGAGAAGC/ | ::: ::::: ::::: UGCAGUUGCITranslation | pacid=371754 |
| 29 | 1302 | 1321 UGGAGAAGC/ | ::: ::::: ::::: AGCAUGUGCCCleavage | pacid=371566 |
| 30 | 1139 | 1159 UGGAGAAGC/ | ::: ::::: ::::: UGCACUGGCCCleavage | pacid=371699 |
| 31 | 998 | 1018 UGGAGAAGC/ | ::: ::::: ::::: UGUAGGAGCICleavage | pacid=371749 |
| 32 | 564 | 584 UGGAGAAGC/ | ::: ::::: ::::: CGAACGUGCCCleavage | pacid=371759 |
| 33 | 564 | 584 UGGAGAAGC/ | ::: ::::: ::::: CGAACGUGCCCleavage | pacid=371759 |
| 34 | 78 | 97 UGGAGAAGC/ | ::: ::::: ::::: UGCAUGU-UCleavage | pacid=371675 |
| 35 | 49 | 69 UGGAGAAGC/ | ::: ::::: ::::: GGUACAUGUICleavage | pacid=371422 |
| 36 | 49 | 69 UGGAGAAGC/ | ::: ::::: ::::: GGUACAUGUICleavage | pacid=371422 |
| 37 | 3477 | 3497 UGGAGAAGC/ | ::: ::::: ::::: GGGCUGUGCICleavage | pacid=371724 |
| 38 | 372 | 392 UGGAGAAGC/ | ::: ::::: ::::: AGCGUUUGCICleavage | pacid=371721 |
| 39 | 304 | 324 UGGAGAAGC/ | ::: ::::: ::::: UCUCGUGCICleavage | pacid=371530 |
| 40 | 2017 | 2037 UGGAGAAGC/ | ::: ::::: ::::: GGCAUGUCUICleavage | pacid=371461 |
| 41 | 1749 | 1769 UGGAGAAGC/ | ::: ::::: ::::: GGCAUGUCUICleavage | pacid=371461 |
| 42 | 151 | 171 UGGAGAAGC/ | ::: ::::: ::::: GCCGCUUGCICleavage | pacid=371589 |
| 43 | 151 | 171 UGGAGAAGC/ | ::: ::::: ::::: GCCGCUUGCICleavage | pacid=371589 |
| 44 | 1700 | 1720 UGGAGAAGC/ | ::: ::::: ::::: GGCAUGUCUICleavage | pacid=371461 |
| 45 | 1369 | 1389 UGGAGAAGC/ | ::: ::::: ::::: CGCAUCUGCCCleavage | pacid=371646 |
| 46 | 775 | 795 UGGAGAAGC/ | ::: ::::: ::::: AGUUCGUGU Translation | pacid=371518 |
| 47 | 1011 | 1031 UGGAGAAGC/ | ::: ::::: ::::: AGUACGGGC/Cleavage | pacid=371742 |

| | | | |
|----|------|--|--------------|
| 1 | | | |
| 2 | 879 | 899 UGGAGAAGC/ :::: : : :::::.. AGUACGGGC/ Cleavage | pacid=371742 |
| 3 | 772 | 792 UGGAGAAGC/ :.. : ::::: : : AGUGCAUGC(Cleavage | pacid=371577 |
| 4 | 526 | 546 UGGAGAAGC/ : ::::: : : : : : : : UGCAUGUGC(Cleavage | pacid=371422 |
| 5 | 220 | 240 UGGAGAAGC/ : ::::: : : : : : : : ACCACGUGC(Cleavage | pacid=371515 |
| 6 | 1359 | 1379 UGGAGAAGC/ : ::::: : : : : : : : UGCACUUGG(Cleavage | pacid=371586 |
| 7 | 1415 | 1435 UGGAGAAGC/ :.. : ::::: : : : : : : : UGUUUGUGU Cleavage | pacid=371487 |
| 8 | 1237 | 1257 UGGAGAAGC/ :.. : ::::: : : : : : : : UGUUCGUGC(Translation | pacid=371708 |
| 9 | 1208 | 1228 UGGAGAAGC/ :.. : ::::: : : : : : : : UGUUCGUGC(Translation | pacid=371708 |
| 10 | 238 | 257 UGGAGAAGC/ : ::::: : : : : : : : CGCACGUGCC Cleavage | pacid=371484 |
| 11 | 182 | 202 UGGAGAAGC/ :.. : : : : : : : : : GGUAUGUGC. Cleavage | pacid=371500 |
| 12 | 210 | 230 UGGAGAAGC/ : ::::: : : : : : : : ... AGCACGUGCC Translation | pacid=371623 |
| 13 | 676 | 696 UGGAGAAGC/ :.. : : : : : : : : : UGCGAGGGU(Cleavage | pacid=371516 |
| 14 | 1409 | 1429 UGGAGAAGC/ :.. : ::::: : : : : : : : UGCUGGUGC(Cleavage | pacid=371770 |
| 15 | 480 | 500 UGGAGAAGC/ :.. : : : : : : : : : UGCAAGUUU(Cleavage | pacid=371764 |
| 16 | 876 | 896 UGGAGAAGC/ :.. : : : : : : : : : UGCAGUUGC(Translation | pacid=371754 |
| 17 | 1302 | 1321 UGGAGAAGC/ : ::::: : : : : : : : AGCAUGUGC(Cleavage | pacid=371566 |
| 18 | 1139 | 1159 UGGAGAAGC/ : ::::: : : : : : : : .. UGCACUGGCC(Cleavage | pacid=371699 |
| 19 | 998 | 1018 UGGAGAAGC/ :.. : : : : : : : : : UGUAGGAGC(Cleavage | pacid=371749 |
| 20 | 564 | 584 UGGAGAAGC/ : : : : : : : : : : . CGAACGUGCC Cleavage | pacid=371759 |
| 21 | 564 | 584 UGGAGAAGC/ : : : : : : : : : : . CGAACGUGCC Cleavage | pacid=371759 |
| 22 | 78 | 97 UGGAGAAGC/ :.. : : : : : : : : : UGCAUGU-UC Cleavage | pacid=371675 |
| 23 | 49 | 69 UGGAGAAGC/ :.. : : : : : : : : : GGUACAUGU(Cleavage | pacid=371422 |
| 24 | 49 | 69 UGGAGAAGC/ :.. : : : : : : : : : GGUACAUGU(Cleavage | pacid=371422 |
| 25 | 3477 | 3497 UGGAGAAGC/ : : : : : : : : : : GGGCUGUGC(Cleavage | pacid=371724 |
| 26 | 372 | 392 UGGAGAAGC/ :.. : : : : : : : : : AGCGUUUGC(Cleavage | pacid=371721 |
| 27 | 304 | 324 UGGAGAAGC/ : : : : : : : : : : UCUCGUGC(Cleavage | pacid=371530 |
| 28 | 2017 | 2037 UGGAGAAGC/ :.. : : : : : : : : : GGCAUGUCU(Cleavage | pacid=371461 |
| 29 | 1749 | 1769 UGGAGAAGC/ :.. : : : : : : : : : GGCAUGUCU(Cleavage | pacid=371461 |
| 30 | 151 | 171 UGGAGAAGC/ :.. : : : : : : : : : GCCGCUUGC(Cleavage | pacid=371589 |
| 31 | 151 | 171 UGGAGAAGC/ :.. : : : : : : : : : GCCGCUUGC(Cleavage | pacid=371589 |
| 32 | 1700 | 1720 UGGAGAAGC/ :.. : : : : : : : : : GGCAUGUCU(Cleavage | pacid=371461 |
| 33 | 1369 | 1389 UGGAGAAGC/ :.. : : : : : : : : : CGCAUCUGCC Cleavage | pacid=371646 |
| 34 | 775 | 795 UGGAGAAGC/ : : : : : : : : : : . AGUUCGUGU(Translation | pacid=371518 |
| 35 | 1011 | 1031 UGGAGAAGC/ :.. : : : : : : : : : AGUACGGGC/ Cleavage | pacid=371742 |
| 36 | 879 | 899 UGGAGAAGC/ :.. : : : : : : : : : AGUACGGGC/ Cleavage | pacid=371742 |
| 37 | 772 | 792 UGGAGAAGC/ :.. : : : : : : : : : AGUGCAUGC(Cleavage | pacid=371577 |
| 38 | 526 | 546 UGGAGAAGC/ : ::::: : : : : : : : UGCAUGUGC(Cleavage | pacid=371422 |
| 39 | 220 | 240 UGGAGAAGC/ : ::::: : : : : : : : ACCACGUGC(Cleavage | pacid=371515 |
| 40 | 1359 | 1379 UGGAGAAGC/ : ::::: : : : : : : : UGCACUUGG(Cleavage | pacid=371586 |
| 41 | 1415 | 1435 UGGAGAAGC/ :.. : ::::: : : : : : : : UGUUUGUGU Cleavage | pacid=371487 |
| 42 | 1237 | 1257 UGGAGAAGC/ :.. : ::::: : : : : : : : UGUUCGUGC(Translation | pacid=371708 |
| 43 | 1208 | 1228 UGGAGAAGC/ :.. : ::::: : : : : : : : UGUUCGUGC(Translation | pacid=371708 |
| 44 | 238 | 257 UGGAGAAGC/ : ::::: : : : : : : : CGCACGUGCC Cleavage | pacid=371484 |
| 45 | 182 | 202 UGGAGAAGC/ :.. : : : : : : : : : GGUAUGUGC. Cleavage | pacid=371500 |
| 46 | 210 | 230 UGGAGAAGC/ : ::::: : : : : : : : ... AGCACGUGCC Translation | pacid=371623 |
| 47 | 676 | 696 UGGAGAAGC/ :.. : : : : : : : : : UGCGAGGGU(Cleavage | pacid=371516 |

| | | | | |
|----|------|-----------------|-------------------------------|--------------|
| 1 | | | | |
| 2 | 372 | 392 UGGAGAAGC/ | ... ::::: AGCGUUUGC(Cleavage | pacid=371721 |
| 3 | 304 | 324 UGGAGAAGC/ | ::::: UCUCGUGC(Cleavage | pacid=371530 |
| 4 | 2017 | 2037 UGGAGAAGC/ | ::::: GGCAUGUCU(Cleavage | pacid=371461 |
| 5 | 1749 | 1769 UGGAGAAGC/ | ::::: GGCAUGUCU(Cleavage | pacid=371461 |
| 6 | 151 | 171 UGGAGAAGC/ | ::: GCCGCUUGC(Cleavage | pacid=371589 |
| 7 | 151 | 171 UGGAGAAGC/ | ::: GCCGCUUGC(Cleavage | pacid=371589 |
| 8 | 1700 | 1720 UGGAGAAGC/ | ::::: GGCAUGUCU(Cleavage | pacid=371461 |
| 9 | 1369 | 1389 UGGAGAAGC/ | ::: CGCAUCUGCC(Cleavage | pacid=371646 |
| 10 | 775 | 795 UGGAGAAGC/ | : ::::: AGUUCGUGU(Translation | pacid=371518 |
| 11 | 1011 | 1031 UGGAGAAGC/ | ::: AGUACGGGC(Cleavage | pacid=371742 |
| 12 | 879 | 899 UGGAGAAGC/ | ::: AGUACGGGC(Cleavage | pacid=371742 |
| 13 | 772 | 792 UGGAGAAGC/ | ::: AGUGCAUGC(Cleavage | pacid=371577 |
| 14 | 526 | 546 UGGAGAAGC/ | ::::: UGCAUGUGC(Cleavage | pacid=371422 |
| 15 | 220 | 240 UGGAGAAGC/ | ::::: ACCACGUGC(Cleavage | pacid=371515 |
| 16 | 1359 | 1379 UGGAGAAGC/ | ::: UGCACUUGG(Cleavage | pacid=371586 |
| 17 | 1415 | 1435 UGGAGAAGC/ | ::: UGUUUGUGU(Cleavage | pacid=371487 |
| 18 | 1237 | 1257 UGGAGAAGC/ | ::: UGUUCGUGC(Translation | pacid=371708 |
| 19 | 1208 | 1228 UGGAGAAGC/ | ::: UGUUCGUGC(Translation | pacid=371708 |
| 20 | 238 | 257 UGGAGAAGC/ | ::::: CGCACGUGCC(Cleavage | pacid=371484 |
| 21 | 182 | 202 UGGAGAAGC/ | ::: GGU AUGUGC(Cleavage | pacid=371500 |
| 22 | 210 | 230 UGGAGAAGC/ | ::: AGCACGUGCC(Translation | pacid=371623 |
| 23 | 676 | 696 UGGAGAAGC/ | ::: UGCGAGGUG(Cleavage | pacid=371516 |
| 24 | 1409 | 1429 UGGAGAAGC/ | ::: UGCUGGUGC(Cleavage | pacid=371770 |
| 25 | 480 | 500 UGGAGAAGC/ | ::: UGCAAGUUU(Cleavage | pacid=371764 |
| 26 | 876 | 896 UGGAGAAGC/ | ::: UGCAGUUGC(Translation | pacid=371754 |
| 27 | 1302 | 1321 UGGAGAAGC/ | ::::: AGCAUGUGC(Cleavage | pacid=371566 |
| 28 | 1139 | 1159 UGGAGAAGC/ | ::: UGCACUGGC(Cleavage | pacid=371699 |
| 29 | 998 | 1018 UGGAGAAGC/ | ::: UGUAGGAGC(Cleavage | pacid=371749 |
| 30 | 564 | 584 UGGAGAAGC/ | ::: CGAACGUGCC(Cleavage | pacid=371759 |
| 31 | 564 | 584 UGGAGAAGC/ | ::: CGAACGUGCC(Cleavage | pacid=371759 |
| 32 | 78 | 97 UGGAGAAGC/ | ::: UGCAUGU-UC(Cleavage | pacid=371675 |
| 33 | 49 | 69 UGGAGAAGC/ | ::: GGUACAUGU(Cleavage | pacid=371422 |
| 34 | 49 | 69 UGGAGAAGC/ | ::: GGUACAUGU(Cleavage | pacid=371422 |
| 35 | 3477 | 3497 UGGAGAAGC/ | ::::: GGGCUGUGC(Cleavage | pacid=371724 |
| 36 | 372 | 392 UGGAGAAGC/ | ... ::::: AGCGUUUGC(Cleavage | pacid=371721 |
| 37 | 304 | 324 UGGAGAAGC/ | ::::: UCUCGUGC(Cleavage | pacid=371530 |
| 38 | 2017 | 2037 UGGAGAAGC/ | ::::: GGCAUGUCU(Cleavage | pacid=371461 |
| 39 | 1749 | 1769 UGGAGAAGC/ | ::::: GGCAUGUCU(Cleavage | pacid=371461 |
| 40 | 151 | 171 UGGAGAAGC/ | ::: GCCGCUUGC(Cleavage | pacid=371589 |
| 41 | 151 | 171 UGGAGAAGC/ | ::: GCCGCUUGC(Cleavage | pacid=371589 |
| 42 | 1700 | 1720 UGGAGAAGC/ | ::::: GGCAUGUCU(Cleavage | pacid=371461 |
| 43 | 1369 | 1389 UGGAGAAGC/ | ::: CGCAUCUGCC(Cleavage | pacid=371646 |
| 44 | 775 | 795 UGGAGAAGC/ | : ::::: AGUUCGUGU(Translation | pacid=371518 |
| 45 | 1011 | 1031 UGGAGAAGC/ | ::: AGUACGGGC(Cleavage | pacid=371742 |
| 46 | 879 | 899 UGGAGAAGC/ | ::: AGUACGGGC(Cleavage | pacid=371742 |
| 47 | 772 | 792 UGGAGAAGC/ | ::: AGUGCAUGC(Cleavage | pacid=371577 |

| | | | |
|----|------|---|--------------|
| 1 | | | |
| 2 | 526 | 546 UGGAGAAGC/ ::::::::::: ::... UGCAUGUGC Cleavage | pacid=371422 |
| 3 | 220 | 240 UGGAGAAGC/ ::::::::::: ACCACGUGCL Cleavage | pacid=371515 |
| 4 | 1359 | 1379 UGGAGAAGC/ ::::: : : : ::::: UGCACUUGG Cleavage | pacid=371586 |
| 5 | 1415 | 1435 UGGAGAAGC/ :. : ::::::::::: UGUUUGUGU Cleavage | pacid=371487 |
| 6 | 1237 | 1257 UGGAGAAGC/ :. : ::::: : ::::: UGUUCGUGC Translation | pacid=371708 |
| 7 | 1208 | 1228 UGGAGAAGC/ :. : ::::: : ::::: UGUUCGUGC Translation | pacid=371708 |
| 8 | | | |
| 9 | 238 | 257 UGGAGAAGC/ ::::::::::: ::::: CGCACGUGCC Cleavage | pacid=371484 |
| 10 | 182 | 202 UGGAGAAGC/ : ::::: : : ::::: GGU AUGUGC. Cleavage | pacid=371500 |
| 11 | 210 | 230 UGGAGAAGC/ ::::::::::: ::::: ... AGCACGUGCC Translation | pacid=371623 |
| 12 | 676 | 696 UGGAGAAGC/ :. : : ::::::::::: UGCGAGGGU Cleavage | pacid=371516 |
| 13 | 1409 | 1429 UGGAGAAGC/ : : : ::::::::::: : UGCUGGUGC Cleavage | pacid=371770 |
| 14 | 480 | 500 UGGAGAAGC/ : : : : ::::::::::: : UGCAAGUUU Cleavage | pacid=371764 |
| 15 | 876 | 896 UGGAGAAGC/ : : : : ::::::::::: UGCAGUUGC Translation | pacid=371754 |
| 16 | 1302 | 1321 UGGAGAAGC/ : ::::::::::: : : : AGCAUGUGC Cleavage | pacid=371566 |
| 17 | 1139 | 1159 UGGAGAAGC/ : : : : ::::::::::: : UGCACUGGCC Cleavage | pacid=371699 |
| 18 | 998 | 1018 UGGAGAAGC/ : : : : ::::::::::: UGUAGGAGC Cleavage | pacid=371749 |
| 19 | 564 | 584 UGGAGAAGC/ : ::::::::::: : CGAACGUGCC Cleavage | pacid=371759 |
| 20 | 564 | 584 UGGAGAAGC/ : ::::::::::: : CGAACGUGCC Cleavage | pacid=371759 |
| 21 | 78 | 97 UGGAGAAGC/ : : : : ::::::::::: UGCAUGU-UC Cleavage | pacid=371675 |
| 22 | 49 | 69 UGGAGAAGC/ : : : : ::::::::::: GGUACAUGU Cleavage | pacid=371422 |
| 23 | 49 | 69 UGGAGAAGC/ : : : : ::::::::::: GGUACAUGU Cleavage | pacid=371422 |
| 24 | 3477 | 3497 UGGAGAAGC/ : ::::::::::: : : GGCUGUGC Cleavage | pacid=371724 |
| 25 | 372 | 392 UGGAGAAGC/ :. : ::::::::::: : AGCGUUUGC Cleavage | pacid=371721 |
| 26 | 304 | 324 UGGAGAAGC/ : ::::::::::: : UCUCGUGCL Cleavage | pacid=371530 |
| 27 | 2017 | 2037 UGGAGAAGC/ : : : : ::::::::::: : GGCAUGUCU Cleavage | pacid=371461 |
| 28 | 1749 | 1769 UGGAGAAGC/ : : : : ::::::::::: : GGCAUGUCU Cleavage | pacid=371461 |
| 29 | 151 | 171 UGGAGAAGC/ : : : : ::::::::::: GCCGCUUGCL Cleavage | pacid=371589 |
| 30 | 151 | 171 UGGAGAAGC/ : : : : ::::::::::: GCCGCUUGCL Cleavage | pacid=371589 |
| 31 | 1700 | 1720 UGGAGAAGC/ : : : : ::::::::::: : GGCAUGUCU Cleavage | pacid=371461 |
| 32 | 1369 | 1389 UGGAGAAGC/ :. : ::::::::::: : CGCAUCUGCC Cleavage | pacid=371646 |
| 33 | 775 | 795 UGGAGAAGC/ :. : ::::: : ::::: AGUUCGUGU Translation | pacid=371518 |
| 34 | 1011 | 1031 UGGAGAAGC/ : : : : ::::::::::: AGUACGGGC Cleavage | pacid=371742 |
| 35 | 879 | 899 UGGAGAAGC/ : : : : ::::::::::: AGUACGGGC Cleavage | pacid=371742 |
| 36 | 772 | 792 UGGAGAAGC/ :. : ::::::::::: : AGUGCAUGC Cleavage | pacid=371577 |
| 37 | 526 | 546 UGGAGAAGC/ ::::::::::: ::... UGCAUGUGC Cleavage | pacid=371422 |
| 38 | 220 | 240 UGGAGAAGC/ ::::::::::: ACCACGUGCL Cleavage | pacid=371515 |
| 39 | 1359 | 1379 UGGAGAAGC/ ::::: : : : ::::: UGCACUUGG Cleavage | pacid=371586 |
| 40 | 1415 | 1435 UGGAGAAGC/ :. : ::::::::::: UGUUUGUGU Cleavage | pacid=371487 |
| 41 | 1237 | 1257 UGGAGAAGC/ :. : ::::: : ::::: UGUUCGUGC Translation | pacid=371708 |
| 42 | 1208 | 1228 UGGAGAAGC/ :. : ::::: : ::::: UGUUCGUGC Translation | pacid=371708 |
| 43 | | | |
| 44 | 238 | 257 UGGAGAAGC/ ::::::::::: ::::: CGCACGUGCC Cleavage | pacid=371484 |
| 45 | 182 | 202 UGGAGAAGC/ : ::::: : : ::::: GGU AUGUGC. Cleavage | pacid=371500 |
| 46 | 210 | 230 UGGAGAAGC/ ::::::::::: ::::: ... AGCACGUGCC Translation | pacid=371623 |
| 47 | 676 | 696 UGGAGAAGC/ :. : : ::::::::::: UGCGAGGGU Cleavage | pacid=371516 |
| 48 | 1409 | 1429 UGGAGAAGC/ : : : ::::::::::: : UGCUGGUGC Cleavage | pacid=371770 |
| 49 | 480 | 500 UGGAGAAGC/ : : : : ::::::::::: : UGCAAGUUU Cleavage | pacid=371764 |

| | | | | |
|----|------|-----------------|----------------------------------|--------------|
| 1 | | | | |
| 2 | 2017 | 2037 UGGAGAAGC/ | ::: :: :: GGCAUGUCU(Cleavage | pacid=371461 |
| 3 | 1749 | 1769 UGGAGAAGC/ | ::: :: :: GGCAUGUCU(Cleavage | pacid=371461 |
| 4 | 151 | 171 UGGAGAAGC/ | :: ::::: GCCGCUUGCL Cleavage | pacid=371589 |
| 5 | 151 | 171 UGGAGAAGC/ | :: ::::: GCCGCUUGCL Cleavage | pacid=371589 |
| 6 | 1700 | 1720 UGGAGAAGC/ | ::: :: :: GGCAUGUCU(Cleavage | pacid=371461 |
| 7 | 1369 | 1389 UGGAGAAGC/ | :: ::::: CGCAUCUGCC Cleavage | pacid=371646 |
| 8 | 775 | 795 UGGAGAAGC/ | :: ::::: AGUUCGUGU Translation | pacid=371518 |
| 9 | 1011 | 1031 UGGAGAAGC/ | ::: :: ::::: AGUACGGGC/ Cleavage | pacid=371742 |
| 10 | 879 | 899 UGGAGAAGC/ | ::: :: ::::: AGUACGGGC/ Cleavage | pacid=371742 |
| 11 | 772 | 792 UGGAGAAGC/ | ::: ::::: AGUGCAUGC(Cleavage | pacid=371577 |
| 12 | 526 | 546 UGGAGAAGC/ | ::: ::::: UGCAUGUGC(Cleavage | pacid=371422 |
| 13 | 220 | 240 UGGAGAAGC/ | ::: ::::: ACCACGUGCL Cleavage | pacid=371515 |
| 14 | 1359 | 1379 UGGAGAAGC/ | ::: :: ::::: UGCACUUGG(Cleavage | pacid=371586 |
| 15 | 1415 | 1435 UGGAGAAGC/ | ::: ::::: UGUUUGUGU Cleavage | pacid=371487 |
| 16 | 1237 | 1257 UGGAGAAGC/ | ::: ::::: UGUUCGUGC(Translation | pacid=371708 |
| 17 | 1208 | 1228 UGGAGAAGC/ | ::: ::::: UGUUCGUGC(Translation | pacid=371708 |
| 18 | 238 | 257 UGGAGAAGC/ | ::: ::::: CGCACGUGCC Cleavage | pacid=371484 |
| 19 | 182 | 202 UGGAGAAGC/ | ::: ::::: GGU AUGUGC Cleavage | pacid=371500 |
| 20 | 210 | 230 UGGAGAAGC/ | ::: ::::: AGCACGUGCC Translation | pacid=371623 |
| 21 | 676 | 696 UGGAGAAGC/ | ::: ::::: UGCGAGGGU(Cleavage | pacid=371516 |
| 22 | 1409 | 1429 UGGAGAAGC/ | ::: ::::: UGCUUGUGC(Cleavage | pacid=371770 |
| 23 | 480 | 500 UGGAGAAGC/ | ::: ::::: UGCAAGUUU(Cleavage | pacid=371764 |
| 24 | 876 | 896 UGGAGAAGC/ | ::: ::::: UGCAGUUGC(Translation | pacid=371754 |
| 25 | 1302 | 1321 UGGAGAAGC/ | ::: ::::: AGCAUGUGC(Cleavage | pacid=371566 |
| 26 | 1139 | 1159 UGGAGAAGC/ | ::: ::::: UGCACUGCC Cleavage | pacid=371699 |
| 27 | 998 | 1018 UGGAGAAGC/ | ::: ::::: UGUAGGAGC(Cleavage | pacid=371749 |
| 28 | 564 | 584 UGGAGAAGC/ | ::: ::::: CGAACGUGCC Cleavage | pacid=371759 |
| 29 | 564 | 584 UGGAGAAGC/ | ::: ::::: CGAACGUGCC Cleavage | pacid=371759 |
| 30 | 78 | 97 UGGAGAAGC/ | ::: ::::: UGCAUGU-UC Cleavage | pacid=371675 |
| 31 | 49 | 69 UGGAGAAGC/ | ::: ::::: GGUACAUGU(Cleavage | pacid=371422 |
| 32 | 49 | 69 UGGAGAAGC/ | ::: ::::: GGUACAUGU(Cleavage | pacid=371422 |
| 33 | 3477 | 3497 UGGAGAAGC/ | ::: ::::: GGGCUGUGC(Cleavage | pacid=371724 |
| 34 | 372 | 392 UGGAGAAGC/ | ::: ::::: AGCGUUUGC(Cleavage | pacid=371721 |
| 35 | 304 | 324 UGGAGAAGC/ | ::: ::::: UCUCGUGCL Cleavage | pacid=371530 |
| 36 | 2017 | 2037 UGGAGAAGC/ | ::: :: :: GGCAUGUCU(Cleavage | pacid=371461 |
| 37 | 1749 | 1769 UGGAGAAGC/ | ::: :: :: GGCAUGUCU(Cleavage | pacid=371461 |
| 38 | 151 | 171 UGGAGAAGC/ | :: ::::: GCCGCUUGCL Cleavage | pacid=371589 |
| 39 | 151 | 171 UGGAGAAGC/ | :: ::::: GCCGCUUGCL Cleavage | pacid=371589 |
| 40 | 1700 | 1720 UGGAGAAGC/ | ::: :: :: GGCAUGUCU(Cleavage | pacid=371461 |
| 41 | 1369 | 1389 UGGAGAAGC/ | :: ::::: CGCAUCUGCC Cleavage | pacid=371646 |
| 42 | 775 | 795 UGGAGAAGC/ | :: ::::: AGUUCGUGU Translation | pacid=371518 |
| 43 | 1011 | 1031 UGGAGAAGC/ | ::: :: ::::: AGUACGGGC/ Cleavage | pacid=371742 |
| 44 | 879 | 899 UGGAGAAGC/ | ::: :: ::::: AGUACGGGC/ Cleavage | pacid=371742 |
| 45 | 772 | 792 UGGAGAAGC/ | ::: ::::: AGUGCAUGC(Cleavage | pacid=371577 |
| 46 | 526 | 546 UGGAGAAGC/ | ::: ::::: UGCAUGUGC(Cleavage | pacid=371422 |
| 47 | 220 | 240 UGGAGAAGC/ | ::: ::::: ACCACGUGCL Cleavage | pacid=371515 |

| | | | |
|----|------|---|--------------|
| 1 | | | |
| 2 | 1359 | 1379 UGGAGAAGC/ ::::: : : : ::::: UGCACUUGG(Cleavage | pacid=371586 |
| 3 | 1415 | 1435 UGGAGAAGC/ :. :.....: UGUUUGUGUCleavage | pacid=371487 |
| 4 | 1237 | 1257 UGGAGAAGC/ :. :.....: UGUUCGUGC(Translation | pacid=371708 |
| 5 | | | |
| 6 | 1208 | 1228 UGGAGAAGC/ :. :.....: UGUUCGUGC(Translation | pacid=371708 |
| 7 | 238 | 257 UGGAGAAGC/ :.....: : : : : CGCACGUGCC Cleavage | pacid=371484 |
| 8 | 182 | 202 UGGAGAAGC/ :.....: : : : : GGU AUGUGC.Cleavage | pacid=371500 |
| 9 | | | |
| 10 | 210 | 230 UGGAGAAGC/ :.....: : : : : ... AGCACGUGCC Translation | pacid=371623 |
| 11 | 676 | 696 UGGAGAAGC/ :. : :.....: UGCGAGGGU(Cleavage | pacid=371516 |
| 12 | 1409 | 1429 UGGAGAAGC/ :. :.....: : : : : UGCUGGUGC(Cleavage | pacid=371770 |
| 13 | | | |
| 14 | 480 | 500 UGGAGAAGC/ :. : :.....: : : : : UGCAAGUUU(Cleavage | pacid=371764 |
| 15 | 876 | 896 UGGAGAAGC/ :. : :.....: : : : : UGCAGUUGC(Translation | pacid=371754 |
| 16 | 1302 | 1321 UGGAGAAGC/ :.....: : : : : AGCAUGUGC(Cleavage | pacid=371566 |
| 17 | | | |
| 18 | 1139 | 1159 UGGAGAAGC/ :.....: : : : : ... UGCACUGGCC Cleavage | pacid=371699 |
| 19 | 998 | 1018 UGGAGAAGC/ :. : :.....: UGUAGGAGC(Cleavage | pacid=371749 |
| 20 | 564 | 584 UGGAGAAGC/ :.....: : : : : CGAACGUGCC Cleavage | pacid=371759 |
| 21 | | | |
| 22 | 564 | 584 UGGAGAAGC/ :.....: : : : : CGAACGUGCC Cleavage | pacid=371759 |
| 23 | 78 | 97 UGGAGAAGC/ :.....: : : : : UGCAUGU-UC Cleavage | pacid=371675 |
| 24 | 49 | 69 UGGAGAAGC/ :. : :.....: : : : : GGUACAUGU(Cleavage | pacid=371422 |
| 25 | | | |
| 26 | 49 | 69 UGGAGAAGC/ :. : :.....: : : : : GGUACAUGU(Cleavage | pacid=371422 |
| 27 | 3477 | 3497 UGGAGAAGC/ :.....: : : : : GGGCUGUGC(Cleavage | pacid=371724 |
| 28 | 372 | 392 UGGAGAAGC/ :. :.....: : : : : AGCGUUUGC(Cleavage | pacid=371721 |
| 29 | | | |
| 30 | 304 | 324 UGGAGAAGC/ :.....: : : : : UCUCGUGC(Cleavage | pacid=371530 |
| 31 | 2017 | 2037 UGGAGAAGC/ :. : :.....: : : : : GGCAUGUCU(Cleavage | pacid=371461 |
| 32 | 1749 | 1769 UGGAGAAGC/ :. : :.....: : : : : GGCAUGUCU(Cleavage | pacid=371461 |
| 33 | | | |
| 34 | 151 | 171 UGGAGAAGC/ :. :.....: : : : : GCCGCUUGC(Cleavage | pacid=371589 |
| 35 | 151 | 171 UGGAGAAGC/ :. :.....: : : : : GCCGCUUGC(Cleavage | pacid=371589 |
| 36 | 1700 | 1720 UGGAGAAGC/ :. : :.....: : : : : GGCAUGUCU(Cleavage | pacid=371461 |
| 37 | | | |
| 38 | 1369 | 1389 UGGAGAAGC/ :. :.....: : : : : CGCAUCUGCC Cleavage | pacid=371646 |
| 39 | 775 | 795 UGGAGAAGC/ :. :.....: : : : : AGUUCGUGU(Translation | pacid=371518 |
| 40 | 1011 | 1031 UGGAGAAGC/ :. : :.....: : : : : AGUACGGGC(Cleavage | pacid=371742 |
| 41 | | | |
| 42 | 879 | 899 UGGAGAAGC/ :. : :.....: : : : : AGUACGGGC(Cleavage | pacid=371742 |
| 43 | 772 | 792 UGGAGAAGC/ :. : :.....: : : : : AGUGCAUGC(Cleavage | pacid=371577 |
| 44 | 526 | 546 UGGAGAAGC/ :.....: : : : : UGCAUGUGC(Cleavage | pacid=371422 |
| 45 | 220 | 240 UGGAGAAGC/ :.....: : : : : ACCACGUGC(Cleavage | pacid=371515 |
| 46 | | | |
| 47 | 1359 | 1379 UGGAGAAGC/ :.....: : : : : UGCACUUGG(Cleavage | pacid=371586 |
| 48 | 1415 | 1435 UGGAGAAGC/ :. :.....: : : : : UGUUUGUGUCleavage | pacid=371487 |
| 49 | 1237 | 1257 UGGAGAAGC/ :. :.....: : : : : UGUUCGUGC(Translation | pacid=371708 |
| 50 | | | |
| 51 | 1208 | 1228 UGGAGAAGC/ :. :.....: : : : : UGUUCGUGC(Translation | pacid=371708 |
| 52 | 238 | 257 UGGAGAAGC/ :.....: : : : : CGCACGUGCC Cleavage | pacid=371484 |
| 53 | 182 | 202 UGGAGAAGC/ :.....: : : : : GGU AUGUGC.Cleavage | pacid=371500 |
| 54 | | | |
| 55 | 210 | 230 UGGAGAAGC/ :.....: : : : : ... AGCACGUGCC Translation | pacid=371623 |
| 56 | 676 | 696 UGGAGAAGC/ :. : :.....: UGCGAGGGU(Cleavage | pacid=371516 |
| 57 | 1409 | 1429 UGGAGAAGC/ :. :.....: : : : : UGCUGGUGC(Cleavage | pacid=371770 |
| 58 | | | |
| 59 | 480 | 500 UGGAGAAGC/ :. : :.....: : : : : UGCAAGUUU(Cleavage | pacid=371764 |
| 60 | 876 | 896 UGGAGAAGC/ :. : :.....: : : : : UGCAGUUGC(Translation | pacid=371754 |
| | 1302 | 1321 UGGAGAAGC/ :.....: : : : : AGCAUGUGC(Cleavage | pacid=371566 |

| | | | | | |
|----|------|-----------------|----------------------|--------------|--------------|
| 1 | | | | | |
| 2 | 151 | 171 UGGAGAAGC/ | :: ::::: GCCGCUUGCL | Cleavage | pacid=371589 |
| 3 | 151 | 171 UGGAGAAGC/ | :: ::::: GCCGCUUGCL | Cleavage | pacid=371589 |
| 4 | 1700 | 1720 UGGAGAAGC/ | ::: : : : GGCAUGUCU | (Cleavage | pacid=371461 |
| 5 | 1369 | 1389 UGGAGAAGC/ | ::: : : : CGCAUCUGCC | Cleavage | pacid=371646 |
| 6 | 775 | 795 UGGAGAAGC/ | : : : : : AGUUCGUGU | Translation | pacid=371518 |
| 7 | 1011 | 1031 UGGAGAAGC/ | ::: : : : AGUACGGGC/ | Cleavage | pacid=371742 |
| 8 | 879 | 899 UGGAGAAGC/ | ::: : : : AGUACGGGC/ | Cleavage | pacid=371742 |
| 9 | 772 | 792 UGGAGAAGC/ | ::: : : : AGUGCAUGCC | (Cleavage | pacid=371577 |
| 10 | 526 | 546 UGGAGAAGC/ | ::: : : : UGCAUGUGCI | Cleavage | pacid=371422 |
| 11 | 220 | 240 UGGAGAAGC/ | ::: : : : ACCACGUGCL | Cleavage | pacid=371515 |
| 12 | 1359 | 1379 UGGAGAAGC/ | ::: : : : UGCACUUGG | (Cleavage | pacid=371586 |
| 13 | 1415 | 1435 UGGAGAAGC/ | ::: : : : UGUUUGUGU | Cleavage | pacid=371487 |
| 14 | 1237 | 1257 UGGAGAAGC/ | ::: : : : UGUUCGUGC | (Translation | pacid=371708 |
| 15 | 1208 | 1228 UGGAGAAGC/ | ::: : : : UGUUCGUGC | (Translation | pacid=371708 |
| 16 | 238 | 257 UGGAGAAGC/ | ::: : : : CGCACGUGCC | Cleavage | pacid=371484 |
| 17 | 182 | 202 UGGAGAAGC/ | ::: : : : GGU AUGUGC | Cleavage | pacid=371500 |
| 18 | 210 | 230 UGGAGAAGC/ | ::: : : : AGCACGUGCC | Translation | pacid=371623 |
| 19 | 676 | 696 UGGAGAAGC/ | ::: : : : UGCGAGGGU | (Cleavage | pacid=371516 |
| 20 | 1409 | 1429 UGGAGAAGC/ | ::: : : : UGCUGGUGCI | Cleavage | pacid=371770 |
| 21 | 480 | 500 UGGAGAAGC/ | ::: : : : UGCAAGUUU | (Cleavage | pacid=371764 |
| 22 | 876 | 896 UGGAGAAGC/ | ::: : : : UGCAGUUGCI | Translation | pacid=371754 |
| 23 | 1302 | 1321 UGGAGAAGC/ | ::: : : : AGCAUGUGCC | (Cleavage | pacid=371566 |
| 24 | 1139 | 1159 UGGAGAAGC/ | ::: : : : UGCACUGGCC | Cleavage | pacid=371699 |
| 25 | 998 | 1018 UGGAGAAGC/ | ::: : : : UGUAGGAGCI | Cleavage | pacid=371749 |
| 26 | 564 | 584 UGGAGAAGC/ | ::: : : : CGAACGUGCC | Cleavage | pacid=371759 |
| 27 | 564 | 584 UGGAGAAGC/ | ::: : : : CGAACGUGCC | Cleavage | pacid=371759 |
| 28 | 78 | 97 UGGAGAAGC/ | ::: : : : UGCAUGU-UC | Cleavage | pacid=371675 |
| 29 | 49 | 69 UGGAGAAGC/ | ::: : : : GGUACAUGUI | Cleavage | pacid=371422 |
| 30 | 49 | 69 UGGAGAAGC/ | ::: : : : GGUACAUGUI | Cleavage | pacid=371422 |
| 31 | 3477 | 3497 UGGAGAAGC/ | ::: : : : GGGCUGUGCI | Cleavage | pacid=371724 |
| 32 | 372 | 392 UGGAGAAGC/ | ::: : : : AGCGUUUGCC | (Cleavage | pacid=371721 |
| 33 | 304 | 324 UGGAGAAGC/ | ::: : : : UCUCGUGCL | Cleavage | pacid=371530 |
| 34 | 2017 | 2037 UGGAGAAGC/ | ::: : : : GGCAUGUCU | (Cleavage | pacid=371461 |
| 35 | 1749 | 1769 UGGAGAAGC/ | ::: : : : GGCAUGUCU | (Cleavage | pacid=371461 |
| 36 | 151 | 171 UGGAGAAGC/ | ::: : : : GCCGCUUGCL | Cleavage | pacid=371589 |
| 37 | 151 | 171 UGGAGAAGC/ | ::: : : : GCCGCUUGCL | Cleavage | pacid=371589 |
| 38 | 1700 | 1720 UGGAGAAGC/ | ::: : : : GGCAUGUCU | (Cleavage | pacid=371461 |
| 39 | 1369 | 1389 UGGAGAAGC/ | ::: : : : CGCAUCUGCC | Cleavage | pacid=371646 |
| 40 | 775 | 795 UGGAGAAGC/ | : : : : : AGUUCGUGU | Translation | pacid=371518 |
| 41 | 1011 | 1031 UGGAGAAGC/ | ::: : : : AGUACGGGC/ | Cleavage | pacid=371742 |
| 42 | 879 | 899 UGGAGAAGC/ | ::: : : : AGUACGGGC/ | Cleavage | pacid=371742 |
| 43 | 772 | 792 UGGAGAAGC/ | ::: : : : AGUGCAUGCC | (Cleavage | pacid=371577 |
| 44 | 526 | 546 UGGAGAAGC/ | ::: : : : UGCAUGUGCI | Cleavage | pacid=371422 |
| 45 | 220 | 240 UGGAGAAGC/ | ::: : : : ACCACGUGCL | Cleavage | pacid=371515 |
| 46 | 1359 | 1379 UGGAGAAGC/ | ::: : : : UGCACUUGG | (Cleavage | pacid=371586 |
| 47 | 1415 | 1435 UGGAGAAGC/ | ::: : : : UGUUUGUGU | Cleavage | pacid=371487 |

| | | | | |
|----|------|---|--------------|--|
| 1 | | | | |
| 2 | 564 | 584 UGGAGAAGC/ : ::::: : . CGAACGUGCC Cleavage | pacid=371759 | |
| 3 | 564 | 584 UGGAGAAGC/ : ::::: : . CGAACGUGCC Cleavage | pacid=371759 | |
| 4 | 78 | 97 UGGAGAAGC/ ::::: : : : : : : UGCAUGU-UC Cleavage | pacid=371675 | |
| 5 | 49 | 69 UGGAGAAGC/ : : : : : : : : : GGUACAUGU Cleavage | pacid=371422 | |
| 6 | 49 | 69 UGGAGAAGC/ : : : : : : : : : GGUACAUGU Cleavage | pacid=371422 | |
| 7 | 3477 | 3497 UGGAGAAGC/ : : : : : : : : : GGGCUGUGC Cleavage | pacid=371724 | |
| 8 | 372 | 392 UGGAGAAGC/ : : : : : : : : : AGCGUUUGC Cleavage | pacid=371721 | |
| 9 | 304 | 324 UGGAGAAGC/ : : : : : : : : : UCUCGUGC Cleavage | pacid=371530 | |
| 10 | 2017 | 2037 UGGAGAAGC/ : : : : : : : : : GGCAUGUCU Cleavage | pacid=371461 | |
| 11 | 1749 | 1769 UGGAGAAGC/ : : : : : : : : : GGCAUGUCU Cleavage | pacid=371461 | |
| 12 | 151 | 171 UGGAGAAGC/ : : : : : : : : : GCCGCUUGC Cleavage | pacid=371589 | |
| 13 | 151 | 171 UGGAGAAGC/ : : : : : : : : : GCCGCUUGC Cleavage | pacid=371589 | |
| 14 | 1700 | 1720 UGGAGAAGC/ : : : : : : : : : GGCAUGUCU Cleavage | pacid=371461 | |
| 15 | 1369 | 1389 UGGAGAAGC/ : : : : : : : : : CGCAUCUGCC Cleavage | pacid=371646 | |
| 16 | 775 | 795 UGGAGAAGC/ : : : : : : : : : AGUUCGUGU Translation | pacid=371518 | |
| 17 | 1011 | 1031 UGGAGAAGC/ : : : : : : : : : AGUACGGGC Cleavage | pacid=371742 | |
| 18 | 879 | 899 UGGAGAAGC/ : : : : : : : : : AGUACGGGC Cleavage | pacid=371742 | |
| 19 | 772 | 792 UGGAGAAGC/ : : : : : : : : : AGUGCAUGC Cleavage | pacid=371577 | |
| 20 | 525 | 546 UGGAGAAGC/ : : : : : : : : : AUGCAUGUG Cleavage | pacid=371422 | |
| 21 | 675 | 696 UGGAGAAGC/ : : : : : : : : : UUGCGAGGG Cleavage | pacid=371516 | |
| 22 | 219 | 240 UGGAGAAGC/ : : : : : : : : : AACCAGUGC Cleavage | pacid=371515 | |
| 23 | 77 | 97 UGGAGAAGC/ : : : : : : : : : UUGCAUGU-L Cleavage | pacid=371675 | |
| 24 | 1358 | 1379 UGGAGAAGC/ : : : : : : : : : CUGCACUUG Cleavage | pacid=371586 | |
| 25 | 1414 | 1435 UGGAGAAGC/ : : : : : : : : : CUGUUUGUG Cleavage | pacid=371487 | |
| 26 | 1236 | 1257 UGGAGAAGC/ : : : : : : : : : AUGUUCGUG Translation | pacid=371708 | |
| 27 | 1207 | 1228 UGGAGAAGC/ : : : : : : : : : AUGUUCGUG Translation | pacid=371708 | |
| 28 | 784 | 805 UGGAGAAGC/ : : : : : : : : : UUCCACGUG Translation | pacid=371513 | |
| 29 | 237 | 257 UGGAGAAGC/ : : : : : : : : : ACGCACGUGC Cleavage | pacid=371484 | |
| 30 | 819 | 839 UGGAGAAGC/ : : : : : : : : : UUGCACCU-C Cleavage | pacid=371743 | |
| 31 | 819 | 839 UGGAGAAGC/ : : : : : : : : : UUGCACCU-C Cleavage | pacid=371743 | |
| 32 | 181 | 202 UGGAGAAGC/ : : : : : : : : : CGGUAUGUG Cleavage | pacid=371500 | |
| 33 | 209 | 230 UGGAGAAGC/ : : : : : : : : : ...AAGCACGUG Translation | pacid=371623 | |
| 34 | 1408 | 1429 UGGAGAAGC/ : : : : : : : : : CUGCUGGUG Cleavage | pacid=371770 | |
| 35 | 479 | 500 UGGAGAAGC/ : : : : : : : : : CUGCAAGUUC Cleavage | pacid=371764 | |
| 36 | 875 | 896 UGGAGAAGC/ : : : : : : : : : GUGCAGUUG Translation | pacid=371754 | |
| 37 | 1301 | 1321 UGGAGAAGC/ : : : : : : : : : CAGCAUGUG Cleavage | pacid=371566 | |
| 38 | 1222 | 1243 UGGAGAAGC/ : : : : : : : : : AACC GGUG Cleavage | pacid=371718 | |
| 39 | 1138 | 1159 UGGAGAAGC/ : : : : : : : : : CUGCACUGG Cleavage | pacid=371699 | |
| 40 | 997 | 1018 UGGAGAAGC/ : : : : : : : : : CUGUAGGAG Cleavage | pacid=371749 | |
| 41 | 48 | 69 UGGAGAAGC/ : : : : : : : : : UGGUACAUG Cleavage | pacid=371422 | |
| 42 | 48 | 69 UGGAGAAGC/ : : : : : : : : : UGGUACAUG Cleavage | pacid=371422 | |
| 43 | 3461 | 3482 UGGAGAAGC/ : : : : : : : : : UUCUAUCUG Cleavage | pacid=371775 | |
| 44 | 890 | 911 UGGAGAAGC/ : : : : : : : : : UGCACCGCC Translation | pacid=371489 | |
| 45 | 273 | 293 UGGAGAAGC/ : : : : : : : : : UGUGUGUGU Cleavage | pacid=371747 | |
| 46 | 894 | 914 UGGAGAAGC/ : : : : : : : : : UGCAUGUGU Translation | pacid=371531 | |
| 47 | 81 | 100 UGGAGAAGC/ : : : : : : : : : UGCAUGUGU Translation | pacid=371483 | |

| | | | | |
|----|------|-----------------|------------------------|--------------|
| 1 | | | | |
| 2 | 81 | 100 UGGAGAAGC/ | UGCAUGUGC(Translation | pacid=371483 |
| 3 | 210 | 229 UGGAGAAGC/ | UGCACGUGCC Cleavage | pacid=371445 |
| 4 | 210 | 229 UGGAGAAGC/ | UGCACGUGCC Cleavage | pacid=371445 |
| 5 | | | | |
| 6 | 67 | 88 UGGAGAAGC/ | UGCAACGUGI Cleavage | pacid=371715 |
| 7 | 2692 | 2712 UGGAGAAGC/ | UGCAUCUGU(Cleavage | pacid=371592 |
| 8 | 1441 | 1461 UGGAGAAGC/ | UGCUGUGU Translation | pacid=371656 |
| 9 | | | | |
| 10 | 393 | 413 UGGAGAAGC/ | UGUCUGUGU Cleavage | pacid=371678 |
| 11 | 1867 | 1887 UGGAGAAGC/ | UGUAUUUGC.Cleavage | pacid=371738 |
| 12 | 1795 | 1815 UGGAGAAGC/ | UGUAUUUGC.Cleavage | pacid=371738 |
| 13 | | | | |
| 14 | 2809 | 2829 UGGAGAAGC/ | GGCACGUGCC(Translation | pacid=371462 |
| 15 | 639 | 659 UGGAGAAGC/ | UAGACGUGUI Cleavage | pacid=371520 |
| 16 | 1429 | 1450 UGGAGAAGC/ | UGCUCAGUG(Cleavage | pacid=371468 |
| 17 | | | | |
| 18 | 1429 | 1450 UGGAGAAGC/ | UGCUCAGUG(Cleavage | pacid=371468 |
| 19 | 1946 | 1966 UGGAGAAGC/ | UGCAGUUGC(Cleavage | pacid=371764 |
| 20 | 1712 | 1732 UGGAGAAGC/ | UGCAGUUGC(Cleavage | pacid=371764 |
| 21 | | | | |
| 22 | 4127 | 4147 UGGAGAAGC/ | ACCAUGUGCC Cleavage | pacid=371756 |
| 23 | 3713 | 3733 UGGAGAAGC/ | ACCAUGUGCC Cleavage | pacid=371756 |
| 24 | 2142 | 2165 UGGAGAAGC/ | GGCACGUCCC Cleavage | pacid=371647 |
| 25 | | | | |
| 26 | 729 | 749 UGGAGAAGC/ | AGCAUGUGU(Cleavage | pacid=371776 |
| 27 | 729 | 749 UGGAGAAGC/ | AGCAUGUGU(Cleavage | pacid=371776 |
| 28 | 1576 | 1596 UGGAGAAGC/ | UUCUCUUGCI Translation | pacid=371530 |
| 29 | | | | |
| 30 | 549 | 569 UGGAGAAGC/ | AGCAUGUGU(Cleavage | pacid=371777 |
| 31 | 444 | 464 UGGAGAAGC/ | GACAUGUGCC(Translation | pacid=371607 |
| 32 | 449 | 469 UGGAGAAGC/ | AGCAUGUGCI Cleavage | pacid=371663 |
| 33 | | | | |
| 34 | 417 | 437 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371656 |
| 35 | 1075 | 1095 UGGAGAAGC/ | ACAACGUGCL Cleavage | pacid=371656 |
| 36 | 331 | 351 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371656 |
| 37 | | | | |
| 38 | 989 | 1009 UGGAGAAGC/ | ACAACGUGCL Cleavage | pacid=371656 |
| 39 | 1100 | 1120 UGGAGAAGC/ | AACACGUGU(Cleavage | pacid=371470 |
| 40 | 99 | 119 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371656 |
| 41 | | | | |
| 42 | 977 | 997 UGGAGAAGC/ | ACAACGUGCL Cleavage | pacid=371656 |
| 43 | 278 | 298 UGGAGAAGC/ | UGCACCUCCC Cleavage | pacid=371740 |
| 44 | 249 | 269 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371656 |
| 45 | | | | |
| 46 | 907 | 927 UGGAGAAGC/ | ACAACGUGCL Cleavage | pacid=371656 |
| 47 | 420 | 440 UGGAGAAGC/ | UGCUCUGCC Cleavage | pacid=371532 |
| 48 | 161 | 181 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371656 |
| 49 | | | | |
| 50 | 819 | 839 UGGAGAAGC/ | ACAACGUGCL Cleavage | pacid=371656 |
| 51 | 285 | 305 UGGAGAAGC/ | UGCUCUGCC Cleavage | pacid=371528 |
| 52 | 501 | 521 UGGAGAAGC/ | AGCAUGUGC(Cleavage | pacid=371779 |
| 53 | | | | |
| 54 | 611 | 631 UGGAGAAGC/ | UGCAAGUCUI Cleavage | pacid=371590 |
| 55 | 205 | 225 UGGAGAAGC/ | AGCAUGUGCI Cleavage | pacid=371599 |
| 56 | 179 | 200 UGGAGAAGC/ | ACCACGUGAC Cleavage | pacid=371457 |
| 57 | 4269 | 4289 UGGAGAAGC/ | UGAACAUGA(Cleavage | pacid=371579 |
| 58 | | | | |
| 59 | 4266 | 4286 UGGAGAAGC/ | UGAACAUGA(Cleavage | pacid=371579 |
| 60 | 1610 | 1630 UGGAGAAGC/ | UGCAGCUGC/ Cleavage | pacid=371622 |
| | 1571 | 1591 UGGAGAAGC/ | UGCAGCUGC/ Cleavage | pacid=371622 |

| | | | |
|----|------|---|--------------|
| 1 | | | |
| 2 | 1531 | 1551 UGGAGAAGC/::: :: :..... UGCAGCUGC/ Cleavage | pacid=371622 |
| 3 | 3830 | 3850 UGGAGAAGC/:: : :..... UGAACAUGUI Cleavage | pacid=371514 |
| 4 | 2950 | 2970 UGGAGAAGC/:: . :..... UGUUUGGGU Cleavage | pacid=371537 |
| 5 | 2890 | 2910 UGGAGAAGC/:: . :..... UGUUUGGGU Cleavage | pacid=371537 |
| 6 | 3661 | 3681 UGGAGAAGC/:: : :..... UGAACAUGUI Cleavage | pacid=371514 |
| 7 | 1224 | 1244 UGGAGAAGC/::: :: :..... UGCAGCUGC/ Cleavage | pacid=371622 |
| 8 | 890 | 911 UGGAGAAGC/::: : :..... UGCACCUGCC Translation | pacid=371489 |
| 9 | 273 | 293 UGGAGAAGC/::..... :..... UGUGUGUGU Cleavage | pacid=371747 |
| 10 | 894 | 914 UGGAGAAGC/::..... :..... UGCAUGUGU Translation | pacid=371531 |
| 11 | 81 | 100 UGGAGAAGC/::..... :..... UGCAUGUGC(Translation | pacid=371483 |
| 12 | 81 | 100 UGGAGAAGC/::..... :..... UGCAUGUGC(Translation | pacid=371483 |
| 13 | 210 | 229 UGGAGAAGC/::..... :..... UGCACGUGCC Cleavage | pacid=371445 |
| 14 | 210 | 229 UGGAGAAGC/::..... :..... UGCACGUGCC Cleavage | pacid=371445 |
| 15 | 67 | 88 UGGAGAAGC/::: :..... UGCAACGUGI Cleavage | pacid=371715 |
| 16 | 2692 | 2712 UGGAGAAGC/::: . :..... UGCAUCUGU(Cleavage | pacid=371592 |
| 17 | 1441 | 1461 UGGAGAAGC/:: :..... :..... UGCUUGUGU Translation | pacid=371656 |
| 18 | 393 | 413 UGGAGAAGC/:: . :..... UGUCUGUGU Cleavage | pacid=371678 |
| 19 | 1867 | 1887 UGGAGAAGC/::.. : :..... UGUUUUUGC Cleavage | pacid=371738 |
| 20 | 1795 | 1815 UGGAGAAGC/::.. : :..... UGUUUUUGC Cleavage | pacid=371738 |
| 21 | 2809 | 2829 UGGAGAAGC/ :..... :..... GGCACGUGCC Translation | pacid=371462 |
| 22 | 639 | 659 UGGAGAAGC/ :..... :..... UAGACGUGUI Cleavage | pacid=371520 |
| 23 | 1429 | 1450 UGGAGAAGC/:: : :..... UGCUCAGUG(Cleavage | pacid=371468 |
| 24 | 1429 | 1450 UGGAGAAGC/:: : :..... UGCUCAGUG(Cleavage | pacid=371468 |
| 25 | 1946 | 1966 UGGAGAAGC/::: :..... : UGCAGUUGC(Cleavage | pacid=371764 |
| 26 | 1712 | 1732 UGGAGAAGC/::: :..... : UGCAGUUGC(Cleavage | pacid=371764 |
| 27 | 4127 | 4147 UGGAGAAGC/ :..... :..... ACCAUGUGCC Cleavage | pacid=371756 |
| 28 | 3713 | 3733 UGGAGAAGC/ :..... :..... ACCAUGUGCC Cleavage | pacid=371756 |
| 29 | 2142 | 2165 UGGAGAAGC/ :..... :..... GGCACGUCCC Cleavage | pacid=371647 |
| 30 | 729 | 749 UGGAGAAGC/ :..... :..... AGCAUGUGU(Cleavage | pacid=371776 |
| 31 | 729 | 749 UGGAGAAGC/ :..... :..... AGCAUGUGU(Cleavage | pacid=371776 |
| 32 | 1576 | 1596 UGGAGAAGC/:: : :..... UUCUCUUGC(Translation | pacid=371530 |
| 33 | 549 | 569 UGGAGAAGC/ :..... :..... AGCAUGUGU(Cleavage | pacid=371777 |
| 34 | 444 | 464 UGGAGAAGC/ :..... :..... GACAUGUGC(Translation | pacid=371607 |
| 35 | 449 | 469 UGGAGAAGC/ :..... :..... AGCAUGUGC(Cleavage | pacid=371663 |
| 36 | 417 | 437 UGGAGAAGC/ :..... :..... AGCACGUGU(Cleavage | pacid=371656 |
| 37 | 1075 | 1095 UGGAGAAGC/ :..... :..... ACAACGUGC(Cleavage | pacid=371656 |
| 38 | 331 | 351 UGGAGAAGC/ :..... :..... AGCACGUGU(Cleavage | pacid=371656 |
| 39 | 989 | 1009 UGGAGAAGC/ :..... :..... ACAACGUGC(Cleavage | pacid=371656 |
| 40 | 1100 | 1120 UGGAGAAGC/ :..... :..... AACACGUGU(Cleavage | pacid=371470 |
| 41 | 99 | 119 UGGAGAAGC/ :..... :..... AGCACGUGU(Cleavage | pacid=371656 |
| 42 | 977 | 997 UGGAGAAGC/ :..... :..... ACAACGUGC(Cleavage | pacid=371656 |
| 43 | 278 | 298 UGGAGAAGC/::: : :..... UGCACCUCCC Cleavage | pacid=371740 |
| 44 | 249 | 269 UGGAGAAGC/ :..... :..... AGCACGUGU(Cleavage | pacid=371656 |
| 45 | 907 | 927 UGGAGAAGC/ :..... :..... ACAACGUGC(Cleavage | pacid=371656 |
| 46 | 420 | 440 UGGAGAAGC/:: : :..... : UGCUCUGCC Cleavage | pacid=371532 |
| 47 | 161 | 181 UGGAGAAGC/ :..... :..... AGCACGUGU(Cleavage | pacid=371656 |

| | | | | |
|----|------|-----------------|---|--------------|
| 1 | | | | |
| 2 | 819 | 839 UGGAGAAGC/ |: :... ACAACGUGCL Cleavage | pacid=371656 |
| 3 | 285 | 305 UGGAGAAGC/ | ::: : : : : : : : : UGCUCCUGCC Cleavage | pacid=371528 |
| 4 | 501 | 521 UGGAGAAGC/ |: : : : : : : : : AGCAUGUGC(Cleavage | pacid=371779 |
| 5 | 611 | 631 UGGAGAAGC/ | ::: : : : : : : : : UGCAAGUCUI Cleavage | pacid=371590 |
| 6 | 205 | 225 UGGAGAAGC/ |: . : : : : : : : : AGCAUGUGC(Cleavage | pacid=371599 |
| 7 | 179 | 200 UGGAGAAGC/ |: : : : : : : : : ACCACGUGAC Cleavage | pacid=371457 |
| 8 | | | | |
| 9 | | | | |
| 10 | 4269 | 4289 UGGAGAAGC/ | ::: : : : : : : : : UGAACAUGA(Cleavage | pacid=371579 |
| 11 | 4266 | 4286 UGGAGAAGC/ | ::: : : : : : : : : UGAACAUGA(Cleavage | pacid=371579 |
| 12 | 1610 | 1630 UGGAGAAGC/ | ::: : : : : : : : : UGCAGCUGC/ Cleavage | pacid=371622 |
| 13 | | | | |
| 14 | 1571 | 1591 UGGAGAAGC/ | ::: : : : : : : : : UGCAGCUGC/ Cleavage | pacid=371622 |
| 15 | 1531 | 1551 UGGAGAAGC/ | ::: : : : : : : : : UGCAGCUGC/ Cleavage | pacid=371622 |
| 16 | 3830 | 3850 UGGAGAAGC/ | ::: : : : : : : : : UGAACAUGUI Cleavage | pacid=371514 |
| 17 | | | | |
| 18 | 2950 | 2970 UGGAGAAGC/ | ::: . : : : : : : : : : UGUUUGGGU Cleavage | pacid=371537 |
| 19 | 2890 | 2910 UGGAGAAGC/ | ::: . : : : : : : : : : UGUUUGGGU Cleavage | pacid=371537 |
| 20 | 3661 | 3681 UGGAGAAGC/ | ::: : : : : : : : : UGAACAUGUI Cleavage | pacid=371514 |
| 21 | | | | |
| 22 | 1224 | 1244 UGGAGAAGC/ | ::: : : : : : : : : UGCAGCUGC/ Cleavage | pacid=371622 |
| 23 | 890 | 911 UGGAGAAGC/ |: : : : : : : : : UGCACCUGCC Translation | pacid=371489 |
| 24 | 273 | 293 UGGAGAAGC/ |: : : : : : : : : UGUGUGUGU Cleavage | pacid=371747 |
| 25 | | | | |
| 26 | 894 | 914 UGGAGAAGC/ |: : : : : : : : : UGCAUGUGU(Translation | pacid=371531 |
| 27 | 81 | 100 UGGAGAAGC/ |: : : : : : : : : UGCAUGUGC(Translation | pacid=371483 |
| 28 | 81 | 100 UGGAGAAGC/ |: : : : : : : : : UGCAUGUGC(Translation | pacid=371483 |
| 29 | | | | |
| 30 | 210 | 229 UGGAGAAGC/ |: : : : : : : : : UGCACGUGC(Cleavage | pacid=371445 |
| 31 | 210 | 229 UGGAGAAGC/ |: : : : : : : : : UGCACGUGC(Cleavage | pacid=371445 |
| 32 | 67 | 88 UGGAGAAGC/ |: : : : : : : : : UGCAACGUG(Cleavage | pacid=371715 |
| 33 | | | | |
| 34 | 2692 | 2712 UGGAGAAGC/ |: : : : : : : : : UGCAUCUGU(Cleavage | pacid=371592 |
| 35 | 1441 | 1461 UGGAGAAGC/ | ::: : : : : : : : : UGCUUGUGU Translation | pacid=371656 |
| 36 | 393 | 413 UGGAGAAGC/ | ::: . : : : : : : : : : UGUCUGUGU Cleavage | pacid=371678 |
| 37 | | | | |
| 38 | 1867 | 1887 UGGAGAAGC/ | ::: . : : : : : : : : : UGUUUUUGC(Cleavage | pacid=371738 |
| 39 | 1795 | 1815 UGGAGAAGC/ | ::: . : : : : : : : : : UGUUUUUGC(Cleavage | pacid=371738 |
| 40 | 2809 | 2829 UGGAGAAGC/ |: : : : : : : : : GGCACGUGC(Translation | pacid=371462 |
| 41 | 639 | 659 UGGAGAAGC/ |: : : : : : : : : UAGACGUGUI Cleavage | pacid=371520 |
| 42 | | | | |
| 43 | 1429 | 1450 UGGAGAAGC/ | ::: : : : : : : : : UGCUCAGUG(Cleavage | pacid=371468 |
| 44 | 1429 | 1450 UGGAGAAGC/ | ::: : : : : : : : : UGCUCAGUG(Cleavage | pacid=371468 |
| 45 | 1946 | 1966 UGGAGAAGC/ | ::: : : : : : : : : UGCAGUUGC(Cleavage | pacid=371764 |
| 46 | | | | |
| 47 | 1712 | 1732 UGGAGAAGC/ | ::: : : : : : : : : UGCAGUUGC(Cleavage | pacid=371764 |
| 48 | 4127 | 4147 UGGAGAAGC/ |: : : : : : : : : ACCAUGUGCC Cleavage | pacid=371756 |
| 49 | 3713 | 3733 UGGAGAAGC/ |: : : : : : : : : ACCAUGUGCC Cleavage | pacid=371756 |
| 50 | | | | |
| 51 | 2142 | 2165 UGGAGAAGC/ |: : : : : : : : : GGCACGUCCC Cleavage | pacid=371647 |
| 52 | 729 | 749 UGGAGAAGC/ |: : : : : : : : : AGCAUGUGU(Cleavage | pacid=371776 |
| 53 | 729 | 749 UGGAGAAGC/ |: : : : : : : : : AGCAUGUGU(Cleavage | pacid=371776 |
| 54 | | | | |
| 55 | 1576 | 1596 UGGAGAAGC/ | ::: : : : : : : : : UUCUCUUGC(Translation | pacid=371530 |
| 56 | 549 | 569 UGGAGAAGC/ |: : : : : : : : : AGCAUGUGU(Cleavage | pacid=371777 |
| 57 | 444 | 464 UGGAGAAGC/ |: : : : : : : : : GACAUGUGC(Translation | pacid=371607 |
| 58 | | | | |
| 59 | 449 | 469 UGGAGAAGC/ |: : : : : : : : : AGCAUGUGC(Cleavage | pacid=371663 |
| 60 | 417 | 437 UGGAGAAGC/ |: : : : : : : : : AGCACGUGU(Cleavage | pacid=371656 |
| | 1075 | 1095 UGGAGAAGC/ |: : : : : : : : : ACAACGUGCL Cleavage | pacid=371656 |

| | | | | |
|----|------|-----------------|------------------------|--------------|
| 1 | | | | |
| 2 | 331 | 351 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371656 |
| 3 | 989 | 1009 UGGAGAAGC/ | ACAACGUGCL Cleavage | pacid=371656 |
| 4 | 1100 | 1120 UGGAGAAGC/ | AACACGUGU(Cleavage | pacid=371470 |
| 5 | | | | |
| 6 | 99 | 119 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371656 |
| 7 | 977 | 997 UGGAGAAGC/ | ACAACGUGCL Cleavage | pacid=371656 |
| 8 | 278 | 298 UGGAGAAGC/ | UGCACCUCCC Cleavage | pacid=371740 |
| 9 | | | | |
| 10 | 249 | 269 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371656 |
| 11 | 907 | 927 UGGAGAAGC/ | ACAACGUGCL Cleavage | pacid=371656 |
| 12 | 420 | 440 UGGAGAAGC/ | UGCUCUGCC Cleavage | pacid=371532 |
| 13 | | | | |
| 14 | 161 | 181 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371656 |
| 15 | 819 | 839 UGGAGAAGC/ | ACAACGUGCL Cleavage | pacid=371656 |
| 16 | 285 | 305 UGGAGAAGC/ | UGCUCUGCC Cleavage | pacid=371528 |
| 17 | | | | |
| 18 | 501 | 521 UGGAGAAGC/ | AGCAUGUGC(Cleavage | pacid=371779 |
| 19 | 611 | 631 UGGAGAAGC/ | UGCAAGUCUI Cleavage | pacid=371590 |
| 20 | 205 | 225 UGGAGAAGC/ | AGCAUGUGC Cleavage | pacid=371599 |
| 21 | | | | |
| 22 | 179 | 200 UGGAGAAGC/ | ACCACGUGAC Cleavage | pacid=371457 |
| 23 | 4269 | 4289 UGGAGAAGC/ | UGAACAUGA(Cleavage | pacid=371579 |
| 24 | 4266 | 4286 UGGAGAAGC/ | UGAACAUGA(Cleavage | pacid=371579 |
| 25 | | | | |
| 26 | 1610 | 1630 UGGAGAAGC/ | UGCAGCUGC/ Cleavage | pacid=371622 |
| 27 | 1571 | 1591 UGGAGAAGC/ | UGCAGCUGC/ Cleavage | pacid=371622 |
| 28 | 1531 | 1551 UGGAGAAGC/ | UGCAGCUGC/ Cleavage | pacid=371622 |
| 29 | | | | |
| 30 | 3830 | 3850 UGGAGAAGC/ | UGAACAUGUI Cleavage | pacid=371514 |
| 31 | 2950 | 2970 UGGAGAAGC/ | UGUUUGGGU Cleavage | pacid=371537 |
| 32 | 2890 | 2910 UGGAGAAGC/ | UGUUUGGGU Cleavage | pacid=371537 |
| 33 | | | | |
| 34 | 3661 | 3681 UGGAGAAGC/ | UGAACAUGUI Cleavage | pacid=371514 |
| 35 | 1224 | 1244 UGGAGAAGC/ | UGCAGCUGC/ Cleavage | pacid=371622 |
| 36 | 890 | 911 UGGAGAAGC/ | UGCACCUGCC Translation | pacid=371489 |
| 37 | | | | |
| 38 | 273 | 293 UGGAGAAGC/ | UGUGUGUGU Cleavage | pacid=371747 |
| 39 | 894 | 914 UGGAGAAGC/ | UGCAUGUGU Translation | pacid=371531 |
| 40 | 81 | 100 UGGAGAAGC/ | UGCAUGUGC(Translation | pacid=371483 |
| 41 | 81 | 100 UGGAGAAGC/ | UGCAUGUGC(Translation | pacid=371483 |
| 42 | | | | |
| 43 | 210 | 229 UGGAGAAGC/ | UGCACGUGCC Cleavage | pacid=371445 |
| 44 | 210 | 229 UGGAGAAGC/ | UGCACGUGCC Cleavage | pacid=371445 |
| 45 | 67 | 88 UGGAGAAGC/ | UGCAACGUGI Cleavage | pacid=371715 |
| 46 | | | | |
| 47 | 2692 | 2712 UGGAGAAGC/ | UGCAUCUGU(Cleavage | pacid=371592 |
| 48 | 1441 | 1461 UGGAGAAGC/ | UGCUUGUGU Translation | pacid=371656 |
| 49 | 393 | 413 UGGAGAAGC/ | UGUCUGUGU Cleavage | pacid=371678 |
| 50 | | | | |
| 51 | 1867 | 1887 UGGAGAAGC/ | UGUAAUUGC Cleavage | pacid=371738 |
| 52 | 1795 | 1815 UGGAGAAGC/ | UGUAAUUGC Cleavage | pacid=371738 |
| 53 | 2809 | 2829 UGGAGAAGC/ | GGCACGUGCC Translation | pacid=371462 |
| 54 | | | | |
| 55 | 639 | 659 UGGAGAAGC/ | UAGACGUGUI Cleavage | pacid=371520 |
| 56 | 1429 | 1450 UGGAGAAGC/ | UGCUCAGUG(Cleavage | pacid=371468 |
| 57 | 1429 | 1450 UGGAGAAGC/ | UGCUCAGUG(Cleavage | pacid=371468 |
| 58 | | | | |
| 59 | 1946 | 1966 UGGAGAAGC/ | UGCAGUUGC(Cleavage | pacid=371764 |
| 60 | 1712 | 1732 UGGAGAAGC/ | UGCAGUUGC(Cleavage | pacid=371764 |
| | 4127 | 4147 UGGAGAAGC/ | ACCAUGUGCC Cleavage | pacid=371756 |

| | | | | | |
|----|------|-----------------|---------------------|------------------------|--------------|
| 1 | | | | | |
| 2 | 3713 | 3733 UGGAGAAGC/ | :::.....: ::::: | ACCAUGUGCC Cleavage | pacid=371756 |
| 3 | 2142 | 2165 UGGAGAAGC/ | :::.....: :::..... | GGCACGUCCC Cleavage | pacid=371647 |
| 4 | 729 | 749 UGGAGAAGC/ | :::.....: : : ..: | AGCAUGUGU(Cleavage | pacid=371776 |
| 5 | 729 | 749 UGGAGAAGC/ | :::.....: : : ..: | AGCAUGUGU(Cleavage | pacid=371776 |
| 6 | 1576 | 1596 UGGAGAAGC/ | ::: : : ..: ..: ..: | UUCUCUUGC(Translation | pacid=371530 |
| 7 | 549 | 569 UGGAGAAGC/ | :::.....: : : ..: | AGCAUGUGU(Cleavage | pacid=371777 |
| 8 | 444 | 464 UGGAGAAGC/ | :::.....: :::..... | GACAUGUGC(Translation | pacid=371607 |
| 9 | 449 | 469 UGGAGAAGC/ | :::.....: :::..... | : AGCAUGUGC(Cleavage | pacid=371663 |
| 10 | 417 | 437 UGGAGAAGC/ | :::.....: : : ..: | AGCACGUGU(Cleavage | pacid=371656 |
| 11 | 1075 | 1095 UGGAGAAGC/ | :::.....: : ..: | ACAACGUGC(Cleavage | pacid=371656 |
| 12 | 331 | 351 UGGAGAAGC/ | :::.....: : ..: | AGCACGUGU(Cleavage | pacid=371656 |
| 13 | 989 | 1009 UGGAGAAGC/ | :::.....: : ..: | ACAACGUGC(Cleavage | pacid=371656 |
| 14 | 1100 | 1120 UGGAGAAGC/ | :::.....: : : ..: | AACACGUGU(Cleavage | pacid=371470 |
| 15 | 99 | 119 UGGAGAAGC/ | :::.....: : : ..: | AGCACGUGU(Cleavage | pacid=371656 |
| 16 | 977 | 997 UGGAGAAGC/ | :::.....: : ..: | ACAACGUGC(Cleavage | pacid=371656 |
| 17 | 278 | 298 UGGAGAAGC/ | ::: : : ..: ..: ..: | UGCACCUCCC Cleavage | pacid=371740 |
| 18 | 249 | 269 UGGAGAAGC/ | :::.....: : : ..: | AGCACGUGU(Cleavage | pacid=371656 |
| 19 | 907 | 927 UGGAGAAGC/ | :::.....: : ..: | ACAACGUGC(Cleavage | pacid=371656 |
| 20 | 420 | 440 UGGAGAAGC/ | ::: : : ..: ..: ..: | UGCUCUGCC Cleavage | pacid=371532 |
| 21 | 161 | 181 UGGAGAAGC/ | :::.....: : : ..: | AGCACGUGU(Cleavage | pacid=371656 |
| 22 | 819 | 839 UGGAGAAGC/ | :::.....: : ..: | ACAACGUGC(Cleavage | pacid=371656 |
| 23 | 285 | 305 UGGAGAAGC/ | ::: : : ..: ..: ..: | UGCUCUGCC Cleavage | pacid=371528 |
| 24 | 501 | 521 UGGAGAAGC/ | :::.....: : : ..: | AGCAUGUGC(Cleavage | pacid=371779 |
| 25 | 611 | 631 UGGAGAAGC/ | ::: : : ..: ..: ..: | UGCAAGUCU(Cleavage | pacid=371590 |
| 26 | 205 | 225 UGGAGAAGC/ | :::.....: : : ..: | AGCAUGUGC(Cleavage | pacid=371599 |
| 27 | 179 | 200 UGGAGAAGC/ | :::.....: : ..: | ACCACGUGAC Cleavage | pacid=371457 |
| 28 | 4269 | 4289 UGGAGAAGC/ | ::: : : ..: ..: ..: | UGAACAUGA(Cleavage | pacid=371579 |
| 29 | 4266 | 4286 UGGAGAAGC/ | ::: : : ..: ..: ..: | UGAACAUGA(Cleavage | pacid=371579 |
| 30 | 1610 | 1630 UGGAGAAGC/ | ::: : : ..: ..: ..: | UGCAGCUGC/ Cleavage | pacid=371622 |
| 31 | 1571 | 1591 UGGAGAAGC/ | ::: : : ..: ..: ..: | UGCAGCUGC/ Cleavage | pacid=371622 |
| 32 | 1531 | 1551 UGGAGAAGC/ | ::: : : ..: ..: ..: | UGCAGCUGC/ Cleavage | pacid=371622 |
| 33 | 3830 | 3850 UGGAGAAGC/ | ::: : : ..: ..: ..: | UGAACAUGU(Cleavage | pacid=371514 |
| 34 | 2950 | 2970 UGGAGAAGC/ | ::: : : ..: ..: ..: | UGUUUGGGU Cleavage | pacid=371537 |
| 35 | 2890 | 2910 UGGAGAAGC/ | ::: : : ..: ..: ..: | UGUUUGGGU Cleavage | pacid=371537 |
| 36 | 3661 | 3681 UGGAGAAGC/ | ::: : : ..: ..: ..: | UGAACAUGU(Cleavage | pacid=371514 |
| 37 | 1224 | 1244 UGGAGAAGC/ | ::: : : ..: ..: ..: | UGCAGCUGC/ Cleavage | pacid=371622 |
| 38 | 890 | 911 UGGAGAAGC/ | :::.....: : ..: | UGCACCUGCC Translation | pacid=371489 |
| 39 | 273 | 293 UGGAGAAGC/ | :::.....: : ..: | UGUGUGUGU Cleavage | pacid=371747 |
| 40 | 894 | 914 UGGAGAAGC/ | :::.....: : ..: | UGCAUGUGU(Translation | pacid=371531 |
| 41 | 81 | 100 UGGAGAAGC/ | :::.....: : ..: | UGCAUGUGC(Translation | pacid=371483 |
| 42 | 81 | 100 UGGAGAAGC/ | :::.....: : ..: | UGCAUGUGC(Translation | pacid=371483 |
| 43 | 210 | 229 UGGAGAAGC/ | :::.....: : ..: | UGCACGUGC(Cleavage | pacid=371445 |
| 44 | 210 | 229 UGGAGAAGC/ | :::.....: : ..: | UGCACGUGC(Cleavage | pacid=371445 |
| 45 | 67 | 88 UGGAGAAGC/ | ::: : : ..: ..: ..: | UGCAACGUG(Cleavage | pacid=371715 |
| 46 | 2692 | 2712 UGGAGAAGC/ | ::: : : ..: ..: ..: | UGCAUCUGU(Cleavage | pacid=371592 |
| 47 | 1441 | 1461 UGGAGAAGC/ | ::: : : ..: ..: ..: | UGCUCUGUGU Translation | pacid=371656 |

| | | | |
|----|------|--|--------------|
| 1 | | | |
| 2 | 393 | 413 UGGAGAAGC/ :: : ::::: : UGUCUGUGU Cleavage | pacid=371678 |
| 3 | 1867 | 1887 UGGAGAAGC/ : : : : : UGUUUUUGC. Cleavage | pacid=371738 |
| 4 | 1795 | 1815 UGGAGAAGC/ : : : : : UGUUUUUGC. Cleavage | pacid=371738 |
| 5 | | | |
| 6 | 2809 | 2829 UGGAGAAGC/ : : : : : GGCACGUGCC Translation | pacid=371462 |
| 7 | 639 | 659 UGGAGAAGC/ : : : : : UAGACGUGU Cleavage | pacid=371520 |
| 8 | 1429 | 1450 UGGAGAAGC/ : : : : : UGCUCAGUG(Cleavage | pacid=371468 |
| 9 | | | |
| 10 | 1429 | 1450 UGGAGAAGC/ : : : : : UGCUCAGUG(Cleavage | pacid=371468 |
| 11 | 1946 | 1966 UGGAGAAGC/ : : : : : UGCAGUUGC(Cleavage | pacid=371764 |
| 12 | 1712 | 1732 UGGAGAAGC/ : : : : : UGCAGUUGC(Cleavage | pacid=371764 |
| 13 | | | |
| 14 | 4127 | 4147 UGGAGAAGC/ : : : : : ACCAUGUGCC Cleavage | pacid=371756 |
| 15 | 3713 | 3733 UGGAGAAGC/ : : : : : ACCAUGUGCC Cleavage | pacid=371756 |
| 16 | 2142 | 2165 UGGAGAAGC/ : : : : : GGCACGUCCC Cleavage | pacid=371647 |
| 17 | | | |
| 18 | 729 | 749 UGGAGAAGC/ : : : : : AGCAUGUGU(Cleavage | pacid=371776 |
| 19 | 729 | 749 UGGAGAAGC/ : : : : : AGCAUGUGU(Cleavage | pacid=371776 |
| 20 | 1576 | 1596 UGGAGAAGC/ : : : : : UUCUCUUGC(Translation | pacid=371530 |
| 21 | | | |
| 22 | 549 | 569 UGGAGAAGC/ : : : : : AGCAUGUGU(Cleavage | pacid=371777 |
| 23 | 444 | 464 UGGAGAAGC/ : : : : : GACAUGUGCC Translation | pacid=371607 |
| 24 | 449 | 469 UGGAGAAGC/ : : : : : AGCAUGUGU(Cleavage | pacid=371663 |
| 25 | | | |
| 26 | 417 | 437 UGGAGAAGC/ : : : : : AGCACGUGU(Cleavage | pacid=371656 |
| 27 | 1075 | 1095 UGGAGAAGC/ : : : : : ACAACGUGU(Cleavage | pacid=371656 |
| 28 | 331 | 351 UGGAGAAGC/ : : : : : AGCACGUGU(Cleavage | pacid=371656 |
| 29 | | | |
| 30 | 989 | 1009 UGGAGAAGC/ : : : : : ACAACGUGU(Cleavage | pacid=371656 |
| 31 | 1100 | 1120 UGGAGAAGC/ : : : : : AACACGUGU(Cleavage | pacid=371470 |
| 32 | 99 | 119 UGGAGAAGC/ : : : : : AGCACGUGU(Cleavage | pacid=371656 |
| 33 | | | |
| 34 | 977 | 997 UGGAGAAGC/ : : : : : ACAACGUGU(Cleavage | pacid=371656 |
| 35 | 278 | 298 UGGAGAAGC/ : : : : : UGCACCUCCC Cleavage | pacid=371740 |
| 36 | 249 | 269 UGGAGAAGC/ : : : : : AGCACGUGU(Cleavage | pacid=371656 |
| 37 | | | |
| 38 | 907 | 927 UGGAGAAGC/ : : : : : ACAACGUGU(Cleavage | pacid=371656 |
| 39 | 420 | 440 UGGAGAAGC/ : : : : : UGCUCUGCC Cleavage | pacid=371532 |
| 40 | 161 | 181 UGGAGAAGC/ : : : : : AGCACGUGU(Cleavage | pacid=371656 |
| 41 | 819 | 839 UGGAGAAGC/ : : : : : ACAACGUGU(Cleavage | pacid=371656 |
| 42 | | | |
| 43 | 285 | 305 UGGAGAAGC/ : : : : : UGCUCUGCC Cleavage | pacid=371528 |
| 44 | 501 | 521 UGGAGAAGC/ : : : : : AGCAUGUGU(Cleavage | pacid=371779 |
| 45 | 611 | 631 UGGAGAAGC/ : : : : : UGCAAGUCU(Cleavage | pacid=371590 |
| 46 | | | |
| 47 | 205 | 225 UGGAGAAGC/ : : : : : AGCAUGUGU(Cleavage | pacid=371599 |
| 48 | 179 | 200 UGGAGAAGC/ : : : : : ACCACGUGAC Cleavage | pacid=371457 |
| 49 | 4269 | 4289 UGGAGAAGC/ : : : : : UGAACAUGA(Cleavage | pacid=371579 |
| 50 | 4266 | 4286 UGGAGAAGC/ : : : : : UGAACAUGA(Cleavage | pacid=371579 |
| 51 | | | |
| 52 | 1610 | 1630 UGGAGAAGC/ : : : : : UGCAGCUGC/ Cleavage | pacid=371622 |
| 53 | 1571 | 1591 UGGAGAAGC/ : : : : : UGCAGCUGC/ Cleavage | pacid=371622 |
| 54 | | | |
| 55 | 1531 | 1551 UGGAGAAGC/ : : : : : UGCAGCUGC/ Cleavage | pacid=371622 |
| 56 | 3830 | 3850 UGGAGAAGC/ : : : : : UGAACAUGU(Cleavage | pacid=371514 |
| 57 | 2950 | 2970 UGGAGAAGC/ : : : : : UGUUUUGGU Cleavage | pacid=371537 |
| 58 | | | |
| 59 | 2890 | 2910 UGGAGAAGC/ : : : : : UGUUUUGGU Cleavage | pacid=371537 |
| 60 | 3661 | 3681 UGGAGAAGC/ : : : : : UGAACAUGU(Cleavage | pacid=371514 |
| | 1224 | 1244 UGGAGAAGC/ : : : : : UGCAGCUGC/ Cleavage | pacid=371622 |

| | | | |
|----|------|--|--------------|
| 1 | | | |
| 2 | 890 | 911 UGGAGAAGC/::::: ::::: ::::: UGCACCUGCC Translation | pacid=371489 |
| 3 | 273 | 293 UGGAGAAGC/::.....: ::::: UGUGUGUGU Cleavage | pacid=371747 |
| 4 | 894 | 914 UGGAGAAGC/::::: ::::: UGCAUGUGU Translation | pacid=371531 |
| 5 | | | |
| 6 | 81 | 100 UGGAGAAGC/::::: ::::: UGCAUGUGC(Translation | pacid=371483 |
| 7 | 81 | 100 UGGAGAAGC/::::: ::::: UGCAUGUGC(Translation | pacid=371483 |
| 8 | | | |
| 9 | 210 | 229 UGGAGAAGC/::::: ::::: UGCACGUGCC Cleavage | pacid=371445 |
| 10 | 210 | 229 UGGAGAAGC/::::: ::::: UGCACGUGCC Cleavage | pacid=371445 |
| 11 | 67 | 88 UGGAGAAGC/::::: ::::: UGCAACGUGI Cleavage | pacid=371715 |
| 12 | 2692 | 2712 UGGAGAAGC/::::: ::::: UGCAUCUGU(Cleavage | pacid=371592 |
| 13 | | | |
| 14 | 1441 | 1461 UGGAGAAGC/::: ::::: UGCUUGUGU Translation | pacid=371656 |
| 15 | 393 | 413 UGGAGAAGC/::: ::::: UGUCUGUGU Cleavage | pacid=371678 |
| 16 | 1867 | 1887 UGGAGAAGC/::: ::::: UGUUUUUGC.Cleavage | pacid=371738 |
| 17 | | | |
| 18 | 1795 | 1815 UGGAGAAGC/::: ::::: UGUUUUUGC.Cleavage | pacid=371738 |
| 19 | 2809 | 2829 UGGAGAAGC/::::: ::::: GGCACGUGCC Translation | pacid=371462 |
| 20 | 639 | 659 UGGAGAAGC/::::: ::::: UAGACGUGU(Cleavage | pacid=371520 |
| 21 | | | |
| 22 | 1429 | 1450 UGGAGAAGC/::: ::::: UGCUCAGUG(Cleavage | pacid=371468 |
| 23 | 1429 | 1450 UGGAGAAGC/::: ::::: UGCUCAGUG(Cleavage | pacid=371468 |
| 24 | 1946 | 1966 UGGAGAAGC/::: ::::: UGCAGUUGC(Cleavage | pacid=371764 |
| 25 | | | |
| 26 | 1712 | 1732 UGGAGAAGC/::: ::::: UGCAGUUGC(Cleavage | pacid=371764 |
| 27 | 4127 | 4147 UGGAGAAGC/::::: ::::: ACCAUGUGCC Cleavage | pacid=371756 |
| 28 | 3713 | 3733 UGGAGAAGC/::::: ::::: ACCAUGUGCC Cleavage | pacid=371756 |
| 29 | | | |
| 30 | 2142 | 2165 UGGAGAAGC/::::: ::::: GGCACGUCCC Cleavage | pacid=371647 |
| 31 | 729 | 749 UGGAGAAGC/::::: ::::: AGCAUGUGU(Cleavage | pacid=371776 |
| 32 | 729 | 749 UGGAGAAGC/::::: ::::: AGCAUGUGU(Cleavage | pacid=371776 |
| 33 | | | |
| 34 | 1576 | 1596 UGGAGAAGC/::: ::::: UUCUCUUGC(Translation | pacid=371530 |
| 35 | 549 | 569 UGGAGAAGC/::::: ::::: AGCAUGUGU(Cleavage | pacid=371777 |
| 36 | 444 | 464 UGGAGAAGC/::::: ::::: GACAUGUGC(Translation | pacid=371607 |
| 37 | | | |
| 38 | 449 | 469 UGGAGAAGC/::::: ::::: AGCAUGUGC(Cleavage | pacid=371663 |
| 39 | 417 | 437 UGGAGAAGC/::::: ::::: AGCACGUGU(Cleavage | pacid=371656 |
| 40 | 1075 | 1095 UGGAGAAGC/::::: ::::: ACAACGUGCL Cleavage | pacid=371656 |
| 41 | | | |
| 42 | 331 | 351 UGGAGAAGC/::::: ::::: AGCACGUGU(Cleavage | pacid=371656 |
| 43 | 989 | 1009 UGGAGAAGC/::::: ::::: ACAACGUGCL Cleavage | pacid=371656 |
| 44 | 1100 | 1120 UGGAGAAGC/::::: ::::: AACACGUGU(Cleavage | pacid=371470 |
| 45 | 99 | 119 UGGAGAAGC/::::: ::::: AGCACGUGU(Cleavage | pacid=371656 |
| 46 | | | |
| 47 | 977 | 997 UGGAGAAGC/::::: ::::: ACAACGUGCL Cleavage | pacid=371656 |
| 48 | 278 | 298 UGGAGAAGC/::::: ::::: UGCACCUCCC Cleavage | pacid=371740 |
| 49 | 249 | 269 UGGAGAAGC/::::: ::::: AGCACGUGU(Cleavage | pacid=371656 |
| 50 | | | |
| 51 | 907 | 927 UGGAGAAGC/::::: ::::: ACAACGUGCL Cleavage | pacid=371656 |
| 52 | 420 | 440 UGGAGAAGC/::: ::::: UGCUCCUGCC Cleavage | pacid=371532 |
| 53 | 161 | 181 UGGAGAAGC/::::: ::::: AGCACGUGU(Cleavage | pacid=371656 |
| 54 | | | |
| 55 | 819 | 839 UGGAGAAGC/::::: ::::: ACAACGUGCL Cleavage | pacid=371656 |
| 56 | 285 | 305 UGGAGAAGC/::: ::::: UGCUCCUGCC Cleavage | pacid=371528 |
| 57 | 501 | 521 UGGAGAAGC/::::: ::::: AGCAUGUGC(Cleavage | pacid=371779 |
| 58 | | | |
| 59 | 611 | 631 UGGAGAAGC/::: ::::: UGCAAGUCU(Cleavage | pacid=371590 |
| 60 | 205 | 225 UGGAGAAGC/::::: ::::: AGCAUGUGC(Cleavage | pacid=371599 |
| | 179 | 200 UGGAGAAGC/::::: ::::: ACCACGUGAC Cleavage | pacid=371457 |

| | | | |
|----|------|--|--------------|
| 1 | | | |
| 2 | 4269 | 4289 UGGAGAAGC/ :: : : ::::: : UGAACAUGA(Cleavage | pacid=371579 |
| 3 | 4266 | 4286 UGGAGAAGC/ :: : : ::::: : UGAACAUGA(Cleavage | pacid=371579 |
| 4 | 1610 | 1630 UGGAGAAGC/ :::: : : ::::: : UGCAGCUGC(Cleavage | pacid=371622 |
| 5 | 1571 | 1591 UGGAGAAGC/ :::: : : ::::: : UGCAGCUGC(Cleavage | pacid=371622 |
| 6 | 1531 | 1551 UGGAGAAGC/ :::: : : ::::: : UGCAGCUGC(Cleavage | pacid=371622 |
| 7 | 3830 | 3850 UGGAGAAGC/ :: : : ::::: : UGAACAUGU(Cleavage | pacid=371514 |
| 8 | 2950 | 2970 UGGAGAAGC/ :: : : ::::: : UGUUUGGGU(Cleavage | pacid=371537 |
| 9 | 2890 | 2910 UGGAGAAGC/ :: : : ::::: : UGUUUGGGU(Cleavage | pacid=371537 |
| 10 | 3661 | 3681 UGGAGAAGC/ :: : : ::::: : UGAACAUGU(Cleavage | pacid=371514 |
| 11 | 1224 | 1244 UGGAGAAGC/ :::: : : ::::: : UGCAGCUGC(Cleavage | pacid=371622 |
| 12 | 890 | 911 UGGAGAAGC/ :::: : : ::::: : UGCACCUGCC(Translation | pacid=371489 |
| 13 | 273 | 293 UGGAGAAGC/ ::::: : ::::: : UGUGUGUGU(Cleavage | pacid=371747 |
| 14 | 894 | 914 UGGAGAAGC/ ::::: : ::::: : UGCAUGUGU(Translation | pacid=371531 |
| 15 | 81 | 100 UGGAGAAGC/ ::::: : ::::: : UGCAUGUGC(Translation | pacid=371483 |
| 16 | 81 | 100 UGGAGAAGC/ ::::: : ::::: : UGCAUGUGC(Translation | pacid=371483 |
| 17 | 210 | 229 UGGAGAAGC/ ::::: : ::::: : UGCACGUGCC(Cleavage | pacid=371445 |
| 18 | 210 | 229 UGGAGAAGC/ ::::: : ::::: : UGCACGUGCC(Cleavage | pacid=371445 |
| 19 | 67 | 88 UGGAGAAGC/ :::: : : ::::: : UGCAACGUGI(Cleavage | pacid=371715 |
| 20 | 2692 | 2712 UGGAGAAGC/ :::: : : ::::: : UGCAUCUGU(Cleavage | pacid=371592 |
| 21 | 1441 | 1461 UGGAGAAGC/ :: : : ::::: : UGCUUGUGU(Translation | pacid=371656 |
| 22 | 393 | 413 UGGAGAAGC/ :: : : ::::: : UGUCUGUGU(Cleavage | pacid=371678 |
| 23 | 1867 | 1887 UGGAGAAGC/ :: : : ::::: : UGUUUUGC(Cleavage | pacid=371738 |
| 24 | 1795 | 1815 UGGAGAAGC/ :: : : ::::: : UGUUUUGC(Cleavage | pacid=371738 |
| 25 | 2809 | 2829 UGGAGAAGC/ ::::: : ::::: : GGCACGUGCC(Translation | pacid=371462 |
| 26 | 639 | 659 UGGAGAAGC/ ::::: : ::::: : UAGACGUGU(Cleavage | pacid=371520 |
| 27 | 1429 | 1450 UGGAGAAGC/ :: : : ::::: : UGCUCAGUG(Cleavage | pacid=371468 |
| 28 | 1429 | 1450 UGGAGAAGC/ :: : : ::::: : UGCUCAGUG(Cleavage | pacid=371468 |
| 29 | 1946 | 1966 UGGAGAAGC/ :::: : : ::::: : UGCAGUUGC(Cleavage | pacid=371764 |
| 30 | 1712 | 1732 UGGAGAAGC/ :::: : : ::::: : UGCAGUUGC(Cleavage | pacid=371764 |
| 31 | 4127 | 4147 UGGAGAAGC/ ::::: : ::::: : ACCAUGUGCC(Cleavage | pacid=371756 |
| 32 | 3713 | 3733 UGGAGAAGC/ ::::: : ::::: : ACCAUGUGCC(Cleavage | pacid=371756 |
| 33 | 2142 | 2165 UGGAGAAGC/ :::: : : ::::: : GGCACGUCCC(Cleavage | pacid=371647 |
| 34 | 729 | 749 UGGAGAAGC/ ::::: : ::::: : AGCAUGUGU(Cleavage | pacid=371776 |
| 35 | 729 | 749 UGGAGAAGC/ ::::: : ::::: : AGCAUGUGU(Cleavage | pacid=371776 |
| 36 | 1576 | 1596 UGGAGAAGC/ :: : : ::::: : UUCUCUUGU(Translation | pacid=371530 |
| 37 | 549 | 569 UGGAGAAGC/ ::::: : ::::: : AGCAUGUGU(Cleavage | pacid=371777 |
| 38 | 444 | 464 UGGAGAAGC/ ::::: : ::::: : GACAUGUGU(Translation | pacid=371607 |
| 39 | 449 | 469 UGGAGAAGC/ ::::: : ::::: : AGCAUGUGU(Cleavage | pacid=371663 |
| 40 | 417 | 437 UGGAGAAGC/ ::::: : ::::: : AGCACGUGU(Cleavage | pacid=371656 |
| 41 | 1075 | 1095 UGGAGAAGC/ ::::: : ::::: : ACAACGUGU(Cleavage | pacid=371656 |
| 42 | 331 | 351 UGGAGAAGC/ ::::: : ::::: : AGCACGUGU(Cleavage | pacid=371656 |
| 43 | 989 | 1009 UGGAGAAGC/ ::::: : ::::: : ACAACGUGU(Cleavage | pacid=371656 |
| 44 | 1100 | 1120 UGGAGAAGC/ ::::: : ::::: : AACACGUGU(Cleavage | pacid=371470 |
| 45 | 99 | 119 UGGAGAAGC/ ::::: : ::::: : AGCACGUGU(Cleavage | pacid=371656 |
| 46 | 977 | 997 UGGAGAAGC/ ::::: : ::::: : ACAACGUGU(Cleavage | pacid=371656 |
| 47 | 278 | 298 UGGAGAAGC/ :::: : : ::::: : UGCACCUCCC(Cleavage | pacid=371740 |

| | | | |
|----|------|---|--------------|
| 1 | | | |
| 2 | 249 | 269 UGGAGAAGC/ ::::::::::: ::::: AGCACGUGU(Cleavage | pacid=371656 |
| 3 | 907 | 927 UGGAGAAGC/ ::::::::::: ::::: ACAACGUGCL Cleavage | pacid=371656 |
| 4 | 420 | 440 UGGAGAAGC/ :::: : ::::::::::: : UGCUCCUGCC Cleavage | pacid=371532 |
| 5 | | | |
| 6 | 161 | 181 UGGAGAAGC/ ::::::::::: ::::: AGCACGUGU(Cleavage | pacid=371656 |
| 7 | 819 | 839 UGGAGAAGC/ ::::::::::: ::::: ACAACGUGCL Cleavage | pacid=371656 |
| 8 | | | |
| 9 | 285 | 305 UGGAGAAGC/ :::: : ::::::::::: : UGCUCCUGCC Cleavage | pacid=371528 |
| 10 | 501 | 521 UGGAGAAGC/ ::::::::::: :: : AGCAUGUGC(Cleavage | pacid=371779 |
| 11 | 611 | 631 UGGAGAAGC/ :::: : ..::::::::: UGCAAGUCUI Cleavage | pacid=371590 |
| 12 | | | |
| 13 | 205 | 225 UGGAGAAGC/ ::::::::::: . ::::: AGCAUGUGCL Cleavage | pacid=371599 |
| 14 | 179 | 200 UGGAGAAGC/ ::::: ::::::::::: ACCACGUGAC Cleavage | pacid=371457 |
| 15 | 4269 | 4289 UGGAGAAGC/ :::: : : ::::::::::: : UGAACAUGA(Cleavage | pacid=371579 |
| 16 | 4266 | 4286 UGGAGAAGC/ :::: : : ::::::::::: : UGAACAUGA(Cleavage | pacid=371579 |
| 17 | | | |
| 18 | 1610 | 1630 UGGAGAAGC/ :::: : : ::::::::::: UGCAGCUGC/ Cleavage | pacid=371622 |
| 19 | 1571 | 1591 UGGAGAAGC/ :::: : : ::::::::::: UGCAGCUGC/ Cleavage | pacid=371622 |
| 20 | 1531 | 1551 UGGAGAAGC/ :::: : : ::::::::::: UGCAGCUGC/ Cleavage | pacid=371622 |
| 21 | | | |
| 22 | 3830 | 3850 UGGAGAAGC/ :: : : ..::::::::: UGAACAUGUI Cleavage | pacid=371514 |
| 23 | 2950 | 2970 UGGAGAAGC/ :: . : ..::::::::: UGUUUGGGU Cleavage | pacid=371537 |
| 24 | 2890 | 2910 UGGAGAAGC/ :: . : ..::::::::: UGUUUGGGU Cleavage | pacid=371537 |
| 25 | | | |
| 26 | 3661 | 3681 UGGAGAAGC/ :: : : ..::::::::: UGAACAUGUI Cleavage | pacid=371514 |
| 27 | 1224 | 1244 UGGAGAAGC/ :::: : : ::::::::::: UGCAGCUGC/ Cleavage | pacid=371622 |
| 28 | 890 | 911 UGGAGAAGC/ ::::: ::::: ::::::::::: UGCACCUGCC Translation | pacid=371489 |
| 29 | | | |
| 30 | 273 | 293 UGGAGAAGC/ ::.....: ::::::::::: UGUGUGUGU Cleavage | pacid=371747 |
| 31 | 894 | 914 UGGAGAAGC/ ::::::::::: ::::: UGCAUGUGU Translation | pacid=371531 |
| 32 | 81 | 100 UGGAGAAGC/ ::::::::::: ::::::::::: UGCAUGUGC(Translation | pacid=371483 |
| 33 | | | |
| 34 | 81 | 100 UGGAGAAGC/ ::::::::::: ::::::::::: UGCAUGUGC(Translation | pacid=371483 |
| 35 | 210 | 229 UGGAGAAGC/ ::::::::::: ::::: UGCACGUGCC Cleavage | pacid=371445 |
| 36 | 210 | 229 UGGAGAAGC/ ::::::::::: ::::: UGCACGUGCC Cleavage | pacid=371445 |
| 37 | | | |
| 38 | 67 | 88 UGGAGAAGC/ ::::: ::.....: ::::::::::: UGCAACGUGI Cleavage | pacid=371715 |
| 39 | 2692 | 2712 UGGAGAAGC/ :::: . : ..::::::::: : UGCAUCUGU(Cleavage | pacid=371592 |
| 40 | 1441 | 1461 UGGAGAAGC/ :: : ..::: ..::::::::: UGCUUGUGU Translation | pacid=371656 |
| 41 | 393 | 413 UGGAGAAGC/ :: . : ..::::::::: : UGUCUGUGU Cleavage | pacid=371678 |
| 42 | | | |
| 43 | 1867 | 1887 UGGAGAAGC/ ::. : : ::::::::::: UGUUUUUGC Cleavage | pacid=371738 |
| 44 | 1795 | 1815 UGGAGAAGC/ ::. : : ::::::::::: UGUUUUUGC Cleavage | pacid=371738 |
| 45 | 2809 | 2829 UGGAGAAGC/ ::::::::::: ::::: GGCACGUGCC(Translation | pacid=371462 |
| 46 | | | |
| 47 | 639 | 659 UGGAGAAGC/ ::.....: ::::::::::: UAGACGUGUI Cleavage | pacid=371520 |
| 48 | 1429 | 1450 UGGAGAAGC/ :::: : ..::::::::: : UGCUCAGUG(Cleavage | pacid=371468 |
| 49 | 1429 | 1450 UGGAGAAGC/ :::: : ..::::::::: : UGCUCAGUG(Cleavage | pacid=371468 |
| 50 | | | |
| 51 | 1946 | 1966 UGGAGAAGC/ :::: : ..::::::::: : UGCAGUUGC(Cleavage | pacid=371764 |
| 52 | 1712 | 1732 UGGAGAAGC/ :::: : ..::::::::: : UGCAGUUGC(Cleavage | pacid=371764 |
| 53 | 4127 | 4147 UGGAGAAGC/ ::::::::::: ::::: ACCAUGUGCC Cleavage | pacid=371756 |
| 54 | | | |
| 55 | 3713 | 3733 UGGAGAAGC/ ::::::::::: ::::: ACCAUGUGCC Cleavage | pacid=371756 |
| 56 | 2142 | 2165 UGGAGAAGC/ ::::: ..::::::::: GGCACGUCCC Cleavage | pacid=371647 |
| 57 | 729 | 749 UGGAGAAGC/ ::::::::::: : ::::: AGCAUGUGU(Cleavage | pacid=371776 |
| 58 | | | |
| 59 | 729 | 749 UGGAGAAGC/ ::::::::::: : ::::: AGCAUGUGU(Cleavage | pacid=371776 |
| 60 | 1576 | 1596 UGGAGAAGC/ :: : ..::: ..::::::::: UUCUCUUGCI Translation | pacid=371530 |
| | 549 | 569 UGGAGAAGC/ ::::::::::: : ::::: AGCAUGUGU(Cleavage | pacid=371777 |

| | | | | |
|----|------|-----------------|-------------------------------------|--------------|
| 1 | | | | |
| 2 | 444 | 464 UGGAGAAGC/ | ::: ::: : GACAUGUGC(Translation | pacid=371607 |
| 3 | 449 | 469 UGGAGAAGC/ | ::: ::: : AGCAUGUGC(Cleavage | pacid=371663 |
| 4 | 417 | 437 UGGAGAAGC/ | ::: ::: : AGCACGUGU(Cleavage | pacid=371656 |
| 5 | | | | |
| 6 | 1075 | 1095 UGGAGAAGC/ | ::: ::: : ACAACGUGC(Cleavage | pacid=371656 |
| 7 | 331 | 351 UGGAGAAGC/ | ::: ::: : AGCACGUGU(Cleavage | pacid=371656 |
| 8 | 989 | 1009 UGGAGAAGC/ | ::: ::: : ACAACGUGC(Cleavage | pacid=371656 |
| 9 | | | | |
| 10 | 1100 | 1120 UGGAGAAGC/ | ::: ::: : AACACGUGU(Cleavage | pacid=371470 |
| 11 | 99 | 119 UGGAGAAGC/ | ::: ::: : AGCACGUGU(Cleavage | pacid=371656 |
| 12 | 977 | 997 UGGAGAAGC/ | ::: ::: : ACAACGUGC(Cleavage | pacid=371656 |
| 13 | | | | |
| 14 | 278 | 298 UGGAGAAGC/ | ::: : ::: : UGCACCUCCC Cleavage | pacid=371740 |
| 15 | 249 | 269 UGGAGAAGC/ | ::: ::: : AGCACGUGU(Cleavage | pacid=371656 |
| 16 | 907 | 927 UGGAGAAGC/ | ::: ::: : ACAACGUGC(Cleavage | pacid=371656 |
| 17 | | | | |
| 18 | 420 | 440 UGGAGAAGC/ | ::: : ::: : UGCUCCUGCC Cleavage | pacid=371532 |
| 19 | 161 | 181 UGGAGAAGC/ | ::: ::: : AGCACGUGU(Cleavage | pacid=371656 |
| 20 | 819 | 839 UGGAGAAGC/ | ::: ::: : ACAACGUGC(Cleavage | pacid=371656 |
| 21 | | | | |
| 22 | 285 | 305 UGGAGAAGC/ | ::: : ::: : UGCUCCUGCC Cleavage | pacid=371528 |
| 23 | 501 | 521 UGGAGAAGC/ | ::: ::: : AGCAUGUGC(Cleavage | pacid=371779 |
| 24 | 611 | 631 UGGAGAAGC/ | ::: : ::: : UGCAAGUCU(Cleavage | pacid=371590 |
| 25 | | | | |
| 26 | 205 | 225 UGGAGAAGC/ | ::: ::: : AGCAUGUGC(Cleavage | pacid=371599 |
| 27 | 179 | 200 UGGAGAAGC/ | ::: : ::: : ACCACGUGAC Cleavage | pacid=371457 |
| 28 | 4269 | 4289 UGGAGAAGC/ | ::: : ::: : UGAACAUGA(Cleavage | pacid=371579 |
| 29 | | | | |
| 30 | 4266 | 4286 UGGAGAAGC/ | ::: : ::: : UGAACAUGA(Cleavage | pacid=371579 |
| 31 | 1610 | 1630 UGGAGAAGC/ | ::: : ::: : UGCAGCUGC/ Cleavage | pacid=371622 |
| 32 | 1571 | 1591 UGGAGAAGC/ | ::: : ::: : UGCAGCUGC/ Cleavage | pacid=371622 |
| 33 | | | | |
| 34 | 1531 | 1551 UGGAGAAGC/ | ::: : ::: : UGCAGCUGC/ Cleavage | pacid=371622 |
| 35 | 3830 | 3850 UGGAGAAGC/ | ::: : ::: : UGAACAUGU(Cleavage | pacid=371514 |
| 36 | 2950 | 2970 UGGAGAAGC/ | ::: : ::: : UGUUUGGGU(Cleavage | pacid=371537 |
| 37 | | | | |
| 38 | 2890 | 2910 UGGAGAAGC/ | ::: : ::: : UGUUUGGGU(Cleavage | pacid=371537 |
| 39 | 3661 | 3681 UGGAGAAGC/ | ::: : ::: : UGAACAUGU(Cleavage | pacid=371514 |
| 40 | 1224 | 1244 UGGAGAAGC/ | ::: : ::: : UGCAGCUGC/ Cleavage | pacid=371622 |
| 41 | | | | |
| 42 | 890 | 911 UGGAGAAGC/ | ::: : ::: : UGCACCUGCC(Translation | pacid=371489 |
| 43 | 273 | 293 UGGAGAAGC/ | ::: ::: : UGUGUGUGU(Cleavage | pacid=371747 |
| 44 | 894 | 914 UGGAGAAGC/ | ::: ::: : UGCAUGUGU(Translation | pacid=371531 |
| 45 | 81 | 100 UGGAGAAGC/ | ::: ::: : UGCAUGUGC(Translation | pacid=371483 |
| 46 | | | | |
| 47 | 81 | 100 UGGAGAAGC/ | ::: ::: : UGCAUGUGC(Translation | pacid=371483 |
| 48 | 210 | 229 UGGAGAAGC/ | ::: ::: : UGCACGUGC(Cleavage | pacid=371445 |
| 49 | 210 | 229 UGGAGAAGC/ | ::: ::: : UGCACGUGC(Cleavage | pacid=371445 |
| 50 | | | | |
| 51 | 67 | 88 UGGAGAAGC/ | ::: : ::: : UGCAACGUG(Cleavage | pacid=371715 |
| 52 | 2692 | 2712 UGGAGAAGC/ | ::: : ::: : UGCAUCUGU(Cleavage | pacid=371592 |
| 53 | 1441 | 1461 UGGAGAAGC/ | ::: : ::: : UGCUUGUGU(Translation | pacid=371656 |
| 54 | | | | |
| 55 | 393 | 413 UGGAGAAGC/ | ::: : ::: : UGUCUGUGU(Cleavage | pacid=371678 |
| 56 | 1867 | 1887 UGGAGAAGC/ | ::: : ::: : UGUUUUGC(Cleavage | pacid=371738 |
| 57 | 1795 | 1815 UGGAGAAGC/ | ::: : ::: : UGUUUUGC(Cleavage | pacid=371738 |
| 58 | | | | |
| 59 | 2809 | 2829 UGGAGAAGC/ | ::: ::: : GGCACGUGC(Translation | pacid=371462 |
| 60 | 639 | 659 UGGAGAAGC/ | ::: ::: : UAGACGUGU(Cleavage | pacid=371520 |
| | 1429 | 1450 UGGAGAAGC/ | ::: : ::: : UGCUAGUG(Cleavage | pacid=371468 |

| | | | |
|----|------|--|--------------|
| 1 | | | |
| 2 | 1429 | 1450 UGGAGAAGC/:: : ::::: :UGCUCAGUG(Cleavage | pacid=371468 |
| 3 | 1946 | 1966 UGGAGAAGC/::: : ::::: : :: UGCAGUUGC(Cleavage | pacid=371764 |
| 4 | 1712 | 1732 UGGAGAAGC/::: : ::::: : :: UGCAGUUGC(Cleavage | pacid=371764 |
| 5 | | | |
| 6 | 4127 | 4147 UGGAGAAGC/ : ::::: : ::::: ACCAUGUGCC Cleavage | pacid=371756 |
| 7 | 3713 | 3733 UGGAGAAGC/ : ::::: : ::::: ACCAUGUGCC Cleavage | pacid=371756 |
| 8 | | | |
| 9 | 2142 | 2165 UGGAGAAGC/ ::::: : ::::: GGCACGUCCC Cleavage | pacid=371647 |
| 10 | 729 | 749 UGGAGAAGC/ : ::::: : : AGCAUGUGU(Cleavage | pacid=371776 |
| 11 | 729 | 749 UGGAGAAGC/ : ::::: : : AGCAUGUGU(Cleavage | pacid=371776 |
| 12 | 1576 | 1596 UGGAGAAGC/ : : : : ::::: UUCUCUUGC(Translation | pacid=371530 |
| 13 | | | |
| 14 | 549 | 569 UGGAGAAGC/ : ::::: : : AGCAUGUGU(Cleavage | pacid=371777 |
| 15 | 444 | 464 UGGAGAAGC/ : ::::: : ::::: GACAUGUGC(Translation | pacid=371607 |
| 16 | 449 | 469 UGGAGAAGC/ : ::::: : : : AGCAUGUGC(Translation | pacid=371663 |
| 17 | | | |
| 18 | 417 | 437 UGGAGAAGC/ : ::::: : : : AGCACGUGU(Cleavage | pacid=371656 |
| 19 | 1075 | 1095 UGGAGAAGC/ : ::::: : : : ACAACGUGC(Translation | pacid=371656 |
| 20 | 331 | 351 UGGAGAAGC/ : ::::: : : : AGCACGUGU(Cleavage | pacid=371656 |
| 21 | | | |
| 22 | 989 | 1009 UGGAGAAGC/ : ::::: : : : ACAACGUGC(Translation | pacid=371656 |
| 23 | 1100 | 1120 UGGAGAAGC/ : ::::: : : : AACACGUGU(Cleavage | pacid=371470 |
| 24 | 99 | 119 UGGAGAAGC/ : ::::: : : : AGCACGUGU(Cleavage | pacid=371656 |
| 25 | | | |
| 26 | 977 | 997 UGGAGAAGC/ : ::::: : : : ACAACGUGC(Translation | pacid=371656 |
| 27 | 278 | 298 UGGAGAAGC/ ::::: : : : UGCACCUCCC Cleavage | pacid=371740 |
| 28 | 249 | 269 UGGAGAAGC/ : ::::: : : : AGCACGUGU(Cleavage | pacid=371656 |
| 29 | | | |
| 30 | 907 | 927 UGGAGAAGC/ : ::::: : : : ACAACGUGC(Translation | pacid=371656 |
| 31 | 420 | 440 UGGAGAAGC/ : : : : ::::: : UGCUCUGCC Cleavage | pacid=371532 |
| 32 | 161 | 181 UGGAGAAGC/ : ::::: : : : AGCACGUGU(Cleavage | pacid=371656 |
| 33 | | | |
| 34 | 819 | 839 UGGAGAAGC/ : ::::: : : : ACAACGUGC(Translation | pacid=371656 |
| 35 | 285 | 305 UGGAGAAGC/ : : : : ::::: : UGCUCUGCC Cleavage | pacid=371528 |
| 36 | 501 | 521 UGGAGAAGC/ : ::::: : : : AGCAUGUGC(Cleavage | pacid=371779 |
| 37 | 611 | 631 UGGAGAAGC/ ::::: : : : UGCAAGUC(Translation | pacid=371590 |
| 38 | | | |
| 39 | 205 | 225 UGGAGAAGC/ : ::::: : : : AGCAUGUGC(Translation | pacid=371599 |
| 40 | 179 | 200 UGGAGAAGC/ : ::::: : : : ACCACGUGAC Cleavage | pacid=371457 |
| 41 | | | |
| 42 | 4269 | 4289 UGGAGAAGC/ : : : : ::::: : UGAACAUGA(Cleavage | pacid=371579 |
| 43 | 4266 | 4286 UGGAGAAGC/ : : : : ::::: : UGAACAUGA(Cleavage | pacid=371579 |
| 44 | 1610 | 1630 UGGAGAAGC/ ::::: : : : UGCAGCUGC(Cleavage | pacid=371622 |
| 45 | 1571 | 1591 UGGAGAAGC/ ::::: : : : UGCAGCUGC(Cleavage | pacid=371622 |
| 46 | 1531 | 1551 UGGAGAAGC/ ::::: : : : UGCAGCUGC(Cleavage | pacid=371622 |
| 47 | | | |
| 48 | 3830 | 3850 UGGAGAAGC/ : : : : : : UGAACAUGU(Cleavage | pacid=371514 |
| 49 | 2950 | 2970 UGGAGAAGC/ : . : : : : : UGUUUGGGU(Cleavage | pacid=371537 |
| 50 | | | |
| 51 | 2890 | 2910 UGGAGAAGC/ : . : : : : : UGUUUGGGU(Cleavage | pacid=371537 |
| 52 | 3661 | 3681 UGGAGAAGC/ : : : : : : UGAACAUGU(Cleavage | pacid=371514 |
| 53 | 1224 | 1244 UGGAGAAGC/ ::::: : : : UGCAGCUGC(Cleavage | pacid=371622 |
| 54 | | | |
| 55 | 890 | 911 UGGAGAAGC/ ::::: : : : UGCACCUCC(Translation | pacid=371489 |
| 56 | 273 | 293 UGGAGAAGC/ : : : : : : UGUUGUGU(Cleavage | pacid=371747 |
| 57 | 894 | 914 UGGAGAAGC/ : : : : : : UGCAUGUGU(Translation | pacid=371531 |
| 58 | | | |
| 59 | 81 | 100 UGGAGAAGC/ : : : : : : UGCAUGUGC(Translation | pacid=371483 |
| 60 | 81 | 100 UGGAGAAGC/ : : : : : : UGCAUGUGC(Translation | pacid=371483 |
| | 210 | 229 UGGAGAAGC/ : : : : : : UGCACGUGC(Cleavage | pacid=371445 |

| | | | | |
|----|------|---|------------------------|--------------|
| 1 | | | | |
| 2 | 210 | 229 UGGAGAAGC/ ::::::::::: ::::: | UGCACGUGCC Cleavage | pacid=371445 |
| 3 | 67 | 88 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UGCAACGUGI Cleavage | pacid=371715 |
| 4 | 2692 | 2712 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UGCAUCUGU(Cleavage | pacid=371592 |
| 5 | 1441 | 1461 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UGCUUGUGU Translation | pacid=371656 |
| 6 | 393 | 413 UGGAGAAGC/ ::: ::::: ::::: ::::: | UGUCUGUGU Cleavage | pacid=371678 |
| 7 | 1867 | 1887 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UGUAUUUGC. Cleavage | pacid=371738 |
| 8 | 1795 | 1815 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UGUAUUUGC. Cleavage | pacid=371738 |
| 9 | 2809 | 2829 UGGAGAAGC/ ::::::::::: ::::: | GGCACGUGCC Translation | pacid=371462 |
| 10 | 639 | 659 UGGAGAAGC/ ::::::::::: ::::: | UAGACGUGUI Cleavage | pacid=371520 |
| 11 | 1429 | 1450 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UGCUCAGUG(Cleavage | pacid=371468 |
| 12 | 1429 | 1450 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UGCUCAGUG(Cleavage | pacid=371468 |
| 13 | 1946 | 1966 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UGCAGUUGC(Cleavage | pacid=371764 |
| 14 | 1712 | 1732 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UGCAGUUGC(Cleavage | pacid=371764 |
| 15 | 4127 | 4147 UGGAGAAGC/ ::::::::::: ::::: | ACCAUGUGCC Cleavage | pacid=371756 |
| 16 | 3713 | 3733 UGGAGAAGC/ ::::::::::: ::::: | ACCAUGUGCC Cleavage | pacid=371756 |
| 17 | 2142 | 2165 UGGAGAAGC/ ::::: ::::: ::::: ::::: | GGCACGUCCC Cleavage | pacid=371647 |
| 18 | 729 | 749 UGGAGAAGC/ ::::::::::: ::::: | AGCAUGUGUI Cleavage | pacid=371776 |
| 19 | 729 | 749 UGGAGAAGC/ ::::::::::: ::::: | AGCAUGUGUI Cleavage | pacid=371776 |
| 20 | 1576 | 1596 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UUCUCUUGCI Translation | pacid=371530 |
| 21 | 549 | 569 UGGAGAAGC/ ::::::::::: ::::: | AGCAUGUGUI Cleavage | pacid=371777 |
| 22 | 444 | 464 UGGAGAAGC/ ::::::::::: ::::: | GACAUGUGC(Translation | pacid=371607 |
| 23 | 449 | 469 UGGAGAAGC/ ::::::::::: ::::: | AGCAUGUGCI Cleavage | pacid=371663 |
| 24 | 417 | 437 UGGAGAAGC/ ::::::::::: ::::: | AGCACGUGU(Cleavage | pacid=371656 |
| 25 | 1075 | 1095 UGGAGAAGC/ ::::::::::: ::::: | ACAACGUGCL Cleavage | pacid=371656 |
| 26 | 331 | 351 UGGAGAAGC/ ::::::::::: ::::: | AGCACGUGU(Cleavage | pacid=371656 |
| 27 | 989 | 1009 UGGAGAAGC/ ::::::::::: ::::: | ACAACGUGCL Cleavage | pacid=371656 |
| 28 | 1100 | 1120 UGGAGAAGC/ ::::::::::: ::::: | AACACGUGU(Cleavage | pacid=371470 |
| 29 | 99 | 119 UGGAGAAGC/ ::::::::::: ::::: | AGCACGUGU(Cleavage | pacid=371656 |
| 30 | 977 | 997 UGGAGAAGC/ ::::::::::: ::::: | ACAACGUGCL Cleavage | pacid=371656 |
| 31 | 278 | 298 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UGCACCUCCC Cleavage | pacid=371740 |
| 32 | 249 | 269 UGGAGAAGC/ ::::::::::: ::::: | AGCACGUGU(Cleavage | pacid=371656 |
| 33 | 907 | 927 UGGAGAAGC/ ::::::::::: ::::: | ACAACGUGCL Cleavage | pacid=371656 |
| 34 | 420 | 440 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UGCUCUGCC Cleavage | pacid=371532 |
| 35 | 161 | 181 UGGAGAAGC/ ::::::::::: ::::: | AGCACGUGU(Cleavage | pacid=371656 |
| 36 | 819 | 839 UGGAGAAGC/ ::::::::::: ::::: | ACAACGUGCL Cleavage | pacid=371656 |
| 37 | 285 | 305 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UGCUCUGCC Cleavage | pacid=371528 |
| 38 | 501 | 521 UGGAGAAGC/ ::::::::::: ::::: | AGCAUGUGC(Cleavage | pacid=371779 |
| 39 | 611 | 631 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UGCAAGUCUI Cleavage | pacid=371590 |
| 40 | 205 | 225 UGGAGAAGC/ ::::::::::: ::::: | AGCAUGUGCI Cleavage | pacid=371599 |
| 41 | 179 | 200 UGGAGAAGC/ ::::: ::::: ::::: ::::: | ACCACGUGAC Cleavage | pacid=371457 |
| 42 | 4269 | 4289 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UGAACAUGA(Cleavage | pacid=371579 |
| 43 | 4266 | 4286 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UGAACAUGA(Cleavage | pacid=371579 |
| 44 | 1610 | 1630 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UGCAGCUGC/ Cleavage | pacid=371622 |
| 45 | 1571 | 1591 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UGCAGCUGC/ Cleavage | pacid=371622 |
| 46 | 1531 | 1551 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UGCAGCUGC/ Cleavage | pacid=371622 |
| 47 | 3830 | 3850 UGGAGAAGC/ ::::: ::::: ::::: ::::: | UGAACAUGUI Cleavage | pacid=371514 |

| | | | |
|----|------|--|--------------|
| 1 | | | |
| 2 | 501 | 521 UGGAGAAGC/ ::::::::::: :: : AGCAUGUGC(Cleavage | pacid=371779 |
| 3 | 611 | 631 UGGAGAAGC/ :::: : ..::::::::: UGCAAGUCU(Cleavage | pacid=371590 |
| 4 | 205 | 225 UGGAGAAGC/ ::::::::::: . ::::: AGCAUGUGC(Cleavage | pacid=371599 |
| 5 | 179 | 200 UGGAGAAGC/ ::::: ::::::::::: ACCACGUGAC(Cleavage | pacid=371457 |
| 6 | 4269 | 4289 UGGAGAAGC/ :: : : ::::::::::: :: UGAACAUGA(Cleavage | pacid=371579 |
| 7 | 4266 | 4286 UGGAGAAGC/ :: : : ::::::::::: :: UGAACAUGA(Cleavage | pacid=371579 |
| 8 | 1610 | 1630 UGGAGAAGC/ :::: : : ::::::::::: UGCAGCUGC/ Cleavage | pacid=371622 |
| 9 | 1571 | 1591 UGGAGAAGC/ :::: : : ::::::::::: UGCAGCUGC/ Cleavage | pacid=371622 |
| 10 | 1531 | 1551 UGGAGAAGC/ :::: : : ::::::::::: UGCAGCUGC/ Cleavage | pacid=371622 |
| 11 | 3830 | 3850 UGGAGAAGC/ :: : : ..:::::::::.. UGAACAUGU(Cleavage | pacid=371514 |
| 12 | 2950 | 2970 UGGAGAAGC/ :: . : ..::::::::: UGUUUGGGU(Cleavage | pacid=371537 |
| 13 | 2890 | 2910 UGGAGAAGC/ :: . : ..::::::::: UGUUUGGGU(Cleavage | pacid=371537 |
| 14 | 3661 | 3681 UGGAGAAGC/ :: : : ..:::::::::.. UGAACAUGU(Cleavage | pacid=371514 |
| 15 | 1224 | 1244 UGGAGAAGC/ :::: : : ::::::::::: UGCAGCUGC/ Cleavage | pacid=371622 |
| 16 | 890 | 911 UGGAGAAGC/ ::::: ::::: ::::::::::: UGCACCUGCC(Translation | pacid=371489 |
| 17 | 273 | 293 UGGAGAAGC/ :::::..: ::::::::::: UGUGUGUGU(Cleavage | pacid=371747 |
| 18 | 894 | 914 UGGAGAAGC/ :::::..: ::::::::::: UGCAUGUGU(Translation | pacid=371531 |
| 19 | 81 | 100 UGGAGAAGC/ :::::..: ::::::::::: UGCAUGUGC(Translation | pacid=371483 |
| 20 | 81 | 100 UGGAGAAGC/ :::::..: ::::::::::: UGCAUGUGC(Translation | pacid=371483 |
| 21 | 210 | 229 UGGAGAAGC/ :::::..: ::::::::::: UGCACGUGC(Cleavage | pacid=371445 |
| 22 | 210 | 229 UGGAGAAGC/ :::::..: ::::::::::: UGCACGUGC(Cleavage | pacid=371445 |
| 23 | 67 | 88 UGGAGAAGC/ :::::..: ::::::::::: UGCAACGUG(Cleavage | pacid=371715 |
| 24 | 2692 | 2712 UGGAGAAGC/ ::::: ..::::::::: . UGCAUCUGU(Cleavage | pacid=371592 |
| 25 | 1441 | 1461 UGGAGAAGC/ :: : ..::: ..::::::::: UGCUUGUGU(Translation | pacid=371656 |
| 26 | 393 | 413 UGGAGAAGC/ :: . : ..:::::::::.. UGUCUGUGU(Cleavage | pacid=371678 |
| 27 | 1867 | 1887 UGGAGAAGC/ ::..: : : ::::::::::: UGUUUUGC(Cleavage | pacid=371738 |
| 28 | 1795 | 1815 UGGAGAAGC/ ::..: : : ::::::::::: UGUUUUGC(Cleavage | pacid=371738 |
| 29 | 2809 | 2829 UGGAGAAGC/ :::::..: ::::::::::: GGCACGUGC(Translation | pacid=371462 |
| 30 | 639 | 659 UGGAGAAGC/ :::::..: ::::::::::: UAGACGUGU(Cleavage | pacid=371520 |
| 31 | 1429 | 1450 UGGAGAAGC/ :: : : ..:::::::::.. UGCUCAGUG(Cleavage | pacid=371468 |
| 32 | 1429 | 1450 UGGAGAAGC/ :: : : ..:::::::::.. UGCUCAGUG(Cleavage | pacid=371468 |
| 33 | 1946 | 1966 UGGAGAAGC/ :::: : ..::::::::: :: UGCAGUUGC(Cleavage | pacid=371764 |
| 34 | 1712 | 1732 UGGAGAAGC/ :::: : ..::::::::: :: UGCAGUUGC(Cleavage | pacid=371764 |
| 35 | 4127 | 4147 UGGAGAAGC/ :::::..: ::::::::::: ACCAUGUGC(Cleavage | pacid=371756 |
| 36 | 3713 | 3733 UGGAGAAGC/ :::::..: ::::::::::: ACCAUGUGC(Cleavage | pacid=371756 |
| 37 | 2142 | 2165 UGGAGAAGC/ ::::: ..::::::::: GGCACGUCCC(Cleavage | pacid=371647 |
| 38 | 729 | 749 UGGAGAAGC/ :::::..: : : : AGCAUGUGU(Cleavage | pacid=371776 |
| 39 | 729 | 749 UGGAGAAGC/ :::::..: : : : AGCAUGUGU(Cleavage | pacid=371776 |
| 40 | 1576 | 1596 UGGAGAAGC/ :: : ..::: ..::::::::: UUCUCUUGC(Translation | pacid=371530 |
| 41 | 549 | 569 UGGAGAAGC/ :::::..: : : : AGCAUGUGU(Cleavage | pacid=371777 |
| 42 | 444 | 464 UGGAGAAGC/ :::::..: ::::::::::: GACAUGUGC(Translation | pacid=371607 |
| 43 | 449 | 469 UGGAGAAGC/ :::::..: : : : AGCAUGUGC(Cleavage | pacid=371663 |
| 44 | 417 | 437 UGGAGAAGC/ :::::..: : : : AGCACGUGU(Cleavage | pacid=371656 |
| 45 | 1075 | 1095 UGGAGAAGC/ :::::..: : : : ACAACGUGC(Cleavage | pacid=371656 |
| 46 | 331 | 351 UGGAGAAGC/ :::::..: : : : AGCACGUGU(Cleavage | pacid=371656 |
| 47 | 989 | 1009 UGGAGAAGC/ :::::..: : : : ACAACGUGC(Cleavage | pacid=371656 |

| | | | | |
|----|------|-----------------|---------------------|--------------------------|
| 1 | | | | |
| 2 | 1100 | 1120 UGGAGAAGC/ | ::::: :: AACACGUGU(| Cleavage pacid=371470 |
| 3 | 99 | 119 UGGAGAAGC/ | ::::: : AGCACGUGU(| Cleavage pacid=371656 |
| 4 | 977 | 997 UGGAGAAGC/ | ::::: : ACAACGUGCL | Cleavage pacid=371656 |
| 5 | 278 | 298 UGGAGAAGC/ | :::: : UGCACCUCCC | Cleavage pacid=371740 |
| 6 | 249 | 269 UGGAGAAGC/ | ::::: : AGCACGUGU(| Cleavage pacid=371656 |
| 7 | 907 | 927 UGGAGAAGC/ | ::::: : ACAACGUGCL | Cleavage pacid=371656 |
| 8 | 420 | 440 UGGAGAAGC/ | :::: : UGCUCCUGCC | Cleavage pacid=371532 |
| 9 | 161 | 181 UGGAGAAGC/ | ::::: : AGCACGUGU(| Cleavage pacid=371656 |
| 10 | 819 | 839 UGGAGAAGC/ | ::::: : ACAACGUGCL | Cleavage pacid=371656 |
| 11 | 285 | 305 UGGAGAAGC/ | :::: : UGCUCCUGCC | Cleavage pacid=371528 |
| 12 | 501 | 521 UGGAGAAGC/ | ::::: : AGCAUGUGCC | Cleavage pacid=371779 |
| 13 | 611 | 631 UGGAGAAGC/ | :::: : UGCAAGUCUI | Cleavage pacid=371590 |
| 14 | 205 | 225 UGGAGAAGC/ | ::::: : AGCAUGUGC(| Cleavage pacid=371599 |
| 15 | 179 | 200 UGGAGAAGC/ | :::: : ACCACGUGAC | Cleavage pacid=371457 |
| 16 | 4269 | 4289 UGGAGAAGC/ | :::: : UGAACAUGA(| Cleavage pacid=371579 |
| 17 | 4266 | 4286 UGGAGAAGC/ | :::: : UGAACAUGA(| Cleavage pacid=371579 |
| 18 | 1610 | 1630 UGGAGAAGC/ | :::: : UGCAGCUGC/ | Cleavage pacid=371622 |
| 19 | 1571 | 1591 UGGAGAAGC/ | :::: : UGCAGCUGC/ | Cleavage pacid=371622 |
| 20 | 1531 | 1551 UGGAGAAGC/ | :::: : UGCAGCUGC/ | Cleavage pacid=371622 |
| 21 | 3830 | 3850 UGGAGAAGC/ | :::: : UGAACAUGUI | Cleavage pacid=371514 |
| 22 | 2950 | 2970 UGGAGAAGC/ | :::: : UGUUUGGGU | Cleavage pacid=371537 |
| 23 | 2890 | 2910 UGGAGAAGC/ | :::: : UGUUUGGGU | Cleavage pacid=371537 |
| 24 | 3661 | 3681 UGGAGAAGC/ | :::: : UGAACAUGUI | Cleavage pacid=371514 |
| 25 | 1224 | 1244 UGGAGAAGC/ | :::: : UGCAGCUGC/ | Cleavage pacid=371622 |
| 26 | 890 | 911 UGGAGAAGC/ | :::: : UGCACCUGCC | Translation pacid=371489 |
| 27 | 273 | 293 UGGAGAAGC/ | :::: : UGUGUGUGU | Cleavage pacid=371747 |
| 28 | 894 | 914 UGGAGAAGC/ | :::: : UGCAUGUGU(| Translation pacid=371531 |
| 29 | 81 | 100 UGGAGAAGC/ | :::: : UGCAUGUGC(| Translation pacid=371483 |
| 30 | 81 | 100 UGGAGAAGC/ | :::: : UGCAUGUGC(| Translation pacid=371483 |
| 31 | 210 | 229 UGGAGAAGC/ | :::: : UGCACGUGCC | Cleavage pacid=371445 |
| 32 | 210 | 229 UGGAGAAGC/ | :::: : UGCACGUGCC | Cleavage pacid=371445 |
| 33 | 67 | 88 UGGAGAAGC/ | :::: : UGCAACGUG(| Cleavage pacid=371715 |
| 34 | 2692 | 2712 UGGAGAAGC/ | :::: : UGCAUCUGU(| Cleavage pacid=371592 |
| 35 | 1441 | 1461 UGGAGAAGC/ | :::: : UGCUUGUGU | Translation pacid=371656 |
| 36 | 393 | 413 UGGAGAAGC/ | :::: : UGUCUGUGU | Cleavage pacid=371678 |
| 37 | 1867 | 1887 UGGAGAAGC/ | :::: : UGUUUUGC. | Cleavage pacid=371738 |
| 38 | 1795 | 1815 UGGAGAAGC/ | :::: : UGUUUUGC. | Cleavage pacid=371738 |
| 39 | 2809 | 2829 UGGAGAAGC/ | :::: : GGCACGUGCC | Translation pacid=371462 |
| 40 | 639 | 659 UGGAGAAGC/ | :::: : UAGACGUGUI | Cleavage pacid=371520 |
| 41 | 1429 | 1450 UGGAGAAGC/ | :::: : UGCUCAGUG(| Cleavage pacid=371468 |
| 42 | 1429 | 1450 UGGAGAAGC/ | :::: : UGCUCAGUG(| Cleavage pacid=371468 |
| 43 | 1946 | 1966 UGGAGAAGC/ | :::: : UGCAGUUGC(| Cleavage pacid=371764 |
| 44 | 1712 | 1732 UGGAGAAGC/ | :::: : UGCAGUUGC(| Cleavage pacid=371764 |
| 45 | 4127 | 4147 UGGAGAAGC/ | :::: : ACCAUGUGCC | Cleavage pacid=371756 |
| 46 | 3713 | 3733 UGGAGAAGC/ | :::: : ACCAUGUGCC | Cleavage pacid=371756 |
| 47 | 2142 | 2165 UGGAGAAGC/ | :::: : GGCACGUCCC | Cleavage pacid=371647 |

| | | | |
|----|------|---|--------------|
| 1 | | | |
| 2 | 729 | 749 UGGAGAAGC/ ::::: : AGCAUGUGU(Cleavage | pacid=371776 |
| 3 | 729 | 749 UGGAGAAGC/ ::::: : AGCAUGUGU(Cleavage | pacid=371776 |
| 4 | 1576 | 1596 UGGAGAAGC/ : : : : : UUCUCUUGC(Translation | pacid=371530 |
| 5 | 549 | 569 UGGAGAAGC/ ::::: : AGCAUGUGU(Cleavage | pacid=371777 |
| 6 | 444 | 464 UGGAGAAGC/ ::::: : GACAUGUGC(Translation | pacid=371607 |
| 7 | 449 | 469 UGGAGAAGC/ ::::: : AGCAUGUGC(Cleavage | pacid=371663 |
| 8 | 417 | 437 UGGAGAAGC/ ::::: : AGCACGUGU(Cleavage | pacid=371656 |
| 9 | 1075 | 1095 UGGAGAAGC/ ::::: : ACAACGUGC(Cleavage | pacid=371656 |
| 10 | 331 | 351 UGGAGAAGC/ ::::: : AGCACGUGU(Cleavage | pacid=371656 |
| 11 | 989 | 1009 UGGAGAAGC/ ::::: : ACAACGUGC(Cleavage | pacid=371656 |
| 12 | 1100 | 1120 UGGAGAAGC/ ::::: : AACACGUGU(Cleavage | pacid=371470 |
| 13 | 99 | 119 UGGAGAAGC/ ::::: : AGCACGUGU(Cleavage | pacid=371656 |
| 14 | 977 | 997 UGGAGAAGC/ ::::: : ACAACGUGC(Cleavage | pacid=371656 |
| 15 | 278 | 298 UGGAGAAGC/ : : : : : UGCACCUCCC(Cleavage | pacid=371740 |
| 16 | 249 | 269 UGGAGAAGC/ ::::: : AGCACGUGU(Cleavage | pacid=371656 |
| 17 | 907 | 927 UGGAGAAGC/ ::::: : ACAACGUGC(Cleavage | pacid=371656 |
| 18 | 420 | 440 UGGAGAAGC/ : : : : : UGCUCCUGC(Cleavage | pacid=371532 |
| 19 | 161 | 181 UGGAGAAGC/ ::::: : AGCACGUGU(Cleavage | pacid=371656 |
| 20 | 819 | 839 UGGAGAAGC/ ::::: : ACAACGUGC(Cleavage | pacid=371656 |
| 21 | 285 | 305 UGGAGAAGC/ : : : : : UGCUCCUGC(Cleavage | pacid=371528 |
| 22 | 501 | 521 UGGAGAAGC/ ::::: : AGCAUGUGC(Cleavage | pacid=371779 |
| 23 | 611 | 631 UGGAGAAGC/ : : : : : UGCAAGUCU(Cleavage | pacid=371590 |
| 24 | 205 | 225 UGGAGAAGC/ ::::: : AGCAUGUGC(Cleavage | pacid=371599 |
| 25 | 179 | 200 UGGAGAAGC/ ::::: : ACCACGUGAC(Cleavage | pacid=371457 |
| 26 | 4269 | 4289 UGGAGAAGC/ : : : : : UGAACAUGA(Cleavage | pacid=371579 |
| 27 | 4266 | 4286 UGGAGAAGC/ : : : : : UGAACAUGA(Cleavage | pacid=371579 |
| 28 | 1610 | 1630 UGGAGAAGC/ : : : : : UGCAGCUGC(Cleavage | pacid=371622 |
| 29 | 1571 | 1591 UGGAGAAGC/ : : : : : UGCAGCUGC(Cleavage | pacid=371622 |
| 30 | 1531 | 1551 UGGAGAAGC/ : : : : : UGCAGCUGC(Cleavage | pacid=371622 |
| 31 | 3830 | 3850 UGGAGAAGC/ : : : : : UGAACAUGU(Cleavage | pacid=371514 |
| 32 | 2950 | 2970 UGGAGAAGC/ : : : : : UGUUUGGGU(Cleavage | pacid=371537 |
| 33 | 2890 | 2910 UGGAGAAGC/ : : : : : UGUUUGGGU(Cleavage | pacid=371537 |
| 34 | 3661 | 3681 UGGAGAAGC/ : : : : : UGAACAUGU(Cleavage | pacid=371514 |
| 35 | 1224 | 1244 UGGAGAAGC/ : : : : : UGCAGCUGC(Cleavage | pacid=371622 |
| 36 | 890 | 911 UGGAGAAGC/ : : : : : UGCACCUGCC(Translation | pacid=371489 |
| 37 | 273 | 293 UGGAGAAGC/ : : : : : UGUGUGUGU(Cleavage | pacid=371747 |
| 38 | 894 | 914 UGGAGAAGC/ : : : : : UGCAUGUGU(Translation | pacid=371531 |
| 39 | 81 | 100 UGGAGAAGC/ : : : : : UGCAUGUGC(Translation | pacid=371483 |
| 40 | 81 | 100 UGGAGAAGC/ : : : : : UGCAUGUGC(Translation | pacid=371483 |
| 41 | 210 | 229 UGGAGAAGC/ : : : : : UGCACGUGC(Cleavage | pacid=371445 |
| 42 | 210 | 229 UGGAGAAGC/ : : : : : UGCACGUGC(Cleavage | pacid=371445 |
| 43 | 67 | 88 UGGAGAAGC/ : : : : : UGCAACGUG(Cleavage | pacid=371715 |
| 44 | 2692 | 2712 UGGAGAAGC/ : : : : : UGCAUCUGU(Cleavage | pacid=371592 |
| 45 | 1441 | 1461 UGGAGAAGC/ : : : : : UGCUUGUGU(Translation | pacid=371656 |
| 46 | 393 | 413 UGGAGAAGC/ : : : : : UGUCUGUGU(Cleavage | pacid=371678 |
| 47 | 1867 | 1887 UGGAGAAGC/ : : : : : UGUUUUGC(Cleavage | pacid=371738 |

| | | | | |
|----|------|-----------------------------------|-------------------------|--------------|
| 1 | | | | |
| 2 | 1795 | 1815 UGGAGAAGC/ ::.. :: | UGUAAUUUGC.Cleavage | pacid=371738 |
| 3 | 2809 | 2829 UGGAGAAGC/ ::..... ::... | GGCACGUGCC Translation | pacid=371462 |
| 4 | 639 | 659 UGGAGAAGC/ ::..... ::..... | UAGACGUGUI Cleavage | pacid=371520 |
| 5 | | | | |
| 6 | 1429 | 1450 UGGAGAAGC/ :: : | UGCUCAGUG(Cleavage | pacid=371468 |
| 7 | 1429 | 1450 UGGAGAAGC/ :: : | UGCUCAGUG(Cleavage | pacid=371468 |
| 8 | | | | |
| 9 | 1946 | 1966 UGGAGAAGC/ ::.. :: | UGCAGUUGC(Cleavage | pacid=371764 |
| 10 | 1712 | 1732 UGGAGAAGC/ ::.. :: | UGCAGUUGC(Cleavage | pacid=371764 |
| 11 | 4127 | 4147 UGGAGAAGC/ ::..... ::... | ACCAUGUGCC Cleavage | pacid=371756 |
| 12 | 3713 | 3733 UGGAGAAGC/ ::..... ::... | ACCAUGUGCC Cleavage | pacid=371756 |
| 13 | | | | |
| 14 | 2142 | 2165 UGGAGAAGC/ ::.. :: | GGCACGUCCC Cleavage | pacid=371647 |
| 15 | 729 | 749 UGGAGAAGC/ ::..... :: | AGCAUGUGUI(Cleavage | pacid=371776 |
| 16 | 729 | 749 UGGAGAAGC/ ::..... :: | AGCAUGUGUI(Cleavage | pacid=371776 |
| 17 | | | | |
| 18 | 1576 | 1596 UGGAGAAGC/ :: : | UUCUCUUGC(Translation | pacid=371530 |
| 19 | 549 | 569 UGGAGAAGC/ ::..... :: | AGCAUGUGUI(Cleavage | pacid=371777 |
| 20 | 444 | 464 UGGAGAAGC/ ::..... ::... | GACAUGUGCC(Translation | pacid=371607 |
| 21 | | | | |
| 22 | 449 | 469 UGGAGAAGC/ ::..... ::... | AGCAUGUGC(Cleavage | pacid=371663 |
| 23 | 417 | 437 UGGAGAAGC/ ::..... ::... | AGCACGUGU(Cleavage | pacid=371656 |
| 24 | 1075 | 1095 UGGAGAAGC/ ::..... ::... | ACAACGUGC(Cleavage | pacid=371656 |
| 25 | | | | |
| 26 | 331 | 351 UGGAGAAGC/ ::..... ::... | AGCACGUGU(Cleavage | pacid=371656 |
| 27 | 989 | 1009 UGGAGAAGC/ ::..... ::... | ACAACGUGC(Cleavage | pacid=371656 |
| 28 | 1100 | 1120 UGGAGAAGC/ ::..... ::... | AACACGUGU(Cleavage | pacid=371470 |
| 29 | | | | |
| 30 | 99 | 119 UGGAGAAGC/ ::..... ::... | AGCACGUGU(Cleavage | pacid=371656 |
| 31 | 977 | 997 UGGAGAAGC/ ::..... ::... | ACAACGUGC(Cleavage | pacid=371656 |
| 32 | 278 | 298 UGGAGAAGC/ ::.. :: | UGCACCUCCC Cleavage | pacid=371740 |
| 33 | | | | |
| 34 | 249 | 269 UGGAGAAGC/ ::..... ::... | AGCACGUGU(Cleavage | pacid=371656 |
| 35 | 907 | 927 UGGAGAAGC/ ::..... ::... | ACAACGUGC(Cleavage | pacid=371656 |
| 36 | 420 | 440 UGGAGAAGC/ :: : | UGCUCUGCC Cleavage | pacid=371532 |
| 37 | | | | |
| 38 | 161 | 181 UGGAGAAGC/ ::..... ::... | AGCACGUGU(Cleavage | pacid=371656 |
| 39 | 819 | 839 UGGAGAAGC/ ::..... ::... | ACAACGUGC(Cleavage | pacid=371656 |
| 40 | 285 | 305 UGGAGAAGC/ :: : | UGCUCUGCC Cleavage | pacid=371528 |
| 41 | 501 | 521 UGGAGAAGC/ ::..... :: : | AGCAUGUGC(Cleavage | pacid=371779 |
| 42 | | | | |
| 43 | 611 | 631 UGGAGAAGC/ :: : | UGCAAGUCUI Cleavage | pacid=371590 |
| 44 | 205 | 225 UGGAGAAGC/ ::..... :: | AGCAUGUGC(Cleavage | pacid=371599 |
| 45 | 179 | 200 UGGAGAAGC/ ::.. :: | ACCACGUGAC Cleavage | pacid=371457 |
| 46 | | | | |
| 47 | 4269 | 4289 UGGAGAAGC/ :: : | UGAACAUGA(Cleavage | pacid=371579 |
| 48 | 4266 | 4286 UGGAGAAGC/ :: : | UGAACAUGA(Cleavage | pacid=371579 |
| 49 | | | | |
| 50 | 1610 | 1630 UGGAGAAGC/ ::.. :: | UGCAGCUGC/ Cleavage | pacid=371622 |
| 51 | 1571 | 1591 UGGAGAAGC/ ::.. :: | UGCAGCUGC/ Cleavage | pacid=371622 |
| 52 | 1531 | 1551 UGGAGAAGC/ ::.. :: | UGCAGCUGC/ Cleavage | pacid=371622 |
| 53 | 3830 | 3850 UGGAGAAGC/ :: : | UGAACAUGUI Cleavage | pacid=371514 |
| 54 | | | | |
| 55 | 2950 | 2970 UGGAGAAGC/ :: : | UGUUUGGGU Cleavage | pacid=371537 |
| 56 | 2890 | 2910 UGGAGAAGC/ :: : | UGUUUGGGU Cleavage | pacid=371537 |
| 57 | | | | |
| 58 | 3661 | 3681 UGGAGAAGC/ :: : | UGAACAUGUI Cleavage | pacid=371514 |
| 59 | 1224 | 1244 UGGAGAAGC/ ::.. :: | UGCAGCUGC/ Cleavage | pacid=371622 |
| 60 | 890 | 911 UGGAGAAGC/ ::.. :: | UGCACCUGCC Translation | pacid=371489 |
| | 273 | 293 UGGAGAAGC/ ::..... ::..... | UGUGUGUGU Cleavage | pacid=371747 |

| | | | | | |
|----|------|-----------------|------------------------------|--------------|--------------|
| 1 | | | | | |
| 2 | 894 | 914 UGGAGAAGC/ | ::: ::::: ::::: . UGCAUGUGU | Translation | pacid=371531 |
| 3 | 81 | 100 UGGAGAAGC/ | ::: ::::: ::::: . UGCAUGUGC | (Translation | pacid=371483 |
| 4 | 81 | 100 UGGAGAAGC/ | ::: ::::: ::::: . UGCAUGUGC | (Translation | pacid=371483 |
| 5 | | | | | |
| 6 | 210 | 229 UGGAGAAGC/ | ::: ::::: ::::: . UGCACGUGC | (Cleavage | pacid=371445 |
| 7 | 210 | 229 UGGAGAAGC/ | ::: ::::: ::::: . UGCACGUGC | (Cleavage | pacid=371445 |
| 8 | 67 | 88 UGGAGAAGC/ | ::: ::::: ::::: . UGCAACGUG | (Cleavage | pacid=371715 |
| 9 | | | | | |
| 10 | 2692 | 2712 UGGAGAAGC/ | ::: ::::: ::::: . UGCAUCUGU | (Cleavage | pacid=371592 |
| 11 | 1441 | 1461 UGGAGAAGC/ | ::: ::::: ::::: . UGCUUGUGU | Translation | pacid=371656 |
| 12 | 393 | 413 UGGAGAAGC/ | ::: ::::: ::::: . UGUCUGUGU | Cleavage | pacid=371678 |
| 13 | | | | | |
| 14 | 1867 | 1887 UGGAGAAGC/ | ::: ::::: ::::: . UGUUUUGC | (Cleavage | pacid=371738 |
| 15 | 1795 | 1815 UGGAGAAGC/ | ::: ::::: ::::: . UGUUUUGC | (Cleavage | pacid=371738 |
| 16 | 2809 | 2829 UGGAGAAGC/ | ::: ::::: ::::: . GGCACGUGC | (Translation | pacid=371462 |
| 17 | | | | | |
| 18 | 639 | 659 UGGAGAAGC/ | ::: ::::: ::::: . UAGACGUGU | (Cleavage | pacid=371520 |
| 19 | 1429 | 1450 UGGAGAAGC/ | ::: ::::: ::::: . UGCUCAGUG | (Cleavage | pacid=371468 |
| 20 | 1429 | 1450 UGGAGAAGC/ | ::: ::::: ::::: . UGCUCAGUG | (Cleavage | pacid=371468 |
| 21 | | | | | |
| 22 | 1946 | 1966 UGGAGAAGC/ | ::: ::::: ::::: . UGCAGUUGC | (Cleavage | pacid=371764 |
| 23 | 1712 | 1732 UGGAGAAGC/ | ::: ::::: ::::: . UGCAGUUGC | (Cleavage | pacid=371764 |
| 24 | 4127 | 4147 UGGAGAAGC/ | ::: ::::: ::::: . ACCAUGUGC | (Cleavage | pacid=371756 |
| 25 | | | | | |
| 26 | 3713 | 3733 UGGAGAAGC/ | ::: ::::: ::::: . ACCAUGUGC | (Cleavage | pacid=371756 |
| 27 | 2142 | 2165 UGGAGAAGC/ | ::: ::::: ::::: . GGCACGUCCC | (Cleavage | pacid=371647 |
| 28 | 729 | 749 UGGAGAAGC/ | ::: ::::: ::::: . AGCAUGUGU | (Cleavage | pacid=371776 |
| 29 | 729 | 749 UGGAGAAGC/ | ::: ::::: ::::: . AGCAUGUGU | (Cleavage | pacid=371776 |
| 30 | | | | | |
| 31 | 1576 | 1596 UGGAGAAGC/ | ::: ::::: ::::: . UUCUCUUGC | (Translation | pacid=371530 |
| 32 | 549 | 569 UGGAGAAGC/ | ::: ::::: ::::: . AGCAUGUGU | (Cleavage | pacid=371777 |
| 33 | | | | | |
| 34 | 444 | 464 UGGAGAAGC/ | ::: ::::: ::::: . GACAUGUGC | (Translation | pacid=371607 |
| 35 | 449 | 469 UGGAGAAGC/ | ::: ::::: ::::: . AGCAUGUGC | (Cleavage | pacid=371663 |
| 36 | 417 | 437 UGGAGAAGC/ | ::: ::::: ::::: . AGCACGUGU | (Cleavage | pacid=371656 |
| 37 | | | | | |
| 38 | 1075 | 1095 UGGAGAAGC/ | ::: ::::: ::::: . ACAACGUGC | (Cleavage | pacid=371656 |
| 39 | 331 | 351 UGGAGAAGC/ | ::: ::::: ::::: . AGCACGUGU | (Cleavage | pacid=371656 |
| 40 | 989 | 1009 UGGAGAAGC/ | ::: ::::: ::::: . ACAACGUGC | (Cleavage | pacid=371656 |
| 41 | 1100 | 1120 UGGAGAAGC/ | ::: ::::: ::::: . AACACGUGU | (Cleavage | pacid=371470 |
| 42 | | | | | |
| 43 | 99 | 119 UGGAGAAGC/ | ::: ::::: ::::: . AGCACGUGU | (Cleavage | pacid=371656 |
| 44 | 977 | 997 UGGAGAAGC/ | ::: ::::: ::::: . ACAACGUGC | (Cleavage | pacid=371656 |
| 45 | 278 | 298 UGGAGAAGC/ | ::: ::::: ::::: . UGCACCUCCC | (Cleavage | pacid=371740 |
| 46 | 249 | 269 UGGAGAAGC/ | ::: ::::: ::::: . AGCACGUGU | (Cleavage | pacid=371656 |
| 47 | | | | | |
| 48 | 907 | 927 UGGAGAAGC/ | ::: ::::: ::::: . ACAACGUGC | (Cleavage | pacid=371656 |
| 49 | 420 | 440 UGGAGAAGC/ | ::: ::::: ::::: . UGCUCUGCC | (Cleavage | pacid=371532 |
| 50 | | | | | |
| 51 | 161 | 181 UGGAGAAGC/ | ::: ::::: ::::: . AGCACGUGU | (Cleavage | pacid=371656 |
| 52 | 819 | 839 UGGAGAAGC/ | ::: ::::: ::::: . ACAACGUGC | (Cleavage | pacid=371656 |
| 53 | 285 | 305 UGGAGAAGC/ | ::: ::::: ::::: . UGCUCUGCC | (Cleavage | pacid=371528 |
| 54 | | | | | |
| 55 | 501 | 521 UGGAGAAGC/ | ::: ::::: ::::: . AGCAUGUGC | (Cleavage | pacid=371779 |
| 56 | 611 | 631 UGGAGAAGC/ | ::: ::::: ::::: . UGCAAGUCU | (Cleavage | pacid=371590 |
| 57 | 205 | 225 UGGAGAAGC/ | ::: ::::: ::::: . AGCAUGUGC | (Cleavage | pacid=371599 |
| 58 | | | | | |
| 59 | 179 | 200 UGGAGAAGC/ | ::: ::::: ::::: . ACCACGUGAC | (Cleavage | pacid=371457 |
| 60 | 4269 | 4289 UGGAGAAGC/ | ::: ::::: ::::: . UGAACAUGA | (Cleavage | pacid=371579 |
| | 4266 | 4286 UGGAGAAGC/ | ::: ::::: ::::: . UGAACAUGA | (Cleavage | pacid=371579 |

| | | | | |
|----|------|--|--|--------------|
| 1 | | | | |
| 2 | 1610 | 1630 UGGAGAAGC/::: :: :.....: UGCAGCUGC/ Cleavage | | pacid=371622 |
| 3 | 1571 | 1591 UGGAGAAGC/::: :: :.....: UGCAGCUGC/ Cleavage | | pacid=371622 |
| 4 | 1531 | 1551 UGGAGAAGC/::: :: :.....: UGCAGCUGC/ Cleavage | | pacid=371622 |
| 5 | | | | |
| 6 | 3830 | 3850 UGGAGAAGC/:: : :.....: UGAACAUGUI Cleavage | | pacid=371514 |
| 7 | 2950 | 2970 UGGAGAAGC/:: . :.....: UGUUUGGGU Cleavage | | pacid=371537 |
| 8 | 2890 | 2910 UGGAGAAGC/:: . :.....: UGUUUGGGU Cleavage | | pacid=371537 |
| 9 | | | | |
| 10 | 3661 | 3681 UGGAGAAGC/:: : :.....: UGAACAUGUI Cleavage | | pacid=371514 |
| 11 | 1224 | 1244 UGGAGAAGC/::: :: :.....: UGCAGCUGC/ Cleavage | | pacid=371622 |
| 12 | 890 | 911 UGGAGAAGC/::: : :.....: UGCACCUGCC Translation | | pacid=371489 |
| 13 | | | | |
| 14 | 273 | 293 UGGAGAAGC/::.....: :.....: UGUGUGUGU Cleavage | | pacid=371747 |
| 15 | 894 | 914 UGGAGAAGC/::: : :.....: UGCAUGUGU Translation | | pacid=371531 |
| 16 | 81 | 100 UGGAGAAGC/::: : :.....: UGCAUGUGC(Translation | | pacid=371483 |
| 17 | | | | |
| 18 | 81 | 100 UGGAGAAGC/::: : :.....: UGCAUGUGC(Translation | | pacid=371483 |
| 19 | 210 | 229 UGGAGAAGC/::: : :.....: UGCACGUGCC Cleavage | | pacid=371445 |
| 20 | 210 | 229 UGGAGAAGC/::: : :.....: UGCACGUGCC Cleavage | | pacid=371445 |
| 21 | | | | |
| 22 | 67 | 88 UGGAGAAGC/::: : :.....: UGCAACGUGI Cleavage | | pacid=371715 |
| 23 | 2692 | 2712 UGGAGAAGC/::: . :.....: . UGCAUCUGU(Cleavage | | pacid=371592 |
| 24 | 1441 | 1461 UGGAGAAGC/:: : :.....: UGCUUGUGU Translation | | pacid=371656 |
| 25 | | | | |
| 26 | 393 | 413 UGGAGAAGC/:: . :.....: UGUCUGUGU Cleavage | | pacid=371678 |
| 27 | 1867 | 1887 UGGAGAAGC/::.. : :.....: UGUUUUUGC Cleavage | | pacid=371738 |
| 28 | 1795 | 1815 UGGAGAAGC/::.. : :.....: UGUUUUUGC Cleavage | | pacid=371738 |
| 29 | | | | |
| 30 | 2809 | 2829 UGGAGAAGC/ : : :.....: GGCACGUGCC Translation | | pacid=371462 |
| 31 | 639 | 659 UGGAGAAGC/ : : :.....: UAGACGUGUI Cleavage | | pacid=371520 |
| 32 | 1429 | 1450 UGGAGAAGC/:: : :.....: UGCUCAGUG(Cleavage | | pacid=371468 |
| 33 | | | | |
| 34 | 1429 | 1450 UGGAGAAGC/:: : :.....: UGCUCAGUG(Cleavage | | pacid=371468 |
| 35 | 1946 | 1966 UGGAGAAGC/::: : :.....: UGCAGUUGC(Cleavage | | pacid=371764 |
| 36 | 1712 | 1732 UGGAGAAGC/::: : :.....: UGCAGUUGC(Cleavage | | pacid=371764 |
| 37 | | | | |
| 38 | 4127 | 4147 UGGAGAAGC/ : : :.....: ACCAUGUGCC Cleavage | | pacid=371756 |
| 39 | 3713 | 3733 UGGAGAAGC/ : : :.....: ACCAUGUGCC Cleavage | | pacid=371756 |
| 40 | 2142 | 2165 UGGAGAAGC/ : : :.....: GGCACGUCCC Cleavage | | pacid=371647 |
| 41 | | | | |
| 42 | 729 | 749 UGGAGAAGC/ : : :.....: AGCAUGUGUI Cleavage | | pacid=371776 |
| 43 | 729 | 749 UGGAGAAGC/ : : :.....: AGCAUGUGUI Cleavage | | pacid=371776 |
| 44 | 1576 | 1596 UGGAGAAGC/:: : :.....: UUCUCUUGCI Translation | | pacid=371530 |
| 45 | 549 | 569 UGGAGAAGC/ : : :.....: AGCAUGUGUI Cleavage | | pacid=371777 |
| 46 | | | | |
| 47 | 444 | 464 UGGAGAAGC/ : : :.....: GACAUGUGC(Translation | | pacid=371607 |
| 48 | 449 | 469 UGGAGAAGC/ : : :.....: AGCAUGUGCI Cleavage | | pacid=371663 |
| 49 | 417 | 437 UGGAGAAGC/ : : :.....: AGCACGUGU(Cleavage | | pacid=371656 |
| 50 | | | | |
| 51 | 1075 | 1095 UGGAGAAGC/ : : :.....: ACAACGUGCI Cleavage | | pacid=371656 |
| 52 | 331 | 351 UGGAGAAGC/ : : :.....: AGCACGUGU(Cleavage | | pacid=371656 |
| 53 | 989 | 1009 UGGAGAAGC/ : : :.....: ACAACGUGCI Cleavage | | pacid=371656 |
| 54 | | | | |
| 55 | 1100 | 1120 UGGAGAAGC/ : : :.....: AACACGUGU(Cleavage | | pacid=371470 |
| 56 | 99 | 119 UGGAGAAGC/ : : :.....: AGCACGUGU(Cleavage | | pacid=371656 |
| 57 | 977 | 997 UGGAGAAGC/ : : :.....: ACAACGUGCI Cleavage | | pacid=371656 |
| 58 | | | | |
| 59 | 278 | 298 UGGAGAAGC/ : : :.....: UGCACCUCCC Cleavage | | pacid=371740 |
| 60 | 249 | 269 UGGAGAAGC/ : : :.....: AGCACGUGU(Cleavage | | pacid=371656 |
| | 907 | 927 UGGAGAAGC/ : : :.....: ACAACGUGCI Cleavage | | pacid=371656 |

| | | | | |
|----|------|--|--------------|--|
| 1 | | | | |
| 2 | 420 | 440 UGGAGAAGC/ :: : ::::: : : UGCUCCUGCC Cleavage | pacid=371532 | |
| 3 | 161 | 181 UGGAGAAGC/ ::::: : : : AGCACGUGU(Cleavage | pacid=371656 | |
| 4 | 819 | 839 UGGAGAAGC/ ::::: : : : ACAACGUGCL Cleavage | pacid=371656 | |
| 5 | 285 | 305 UGGAGAAGC/ :: : : ::::: : : UGCUCCUGCC Cleavage | pacid=371528 | |
| 6 | 501 | 521 UGGAGAAGC/ ::::: : : : : AGCAUGUGCC Cleavage | pacid=371779 | |
| 7 | 611 | 631 UGGAGAAGC/ ::::: : : : : UGCAAGUCU(Cleavage | pacid=371590 | |
| 8 | 205 | 225 UGGAGAAGC/ ::::: : : : : AGCAUGUGC(Cleavage | pacid=371599 | |
| 9 | 179 | 200 UGGAGAAGC/ ::::: : : : : ACCACGUGAC Cleavage | pacid=371457 | |
| 10 | 4269 | 4289 UGGAGAAGC/ :: : : : ::::: : : UGAACAUGA(Cleavage | pacid=371579 | |
| 11 | 4266 | 4286 UGGAGAAGC/ :: : : : ::::: : : UGAACAUGA(Cleavage | pacid=371579 | |
| 12 | 1610 | 1630 UGGAGAAGC/ ::::: : : : : UGCAGCUGC/ Cleavage | pacid=371622 | |
| 13 | 1571 | 1591 UGGAGAAGC/ ::::: : : : : UGCAGCUGC/ Cleavage | pacid=371622 | |
| 14 | 1531 | 1551 UGGAGAAGC/ ::::: : : : : UGCAGCUGC/ Cleavage | pacid=371622 | |
| 15 | 3830 | 3850 UGGAGAAGC/ :: : : : : : : UGAACAUGU(Cleavage | pacid=371514 | |
| 16 | 2950 | 2970 UGGAGAAGC/ :: : : : : : : UGUUUGGGU Cleavage | pacid=371537 | |
| 17 | 2890 | 2910 UGGAGAAGC/ :: : : : : : : UGUUUGGGU Cleavage | pacid=371537 | |
| 18 | 3661 | 3681 UGGAGAAGC/ :: : : : : : : UGAACAUGU(Cleavage | pacid=371514 | |
| 19 | 1224 | 1244 UGGAGAAGC/ ::::: : : : : UGCAGCUGC/ Cleavage | pacid=371622 | |
| 20 | 890 | 911 UGGAGAAGC/ ::::: : : : : UGCACCUGCC Translation | pacid=371489 | |
| 21 | 273 | 293 UGGAGAAGC/ ::::: : : : : UGUGUGUGU Cleavage | pacid=371747 | |
| 22 | 894 | 914 UGGAGAAGC/ ::::: : : : : UGCAUGUGU(Translation | pacid=371531 | |
| 23 | 81 | 100 UGGAGAAGC/ ::::: : : : : UGCAUGUGC(Translation | pacid=371483 | |
| 24 | 81 | 100 UGGAGAAGC/ ::::: : : : : UGCAUGUGC(Translation | pacid=371483 | |
| 25 | 210 | 229 UGGAGAAGC/ ::::: : : : : UGCACGUGCC Cleavage | pacid=371445 | |
| 26 | 210 | 229 UGGAGAAGC/ ::::: : : : : UGCACGUGCC Cleavage | pacid=371445 | |
| 27 | 67 | 88 UGGAGAAGC/ ::::: : : : : UGCAACGUG(Cleavage | pacid=371715 | |
| 28 | 2692 | 2712 UGGAGAAGC/ ::::: : : : : UGCAUCUGU(Cleavage | pacid=371592 | |
| 29 | 1441 | 1461 UGGAGAAGC/ :: : : : : : : UGCUUGUGU Translation | pacid=371656 | |
| 30 | 393 | 413 UGGAGAAGC/ :: : : : : : : UGUCUGUGU Cleavage | pacid=371678 | |
| 31 | 1867 | 1887 UGGAGAAGC/ :: : : : : : : UGUUUUUGC Cleavage | pacid=371738 | |
| 32 | 1795 | 1815 UGGAGAAGC/ :: : : : : : : UGUUUUUGC Cleavage | pacid=371738 | |
| 33 | 2809 | 2829 UGGAGAAGC/ ::::: : : : : GGCACGUGCC Translation | pacid=371462 | |
| 34 | 639 | 659 UGGAGAAGC/ ::::: : : : : UAGACGUGU(Cleavage | pacid=371520 | |
| 35 | 1429 | 1450 UGGAGAAGC/ :: : : : : : : UGCUCAGUG(Cleavage | pacid=371468 | |
| 36 | 1429 | 1450 UGGAGAAGC/ :: : : : : : : UGCUCAGUG(Cleavage | pacid=371468 | |
| 37 | 1946 | 1966 UGGAGAAGC/ ::::: : : : : UGCAGUUGC(Cleavage | pacid=371764 | |
| 38 | 1712 | 1732 UGGAGAAGC/ ::::: : : : : UGCAGUUGC(Cleavage | pacid=371764 | |
| 39 | 4127 | 4147 UGGAGAAGC/ ::::: : : : : ACCAUGUGCC Cleavage | pacid=371756 | |
| 40 | 3713 | 3733 UGGAGAAGC/ ::::: : : : : ACCAUGUGCC Cleavage | pacid=371756 | |
| 41 | 2142 | 2165 UGGAGAAGC/ ::::: : : : : GGCACGUCCC Cleavage | pacid=371647 | |
| 42 | 729 | 749 UGGAGAAGC/ ::::: : : : : AGCAUGUGU(Cleavage | pacid=371776 | |
| 43 | 729 | 749 UGGAGAAGC/ ::::: : : : : AGCAUGUGU(Cleavage | pacid=371776 | |
| 44 | 1576 | 1596 UGGAGAAGC/ :: : : : : : : UUCUCUUGC(Translation | pacid=371530 | |
| 45 | 549 | 569 UGGAGAAGC/ ::::: : : : : AGCAUGUGU(Cleavage | pacid=371777 | |
| 46 | 444 | 464 UGGAGAAGC/ ::::: : : : : GACAUGUGC(Translation | pacid=371607 | |
| 47 | 449 | 469 UGGAGAAGC/ ::::: : : : : AGCAUGUGC(Cleavage | pacid=371663 | |

| | | | | |
|----|------|-----------------|------------------------|--------------|
| 1 | | | | |
| 2 | 417 | 437 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371656 |
| 3 | 1075 | 1095 UGGAGAAGC/ | ACAACGUGCL Cleavage | pacid=371656 |
| 4 | 331 | 351 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371656 |
| 5 | 989 | 1009 UGGAGAAGC/ | ACAACGUGCL Cleavage | pacid=371656 |
| 6 | 1100 | 1120 UGGAGAAGC/ | AACACGUGU(Cleavage | pacid=371470 |
| 7 | 99 | 119 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371656 |
| 8 | 977 | 997 UGGAGAAGC/ | ACAACGUGCL Cleavage | pacid=371656 |
| 9 | 278 | 298 UGGAGAAGC/ | UGCACCUCCC Cleavage | pacid=371740 |
| 10 | 249 | 269 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371656 |
| 11 | 907 | 927 UGGAGAAGC/ | ACAACGUGCL Cleavage | pacid=371656 |
| 12 | 420 | 440 UGGAGAAGC/ | UGCUCUGCC Cleavage | pacid=371532 |
| 13 | 161 | 181 UGGAGAAGC/ | AGCACGUGU(Cleavage | pacid=371656 |
| 14 | 819 | 839 UGGAGAAGC/ | ACAACGUGCL Cleavage | pacid=371656 |
| 15 | 285 | 305 UGGAGAAGC/ | UGCUCUGCC Cleavage | pacid=371528 |
| 16 | 501 | 521 UGGAGAAGC/ | AGCAUGUGC(Cleavage | pacid=371779 |
| 17 | 611 | 631 UGGAGAAGC/ | UGCAAGUCUI Cleavage | pacid=371590 |
| 18 | 205 | 225 UGGAGAAGC/ | AGCAUGUGCL Cleavage | pacid=371599 |
| 19 | 179 | 200 UGGAGAAGC/ | ACCACGUGAC Cleavage | pacid=371457 |
| 20 | 4269 | 4289 UGGAGAAGC/ | UGAACAUGA(Cleavage | pacid=371579 |
| 21 | 4266 | 4286 UGGAGAAGC/ | UGAACAUGA(Cleavage | pacid=371579 |
| 22 | 1610 | 1630 UGGAGAAGC/ | UGCAGCUGC/ Cleavage | pacid=371622 |
| 23 | 1571 | 1591 UGGAGAAGC/ | UGCAGCUGC/ Cleavage | pacid=371622 |
| 24 | 1531 | 1551 UGGAGAAGC/ | UGCAGCUGC/ Cleavage | pacid=371622 |
| 25 | 3830 | 3850 UGGAGAAGC/ | UGAACAUGUI Cleavage | pacid=371514 |
| 26 | 2950 | 2970 UGGAGAAGC/ | UGUUUGGGU Cleavage | pacid=371537 |
| 27 | 2890 | 2910 UGGAGAAGC/ | UGUUUGGGU Cleavage | pacid=371537 |
| 28 | 3661 | 3681 UGGAGAAGC/ | UGAACAUGUI Cleavage | pacid=371514 |
| 29 | 1224 | 1244 UGGAGAAGC/ | UGCAGCUGC/ Cleavage | pacid=371622 |
| 30 | 66 | 88 UGGAGAAGC/ | UUGCAACGU(Cleavage | pacid=371715 |
| 31 | 2691 | 2712 UGGAGAAGC/ | UUGCAUCUGI Cleavage | pacid=371592 |
| 32 | 1866 | 1887 UGGAGAAGC/ | UUGUAUUUG Cleavage | pacid=371738 |
| 33 | 889 | 911 UGGAGAAGC/ | AUGCACCUGC Translation | pacid=371489 |
| 34 | 1794 | 1815 UGGAGAAGC/ | UUGUAUUUG Cleavage | pacid=371738 |
| 35 | 272 | 293 UGGAGAAGC/ | CUGUGUGUG Cleavage | pacid=371747 |
| 36 | 893 | 914 UGGAGAAGC/ | CUGCAUGUGI Translation | pacid=371531 |
| 37 | 80 | 100 UGGAGAAGC/ | CUGCAUGUG(Translation | pacid=371483 |
| 38 | 80 | 100 UGGAGAAGC/ | CUGCAUGUG(Translation | pacid=371483 |
| 39 | 209 | 229 UGGAGAAGC/ | CUGCACGUG(Cleavage | pacid=371445 |
| 40 | 209 | 229 UGGAGAAGC/ | CUGCACGUG(Cleavage | pacid=371445 |
| 41 | 419 | 440 UGGAGAAGC/ | UUGCUCUG(Cleavage | pacid=371532 |
| 42 | 284 | 305 UGGAGAAGC/ | UUGCUCUG(Cleavage | pacid=371528 |
| 43 | 4268 | 4289 UGGAGAAGC/ | UUGAACAUG/ Cleavage | pacid=371579 |
| 44 | 4265 | 4286 UGGAGAAGC/ | UUGAACAUG/ Cleavage | pacid=371579 |
| 45 | 3829 | 3850 UGGAGAAGC/ | UUGAACAUGI Cleavage | pacid=371514 |
| 46 | 2949 | 2970 UGGAGAAGC/ | UUGUUUGGG Cleavage | pacid=371537 |
| 47 | 2889 | 2910 UGGAGAAGC/ | UUGUUUGGG Cleavage | pacid=371537 |

| | | | | | | |
|----|---|------------------|------------------|---------|--------------------------|---|
| 1 | | | | | | |
| 2 | 1 | Phvul.005G074500 | Phvul.005G074500 | PF02365 | PTHR31744,P ⁻ | 0 |
| 3 | 1 | Phvul.011G160400 | Phvul.011G160400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 4 | 1 | Phvul.005G055400 | Phvul.005G055400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 5 | | | | | | |
| 6 | 1 | Phvul.005G074500 | Phvul.005G074500 | PF02365 | PTHR31744,P ⁻ | 0 |
| 7 | 1 | Phvul.011G160400 | Phvul.011G160400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 8 | 1 | Phvul.005G055400 | Phvul.005G055400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 9 | | | | | | |
| 10 | 1 | Phvul.005G074500 | Phvul.005G074500 | PF02365 | PTHR31744,P ⁻ | 0 |
| 11 | 1 | Phvul.011G160400 | Phvul.011G160400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 12 | 1 | Phvul.005G055400 | Phvul.005G055400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 13 | | | | | | |
| 14 | 1 | Phvul.005G074500 | Phvul.005G074500 | PF02365 | PTHR31744,P ⁻ | 0 |
| 15 | 1 | Phvul.011G160400 | Phvul.011G160400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 16 | 1 | Phvul.005G055400 | Phvul.005G055400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 17 | | | | | | |
| 18 | 1 | Phvul.005G074500 | Phvul.005G074500 | PF02365 | PTHR31744,P ⁻ | 0 |
| 19 | 1 | Phvul.011G160400 | Phvul.011G160400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 20 | 1 | Phvul.005G055400 | Phvul.005G055400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 21 | | | | | | |
| 22 | 1 | Phvul.005G074500 | Phvul.005G074500 | PF02365 | PTHR31744,P ⁻ | 0 |
| 23 | 1 | Phvul.011G160400 | Phvul.011G160400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 24 | 1 | Phvul.005G055400 | Phvul.005G055400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 25 | | | | | | |
| 26 | 1 | Phvul.005G074500 | Phvul.005G074500 | PF02365 | PTHR31744,P ⁻ | 0 |
| 27 | 1 | Phvul.011G160400 | Phvul.011G160400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 28 | 1 | Phvul.005G055400 | Phvul.005G055400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 29 | | | | | | |
| 30 | 1 | Phvul.005G074500 | Phvul.005G074500 | PF02365 | PTHR31744,P ⁻ | 0 |
| 31 | 1 | Phvul.011G160400 | Phvul.011G160400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 32 | 1 | Phvul.005G055400 | Phvul.005G055400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 33 | | | | | | |
| 34 | 1 | Phvul.005G074500 | Phvul.005G074500 | PF02365 | PTHR31744,P ⁻ | 0 |
| 35 | 1 | Phvul.011G160400 | Phvul.011G160400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 36 | 1 | Phvul.005G055400 | Phvul.005G055400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 37 | | | | | | |
| 38 | 1 | Phvul.005G074500 | Phvul.005G074500 | PF02365 | PTHR31744,P ⁻ | 0 |
| 39 | 1 | Phvul.011G160400 | Phvul.011G160400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 40 | 1 | Phvul.005G055400 | Phvul.005G055400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 41 | | | | | | |
| 42 | 1 | Phvul.005G074500 | Phvul.005G074500 | PF02365 | PTHR31744,P ⁻ | 0 |
| 43 | 1 | Phvul.011G160400 | Phvul.011G160400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 44 | 1 | Phvul.005G055400 | Phvul.005G055400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 45 | | | | | | |
| 46 | 1 | Phvul.005G074500 | Phvul.005G074500 | PF02365 | PTHR31744,P ⁻ | 0 |
| 47 | 1 | Phvul.011G160400 | Phvul.011G160400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 48 | 1 | Phvul.005G055400 | Phvul.005G055400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 49 | | | | | | |
| 50 | 1 | Phvul.005G074500 | Phvul.005G074500 | PF02365 | PTHR31744,P ⁻ | 0 |
| 51 | 1 | Phvul.011G160400 | Phvul.011G160400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 52 | 1 | Phvul.005G055400 | Phvul.005G055400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 53 | | | | | | |
| 54 | 1 | Phvul.005G074500 | Phvul.005G074500 | PF02365 | PTHR31744,P ⁻ | 0 |
| 55 | 1 | Phvul.011G160400 | Phvul.011G160400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 56 | 1 | Phvul.005G055400 | Phvul.005G055400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 57 | | | | | | |
| 58 | 1 | Phvul.005G074500 | Phvul.005G074500 | PF02365 | PTHR31744,P ⁻ | 0 |
| 59 | 1 | Phvul.011G160400 | Phvul.011G160400 | PF02365 | PTHR31744,P ⁻ | 0 |
| 60 | 1 | Phvul.005G055400 | Phvul.005G055400 | PF02365 | PTHR31744,P ⁻ | 0 |
| | 1 | Phvul.006G169300 | Phvul.006G169300 | PF00657 | PTHR22835,P ⁻ | 0 |

| | | | | | |
|----|--------------------|------------------|---------|----------------------------------|---|
| 1 | | | | | |
| 2 | 1 Phvul.007G164800 | Phvul.007G164800 | | 0 PTHR33448,P ⁻ | 0 |
| 3 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 4 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 7 | 1 Phvul.004G172600 | Phvul.004G172600 | PF13578 | PTHR10509,P ⁻ KOG1663 | |
| 8 | 1 Phvul.006G169300 | Phvul.006G169300 | PF00657 | PTHR22835,P ⁻ | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.007G164800 | Phvul.007G164800 | | 0 PTHR33448,P ⁻ | 0 |
| 11 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 12 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 15 | 1 Phvul.004G172600 | Phvul.004G172600 | PF13578 | PTHR10509,P ⁻ KOG1663 | |
| 16 | 1 Phvul.006G169300 | Phvul.006G169300 | PF00657 | PTHR22835,P ⁻ | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.007G164800 | Phvul.007G164800 | | 0 PTHR33448,P ⁻ | 0 |
| 19 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 20 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 23 | 1 Phvul.004G172600 | Phvul.004G172600 | PF13578 | PTHR10509,P ⁻ KOG1663 | |
| 24 | 1 Phvul.006G169300 | Phvul.006G169300 | PF00657 | PTHR22835,P ⁻ | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.007G164800 | Phvul.007G164800 | | 0 PTHR33448,P ⁻ | 0 |
| 27 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 28 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 29 | | | | | |
| 30 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 31 | 1 Phvul.004G172600 | Phvul.004G172600 | PF13578 | PTHR10509,P ⁻ KOG1663 | |
| 32 | 1 Phvul.006G169300 | Phvul.006G169300 | PF00657 | PTHR22835,P ⁻ | 0 |
| 33 | | | | | |
| 34 | 1 Phvul.007G164800 | Phvul.007G164800 | | 0 PTHR33448,P ⁻ | 0 |
| 35 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 36 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 37 | | | | | |
| 38 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 39 | 1 Phvul.004G172600 | Phvul.004G172600 | PF13578 | PTHR10509,P ⁻ KOG1663 | |
| 40 | 1 Phvul.006G169300 | Phvul.006G169300 | PF00657 | PTHR22835,P ⁻ | 0 |
| 41 | | | | | |
| 42 | 1 Phvul.007G164800 | Phvul.007G164800 | | 0 PTHR33448,P ⁻ | 0 |
| 43 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 44 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 45 | | | | | |
| 46 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 47 | 1 Phvul.004G172600 | Phvul.004G172600 | PF13578 | PTHR10509,P ⁻ KOG1663 | |
| 48 | 1 Phvul.006G169300 | Phvul.006G169300 | PF00657 | PTHR22835,P ⁻ | 0 |
| 49 | | | | | |
| 50 | 1 Phvul.007G164800 | Phvul.007G164800 | | 0 PTHR33448,P ⁻ | 0 |
| 51 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 52 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 53 | | | | | |
| 54 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 55 | 1 Phvul.004G172600 | Phvul.004G172600 | PF13578 | PTHR10509,P ⁻ KOG1663 | |
| 56 | 1 Phvul.006G169300 | Phvul.006G169300 | PF00657 | PTHR22835,P ⁻ | 0 |
| 57 | | | | | |
| 58 | 1 Phvul.007G164800 | Phvul.007G164800 | | 0 PTHR33448,P ⁻ | 0 |
| 59 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| 60 | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |
| | 1 Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ | 0 |

| | | | | | |
|----|---|------------------|------------------|---------|----------------------------------|
| 1 | | | | | |
| 2 | 1 | Phvul.004G172600 | Phvul.004G172600 | PF13578 | PTHR10509,P ⁻ KOG1663 |
| 3 | 1 | Phvul.006G169300 | Phvul.006G169300 | PF00657 | PTHR22835,P ⁻ 0 |
| 4 | 1 | Phvul.007G164800 | Phvul.007G164800 | | 0 PTHR33448,P ⁻ 0 |
| 5 | | | | | |
| 6 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 7 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 8 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 9 | | | | | |
| 10 | 1 | Phvul.004G172600 | Phvul.004G172600 | PF13578 | PTHR10509,P ⁻ KOG1663 |
| 11 | 1 | Phvul.006G169300 | Phvul.006G169300 | PF00657 | PTHR22835,P ⁻ 0 |
| 12 | 1 | Phvul.007G164800 | Phvul.007G164800 | | 0 PTHR33448,P ⁻ 0 |
| 13 | | | | | |
| 14 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 15 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 16 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 17 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 18 | 1 | Phvul.004G172600 | Phvul.004G172600 | PF13578 | PTHR10509,P ⁻ KOG1663 |
| 19 | 1 | Phvul.006G169300 | Phvul.006G169300 | PF00657 | PTHR22835,P ⁻ 0 |
| 20 | 1 | Phvul.007G164800 | Phvul.007G164800 | | 0 PTHR33448,P ⁻ 0 |
| 21 | | | | | |
| 22 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 23 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 24 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 25 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 26 | 1 | Phvul.004G172600 | Phvul.004G172600 | PF13578 | PTHR10509,P ⁻ KOG1663 |
| 27 | 1 | Phvul.006G169300 | Phvul.006G169300 | PF00657 | PTHR22835,P ⁻ 0 |
| 28 | 1 | Phvul.007G164800 | Phvul.007G164800 | | 0 PTHR33448,P ⁻ 0 |
| 29 | | | | | |
| 30 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 31 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 32 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 33 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 34 | 1 | Phvul.004G172600 | Phvul.004G172600 | PF13578 | PTHR10509,P ⁻ KOG1663 |
| 35 | 1 | Phvul.006G169300 | Phvul.006G169300 | PF00657 | PTHR22835,P ⁻ 0 |
| 36 | 1 | Phvul.007G164800 | Phvul.007G164800 | | 0 PTHR33448,P ⁻ 0 |
| 37 | | | | | |
| 38 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 39 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 40 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 41 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 42 | 1 | Phvul.004G172600 | Phvul.004G172600 | PF13578 | PTHR10509,P ⁻ KOG1663 |
| 43 | 1 | Phvul.006G169300 | Phvul.006G169300 | PF00657 | PTHR22835,P ⁻ 0 |
| 44 | 1 | Phvul.007G164800 | Phvul.007G164800 | | 0 PTHR33448,P ⁻ 0 |
| 45 | | | | | |
| 46 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 47 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 48 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 49 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 50 | 1 | Phvul.004G172600 | Phvul.004G172600 | PF13578 | PTHR10509,P ⁻ KOG1663 |
| 51 | 1 | Phvul.006G169300 | Phvul.006G169300 | PF00657 | PTHR22835,P ⁻ 0 |
| 52 | 1 | Phvul.007G164800 | Phvul.007G164800 | | 0 PTHR33448,P ⁻ 0 |
| 53 | | | | | |
| 54 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 55 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 56 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 57 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 58 | 1 | Phvul.004G172600 | Phvul.004G172600 | PF13578 | PTHR10509,P ⁻ KOG1663 |
| 59 | 1 | Phvul.006G169300 | Phvul.006G169300 | PF00657 | PTHR22835,P ⁻ 0 |
| 60 | 1 | Phvul.007G164800 | Phvul.007G164800 | | 0 PTHR33448,P ⁻ 0 |
| | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |

| | | | | | |
|----|---|------------------|------------------|--------------|----------------------------------|
| 1 | | | | | |
| 2 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 3 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 4 | 1 | Phvul.004G172600 | Phvul.004G172600 | PF13578 | PTHR10509,P ⁻ KOG1663 |
| 5 | 1 | Phvul.006G169300 | Phvul.006G169300 | PF00657 | PTHR22835,P ⁻ 0 |
| 6 | 1 | Phvul.007G164800 | Phvul.007G164800 | | 0 PTHR33448,P ⁻ 0 |
| 7 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 8 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 9 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 10 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 11 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 12 | 1 | Phvul.004G172600 | Phvul.004G172600 | PF13578 | PTHR10509,P ⁻ KOG1663 |
| 13 | 1 | Phvul.006G169300 | Phvul.006G169300 | PF00657 | PTHR22835,P ⁻ 0 |
| 14 | 1 | Phvul.006G169300 | Phvul.006G169300 | PF00657 | PTHR22835,P ⁻ 0 |
| 15 | 1 | Phvul.007G164800 | Phvul.007G164800 | | 0 PTHR33448,P ⁻ 0 |
| 16 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 17 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 18 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 19 | 1 | Phvul.011G065700 | Phvul.011G065700 | PF01073 | PTHR10366,P ⁻ 0 |
| 20 | 1 | Phvul.004G172600 | Phvul.004G172600 | PF13578 | PTHR10509,P ⁻ KOG1663 |
| 21 | 1 | Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P ⁻ 0 |
| 22 | 1 | Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P ⁻ 0 |
| 23 | 1 | Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P ⁻ 0 |
| 24 | 1 | Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P ⁻ 0 |
| 25 | 1 | Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P ⁻ 0 |
| 26 | 1 | Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P ⁻ 0 |
| 27 | 1 | Phvul.008G147100 | Phvul.008G147100 | | 0 0 0 |
| 28 | 1 | Phvul.008G147100 | Phvul.008G147100 | | 0 0 0 |
| 29 | 1 | Phvul.008G147100 | Phvul.008G147100 | | 0 0 0 |
| 30 | 1 | Phvul.008G147100 | Phvul.008G147100 | | 0 0 0 |
| 31 | 1 | Phvul.006G086200 | Phvul.006G086200 | | 0 PTHR32133 0 |
| 32 | 1 | Phvul.010G128500 | Phvul.010G128500 | PF01699 | PTHR12266,P ⁻ KOG2399 |
| 33 | 1 | Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P ⁻ 0 |
| 34 | 1 | Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P ⁻ 0 |
| 35 | 1 | Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P ⁻ 0 |
| 36 | 1 | Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P ⁻ 0 |
| 37 | 1 | Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P ⁻ 0 |
| 38 | 1 | Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P ⁻ 0 |
| 39 | 1 | Phvul.008G147100 | Phvul.008G147100 | | 0 0 0 |
| 40 | 1 | Phvul.008G147100 | Phvul.008G147100 | | 0 0 0 |
| 41 | 1 | Phvul.008G147100 | Phvul.008G147100 | | 0 0 0 |
| 42 | 1 | Phvul.008G147100 | Phvul.008G147100 | | 0 0 0 |
| 43 | 1 | Phvul.006G086200 | Phvul.006G086200 | | 0 PTHR32133 0 |
| 44 | 1 | Phvul.010G128500 | Phvul.010G128500 | PF01699 | PTHR12266,P ⁻ KOG2399 |
| 45 | 1 | Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P ⁻ 0 |
| 46 | 1 | Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P ⁻ 0 |
| 47 | 1 | Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P ⁻ 0 |
| 48 | 1 | Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P ⁻ 0 |
| 49 | 1 | Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P ⁻ 0 |
| 50 | 1 | Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P ⁻ 0 |
| 51 | 1 | Phvul.008G147100 | Phvul.008G147100 | | 0 0 0 |
| 52 | 1 | Phvul.008G147100 | Phvul.008G147100 | | 0 0 0 |
| 53 | 1 | Phvul.008G147100 | Phvul.008G147100 | | 0 0 0 |
| 54 | 1 | Phvul.008G147100 | Phvul.008G147100 | | 0 0 0 |
| 55 | 1 | Phvul.006G086200 | Phvul.006G086200 | | 0 PTHR32133 0 |
| 56 | 1 | Phvul.010G128500 | Phvul.010G128500 | PF01699 | PTHR12266,P ⁻ KOG2399 |
| 57 | 1 | Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P ⁻ 0 |
| 58 | 1 | Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P ⁻ 0 |
| 59 | 1 | Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P ⁻ 0 |
| 60 | 1 | Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P ⁻ 0 |
| | 1 | Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P ⁻ 0 |

| | | | | | |
|----|--------------------|------------------|--------------|-------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 3 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 4 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.006G086200 | Phvul.006G086200 | 0 | PTHR32133 | 0 |
| 7 | 1 Phvul.010G128500 | Phvul.010G128500 | PF01699 | PTHR12266,P | KOG2399 |
| 8 | 1 Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P | 0 |
| 11 | 1 Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P | 0 |
| 12 | 1 Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 15 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 16 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.006G086200 | Phvul.006G086200 | 0 | PTHR32133 | 0 |
| 19 | 1 Phvul.010G128500 | Phvul.010G128500 | PF01699 | PTHR12266,P | KOG2399 |
| 20 | 1 Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P | 0 |
| 23 | 1 Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P | 0 |
| 24 | 1 Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 27 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 28 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 29 | | | | | |
| 30 | 1 Phvul.006G086200 | Phvul.006G086200 | 0 | PTHR32133 | 0 |
| 31 | 1 Phvul.010G128500 | Phvul.010G128500 | PF01699 | PTHR12266,P | KOG2399 |
| 32 | 1 Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P | 0 |
| 33 | | | | | |
| 34 | 1 Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P | 0 |
| 35 | 1 Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P | 0 |
| 36 | 1 Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P | 0 |
| 37 | | | | | |
| 38 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 39 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 40 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 41 | | | | | |
| 42 | 1 Phvul.006G086200 | Phvul.006G086200 | 0 | PTHR32133 | 0 |
| 43 | 1 Phvul.010G128500 | Phvul.010G128500 | PF01699 | PTHR12266,P | KOG2399 |
| 44 | 1 Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P | 0 |
| 45 | 1 Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P | 0 |
| 46 | 1 Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P | 0 |
| 47 | 1 Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P | 0 |
| 48 | | | | | |
| 49 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 50 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 51 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 52 | | | | | |
| 53 | 1 Phvul.006G086200 | Phvul.006G086200 | 0 | PTHR32133 | 0 |
| 54 | | | | | |
| 55 | 1 Phvul.010G128500 | Phvul.010G128500 | PF01699 | PTHR12266,P | KOG2399 |
| 56 | 1 Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P | 0 |
| 57 | 1 Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P | 0 |
| 58 | 1 Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P | 0 |
| 59 | 1 Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P | 0 |
| 60 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |

| | | | | | |
|----|--------------------|------------------|--------------|--------------------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 3 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 4 | 1 Phvul.006G086200 | Phvul.006G086200 | 0 | PTHR32133 | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.010G128500 | Phvul.010G128500 | PF01699 | PTHR12266,P ⁻ | KOG2399 |
| 7 | 1 Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P ⁻ | 0 |
| 8 | 1 Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P ⁻ | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P ⁻ | 0 |
| 11 | 1 Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P ⁻ | 0 |
| 12 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 15 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 16 | 1 Phvul.006G086200 | Phvul.006G086200 | 0 | PTHR32133 | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.010G128500 | Phvul.010G128500 | PF01699 | PTHR12266,P ⁻ | KOG2399 |
| 19 | 1 Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P ⁻ | 0 |
| 20 | 1 Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P ⁻ | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P ⁻ | 0 |
| 23 | 1 Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P ⁻ | 0 |
| 24 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 27 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 28 | 1 Phvul.006G086200 | Phvul.006G086200 | 0 | PTHR32133 | 0 |
| 29 | | | | | |
| 30 | 1 Phvul.010G128500 | Phvul.010G128500 | PF01699 | PTHR12266,P ⁻ | KOG2399 |
| 31 | 1 Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P ⁻ | 0 |
| 32 | 1 Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P ⁻ | 0 |
| 33 | | | | | |
| 34 | 1 Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P ⁻ | 0 |
| 35 | 1 Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P ⁻ | 0 |
| 36 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 37 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 38 | | | | | |
| 39 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 40 | 1 Phvul.006G086200 | Phvul.006G086200 | 0 | PTHR32133 | 0 |
| 41 | | | | | |
| 42 | 1 Phvul.010G128500 | Phvul.010G128500 | PF01699 | PTHR12266,P ⁻ | KOG2399 |
| 43 | 1 Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P ⁻ | 0 |
| 44 | 1 Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P ⁻ | 0 |
| 45 | | | | | |
| 46 | 1 Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P ⁻ | 0 |
| 47 | 1 Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P ⁻ | 0 |
| 48 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 49 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 50 | | | | | |
| 51 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 52 | 1 Phvul.006G086200 | Phvul.006G086200 | 0 | PTHR32133 | 0 |
| 53 | | | | | |
| 54 | 1 Phvul.010G128500 | Phvul.010G128500 | PF01699 | PTHR12266,P ⁻ | KOG2399 |
| 55 | 1 Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P ⁻ | 0 |
| 56 | 1 Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P ⁻ | 0 |
| 57 | | | | | |
| 58 | 1 Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P ⁻ | 0 |
| 59 | 1 Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P ⁻ | 0 |
| 60 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |

| | | | | | |
|----|--------------------|------------------|--------------|--------------------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 3 | 1 Phvul.006G086200 | Phvul.006G086200 | 0 | PTHR32133 | 0 |
| 4 | 1 Phvul.010G128500 | Phvul.010G128500 | PF01699 | PTHR12266,P ⁻ | KOG2399 |
| 5 | 1 Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P ⁻ | 0 |
| 6 | 1 Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P ⁻ | 0 |
| 7 | 1 Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P ⁻ | 0 |
| 8 | 1 Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P ⁻ | 0 |
| 9 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 10 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 11 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 12 | 1 Phvul.006G086200 | Phvul.006G086200 | 0 | PTHR32133 | 0 |
| 13 | 1 Phvul.010G128500 | Phvul.010G128500 | PF01699 | PTHR12266,P ⁻ | KOG2399 |
| 14 | 1 Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P ⁻ | 0 |
| 15 | 1 Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P ⁻ | 0 |
| 16 | 1 Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P ⁻ | 0 |
| 17 | 1 Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P ⁻ | 0 |
| 18 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 19 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 20 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 21 | 1 Phvul.006G086200 | Phvul.006G086200 | 0 | PTHR32133 | 0 |
| 22 | 1 Phvul.010G128500 | Phvul.010G128500 | PF01699 | PTHR12266,P ⁻ | KOG2399 |
| 23 | 1 Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P ⁻ | 0 |
| 24 | 1 Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P ⁻ | 0 |
| 25 | 1 Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P ⁻ | 0 |
| 26 | 1 Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P ⁻ | 0 |
| 27 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 28 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 29 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 30 | 1 Phvul.006G086200 | Phvul.006G086200 | 0 | PTHR32133 | 0 |
| 31 | 1 Phvul.010G128500 | Phvul.010G128500 | PF01699 | PTHR12266,P ⁻ | KOG2399 |
| 32 | 1 Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P ⁻ | 0 |
| 33 | 1 Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P ⁻ | 0 |
| 34 | 1 Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P ⁻ | 0 |
| 35 | 1 Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P ⁻ | 0 |
| 36 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 37 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 38 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 39 | 1 Phvul.006G086200 | Phvul.006G086200 | 0 | PTHR32133 | 0 |
| 40 | 1 Phvul.010G128500 | Phvul.010G128500 | PF01699 | PTHR12266,P ⁻ | KOG2399 |
| 41 | 1 Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P ⁻ | 0 |
| 42 | 1 Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P ⁻ | 0 |
| 43 | 1 Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P ⁻ | 0 |
| 44 | 1 Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P ⁻ | 0 |
| 45 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 46 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 47 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 48 | 1 Phvul.006G086200 | Phvul.006G086200 | 0 | PTHR32133 | 0 |
| 49 | 1 Phvul.010G128500 | Phvul.010G128500 | PF01699 | PTHR12266,P ⁻ | KOG2399 |
| 50 | 1 Phvul.010G089100 | Phvul.010G089100 | PF03634 | PTHR31072,P ⁻ | 0 |
| 51 | 1 Phvul.002G325300 | Phvul.002G325300 | PF03033,PF04 | PTHR21015,P ⁻ | 0 |
| 52 | 1 Phvul.004G139200 | Phvul.004G139200 | PF13355 | PTHR33925,P ⁻ | 0 |
| 53 | 1 Phvul.005G001200 | Phvul.005G001200 | PF00657 | PTHR22835,P ⁻ | 0 |
| 54 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 55 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 56 | 1 Phvul.008G147100 | Phvul.008G147100 | 0 | 0 | 0 |
| 57 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 | PTHR36319,P ⁻ | 0 |
| 58 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 | PTHR36319,P ⁻ | 0 |
| 59 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08 | PTHR24326,P ⁻ | 0 |
| 60 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07 | PTHR27002 | KOG1187 |
| 61 | 1 Phvul.011G110300 | Phvul.011G110300 | 0 | PTHR34056,P ⁻ | 0 |
| 62 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 | PTHR32099 | 0 |
| 63 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00 | PTHR11689,P ⁻ | 0 |
| 64 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06 | PTHR23416,P ⁻ | KOG4750 |
| 65 | 1 Phvul.003G067000 | Phvul.003G067000 | 0 | PTHR34222,P ⁻ | 0 |

| | | | | | |
|----|--------------------|------------------|-------------------------|---------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 | PTHR24089,P | KOG0769 |
| 3 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P | | 0 |
| 4 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P | | KOG0546 |
| 5 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 | PTHR10108,P | 0 |
| 6 | 1 Phvul.005G087600 | Phvul.005G087600 | | 0 PTHR34379,P | 0 |
| 7 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P | | KOG0014 |
| 8 | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 | PTHR10108,P | 0 |
| 9 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | | 0 |
| 10 | 1 Phvul.007G083500 | Phvul.007G083500 | | 0 PTHR36319,P | 0 |
| 11 | 1 Phvul.007G083500 | Phvul.007G083500 | | 0 PTHR36319,P | 0 |
| 12 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P | | 0 |
| 13 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 | | KOG1187 |
| 14 | 1 Phvul.011G110300 | Phvul.011G110300 | | 0 PTHR34056,P | 0 |
| 15 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 | PTHR32099 | 0 |
| 16 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P | | 0 |
| 17 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P | | KOG4750 |
| 18 | 1 Phvul.003G067000 | Phvul.003G067000 | | 0 PTHR34222,P | 0 |
| 19 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 | PTHR24089,P | KOG0769 |
| 20 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P | | 0 |
| 21 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P | | KOG0546 |
| 22 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 | PTHR10108,P | 0 |
| 23 | 1 Phvul.005G087600 | Phvul.005G087600 | | 0 PTHR34379,P | 0 |
| 24 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P | | KOG0014 |
| 25 | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 | PTHR10108,P | 0 |
| 26 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | | 0 |
| 27 | 1 Phvul.007G083500 | Phvul.007G083500 | | 0 PTHR36319,P | 0 |
| 28 | 1 Phvul.007G083500 | Phvul.007G083500 | | 0 PTHR36319,P | 0 |
| 29 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P | | 0 |
| 30 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 | | KOG1187 |
| 31 | 1 Phvul.011G110300 | Phvul.011G110300 | | 0 PTHR34056,P | 0 |
| 32 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 | PTHR32099 | 0 |
| 33 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P | | 0 |
| 34 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P | | KOG4750 |
| 35 | 1 Phvul.003G067000 | Phvul.003G067000 | | 0 PTHR34222,P | 0 |
| 36 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 | PTHR24089,P | KOG0769 |
| 37 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P | | 0 |
| 38 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P | | KOG0546 |
| 39 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 | PTHR10108,P | 0 |
| 40 | 1 Phvul.005G087600 | Phvul.005G087600 | | 0 PTHR34379,P | 0 |
| 41 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P | | KOG0014 |
| 42 | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 | PTHR10108,P | 0 |
| 43 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | | 0 |
| 44 | 1 Phvul.007G083500 | Phvul.007G083500 | | 0 PTHR36319,P | 0 |
| 45 | 1 Phvul.007G083500 | Phvul.007G083500 | | 0 PTHR36319,P | 0 |
| 46 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P | | 0 |
| 47 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 | | KOG1187 |
| 48 | 1 Phvul.011G110300 | Phvul.011G110300 | | 0 PTHR34056,P | 0 |
| 49 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 | PTHR32099 | 0 |
| 50 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P | | 0 |
| 51 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P | | KOG4750 |
| 52 | 1 Phvul.003G067000 | Phvul.003G067000 | | 0 PTHR34222,P | 0 |
| 53 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 | PTHR24089,P | KOG0769 |
| 54 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P | | 0 |
| 55 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P | | KOG0546 |
| 56 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 | PTHR10108,P | 0 |
| 57 | 1 Phvul.005G087600 | Phvul.005G087600 | | 0 PTHR34379,P | 0 |
| 58 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P | | KOG0014 |
| 59 | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 | PTHR10108,P | 0 |
| 60 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | | 0 |
| 61 | 1 Phvul.007G083500 | Phvul.007G083500 | | 0 PTHR36319,P | 0 |
| 62 | 1 Phvul.007G083500 | Phvul.007G083500 | | 0 PTHR36319,P | 0 |
| 63 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P | | 0 |
| 64 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 | | KOG1187 |

| | | | | | |
|----|--------------------|------------------|-------------------------|---------|---|
| 1 | | | | | |
| 2 | 1 Phvul.011G110300 | Phvul.011G110300 | 0 PTHR34056,P | | 0 |
| 3 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 PTHR32099 | | 0 |
| 4 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P | | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P | KOG4750 | |
| 7 | 1 Phvul.003G067000 | Phvul.003G067000 | 0 PTHR34222,P | | 0 |
| 8 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 PTHR24089,P | KOG0769 | |
| 9 | | | | | |
| 10 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P | | 0 |
| 11 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P | KOG0546 | |
| 12 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 PTHR10108,P | | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.005G087600 | Phvul.005G087600 | 0 PTHR34379,P | | 0 |
| 15 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P | KOG0014 | |
| 16 | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 PTHR10108,P | | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | | 0 |
| 19 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P | | 0 |
| 20 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P | | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P | | 0 |
| 23 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 | KOG1187 | |
| 24 | 1 Phvul.011G110300 | Phvul.011G110300 | 0 PTHR34056,P | | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 PTHR32099 | | 0 |
| 27 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P | | 0 |
| 28 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P | KOG4750 | |
| 29 | 1 Phvul.003G067000 | Phvul.003G067000 | 0 PTHR34222,P | | 0 |
| 30 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 PTHR24089,P | KOG0769 | |
| 31 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P | | 0 |
| 32 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P | KOG0546 | |
| 33 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 PTHR10108,P | | 0 |
| 34 | | | | | |
| 35 | 1 Phvul.005G087600 | Phvul.005G087600 | 0 PTHR34379,P | | 0 |
| 36 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P | KOG0014 | |
| 37 | | | | | |
| 38 | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 PTHR10108,P | | 0 |
| 39 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | | 0 |
| 40 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P | | 0 |
| 41 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P | | 0 |
| 42 | | | | | |
| 43 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P | | 0 |
| 44 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 | KOG1187 | |
| 45 | 1 Phvul.011G110300 | Phvul.011G110300 | 0 PTHR34056,P | | 0 |
| 46 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 PTHR32099 | | 0 |
| 47 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P | | 0 |
| 48 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P | KOG4750 | |
| 49 | 1 Phvul.003G067000 | Phvul.003G067000 | 0 PTHR34222,P | | 0 |
| 50 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 PTHR24089,P | KOG0769 | |
| 51 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P | | 0 |
| 52 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P | KOG0546 | |
| 53 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 PTHR10108,P | | 0 |
| 54 | | | | | |
| 55 | 1 Phvul.005G087600 | Phvul.005G087600 | 0 PTHR34379,P | | 0 |
| 56 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P | KOG0014 | |
| 57 | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 PTHR10108,P | | 0 |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | |
|----|--------------------|------------------|----------------------------------|---|
| 1 | | | | |
| 2 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | 0 |
| 3 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P' | 0 |
| 4 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P' | 0 |
| 5 | | | | |
| 6 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P' | 0 |
| 7 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 KOG1187 | |
| 8 | 1 Phvul.011G110300 | Phvul.011G110300 | 0 PTHR34056,P' | 0 |
| 9 | | | | |
| 10 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 PTHR32099 | 0 |
| 11 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P' | 0 |
| 12 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P' KOG4750 | |
| 13 | | | | |
| 14 | 1 Phvul.003G067000 | Phvul.003G067000 | 0 PTHR34222,P' | 0 |
| 15 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 PTHR24089,P' KOG0769 | |
| 16 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P' | 0 |
| 17 | | | | |
| 18 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P' KOG0546 | |
| 19 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 PTHR10108,P' | 0 |
| 20 | 1 Phvul.005G087600 | Phvul.005G087600 | 0 PTHR34379,P' | 0 |
| 21 | | | | |
| 22 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P' KOG0014 | |
| 23 | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 PTHR10108,P' | 0 |
| 24 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | 0 |
| 25 | | | | |
| 26 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P' | 0 |
| 27 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P' | 0 |
| 28 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P' | 0 |
| 29 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 KOG1187 | |
| 30 | 1 Phvul.011G110300 | Phvul.011G110300 | 0 PTHR34056,P' | 0 |
| 31 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 PTHR32099 | 0 |
| 32 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P' | 0 |
| 33 | | | | |
| 34 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P' KOG4750 | |
| 35 | 1 Phvul.003G067000 | Phvul.003G067000 | 0 PTHR34222,P' | 0 |
| 36 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 PTHR24089,P' KOG0769 | |
| 37 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P' | 0 |
| 38 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P' KOG0546 | |
| 39 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 PTHR10108,P' | 0 |
| 40 | 1 Phvul.005G087600 | Phvul.005G087600 | 0 PTHR34379,P' | 0 |
| 41 | | | | |
| 42 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P' KOG0014 | |
| 43 | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 PTHR10108,P' | 0 |
| 44 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | 0 |
| 45 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P' | 0 |
| 46 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P' | 0 |
| 47 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P' | 0 |
| 48 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 KOG1187 | |
| 49 | 1 Phvul.011G110300 | Phvul.011G110300 | 0 PTHR34056,P' | 0 |
| 50 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 PTHR32099 | 0 |
| 51 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P' | 0 |
| 52 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P' KOG4750 | |
| 53 | 1 Phvul.003G067000 | Phvul.003G067000 | 0 PTHR34222,P' | 0 |
| 54 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 PTHR24089,P' KOG0769 | |
| 55 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P' | 0 |
| 56 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P' KOG0546 | |
| 57 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 PTHR10108,P' | 0 |
| 58 | 1 Phvul.005G087600 | Phvul.005G087600 | 0 PTHR34379,P' | 0 |
| 59 | | | | |
| 60 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P' KOG0014 | |
| | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 PTHR10108,P' | 0 |
| | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | 0 |
| | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P' | 0 |
| | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P' | 0 |
| | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P' | 0 |
| | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 KOG1187 | |
| | 1 Phvul.011G110300 | Phvul.011G110300 | 0 PTHR34056,P' | 0 |
| | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 PTHR32099 | 0 |
| | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P' | 0 |
| | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P' KOG4750 | |
| | 1 Phvul.003G067000 | Phvul.003G067000 | 0 PTHR34222,P' | 0 |
| | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 PTHR24089,P' KOG0769 | |
| | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P' | 0 |

| | | | | | |
|----|--------------------|------------------|-------------------------|---------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P | KOG0546 | |
| 3 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 | PTHR10108,P | 0 |
| 4 | 1 Phvul.005G087600 | Phvul.005G087600 | | 0 PTHR34379,P | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P | KOG0014 | |
| 7 | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 | PTHR10108,P | 0 |
| 8 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.007G083500 | Phvul.007G083500 | | 0 PTHR36319,P | 0 |
| 11 | 1 Phvul.007G083500 | Phvul.007G083500 | | 0 PTHR36319,P | 0 |
| 12 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P | | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 | KOG1187 | |
| 15 | 1 Phvul.011G110300 | Phvul.011G110300 | | 0 PTHR34056,P | 0 |
| 16 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 | PTHR32099 | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P | | 0 |
| 19 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P | KOG4750 | |
| 20 | 1 Phvul.003G067000 | Phvul.003G067000 | | 0 PTHR34222,P | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 | PTHR24089,P | KOG0769 |
| 23 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P | | 0 |
| 24 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P | KOG0546 | |
| 25 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 | PTHR10108,P | 0 |
| 26 | 1 Phvul.005G087600 | Phvul.005G087600 | | 0 PTHR34379,P | 0 |
| 27 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P | KOG0014 | |
| 28 | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 | PTHR10108,P | 0 |
| 29 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | | 0 |
| 30 | 1 Phvul.007G083500 | Phvul.007G083500 | | 0 PTHR36319,P | 0 |
| 31 | 1 Phvul.007G083500 | Phvul.007G083500 | | 0 PTHR36319,P | 0 |
| 32 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P | | 0 |
| 33 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 | KOG1187 | |
| 34 | 1 Phvul.011G110300 | Phvul.011G110300 | | 0 PTHR34056,P | 0 |
| 35 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 | PTHR32099 | 0 |
| 36 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P | | 0 |
| 37 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P | KOG4750 | |
| 38 | 1 Phvul.003G067000 | Phvul.003G067000 | | 0 PTHR34222,P | 0 |
| 39 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 | PTHR24089,P | KOG0769 |
| 40 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P | | 0 |
| 41 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P | KOG0546 | |
| 42 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 | PTHR10108,P | 0 |
| 43 | 1 Phvul.005G087600 | Phvul.005G087600 | | 0 PTHR34379,P | 0 |
| 44 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P | KOG0014 | |
| 45 | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 | PTHR10108,P | 0 |
| 46 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | | 0 |
| 47 | 1 Phvul.007G083500 | Phvul.007G083500 | | 0 PTHR36319,P | 0 |
| 48 | 1 Phvul.007G083500 | Phvul.007G083500 | | 0 PTHR36319,P | 0 |
| 49 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P | | 0 |
| 50 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 | KOG1187 | |
| 51 | 1 Phvul.011G110300 | Phvul.011G110300 | | 0 PTHR34056,P | 0 |
| 52 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 | PTHR32099 | 0 |

| | | | | |
|----|--------------------|------------------|--------------------------------------|---------|
| 1 | | | | |
| 2 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P ⁻ | 0 |
| 3 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P ⁻ | KOG4750 |
| 4 | 1 Phvul.003G067000 | Phvul.003G067000 | 0 PTHR34222,P ⁻ | 0 |
| 5 | | | | |
| 6 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 PTHR24089,P ⁻ | KOG0769 |
| 7 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P ⁻ | 0 |
| 8 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P ⁻ | KOG0546 |
| 9 | | | | |
| 10 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 PTHR10108,P ⁻ | 0 |
| 11 | 1 Phvul.005G087600 | Phvul.005G087600 | 0 PTHR34379,P ⁻ | 0 |
| 12 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P ⁻ | KOG0014 |
| 13 | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 PTHR10108,P ⁻ | 0 |
| 14 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | 0 |
| 15 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P ⁻ | 0 |
| 16 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P ⁻ | 0 |
| 17 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P ⁻ | 0 |
| 18 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P ⁻ | 0 |
| 19 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 | KOG1187 |
| 20 | 1 Phvul.011G110300 | Phvul.011G110300 | 0 PTHR34056,P ⁻ | 0 |
| 21 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 PTHR32099 | 0 |
| 22 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 PTHR32099 | 0 |
| 23 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P ⁻ | 0 |
| 24 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P ⁻ | KOG4750 |
| 25 | 1 Phvul.003G067000 | Phvul.003G067000 | 0 PTHR34222,P ⁻ | 0 |
| 26 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 PTHR24089,P ⁻ | KOG0769 |
| 27 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P ⁻ | 0 |
| 28 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P ⁻ | KOG0546 |
| 29 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 PTHR10108,P ⁻ | 0 |
| 30 | 1 Phvul.005G087600 | Phvul.005G087600 | 0 PTHR34379,P ⁻ | 0 |
| 31 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P ⁻ | KOG0014 |
| 32 | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 PTHR10108,P ⁻ | 0 |
| 33 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | 0 |
| 34 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P ⁻ | 0 |
| 35 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P ⁻ | 0 |
| 36 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P ⁻ | 0 |
| 37 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 | KOG1187 |
| 38 | 1 Phvul.011G110300 | Phvul.011G110300 | 0 PTHR34056,P ⁻ | 0 |
| 39 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 PTHR32099 | 0 |
| 40 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P ⁻ | 0 |
| 41 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P ⁻ | KOG4750 |
| 42 | 1 Phvul.003G067000 | Phvul.003G067000 | 0 PTHR34222,P ⁻ | 0 |
| 43 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 PTHR24089,P ⁻ | KOG0769 |
| 44 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P ⁻ | 0 |
| 45 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P ⁻ | KOG0546 |
| 46 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 PTHR10108,P ⁻ | 0 |
| 47 | 1 Phvul.005G087600 | Phvul.005G087600 | 0 PTHR34379,P ⁻ | 0 |
| 48 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P ⁻ | KOG0014 |
| 49 | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 PTHR10108,P ⁻ | 0 |
| 50 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | 0 |
| 51 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P ⁻ | 0 |
| 52 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P ⁻ | 0 |
| 53 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P ⁻ | 0 |
| 54 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 | KOG1187 |
| 55 | 1 Phvul.011G110300 | Phvul.011G110300 | 0 PTHR34056,P ⁻ | 0 |
| 56 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 PTHR32099 | 0 |
| 57 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P ⁻ | 0 |
| 58 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P ⁻ | KOG4750 |
| 59 | 1 Phvul.003G067000 | Phvul.003G067000 | 0 PTHR34222,P ⁻ | 0 |
| 60 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 PTHR24089,P ⁻ | KOG0769 |
| 61 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P ⁻ | 0 |
| 62 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P ⁻ | KOG0546 |
| 63 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 PTHR10108,P ⁻ | 0 |
| 64 | 1 Phvul.005G087600 | Phvul.005G087600 | 0 PTHR34379,P ⁻ | 0 |
| 65 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P ⁻ | KOG0014 |
| 66 | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 PTHR10108,P ⁻ | 0 |
| 67 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | 0 |
| 68 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P ⁻ | 0 |

| | | | | |
|----|--------------------|------------------|--|---|
| 1 | | | | |
| 2 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P ⁻ | 0 |
| 3 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P ⁻ | 0 |
| 4 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 KOG1187 | |
| 5 | | | | |
| 6 | 1 Phvul.011G110300 | Phvul.011G110300 | 0 PTHR34056,P ⁻ | 0 |
| 7 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 PTHR32099 | 0 |
| 8 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P ⁻ | 0 |
| 9 | | | | |
| 10 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P ⁻ KOG4750 | |
| 11 | 1 Phvul.003G067000 | Phvul.003G067000 | 0 PTHR34222,P ⁻ | 0 |
| 12 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 PTHR24089,P ⁻ KOG0769 | |
| 13 | | | | |
| 14 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P ⁻ | 0 |
| 15 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P ⁻ KOG0546 | |
| 16 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 PTHR10108,P ⁻ | 0 |
| 17 | | | | |
| 18 | 1 Phvul.005G087600 | Phvul.005G087600 | 0 PTHR34379,P ⁻ | 0 |
| 19 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P ⁻ KOG0014 | |
| 20 | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 PTHR10108,P ⁻ | 0 |
| 21 | | | | |
| 22 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | 0 |
| 23 | | | | |
| 24 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P ⁻ | 0 |
| 25 | | | | |
| 26 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P ⁻ | 0 |
| 27 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 KOG1187 | |
| 28 | 1 Phvul.011G110300 | Phvul.011G110300 | 0 PTHR34056,P ⁻ | 0 |
| 29 | | | | |
| 30 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 PTHR32099 | 0 |
| 31 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P ⁻ | 0 |
| 32 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P ⁻ KOG4750 | |
| 33 | | | | |
| 34 | 1 Phvul.003G067000 | Phvul.003G067000 | 0 PTHR34222,P ⁻ | 0 |
| 35 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 PTHR24089,P ⁻ KOG0769 | |
| 36 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P ⁻ | 0 |
| 37 | | | | |
| 38 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P ⁻ KOG0546 | |
| 39 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 PTHR10108,P ⁻ | 0 |
| 40 | 1 Phvul.005G087600 | Phvul.005G087600 | 0 PTHR34379,P ⁻ | 0 |
| 41 | | | | |
| 42 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P ⁻ KOG0014 | |
| 43 | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 PTHR10108,P ⁻ | 0 |
| 44 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | 0 |
| 45 | | | | |
| 46 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P ⁻ | 0 |
| 47 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P ⁻ | 0 |
| 48 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P ⁻ | 0 |
| 49 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 KOG1187 | |
| 50 | | | | |
| 51 | 1 Phvul.011G110300 | Phvul.011G110300 | 0 PTHR34056,P ⁻ | 0 |
| 52 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 PTHR32099 | 0 |
| 53 | | | | |
| 54 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P ⁻ | 0 |
| 55 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P ⁻ KOG4750 | |
| 56 | 1 Phvul.003G067000 | Phvul.003G067000 | 0 PTHR34222,P ⁻ | 0 |
| 57 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 PTHR24089,P ⁻ KOG0769 | |
| 58 | | | | |
| 59 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P ⁻ | 0 |
| 60 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P ⁻ KOG0546 | |
| | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 PTHR10108,P ⁻ | 0 |

| | | | | | |
|----|--------------------|------------------|--------------------------------------|--------------------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.005G087600 | Phvul.005G087600 | 0 PTHR34379,P ⁻ | | 0 |
| 3 | 1 Phvul.009G130000 | Phvul.009G130000 | PF01486,PF00PTHR11945,P ⁻ | KOG0014 | |
| 4 | 1 Phvul.011G108000 | Phvul.011G108000 | PF08241 | PTHR10108,P ⁻ | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | | 0 |
| 7 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P ⁻ | | 0 |
| 8 | 1 Phvul.007G083500 | Phvul.007G083500 | 0 PTHR36319,P ⁻ | | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.011G079800 | Phvul.011G079800 | PF00046,PF08PTHR24326,P ⁻ | | 0 |
| 11 | 1 Phvul.011G054900 | Phvul.011G054900 | PF01695,PF00PTHR23069 | | 0 |
| 12 | 1 Phvul.008G077800 | Phvul.008G077800 | PF01657,PF07PTHR27002 | KOG1187 | |
| 13 | | | | | |
| 14 | 1 Phvul.011G110300 | Phvul.011G110300 | 0 PTHR34056,P ⁻ | | 0 |
| 15 | 1 Phvul.008G077700 | Phvul.008G077700 | PF01657 | PTHR32099 | 0 |
| 16 | 1 Phvul.005G005200 | Phvul.005G005200 | PF00571,PF00PTHR11689,P ⁻ | | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.002G073200 | Phvul.002G073200 | PF00892 | PTHR31218,P ⁻ | KOG4510 |
| 19 | 1 Phvul.002G073100 | Phvul.002G073100 | PF00892 | PTHR31218,P ⁻ | KOG4510 |
| 20 | 1 Phvul.002G073100 | Phvul.002G073100 | PF00892 | PTHR31218,P ⁻ | KOG4510 |
| 21 | | | | | |
| 22 | 1 Phvul.008G277800 | Phvul.008G277800 | PF00132,PF06PTHR23416,P ⁻ | KOG4750 | |
| 23 | 1 Phvul.003G067000 | Phvul.003G067000 | 0 PTHR34222,P ⁻ | | 0 |
| 24 | 1 Phvul.001G240500 | Phvul.001G240500 | PF00153 | PTHR24089,P ⁻ | KOG0769 |
| 25 | | | | | |
| 26 | 1 Phvul.008G061000 | Phvul.008G061000 | PF04851,PF08PTHR10799,P ⁻ | | 0 |
| 27 | 1 Phvul.003G246400 | Phvul.003G246400 | PF07719,PF00PTHR11071,P ⁻ | KOG0546 | |
| 28 | 1 Phvul.009G132000 | Phvul.009G132000 | PF03141 | PTHR10108,P ⁻ | 0 |
| 29 | 1 Phvul.004G099100 | Phvul.004G099100 | PF08263,PF00PTHR27004,P ⁻ | KOG0472 | |
| 30 | | | | | |
| 31 | 1 Phvul.002G157300 | Phvul.002G157300 | PF03479 | PTHR31500,P ⁻ | 0 |
| 32 | 1 Phvul.009G146400 | Phvul.009G146400 | PF03360 | PTHR10896,P ⁻ | KOG1476 |
| 33 | 1 Phvul.011G046800 | Phvul.011G046800 | PF00083 | PTHR23500,P ⁻ | KOG0254 |
| 34 | | | | | |
| 35 | 1 Phvul.006G023000 | Phvul.006G023000 | PF00657 | PTHR22835,P ⁻ | 0 |
| 36 | 1 Phvul.006G093600 | Phvul.006G093600 | PF00026 | PTHR13683,P ⁻ | KOG1339 |
| 37 | 1 Phvul.001G151600 | Phvul.001G151600 | 0 PTHR34798,P ⁻ | | 0 |
| 38 | | | | | |
| 39 | 1 Phvul.007G231200 | Phvul.007G231200 | PF07650,PF00PTHR11760,P ⁻ | KOG3181 | |
| 40 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P ⁻ | KOG1187 | |
| 41 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P ⁻ | KOG1187 | |
| 42 | | | | | |
| 43 | 1 Phvul.007G156900 | Phvul.007G156900 | 0 PTHR33981,P ⁻ | | 0 |
| 44 | 1 Phvul.007G157000 | Phvul.007G157000 | 0 PTHR33981,P ⁻ | | 0 |
| 45 | 1 Phvul.007G105700 | Phvul.007G105700 | PF13837,PF00PTHR21499,P ⁻ | | 0 |
| 46 | | | | | |
| 47 | 1 Phvul.008G159000 | Phvul.008G159000 | PF10250 | PTHR31741,P ⁻ | 0 |
| 48 | 1 Phvul.005G114000 | Phvul.005G114000 | PF05634 | PTHR10388,P ⁻ | 0 |
| 49 | 1 Phvul.001G031000 | Phvul.001G031000 | PF08880,PF08PTHR31602,P ⁻ | | 0 |
| 50 | | | | | |
| 51 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 52 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 53 | 1 Phvul.007G084000 | Phvul.007G084000 | PF00230 | PTHR19139,P ⁻ | KOG0223 |
| 54 | | | | | |
| 55 | 1 Phvul.009G119100 | Phvul.009G119100 | PF13386 | PTHR33876,P ⁻ | 0 |
| 56 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P ⁻ | 0 |
| 57 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P ⁻ | 0 |
| 58 | | | | | |
| 59 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P ⁻ | 0 |
| 60 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P ⁻ | 0 |
| | 1 Phvul.008G127800 | Phvul.008G127800 | 0 | 0 | 0 |

| | | | | | | |
|----|--------------------|------------------|-------------------------|---------------|---------|---|
| 1 | | | | | | |
| 2 | 1 Phvul.001G038000 | Phvul.001G038000 | PF01843 | PTHR13140,P | | 0 |
| 3 | 1 Phvul.002G105200 | Phvul.002G105200 | PF00026 | PTHR13683,P | KOG1339 | |
| 4 | 1 Phvul.008G032900 | Phvul.008G032900 | PF07897,PF16PTHR31413,P | | | 0 |
| 5 | 1 Phvul.009G244600 | Phvul.009G244600 | PF08263,PF00PTHR27000 | | KOG1187 | |
| 6 | 1 Phvul.004G099100 | Phvul.004G099100 | PF08263,PF00PTHR27004,P | | KOG0472 | |
| 7 | 1 Phvul.002G157300 | Phvul.002G157300 | PF03479 | PTHR31500,P | | 0 |
| 8 | 1 Phvul.009G146400 | Phvul.009G146400 | PF03360 | PTHR10896,P | KOG1476 | |
| 9 | 1 Phvul.011G046800 | Phvul.011G046800 | PF00083 | PTHR23500,P | KOG0254 | |
| 10 | 1 Phvul.006G023000 | Phvul.006G023000 | PF00657 | PTHR22835,P | | 0 |
| 11 | 1 Phvul.006G093600 | Phvul.006G093600 | PF00026 | PTHR13683,P | KOG1339 | |
| 12 | 1 Phvul.001G151600 | Phvul.001G151600 | | 0 PTHR34798,P | | 0 |
| 13 | 1 Phvul.007G231200 | Phvul.007G231200 | PF07650,PF00PTHR11760,P | | KOG3181 | |
| 14 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P | | KOG1187 | |
| 15 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P | | KOG1187 | |
| 16 | 1 Phvul.007G156900 | Phvul.007G156900 | | 0 PTHR33981,P | | 0 |
| 17 | 1 Phvul.007G157000 | Phvul.007G157000 | | 0 PTHR33981,P | | 0 |
| 18 | 1 Phvul.007G105700 | Phvul.007G105700 | PF13837,PF00PTHR21499,P | | | 0 |
| 19 | 1 Phvul.008G159000 | Phvul.008G159000 | PF10250 | PTHR31741,P | | 0 |
| 20 | 1 Phvul.005G114000 | Phvul.005G114000 | PF05634 | PTHR10388,P | | 0 |
| 21 | 1 Phvul.001G031000 | Phvul.001G031000 | PF08880,PF08PTHR31602,P | | | 0 |
| 22 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | | 0 |
| 23 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | | 0 |
| 24 | 1 Phvul.007G084000 | Phvul.007G084000 | PF00230 | PTHR19139,P | KOG0223 | |
| 25 | 1 Phvul.009G119100 | Phvul.009G119100 | PF13386 | PTHR33876,P | | 0 |
| 26 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P | | 0 |
| 27 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P | | 0 |
| 28 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P | | 0 |
| 29 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P | | 0 |
| 30 | 1 Phvul.008G127800 | Phvul.008G127800 | | 0 | 0 | 0 |
| 31 | 1 Phvul.001G038000 | Phvul.001G038000 | PF01843 | PTHR13140,P | | 0 |
| 32 | 1 Phvul.002G105200 | Phvul.002G105200 | PF00026 | PTHR13683,P | KOG1339 | |
| 33 | 1 Phvul.008G032900 | Phvul.008G032900 | PF07897,PF16PTHR31413,P | | | 0 |
| 34 | 1 Phvul.009G244600 | Phvul.009G244600 | PF08263,PF00PTHR27000 | | KOG1187 | |
| 35 | 1 Phvul.004G099100 | Phvul.004G099100 | PF08263,PF00PTHR27004,P | | KOG0472 | |
| 36 | 1 Phvul.002G157300 | Phvul.002G157300 | PF03479 | PTHR31500,P | | 0 |
| 37 | 1 Phvul.009G146400 | Phvul.009G146400 | PF03360 | PTHR10896,P | KOG1476 | |
| 38 | 1 Phvul.011G046800 | Phvul.011G046800 | PF00083 | PTHR23500,P | KOG0254 | |
| 39 | 1 Phvul.006G023000 | Phvul.006G023000 | PF00657 | PTHR22835,P | | 0 |
| 40 | 1 Phvul.006G093600 | Phvul.006G093600 | PF00026 | PTHR13683,P | KOG1339 | |
| 41 | 1 Phvul.001G151600 | Phvul.001G151600 | | 0 PTHR34798,P | | 0 |
| 42 | 1 Phvul.007G231200 | Phvul.007G231200 | PF07650,PF00PTHR11760,P | | KOG3181 | |
| 43 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P | | KOG1187 | |
| 44 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P | | KOG1187 | |
| 45 | 1 Phvul.007G156900 | Phvul.007G156900 | | 0 PTHR33981,P | | 0 |
| 46 | 1 Phvul.007G157000 | Phvul.007G157000 | | 0 PTHR33981,P | | 0 |
| 47 | 1 Phvul.007G105700 | Phvul.007G105700 | PF13837,PF00PTHR21499,P | | | 0 |

| | | | | | | |
|----|--------------------|------------------|--------------|--------------------------|--------------------------|---|
| 1 | | | | | | |
| 2 | 1 Phvul.008G159000 | Phvul.008G159000 | PF10250 | PTHR31741,P ⁻ | | 0 |
| 3 | 1 Phvul.005G114000 | Phvul.005G114000 | PF05634 | PTHR10388,P ⁻ | | 0 |
| 4 | 1 Phvul.001G031000 | Phvul.001G031000 | PF08880,PF08 | PTHR31602,P ⁻ | | 0 |
| 5 | | | | | | |
| 6 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | | 0 |
| 7 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | | 0 |
| 8 | 1 Phvul.007G084000 | Phvul.007G084000 | PF00230 | PTHR19139,P ⁻ | KOG0223 | |
| 9 | | | | | | |
| 10 | 1 Phvul.009G119100 | Phvul.009G119100 | PF13386 | PTHR33876,P ⁻ | | 0 |
| 11 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P ⁻ | | 0 |
| 12 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P ⁻ | | 0 |
| 13 | | | | | | |
| 14 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P ⁻ | | 0 |
| 15 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P ⁻ | | 0 |
| 16 | 1 Phvul.008G127800 | Phvul.008G127800 | | 0 | 0 | 0 |
| 17 | | | | | | |
| 18 | 1 Phvul.001G038000 | Phvul.001G038000 | PF01843 | PTHR13140,P ⁻ | | 0 |
| 19 | 1 Phvul.002G105200 | Phvul.002G105200 | PF00026 | PTHR13683,P ⁻ | KOG1339 | |
| 20 | 1 Phvul.008G032900 | Phvul.008G032900 | PF07897,PF16 | PTHR31413,P ⁻ | | 0 |
| 21 | | | | | | |
| 22 | 1 Phvul.009G244600 | Phvul.009G244600 | PF08263,PF00 | PTHR27000 | KOG1187 | |
| 23 | 1 Phvul.004G099100 | Phvul.004G099100 | PF08263,PF00 | PTHR27004,P ⁻ | KOG0472 | |
| 24 | 1 Phvul.002G157300 | Phvul.002G157300 | PF03479 | PTHR31500,P ⁻ | | 0 |
| 25 | | | | | | |
| 26 | 1 Phvul.009G146400 | Phvul.009G146400 | PF03360 | PTHR10896,P ⁻ | KOG1476 | |
| 27 | 1 Phvul.011G046800 | Phvul.011G046800 | PF00083 | PTHR23500,P ⁻ | KOG0254 | |
| 28 | 1 Phvul.006G023000 | Phvul.006G023000 | PF00657 | PTHR22835,P ⁻ | | 0 |
| 29 | 1 Phvul.006G093600 | Phvul.006G093600 | PF00026 | PTHR13683,P ⁻ | KOG1339 | |
| 30 | | | | | | |
| 31 | 1 Phvul.001G151600 | Phvul.001G151600 | | 0 | PTHR34798,P ⁻ | 0 |
| 32 | 1 Phvul.007G231200 | Phvul.007G231200 | PF07650,PF00 | PTHR11760,P ⁻ | KOG3181 | |
| 33 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00 | PTHR27000,P ⁻ | KOG1187 | |
| 34 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00 | PTHR27000,P ⁻ | KOG1187 | |
| 35 | 1 Phvul.007G156900 | Phvul.007G156900 | | 0 | PTHR33981,P ⁻ | 0 |
| 36 | 1 Phvul.007G157000 | Phvul.007G157000 | | 0 | PTHR33981,P ⁻ | 0 |
| 37 | | | | | | |
| 38 | 1 Phvul.007G105700 | Phvul.007G105700 | PF13837,PF00 | PTHR21499,P ⁻ | | 0 |
| 39 | 1 Phvul.008G159000 | Phvul.008G159000 | PF10250 | PTHR31741,P ⁻ | | 0 |
| 40 | 1 Phvul.005G114000 | Phvul.005G114000 | PF05634 | PTHR10388,P ⁻ | | 0 |
| 41 | 1 Phvul.001G031000 | Phvul.001G031000 | PF08880,PF08 | PTHR31602,P ⁻ | | 0 |
| 42 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | | 0 |
| 43 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | | 0 |
| 44 | 1 Phvul.007G084000 | Phvul.007G084000 | PF00230 | PTHR19139,P ⁻ | KOG0223 | |
| 45 | 1 Phvul.009G119100 | Phvul.009G119100 | PF13386 | PTHR33876,P ⁻ | | 0 |
| 46 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P ⁻ | | 0 |
| 47 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P ⁻ | | 0 |
| 48 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P ⁻ | | 0 |
| 49 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P ⁻ | | 0 |
| 50 | | | | | | |
| 51 | 1 Phvul.008G127800 | Phvul.008G127800 | | 0 | 0 | 0 |
| 52 | 1 Phvul.001G038000 | Phvul.001G038000 | PF01843 | PTHR13140,P ⁻ | | 0 |
| 53 | 1 Phvul.002G105200 | Phvul.002G105200 | PF00026 | PTHR13683,P ⁻ | KOG1339 | |
| 54 | 1 Phvul.008G032900 | Phvul.008G032900 | PF07897,PF16 | PTHR31413,P ⁻ | | 0 |
| 55 | 1 Phvul.009G244600 | Phvul.009G244600 | PF08263,PF00 | PTHR27000 | KOG1187 | |
| 56 | 1 Phvul.004G099100 | Phvul.004G099100 | PF08263,PF00 | PTHR27004,P ⁻ | KOG0472 | |
| 57 | | | | | | |
| 58 | | | | | | |
| 59 | | | | | | |
| 60 | | | | | | |

| | | | | | |
|----|--------------------|------------------|--------------------------------------|----------------------------------|---|
| 1 | | | | | |
| 2 | 1 Phvul.002G157300 | Phvul.002G157300 | PF03479 | PTHR31500,P ⁻ | 0 |
| 3 | 1 Phvul.009G146400 | Phvul.009G146400 | PF03360 | PTHR10896,P ⁻ KOG1476 | |
| 4 | 1 Phvul.011G046800 | Phvul.011G046800 | PF00083 | PTHR23500,P ⁻ KOG0254 | |
| 5 | | | | | |
| 6 | 1 Phvul.006G023000 | Phvul.006G023000 | PF00657 | PTHR22835,P ⁻ | 0 |
| 7 | 1 Phvul.006G093600 | Phvul.006G093600 | PF00026 | PTHR13683,P ⁻ KOG1339 | |
| 8 | 1 Phvul.001G151600 | Phvul.001G151600 | | 0 PTHR34798,P ⁻ | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.007G231200 | Phvul.007G231200 | PF07650,PF00PTHR11760,P ⁻ | KOG3181 | |
| 11 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P ⁻ | KOG1187 | |
| 12 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P ⁻ | KOG1187 | |
| 13 | | | | | |
| 14 | 1 Phvul.007G156900 | Phvul.007G156900 | | 0 PTHR33981,P ⁻ | 0 |
| 15 | 1 Phvul.007G157000 | Phvul.007G157000 | | 0 PTHR33981,P ⁻ | 0 |
| 16 | 1 Phvul.007G105700 | Phvul.007G105700 | PF13837,PF00PTHR21499,P ⁻ | | 0 |
| 17 | 1 Phvul.008G159000 | Phvul.008G159000 | PF10250 | PTHR31741,P ⁻ | 0 |
| 18 | 1 Phvul.005G114000 | Phvul.005G114000 | PF05634 | PTHR10388,P ⁻ | 0 |
| 19 | 1 Phvul.001G031000 | Phvul.001G031000 | PF08880,PF08PTHR31602,P ⁻ | | 0 |
| 20 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 21 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 22 | | | | | |
| 23 | 1 Phvul.007G084000 | Phvul.007G084000 | PF00230 | PTHR19139,P ⁻ KOG0223 | |
| 24 | 1 Phvul.009G119100 | Phvul.009G119100 | PF13386 | PTHR33876,P ⁻ | 0 |
| 25 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P ⁻ | 0 |
| 26 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P ⁻ | 0 |
| 27 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P ⁻ | 0 |
| 28 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P ⁻ | 0 |
| 29 | 1 Phvul.008G127800 | Phvul.008G127800 | | 0 0 | 0 |
| 30 | 1 Phvul.001G038000 | Phvul.001G038000 | PF01843 | PTHR13140,P ⁻ | 0 |
| 31 | 1 Phvul.002G105200 | Phvul.002G105200 | PF00026 | PTHR13683,P ⁻ KOG1339 | |
| 32 | 1 Phvul.008G032900 | Phvul.008G032900 | PF07897,PF16PTHR31413,P ⁻ | | 0 |
| 33 | 1 Phvul.009G244600 | Phvul.009G244600 | PF08263,PF00PTHR27000 | KOG1187 | |
| 34 | 1 Phvul.004G099100 | Phvul.004G099100 | PF08263,PF00PTHR27004,P ⁻ | KOG0472 | |
| 35 | 1 Phvul.002G157300 | Phvul.002G157300 | PF03479 | PTHR31500,P ⁻ | 0 |
| 36 | 1 Phvul.009G146400 | Phvul.009G146400 | PF03360 | PTHR10896,P ⁻ KOG1476 | |
| 37 | 1 Phvul.011G046800 | Phvul.011G046800 | PF00083 | PTHR23500,P ⁻ KOG0254 | |
| 38 | 1 Phvul.006G023000 | Phvul.006G023000 | PF00657 | PTHR22835,P ⁻ | 0 |
| 39 | 1 Phvul.006G093600 | Phvul.006G093600 | PF00026 | PTHR13683,P ⁻ KOG1339 | |
| 40 | 1 Phvul.001G151600 | Phvul.001G151600 | | 0 PTHR34798,P ⁻ | 0 |
| 41 | 1 Phvul.007G231200 | Phvul.007G231200 | PF07650,PF00PTHR11760,P ⁻ | KOG3181 | |
| 42 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P ⁻ | KOG1187 | |
| 43 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P ⁻ | KOG1187 | |
| 44 | 1 Phvul.007G156900 | Phvul.007G156900 | | 0 PTHR33981,P ⁻ | 0 |
| 45 | 1 Phvul.007G157000 | Phvul.007G157000 | | 0 PTHR33981,P ⁻ | 0 |
| 46 | 1 Phvul.007G105700 | Phvul.007G105700 | PF13837,PF00PTHR21499,P ⁻ | | 0 |
| 47 | 1 Phvul.008G159000 | Phvul.008G159000 | PF10250 | PTHR31741,P ⁻ | 0 |
| 48 | 1 Phvul.005G114000 | Phvul.005G114000 | PF05634 | PTHR10388,P ⁻ | 0 |
| 49 | 1 Phvul.001G031000 | Phvul.001G031000 | PF08880,PF08PTHR31602,P ⁻ | | 0 |
| 50 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 51 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |

| | | | | | |
|----|--------------------|------------------|--------------|----------------------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.007G084000 | Phvul.007G084000 | PF00230 | PTHR19139,P ⁻ | KOG0223 |
| 3 | 1 Phvul.009G119100 | Phvul.009G119100 | PF13386 | PTHR33876,P ⁻ | 0 |
| 4 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P ⁻ | 0 |
| 5 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P ⁻ | 0 |
| 6 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P ⁻ | 0 |
| 7 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P ⁻ | 0 |
| 8 | 1 Phvul.008G127800 | Phvul.008G127800 | | 0 | 0 |
| 9 | 1 Phvul.001G038000 | Phvul.001G038000 | PF01843 | PTHR13140,P ⁻ | 0 |
| 10 | 1 Phvul.002G105200 | Phvul.002G105200 | PF00026 | PTHR13683,P ⁻ | KOG1339 |
| 11 | 1 Phvul.008G032900 | Phvul.008G032900 | PF07897,PF16 | PTHR31413,P ⁻ | 0 |
| 12 | 1 Phvul.009G244600 | Phvul.009G244600 | PF08263,PF00 | PTHR27000 | KOG1187 |
| 13 | 1 Phvul.004G099100 | Phvul.004G099100 | PF08263,PF00 | PTHR27004,P ⁻ | KOG0472 |
| 14 | 1 Phvul.002G157300 | Phvul.002G157300 | PF03479 | PTHR31500,P ⁻ | 0 |
| 15 | 1 Phvul.009G146400 | Phvul.009G146400 | PF03360 | PTHR10896,P ⁻ | KOG1476 |
| 16 | 1 Phvul.011G046800 | Phvul.011G046800 | PF00083 | PTHR23500,P ⁻ | KOG0254 |
| 17 | 1 Phvul.006G023000 | Phvul.006G023000 | PF00657 | PTHR22835,P ⁻ | 0 |
| 18 | 1 Phvul.006G093600 | Phvul.006G093600 | PF00026 | PTHR13683,P ⁻ | KOG1339 |
| 19 | 1 Phvul.001G151600 | Phvul.001G151600 | | 0 PTHR34798,P ⁻ | 0 |
| 20 | 1 Phvul.007G231200 | Phvul.007G231200 | PF07650,PF00 | PTHR11760,P ⁻ | KOG3181 |
| 21 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00 | PTHR27000,P ⁻ | KOG1187 |
| 22 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00 | PTHR27000,P ⁻ | KOG1187 |
| 23 | 1 Phvul.007G156900 | Phvul.007G156900 | | 0 PTHR33981,P ⁻ | 0 |
| 24 | 1 Phvul.007G157000 | Phvul.007G157000 | | 0 PTHR33981,P ⁻ | 0 |
| 25 | 1 Phvul.007G105700 | Phvul.007G105700 | PF13837,PF00 | PTHR21499,P ⁻ | 0 |
| 26 | 1 Phvul.008G159000 | Phvul.008G159000 | PF10250 | PTHR31741,P ⁻ | 0 |
| 27 | 1 Phvul.005G114000 | Phvul.005G114000 | PF05634 | PTHR10388,P ⁻ | 0 |
| 28 | 1 Phvul.001G031000 | Phvul.001G031000 | PF08880,PF08 | PTHR31602,P ⁻ | 0 |
| 29 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 30 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 31 | 1 Phvul.007G084000 | Phvul.007G084000 | PF00230 | PTHR19139,P ⁻ | KOG0223 |
| 32 | 1 Phvul.009G119100 | Phvul.009G119100 | PF13386 | PTHR33876,P ⁻ | 0 |
| 33 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P ⁻ | 0 |
| 34 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P ⁻ | 0 |
| 35 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P ⁻ | 0 |
| 36 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P ⁻ | 0 |
| 37 | 1 Phvul.008G127800 | Phvul.008G127800 | | 0 | 0 |
| 38 | 1 Phvul.001G038000 | Phvul.001G038000 | PF01843 | PTHR13140,P ⁻ | 0 |
| 39 | 1 Phvul.002G105200 | Phvul.002G105200 | PF00026 | PTHR13683,P ⁻ | KOG1339 |
| 40 | 1 Phvul.008G032900 | Phvul.008G032900 | PF07897,PF16 | PTHR31413,P ⁻ | 0 |
| 41 | 1 Phvul.009G244600 | Phvul.009G244600 | PF08263,PF00 | PTHR27000 | KOG1187 |
| 42 | 1 Phvul.004G099100 | Phvul.004G099100 | PF08263,PF00 | PTHR27004,P ⁻ | KOG0472 |
| 43 | 1 Phvul.002G157300 | Phvul.002G157300 | PF03479 | PTHR31500,P ⁻ | 0 |
| 44 | 1 Phvul.009G146400 | Phvul.009G146400 | PF03360 | PTHR10896,P ⁻ | KOG1476 |
| 45 | 1 Phvul.011G046800 | Phvul.011G046800 | PF00083 | PTHR23500,P ⁻ | KOG0254 |
| 46 | 1 Phvul.006G023000 | Phvul.006G023000 | PF00657 | PTHR22835,P ⁻ | 0 |
| 47 | 1 Phvul.006G093600 | Phvul.006G093600 | PF00026 | PTHR13683,P ⁻ | KOG1339 |

| | | | | | |
|----|--------------------|------------------|-------------------------|-------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.001G151600 | Phvul.001G151600 | 0 PTHR34798,P | | 0 |
| 3 | 1 Phvul.007G231200 | Phvul.007G231200 | PF07650,PF00PTHR11760,P | KOG3181 | |
| 4 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P | KOG1187 | |
| 5 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P | KOG1187 | |
| 6 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P | KOG1187 | |
| 7 | 1 Phvul.007G156900 | Phvul.007G156900 | 0 PTHR33981,P | | 0 |
| 8 | 1 Phvul.007G157000 | Phvul.007G157000 | 0 PTHR33981,P | | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.007G105700 | Phvul.007G105700 | PF13837,PF00PTHR21499,P | | 0 |
| 11 | 1 Phvul.008G159000 | Phvul.008G159000 | PF10250 | PTHR31741,P | 0 |
| 12 | 1 Phvul.005G114000 | Phvul.005G114000 | PF05634 | PTHR10388,P | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.001G031000 | Phvul.001G031000 | PF08880,PF08PTHR31602,P | | 0 |
| 15 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 16 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.007G084000 | Phvul.007G084000 | PF00230 | PTHR19139,P | KOG0223 |
| 19 | 1 Phvul.009G119100 | Phvul.009G119100 | PF13386 | PTHR33876,P | 0 |
| 20 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P | 0 |
| 23 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P | 0 |
| 24 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.008G127800 | Phvul.008G127800 | 0 | 0 | 0 |
| 27 | 1 Phvul.001G038000 | Phvul.001G038000 | PF01843 | PTHR13140,P | 0 |
| 28 | 1 Phvul.002G105200 | Phvul.002G105200 | PF00026 | PTHR13683,P | KOG1339 |
| 29 | | | | | |
| 30 | 1 Phvul.008G032900 | Phvul.008G032900 | PF07897,PF16PTHR31413,P | | 0 |
| 31 | 1 Phvul.009G244600 | Phvul.009G244600 | PF08263,PF00PTHR27000 | KOG1187 | |
| 32 | 1 Phvul.004G099100 | Phvul.004G099100 | PF08263,PF00PTHR27004,P | KOG0472 | |
| 33 | 1 Phvul.002G157300 | Phvul.002G157300 | PF03479 | PTHR31500,P | 0 |
| 34 | | | | | |
| 35 | 1 Phvul.009G146400 | Phvul.009G146400 | PF03360 | PTHR10896,P | KOG1476 |
| 36 | 1 Phvul.011G046800 | Phvul.011G046800 | PF00083 | PTHR23500,P | KOG0254 |
| 37 | | | | | |
| 38 | 1 Phvul.006G023000 | Phvul.006G023000 | PF00657 | PTHR22835,P | 0 |
| 39 | 1 Phvul.006G093600 | Phvul.006G093600 | PF00026 | PTHR13683,P | KOG1339 |
| 40 | 1 Phvul.001G151600 | Phvul.001G151600 | 0 PTHR34798,P | | 0 |
| 41 | 1 Phvul.007G231200 | Phvul.007G231200 | PF07650,PF00PTHR11760,P | KOG3181 | |
| 42 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P | KOG1187 | |
| 43 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P | KOG1187 | |
| 44 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P | KOG1187 | |
| 45 | 1 Phvul.007G156900 | Phvul.007G156900 | 0 PTHR33981,P | | 0 |
| 46 | 1 Phvul.007G157000 | Phvul.007G157000 | 0 PTHR33981,P | | 0 |
| 47 | | | | | |
| 48 | 1 Phvul.007G105700 | Phvul.007G105700 | PF13837,PF00PTHR21499,P | | 0 |
| 49 | 1 Phvul.008G159000 | Phvul.008G159000 | PF10250 | PTHR31741,P | 0 |
| 50 | | | | | |
| 51 | 1 Phvul.005G114000 | Phvul.005G114000 | PF05634 | PTHR10388,P | 0 |
| 52 | 1 Phvul.001G031000 | Phvul.001G031000 | PF08880,PF08PTHR31602,P | | 0 |
| 53 | | | | | |
| 54 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 55 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 56 | 1 Phvul.007G084000 | Phvul.007G084000 | PF00230 | PTHR19139,P | KOG0223 |
| 57 | 1 Phvul.009G119100 | Phvul.009G119100 | PF13386 | PTHR33876,P | 0 |
| 58 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P | 0 |
| 59 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P | 0 |
| 60 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P | 0 |

| | | | | | |
|----|--------------------|------------------|--------------|----------------------------------|---|
| 1 | | | | | |
| 2 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P ⁻ | 0 |
| 3 | 1 Phvul.008G127800 | Phvul.008G127800 | | 0 0 | 0 |
| 4 | 1 Phvul.001G038000 | Phvul.001G038000 | PF01843 | PTHR13140,P ⁻ | 0 |
| 5 | 1 Phvul.002G105200 | Phvul.002G105200 | PF00026 | PTHR13683,P ⁻ KOG1339 | |
| 6 | 1 Phvul.008G032900 | Phvul.008G032900 | PF07897,PF16 | PTHR31413,P ⁻ | 0 |
| 7 | 1 Phvul.009G244600 | Phvul.009G244600 | PF08263,PF00 | PTHR27000 KOG1187 | |
| 8 | 1 Phvul.004G099100 | Phvul.004G099100 | PF08263,PF00 | PTHR27004,P ⁻ KOG0472 | |
| 9 | 1 Phvul.002G157300 | Phvul.002G157300 | PF03479 | PTHR31500,P ⁻ | 0 |
| 10 | 1 Phvul.009G146400 | Phvul.009G146400 | PF03360 | PTHR10896,P ⁻ KOG1476 | |
| 11 | 1 Phvul.011G046800 | Phvul.011G046800 | PF00083 | PTHR23500,P ⁻ KOG0254 | |
| 12 | 1 Phvul.006G023000 | Phvul.006G023000 | PF00657 | PTHR22835,P ⁻ | 0 |
| 13 | 1 Phvul.006G093600 | Phvul.006G093600 | PF00026 | PTHR13683,P ⁻ KOG1339 | |
| 14 | 1 Phvul.001G151600 | Phvul.001G151600 | | 0 PTHR34798,P ⁻ | 0 |
| 15 | 1 Phvul.007G231200 | Phvul.007G231200 | PF07650,PF00 | PTHR11760,P ⁻ KOG3181 | |
| 16 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00 | PTHR27000,P ⁻ KOG1187 | |
| 17 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00 | PTHR27000,P ⁻ KOG1187 | |
| 18 | 1 Phvul.007G156900 | Phvul.007G156900 | | 0 PTHR33981,P ⁻ | 0 |
| 19 | 1 Phvul.007G157000 | Phvul.007G157000 | | 0 PTHR33981,P ⁻ | 0 |
| 20 | 1 Phvul.007G105700 | Phvul.007G105700 | PF13837,PF00 | PTHR21499,P ⁻ | 0 |
| 21 | 1 Phvul.008G159000 | Phvul.008G159000 | PF10250 | PTHR31741,P ⁻ | 0 |
| 22 | 1 Phvul.005G114000 | Phvul.005G114000 | PF05634 | PTHR10388,P ⁻ | 0 |
| 23 | 1 Phvul.001G031000 | Phvul.001G031000 | PF08880,PF08 | PTHR31602,P ⁻ | 0 |
| 24 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 25 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 26 | 1 Phvul.007G084000 | Phvul.007G084000 | PF00230 | PTHR19139,P ⁻ KOG0223 | |
| 27 | 1 Phvul.009G119100 | Phvul.009G119100 | PF13386 | PTHR33876,P ⁻ | 0 |
| 28 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P ⁻ | 0 |
| 29 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P ⁻ | 0 |
| 30 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P ⁻ | 0 |
| 31 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P ⁻ | 0 |
| 32 | 1 Phvul.008G127800 | Phvul.008G127800 | | 0 0 | 0 |
| 33 | 1 Phvul.001G038000 | Phvul.001G038000 | PF01843 | PTHR13140,P ⁻ | 0 |
| 34 | 1 Phvul.002G105200 | Phvul.002G105200 | PF00026 | PTHR13683,P ⁻ KOG1339 | |
| 35 | 1 Phvul.008G032900 | Phvul.008G032900 | PF07897,PF16 | PTHR31413,P ⁻ | 0 |
| 36 | 1 Phvul.009G244600 | Phvul.009G244600 | PF08263,PF00 | PTHR27000 KOG1187 | |
| 37 | 1 Phvul.004G099100 | Phvul.004G099100 | PF08263,PF00 | PTHR27004,P ⁻ KOG0472 | |
| 38 | 1 Phvul.002G157300 | Phvul.002G157300 | PF03479 | PTHR31500,P ⁻ | 0 |
| 39 | 1 Phvul.009G146400 | Phvul.009G146400 | PF03360 | PTHR10896,P ⁻ KOG1476 | |
| 40 | 1 Phvul.011G046800 | Phvul.011G046800 | PF00083 | PTHR23500,P ⁻ KOG0254 | |
| 41 | 1 Phvul.006G023000 | Phvul.006G023000 | PF00657 | PTHR22835,P ⁻ | 0 |
| 42 | 1 Phvul.006G093600 | Phvul.006G093600 | PF00026 | PTHR13683,P ⁻ KOG1339 | |
| 43 | 1 Phvul.001G151600 | Phvul.001G151600 | | 0 PTHR34798,P ⁻ | 0 |
| 44 | 1 Phvul.007G231200 | Phvul.007G231200 | PF07650,PF00 | PTHR11760,P ⁻ KOG3181 | |
| 45 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00 | PTHR27000,P ⁻ KOG1187 | |
| 46 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00 | PTHR27000,P ⁻ KOG1187 | |
| 47 | 1 Phvul.007G156900 | Phvul.007G156900 | | 0 PTHR33981,P ⁻ | 0 |

| | | | | | |
|----|--------------------|------------------|---------------------------------|--|---|
| 1 | | | | | |
| 2 | 1 Phvul.007G157000 | Phvul.007G157000 | 0 PTHR33981,P | | 0 |
| 3 | 1 Phvul.007G105700 | Phvul.007G105700 | PF13837,PF00PTHR21499,P | | 0 |
| 4 | 1 Phvul.008G159000 | Phvul.008G159000 | PF10250 PTHR31741,P | | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.005G114000 | Phvul.005G114000 | PF05634 PTHR10388,P | | 0 |
| 7 | 1 Phvul.001G031000 | Phvul.001G031000 | PF08880,PF08PTHR31602,P | | 0 |
| 8 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 PTHR10631 | | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 PTHR10631 | | 0 |
| 11 | 1 Phvul.007G084000 | Phvul.007G084000 | PF00230 PTHR19139,P KOG0223 | | |
| 12 | 1 Phvul.009G119100 | Phvul.009G119100 | PF13386 PTHR33876,P | | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 PTHR31358,P | | 0 |
| 15 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 PTHR31358,P | | 0 |
| 16 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 PTHR31675,P | | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 PTHR31675,P | | 0 |
| 19 | 1 Phvul.008G127800 | Phvul.008G127800 | 0 0 | | 0 |
| 20 | 1 Phvul.001G038000 | Phvul.001G038000 | PF01843 PTHR13140,P | | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.002G105200 | Phvul.002G105200 | PF00026 PTHR13683,P KOG1339 | | |
| 23 | 1 Phvul.008G032900 | Phvul.008G032900 | PF07897,PF16PTHR31413,P | | 0 |
| 24 | 1 Phvul.009G244600 | Phvul.009G244600 | PF08263,PF00PTHR27000 KOG1187 | | |
| 25 | | | | | |
| 26 | 1 Phvul.004G099100 | Phvul.004G099100 | PF08263,PF00PTHR27004,P KOG0472 | | |
| 27 | 1 Phvul.002G157300 | Phvul.002G157300 | PF03479 PTHR31500,P | | 0 |
| 28 | 1 Phvul.009G146400 | Phvul.009G146400 | PF03360 PTHR10896,P KOG1476 | | |
| 29 | 1 Phvul.011G046800 | Phvul.011G046800 | PF00083 PTHR23500,P KOG0254 | | |
| 30 | | | | | |
| 31 | 1 Phvul.006G023000 | Phvul.006G023000 | PF00657 PTHR22835,P | | 0 |
| 32 | 1 Phvul.006G093600 | Phvul.006G093600 | PF00026 PTHR13683,P KOG1339 | | |
| 33 | | | | | |
| 34 | 1 Phvul.001G151600 | Phvul.001G151600 | 0 PTHR34798,P | | 0 |
| 35 | 1 Phvul.007G231200 | Phvul.007G231200 | PF07650,PF00PTHR11760,P KOG3181 | | |
| 36 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P KOG1187 | | |
| 37 | | | | | |
| 38 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P KOG1187 | | |
| 39 | 1 Phvul.007G156900 | Phvul.007G156900 | 0 PTHR33981,P | | 0 |
| 40 | 1 Phvul.007G157000 | Phvul.007G157000 | 0 PTHR33981,P | | 0 |
| 41 | 1 Phvul.007G105700 | Phvul.007G105700 | PF13837,PF00PTHR21499,P | | 0 |
| 42 | | | | | |
| 43 | 1 Phvul.008G159000 | Phvul.008G159000 | PF10250 PTHR31741,P | | 0 |
| 44 | 1 Phvul.005G114000 | Phvul.005G114000 | PF05634 PTHR10388,P | | 0 |
| 45 | | | | | |
| 46 | 1 Phvul.001G031000 | Phvul.001G031000 | PF08880,PF08PTHR31602,P | | 0 |
| 47 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 PTHR10631 | | 0 |
| 48 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 PTHR10631 | | 0 |
| 49 | 1 Phvul.007G084000 | Phvul.007G084000 | PF00230 PTHR19139,P KOG0223 | | |
| 50 | | | | | |
| 51 | 1 Phvul.009G119100 | Phvul.009G119100 | PF13386 PTHR33876,P | | 0 |
| 52 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 PTHR31358,P | | 0 |
| 53 | | | | | |
| 54 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 PTHR31358,P | | 0 |
| 55 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 PTHR31675,P | | 0 |
| 56 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 PTHR31675,P | | 0 |
| 57 | | | | | |
| 58 | 1 Phvul.008G127800 | Phvul.008G127800 | 0 0 | | 0 |
| 59 | 1 Phvul.001G038000 | Phvul.001G038000 | PF01843 PTHR13140,P | | 0 |
| 60 | 1 Phvul.002G105200 | Phvul.002G105200 | PF00026 PTHR13683,P KOG1339 | | |
| | 1 Phvul.008G032900 | Phvul.008G032900 | PF07897,PF16PTHR31413,P | | 0 |

| | | | | | |
|----|--------------------|------------------|-------------------------|---------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.009G244600 | Phvul.009G244600 | PF08263,PF00PTHR27000 | KOG1187 | |
| 3 | 1 Phvul.004G099100 | Phvul.004G099100 | PF08263,PF00PTHR27004,P | KOG0472 | |
| 4 | 1 Phvul.002G157300 | Phvul.002G157300 | PF03479 | PTHR31500,P | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.009G146400 | Phvul.009G146400 | PF03360 | PTHR10896,P | KOG1476 |
| 7 | 1 Phvul.011G046800 | Phvul.011G046800 | PF00083 | PTHR23500,P | KOG0254 |
| 8 | | | | | |
| 9 | 1 Phvul.006G023000 | Phvul.006G023000 | PF00657 | PTHR22835,P | 0 |
| 10 | 1 Phvul.006G093600 | Phvul.006G093600 | PF00026 | PTHR13683,P | KOG1339 |
| 11 | 1 Phvul.001G151600 | Phvul.001G151600 | | 0 PTHR34798,P | 0 |
| 12 | 1 Phvul.007G231200 | Phvul.007G231200 | PF07650,PF00PTHR11760,P | KOG3181 | |
| 13 | | | | | |
| 14 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P | KOG1187 | |
| 15 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P | KOG1187 | |
| 16 | 1 Phvul.007G156900 | Phvul.007G156900 | | 0 PTHR33981,P | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.007G157000 | Phvul.007G157000 | | 0 PTHR33981,P | 0 |
| 19 | 1 Phvul.007G105700 | Phvul.007G105700 | PF13837,PF00PTHR21499,P | | 0 |
| 20 | 1 Phvul.008G159000 | Phvul.008G159000 | PF10250 | PTHR31741,P | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.005G114000 | Phvul.005G114000 | PF05634 | PTHR10388,P | 0 |
| 23 | 1 Phvul.001G031000 | Phvul.001G031000 | PF08880,PF08PTHR31602,P | | 0 |
| 24 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 27 | 1 Phvul.007G084000 | Phvul.007G084000 | PF00230 | PTHR19139,P | KOG0223 |
| 28 | 1 Phvul.009G119100 | Phvul.009G119100 | PF13386 | PTHR33876,P | 0 |
| 29 | | | | | |
| 30 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P | 0 |
| 31 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P | 0 |
| 32 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P | 0 |
| 33 | | | | | |
| 34 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P | 0 |
| 35 | 1 Phvul.008G127800 | Phvul.008G127800 | | 0 | 0 |
| 36 | 1 Phvul.001G038000 | Phvul.001G038000 | PF01843 | PTHR13140,P | 0 |
| 37 | | | | | |
| 38 | 1 Phvul.002G105200 | Phvul.002G105200 | PF00026 | PTHR13683,P | KOG1339 |
| 39 | 1 Phvul.008G032900 | Phvul.008G032900 | PF07897,PF16PTHR31413,P | | 0 |
| 40 | 1 Phvul.009G244600 | Phvul.009G244600 | PF08263,PF00PTHR27000 | KOG1187 | |
| 41 | 1 Phvul.004G099100 | Phvul.004G099100 | PF08263,PF00PTHR27004,P | KOG0472 | |
| 42 | | | | | |
| 43 | 1 Phvul.002G157300 | Phvul.002G157300 | PF03479 | PTHR31500,P | 0 |
| 44 | 1 Phvul.009G146400 | Phvul.009G146400 | PF03360 | PTHR10896,P | KOG1476 |
| 45 | 1 Phvul.011G046800 | Phvul.011G046800 | PF00083 | PTHR23500,P | KOG0254 |
| 46 | | | | | |
| 47 | 1 Phvul.006G023000 | Phvul.006G023000 | PF00657 | PTHR22835,P | 0 |
| 48 | 1 Phvul.006G093600 | Phvul.006G093600 | PF00026 | PTHR13683,P | KOG1339 |
| 49 | 1 Phvul.001G151600 | Phvul.001G151600 | | 0 PTHR34798,P | 0 |
| 50 | | | | | |
| 51 | 1 Phvul.007G231200 | Phvul.007G231200 | PF07650,PF00PTHR11760,P | KOG3181 | |
| 52 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P | KOG1187 | |
| 53 | | | | | |
| 54 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P | KOG1187 | |
| 55 | 1 Phvul.007G156900 | Phvul.007G156900 | | 0 PTHR33981,P | 0 |
| 56 | 1 Phvul.007G157000 | Phvul.007G157000 | | 0 PTHR33981,P | 0 |
| 57 | 1 Phvul.007G105700 | Phvul.007G105700 | PF13837,PF00PTHR21499,P | | 0 |
| 58 | | | | | |
| 59 | 1 Phvul.008G159000 | Phvul.008G159000 | PF10250 | PTHR31741,P | 0 |
| 60 | 1 Phvul.005G114000 | Phvul.005G114000 | PF05634 | PTHR10388,P | 0 |
| | 1 Phvul.001G031000 | Phvul.001G031000 | PF08880,PF08PTHR31602,P | | 0 |

| | | | | | |
|----|--------------------|------------------|--------------|---------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 3 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 4 | 1 Phvul.007G084000 | Phvul.007G084000 | PF00230 | PTHR19139,P | KOG0223 |
| 5 | | | | | |
| 6 | 1 Phvul.009G119100 | Phvul.009G119100 | PF13386 | PTHR33876,P | 0 |
| 7 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P | 0 |
| 8 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P | 0 |
| 11 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P | 0 |
| 12 | 1 Phvul.008G127800 | Phvul.008G127800 | | 0 0 | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.001G038000 | Phvul.001G038000 | PF01843 | PTHR13140,P | 0 |
| 15 | 1 Phvul.002G105200 | Phvul.002G105200 | PF00026 | PTHR13683,P | KOG1339 |
| 16 | 1 Phvul.008G032900 | Phvul.008G032900 | PF07897,PF16 | PTHR31413,P | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.009G244600 | Phvul.009G244600 | PF08263,PF00 | PTHR27000 | KOG1187 |
| 19 | 1 Phvul.004G099100 | Phvul.004G099100 | PF08263,PF00 | PTHR27004,P | KOG0472 |
| 20 | 1 Phvul.002G157300 | Phvul.002G157300 | PF03479 | PTHR31500,P | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.009G146400 | Phvul.009G146400 | PF03360 | PTHR10896,P | KOG1476 |
| 23 | 1 Phvul.011G046800 | Phvul.011G046800 | PF00083 | PTHR23500,P | KOG0254 |
| 24 | 1 Phvul.006G023000 | Phvul.006G023000 | PF00657 | PTHR22835,P | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.006G093600 | Phvul.006G093600 | PF00026 | PTHR13683,P | KOG1339 |
| 27 | 1 Phvul.001G151600 | Phvul.001G151600 | | 0 PTHR34798,P | 0 |
| 28 | 1 Phvul.007G231200 | Phvul.007G231200 | PF07650,PF00 | PTHR11760,P | KOG3181 |
| 29 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00 | PTHR27000,P | KOG1187 |
| 30 | | | | | |
| 31 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00 | PTHR27000,P | KOG1187 |
| 32 | 1 Phvul.007G156900 | Phvul.007G156900 | | 0 PTHR33981,P | 0 |
| 33 | 1 Phvul.007G157000 | Phvul.007G157000 | | 0 PTHR33981,P | 0 |
| 34 | | | | | |
| 35 | 1 Phvul.007G105700 | Phvul.007G105700 | PF13837,PF00 | PTHR21499,P | 0 |
| 36 | 1 Phvul.008G159000 | Phvul.008G159000 | PF10250 | PTHR31741,P | 0 |
| 37 | 1 Phvul.005G114000 | Phvul.005G114000 | PF05634 | PTHR10388,P | 0 |
| 38 | | | | | |
| 39 | 1 Phvul.001G031000 | Phvul.001G031000 | PF08880,PF08 | PTHR31602,P | 0 |
| 40 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 41 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 42 | | | | | |
| 43 | 1 Phvul.007G084000 | Phvul.007G084000 | PF00230 | PTHR19139,P | KOG0223 |
| 44 | 1 Phvul.009G119100 | Phvul.009G119100 | PF13386 | PTHR33876,P | 0 |
| 45 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P | 0 |
| 46 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P | 0 |
| 47 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P | 0 |
| 48 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P | 0 |
| 49 | | | | | |
| 50 | | | | | |
| 51 | 1 Phvul.008G127800 | Phvul.008G127800 | | 0 0 | 0 |
| 52 | 1 Phvul.001G038000 | Phvul.001G038000 | PF01843 | PTHR13140,P | 0 |
| 53 | 1 Phvul.002G105200 | Phvul.002G105200 | PF00026 | PTHR13683,P | KOG1339 |
| 54 | | | | | |
| 55 | 1 Phvul.008G032900 | Phvul.008G032900 | PF07897,PF16 | PTHR31413,P | 0 |
| 56 | 1 Phvul.009G244600 | Phvul.009G244600 | PF08263,PF00 | PTHR27000 | KOG1187 |
| 57 | 1 Phvul.004G099100 | Phvul.004G099100 | PF08263,PF00 | PTHR27004,P | KOG0472 |
| 58 | | | | | |
| 59 | 1 Phvul.002G157300 | Phvul.002G157300 | PF03479 | PTHR31500,P | 0 |
| 60 | 1 Phvul.009G146400 | Phvul.009G146400 | PF03360 | PTHR10896,P | KOG1476 |
| | 1 Phvul.011G046800 | Phvul.011G046800 | PF00083 | PTHR23500,P | KOG0254 |

| | | | | | |
|----|--------------------|------------------|-------------------------|---------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.006G023000 | Phvul.006G023000 | PF00657 | PTHR22835,P | 0 |
| 3 | 1 Phvul.006G093600 | Phvul.006G093600 | PF00026 | PTHR13683,P | KOG1339 |
| 4 | 1 Phvul.001G151600 | Phvul.001G151600 | | 0 PTHR34798,P | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.007G231200 | Phvul.007G231200 | PF07650,PF00PTHR11760,P | | KOG3181 |
| 7 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P | | KOG1187 |
| 8 | | | | | |
| 9 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P | | KOG1187 |
| 10 | 1 Phvul.007G156900 | Phvul.007G156900 | | 0 PTHR33981,P | 0 |
| 11 | 1 Phvul.007G157000 | Phvul.007G157000 | | 0 PTHR33981,P | 0 |
| 12 | | | | | |
| 13 | 1 Phvul.007G105700 | Phvul.007G105700 | PF13837,PF00PTHR21499,P | | 0 |
| 14 | 1 Phvul.008G159000 | Phvul.008G159000 | PF10250 | PTHR31741,P | 0 |
| 15 | 1 Phvul.005G114000 | Phvul.005G114000 | PF05634 | PTHR10388,P | 0 |
| 16 | 1 Phvul.001G031000 | Phvul.001G031000 | PF08880,PF08PTHR31602,P | | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 19 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 20 | 1 Phvul.007G084000 | Phvul.007G084000 | PF00230 | PTHR19139,P | KOG0223 |
| 21 | | | | | |
| 22 | 1 Phvul.009G119100 | Phvul.009G119100 | PF13386 | PTHR33876,P | 0 |
| 23 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P | 0 |
| 24 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P | 0 |
| 27 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P | 0 |
| 28 | 1 Phvul.008G127800 | Phvul.008G127800 | | 0 0 | 0 |
| 29 | | | | | |
| 30 | 1 Phvul.001G038000 | Phvul.001G038000 | PF01843 | PTHR13140,P | 0 |
| 31 | 1 Phvul.002G105200 | Phvul.002G105200 | PF00026 | PTHR13683,P | KOG1339 |
| 32 | 1 Phvul.008G032900 | Phvul.008G032900 | PF07897,PF16PTHR31413,P | | 0 |
| 33 | | | | | |
| 34 | 1 Phvul.009G244600 | Phvul.009G244600 | PF08263,PF00PTHR27000 | | KOG1187 |
| 35 | 1 Phvul.004G099100 | Phvul.004G099100 | PF08263,PF00PTHR27004,P | | KOG0472 |
| 36 | 1 Phvul.002G157300 | Phvul.002G157300 | PF03479 | PTHR31500,P | 0 |
| 37 | 1 Phvul.009G146400 | Phvul.009G146400 | PF03360 | PTHR10896,P | KOG1476 |
| 38 | | | | | |
| 39 | 1 Phvul.011G046800 | Phvul.011G046800 | PF00083 | PTHR23500,P | KOG0254 |
| 40 | 1 Phvul.006G023000 | Phvul.006G023000 | PF00657 | PTHR22835,P | 0 |
| 41 | 1 Phvul.006G093600 | Phvul.006G093600 | PF00026 | PTHR13683,P | KOG1339 |
| 42 | | | | | |
| 43 | 1 Phvul.001G151600 | Phvul.001G151600 | | 0 PTHR34798,P | 0 |
| 44 | 1 Phvul.007G231200 | Phvul.007G231200 | PF07650,PF00PTHR11760,P | | KOG3181 |
| 45 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P | | KOG1187 |
| 46 | | | | | |
| 47 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00PTHR27000,P | | KOG1187 |
| 48 | 1 Phvul.007G156900 | Phvul.007G156900 | | 0 PTHR33981,P | 0 |
| 49 | 1 Phvul.007G157000 | Phvul.007G157000 | | 0 PTHR33981,P | 0 |
| 50 | | | | | |
| 51 | 1 Phvul.007G105700 | Phvul.007G105700 | PF13837,PF00PTHR21499,P | | 0 |
| 52 | 1 Phvul.008G159000 | Phvul.008G159000 | PF10250 | PTHR31741,P | 0 |
| 53 | | | | | |
| 54 | 1 Phvul.005G114000 | Phvul.005G114000 | PF05634 | PTHR10388,P | 0 |
| 55 | 1 Phvul.001G031000 | Phvul.001G031000 | PF08880,PF08PTHR31602,P | | 0 |
| 56 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 57 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 58 | | | | | |
| 59 | 1 Phvul.007G084000 | Phvul.007G084000 | PF00230 | PTHR19139,P | KOG0223 |
| 60 | 1 Phvul.009G119100 | Phvul.009G119100 | PF13386 | PTHR33876,P | 0 |
| | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P | 0 |

| | | | | | |
|----|--------------------|------------------|--------------|----------------------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P ⁻ | 0 |
| 3 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P ⁻ | 0 |
| 4 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P ⁻ | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.008G127800 | Phvul.008G127800 | | 0 0 | 0 |
| 7 | 1 Phvul.001G038000 | Phvul.001G038000 | PF01843 | PTHR13140,P ⁻ | 0 |
| 8 | 1 Phvul.002G105200 | Phvul.002G105200 | PF00026 | PTHR13683,P ⁻ | KOG1339 |
| 9 | | | | | |
| 10 | 1 Phvul.008G032900 | Phvul.008G032900 | PF07897,PF16 | PTHR31413,P ⁻ | 0 |
| 11 | 1 Phvul.009G244600 | Phvul.009G244600 | PF08263,PF00 | PTHR27000 | KOG1187 |
| 12 | 1 Phvul.007G105700 | Phvul.007G105700 | PF13837,PF00 | PTHR21499,P ⁻ | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.011G046800 | Phvul.011G046800 | PF00083 | PTHR23500,P ⁻ | KOG0254 |
| 15 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P ⁻ | 0 |
| 16 | 1 Phvul.006G102900 | Phvul.006G102900 | PF06886 | PTHR31358,P ⁻ | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.006G023000 | Phvul.006G023000 | PF00657 | PTHR22835,P ⁻ | 0 |
| 19 | 1 Phvul.004G099100 | Phvul.004G099100 | PF08263,PF00 | PTHR27004,P ⁻ | KOG0472 |
| 20 | 1 Phvul.002G157300 | Phvul.002G157300 | PF03479 | PTHR31500,P ⁻ | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.009G146400 | Phvul.009G146400 | PF03360 | PTHR10896,P ⁻ | KOG1476 |
| 23 | 1 Phvul.006G093600 | Phvul.006G093600 | PF00026 | PTHR13683,P ⁻ | KOG1339 |
| 24 | 1 Phvul.001G151600 | Phvul.001G151600 | | 0 PTHR34798,P ⁻ | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.009G244600 | Phvul.009G244600 | PF08263,PF00 | PTHR27000 | KOG1187 |
| 27 | 1 Phvul.009G121200 | Phvul.009G121200 | PF02493,PF01 | PTHR23086,P ⁻ | KOG0229 |
| 28 | 1 Phvul.009G121200 | Phvul.009G121200 | PF02493,PF01 | PTHR23086,P ⁻ | KOG0229 |
| 29 | | | | | |
| 30 | 1 Phvul.007G156900 | Phvul.007G156900 | | 0 PTHR33981,P ⁻ | 0 |
| 31 | 1 Phvul.007G157000 | Phvul.007G157000 | | 0 PTHR33981,P ⁻ | 0 |
| 32 | 1 Phvul.008G159000 | Phvul.008G159000 | PF10250 | PTHR31741,P ⁻ | 0 |
| 33 | | | | | |
| 34 | 1 Phvul.007G231200 | Phvul.007G231200 | PF07650,PF00 | PTHR11760,P ⁻ | KOG3181 |
| 35 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00 | PTHR27000,P ⁻ | KOG1187 |
| 36 | 1 Phvul.004G037600 | Phvul.004G037600 | PF00560,PF00 | PTHR27000,P ⁻ | KOG1187 |
| 37 | | | | | |
| 38 | 1 Phvul.005G114000 | Phvul.005G114000 | PF05634 | PTHR10388,P ⁻ | 0 |
| 39 | 1 Phvul.001G031000 | Phvul.001G031000 | PF08880,PF08 | PTHR31602,P ⁻ | 0 |
| 40 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 41 | 1 Phvul.004G041500 | Phvul.004G041500 | PF02005 | PTHR10631 | 0 |
| 42 | | | | | |
| 43 | 1 Phvul.002G105200 | Phvul.002G105200 | PF00026 | PTHR13683,P ⁻ | KOG1339 |
| 44 | 1 Phvul.007G084000 | Phvul.007G084000 | PF00230 | PTHR19139,P ⁻ | KOG0223 |
| 45 | 1 Phvul.009G119100 | Phvul.009G119100 | PF13386 | PTHR33876,P ⁻ | 0 |
| 46 | | | | | |
| 47 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P ⁻ | 0 |
| 48 | 1 Phvul.010G079200 | Phvul.010G079200 | PF04690 | PTHR31675,P ⁻ | 0 |
| 49 | 1 Phvul.008G127800 | Phvul.008G127800 | | 0 0 | 0 |
| 50 | | | | | |
| 51 | 1 Phvul.007G029900 | Phvul.007G029900 | PF00560,PF08 | PTHR27008,P ⁻ | KOG1187 |
| 52 | 1 Phvul.010G156200 | Phvul.010G156200 | PF00487 | PTHR11351,P ⁻ | KOG1600 |
| 53 | 1 Phvul.009G217000 | Phvul.009G217000 | PF04783,PF04 | PTHR21450,P ⁻ | 0 |
| 54 | | | | | |
| 55 | 1 Phvul.008G043500 | Phvul.008G043500 | PF00847 | PTHR32467,P ⁻ | 0 |
| 56 | 1 Phvul.009G079400 | Phvul.009G079400 | PF05254 | PTHR21329 | 0 |
| 57 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 58 | | | | | |
| 59 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 60 | 1 Phvul.003G154400 | Phvul.003G154400 | PF12854,PF14 | PTHR24015,P ⁻ | 0 |
| | 1 Phvul.009G030200 | Phvul.009G030200 | PF08241 | PTHR10108,P ⁻ | 0 |

| | | | | | | |
|----|--------------------|------------------|--------------|----------------------------|---------|---|
| 1 | | | | | | |
| 2 | 1 Phvul.004G166100 | Phvul.004G166100 | PF00578 | PTHR10430 | KOG0541 | |
| 3 | 1 Phvul.009G160200 | Phvul.009G160200 | PF13414 | PTHR16193 | | 0 |
| 4 | 1 Phvul.002G119600 | Phvul.002G119600 | PF11443 | PTHR31373,P ⁻ | | 0 |
| 5 | 1 Phvul.002G150800 | Phvul.002G150800 | PF00155 | PTHR11751,P ⁻ | | 0 |
| 6 | 1 Phvul.002G271400 | Phvul.002G271400 | PF00266 | PTHR11601,P ⁻ | | 0 |
| 7 | 1 Phvul.011G166200 | Phvul.011G166200 | PF10559,PF00 | PTHR10906 | | 0 |
| 8 | 1 Phvul.001G110100 | Phvul.001G110100 | | 0 PTHR11122,P ⁻ | KOG1594 | |
| 9 | 1 Phvul.002G037500 | Phvul.002G037500 | | 0 PTHR17130 | | 0 |
| 10 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁻ | | 0 |
| 11 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁻ | | 0 |
| 12 | 1 Phvul.007G022500 | Phvul.007G022500 | PF00111 | PTHR19370,P ⁻ | | 0 |
| 13 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P ⁻ | | 0 |
| 14 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P ⁻ | | 0 |
| 15 | 1 Phvul.006G154900 | Phvul.006G154900 | | 0 PTHR33739,P ⁻ | | 0 |
| 16 | 1 Phvul.006G047000 | Phvul.006G047000 | PF02922,PF00 | PTHR10357,P ⁻ | | 0 |
| 17 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P ⁻ | | 0 |
| 18 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | | 0 |
| 19 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | | 0 |
| 20 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁻ | KOG1383 | |
| 21 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁻ | KOG1383 | |
| 22 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | | 0 |
| 23 | 1 Phvul.007G106300 | Phvul.007G106300 | PF00067 | PTHR24298,P ⁻ | KOG0156 | |
| 24 | 1 Phvul.009G034400 | Phvul.009G034400 | PF16913 | PTHR31376,P ⁻ | | 0 |
| 25 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | | 0 |
| 26 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | | 0 |
| 27 | 1 Phvul.008G070000 | Phvul.008G070000 | PF01988 | PTHR31851,P ⁻ | KOG4473 | |
| 28 | 1 Phvul.010G156200 | Phvul.010G156200 | PF00487 | PTHR11351,P ⁻ | KOG1600 | |
| 29 | 1 Phvul.009G217000 | Phvul.009G217000 | PF04783,PF04 | PTHR21450,P ⁻ | | 0 |
| 30 | 1 Phvul.008G043500 | Phvul.008G043500 | PF00847 | PTHR32467,P ⁻ | | 0 |
| 31 | 1 Phvul.009G079400 | Phvul.009G079400 | PF05254 | PTHR21329 | | 0 |
| 32 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | | 0 |
| 33 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | | 0 |
| 34 | 1 Phvul.003G154400 | Phvul.003G154400 | PF12854,PF14 | PTHR24015,P ⁻ | | 0 |
| 35 | 1 Phvul.009G030200 | Phvul.009G030200 | PF08241 | PTHR10108,P ⁻ | | 0 |
| 36 | 1 Phvul.004G166100 | Phvul.004G166100 | PF00578 | PTHR10430 | KOG0541 | |
| 37 | 1 Phvul.009G160200 | Phvul.009G160200 | PF13414 | PTHR16193 | | 0 |
| 38 | 1 Phvul.002G119600 | Phvul.002G119600 | PF11443 | PTHR31373,P ⁻ | | 0 |
| 39 | 1 Phvul.002G150800 | Phvul.002G150800 | PF00155 | PTHR11751,P ⁻ | | 0 |
| 40 | 1 Phvul.002G271400 | Phvul.002G271400 | PF00266 | PTHR11601,P ⁻ | | 0 |
| 41 | 1 Phvul.011G166200 | Phvul.011G166200 | PF10559,PF00 | PTHR10906 | | 0 |
| 42 | 1 Phvul.001G110100 | Phvul.001G110100 | | 0 PTHR11122,P ⁻ | KOG1594 | |
| 43 | 1 Phvul.002G037500 | Phvul.002G037500 | | 0 PTHR17130 | | 0 |
| 44 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁻ | | 0 |
| 45 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁻ | | 0 |
| 46 | 1 Phvul.007G022500 | Phvul.007G022500 | PF00111 | PTHR19370,P ⁻ | | 0 |
| 47 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P ⁻ | | 0 |

| | | | | |
|----|--------------------|------------------|--|---|
| 1 | | | | |
| 2 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12PTHR13950,P ⁻ | 0 |
| 3 | 1 Phvul.006G154900 | Phvul.006G154900 | 0 PTHR33739,P ⁻ | 0 |
| 4 | 1 Phvul.006G047000 | Phvul.006G047000 | PF02922,PF00PTHR10357,P ⁻ | 0 |
| 5 | | | | |
| 6 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 PTHR13301,P ⁻ | 0 |
| 7 | 1 Phvul.003G056900 | Phvul.003G056900 | 0 PTHR37243 | 0 |
| 8 | 1 Phvul.003G056900 | Phvul.003G056900 | 0 PTHR37243 | 0 |
| 9 | | | | |
| 10 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 PTHR11999,P ⁻ KOG1383 | |
| 11 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 PTHR11999,P ⁻ KOG1383 | |
| 12 | 1 Phvul.003G056900 | Phvul.003G056900 | 0 PTHR37243 | 0 |
| 13 | | | | |
| 14 | 1 Phvul.007G106300 | Phvul.007G106300 | PF00067 PTHR24298,P ⁻ KOG0156 | |
| 15 | 1 Phvul.009G034400 | Phvul.009G034400 | PF16913 PTHR31376,P ⁻ | 0 |
| 16 | 1 Phvul.L002444 | Phvul.L002444 | 0 PTHR33401 | 0 |
| 17 | | | | |
| 18 | 1 Phvul.L002444 | Phvul.L002444 | 0 PTHR33401 | 0 |
| 19 | 1 Phvul.008G070000 | Phvul.008G070000 | PF01988 PTHR31851,P ⁻ KOG4473 | |
| 20 | 1 Phvul.010G156200 | Phvul.010G156200 | PF00487 PTHR11351,P ⁻ KOG1600 | |
| 21 | | | | |
| 22 | 1 Phvul.009G217000 | Phvul.009G217000 | PF04783,PF04PTHR21450,P ⁻ | 0 |
| 23 | 1 Phvul.008G043500 | Phvul.008G043500 | PF00847 PTHR32467,P ⁻ | 0 |
| 24 | 1 Phvul.009G079400 | Phvul.009G079400 | PF05254 PTHR21329 | 0 |
| 25 | | | | |
| 26 | 1 Phvul.001G193000 | Phvul.001G193000 | 0 PTHR36064 | 0 |
| 27 | 1 Phvul.001G193000 | Phvul.001G193000 | 0 PTHR36064 | 0 |
| 28 | 1 Phvul.003G154400 | Phvul.003G154400 | PF12854,PF14PTHR24015,P ⁻ | 0 |
| 29 | 1 Phvul.009G030200 | Phvul.009G030200 | PF08241 PTHR10108,P ⁻ | 0 |
| 30 | 1 Phvul.004G166100 | Phvul.004G166100 | PF00578 PTHR10430 KOG0541 | |
| 31 | 1 Phvul.009G160200 | Phvul.009G160200 | PF13414 PTHR16193 | 0 |
| 32 | 1 Phvul.002G119600 | Phvul.002G119600 | PF11443 PTHR31373,P ⁻ | 0 |
| 33 | 1 Phvul.002G150800 | Phvul.002G150800 | PF00155 PTHR11751,P ⁻ | 0 |
| 34 | 1 Phvul.002G271400 | Phvul.002G271400 | PF00266 PTHR11601,P ⁻ | 0 |
| 35 | | | | |
| 36 | 1 Phvul.011G166200 | Phvul.011G166200 | PF10559,PF00PTHR10906 | 0 |
| 37 | 1 Phvul.001G110100 | Phvul.001G110100 | 0 PTHR11122,P ⁻ KOG1594 | |
| 38 | 1 Phvul.002G037500 | Phvul.002G037500 | 0 PTHR17130 | 0 |
| 39 | | | | |
| 40 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 PTHR27001,P ⁻ | 0 |
| 41 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 PTHR27001,P ⁻ | 0 |
| 42 | 1 Phvul.007G022500 | Phvul.007G022500 | PF00111 PTHR19370,P ⁻ | 0 |
| 43 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12PTHR13950,P ⁻ | 0 |
| 44 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12PTHR13950,P ⁻ | 0 |
| 45 | 1 Phvul.006G154900 | Phvul.006G154900 | 0 PTHR33739,P ⁻ | 0 |
| 46 | 1 Phvul.006G047000 | Phvul.006G047000 | PF02922,PF00PTHR10357,P ⁻ | 0 |
| 47 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 PTHR13301,P ⁻ | 0 |
| 48 | 1 Phvul.003G056900 | Phvul.003G056900 | 0 PTHR37243 | 0 |
| 49 | 1 Phvul.003G056900 | Phvul.003G056900 | 0 PTHR37243 | 0 |
| 50 | | | | |
| 51 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 PTHR11999,P ⁻ KOG1383 | |
| 52 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 PTHR11999,P ⁻ KOG1383 | |
| 53 | 1 Phvul.003G056900 | Phvul.003G056900 | 0 PTHR37243 | 0 |
| 54 | 1 Phvul.007G106300 | Phvul.007G106300 | PF00067 PTHR24298,P ⁻ KOG0156 | |
| 55 | 1 Phvul.009G034400 | Phvul.009G034400 | PF16913 PTHR31376,P ⁻ | 0 |
| 56 | 1 Phvul.L002444 | Phvul.L002444 | 0 PTHR33401 | 0 |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

| | | | | | |
|----|--------------------|------------------|--------------|------------------------------------|---|
| 1 | | | | | |
| 2 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 3 | 1 Phvul.008G070000 | Phvul.008G070000 | PF01988 | PTHR31851,P ⁺ KOG4473 | |
| 4 | 1 Phvul.010G156200 | Phvul.010G156200 | PF00487 | PTHR11351,P ⁺ KOG1600 | |
| 5 | | | | | |
| 6 | 1 Phvul.009G217000 | Phvul.009G217000 | PF04783,PF04 | PTHR21450,P ⁺ | 0 |
| 7 | 1 Phvul.008G043500 | Phvul.008G043500 | PF00847 | PTHR32467,P ⁺ | 0 |
| 8 | 1 Phvul.009G079400 | Phvul.009G079400 | PF05254 | PTHR21329 | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 11 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 12 | 1 Phvul.003G154400 | Phvul.003G154400 | PF12854,PF14 | PTHR24015,P ⁺ | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.009G030200 | Phvul.009G030200 | PF08241 | PTHR10108,P ⁺ | 0 |
| 15 | 1 Phvul.004G166100 | Phvul.004G166100 | PF00578 | PTHR10430 KOG0541 | |
| 16 | 1 Phvul.009G160200 | Phvul.009G160200 | PF13414 | PTHR16193 | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.002G119600 | Phvul.002G119600 | PF11443 | PTHR31373,P ⁺ | 0 |
| 19 | 1 Phvul.002G150800 | Phvul.002G150800 | PF00155 | PTHR11751,P ⁺ | 0 |
| 20 | 1 Phvul.002G271400 | Phvul.002G271400 | PF00266 | PTHR11601,P ⁺ | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.011G166200 | Phvul.011G166200 | PF10559,PF00 | PTHR10906 | 0 |
| 23 | 1 Phvul.001G110100 | Phvul.001G110100 | | 0 PTHR11122,P ⁺ KOG1594 | |
| 24 | 1 Phvul.002G037500 | Phvul.002G037500 | | 0 PTHR17130 | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁺ | 0 |
| 27 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁺ | 0 |
| 28 | 1 Phvul.007G022500 | Phvul.007G022500 | PF00111 | PTHR19370,P ⁺ | 0 |
| 29 | | | | | |
| 30 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P ⁺ | 0 |
| 31 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P ⁺ | 0 |
| 32 | 1 Phvul.006G154900 | Phvul.006G154900 | | 0 PTHR33739,P ⁺ | 0 |
| 33 | | | | | |
| 34 | 1 Phvul.006G047000 | Phvul.006G047000 | PF02922,PF00 | PTHR10357,P ⁺ | 0 |
| 35 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P ⁺ | 0 |
| 36 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 37 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 38 | | | | | |
| 39 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁺ KOG1383 | |
| 40 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁺ KOG1383 | |
| 41 | | | | | |
| 42 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 43 | 1 Phvul.007G106300 | Phvul.007G106300 | PF00067 | PTHR24298,P ⁺ KOG0156 | |
| 44 | 1 Phvul.009G034400 | Phvul.009G034400 | PF16913 | PTHR31376,P ⁺ | 0 |
| 45 | | | | | |
| 46 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 47 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 48 | 1 Phvul.008G070000 | Phvul.008G070000 | PF01988 | PTHR31851,P ⁺ KOG4473 | |
| 49 | 1 Phvul.010G156200 | Phvul.010G156200 | PF00487 | PTHR11351,P ⁺ KOG1600 | |
| 50 | | | | | |
| 51 | 1 Phvul.009G217000 | Phvul.009G217000 | PF04783,PF04 | PTHR21450,P ⁺ | 0 |
| 52 | 1 Phvul.008G043500 | Phvul.008G043500 | PF00847 | PTHR32467,P ⁺ | 0 |
| 53 | 1 Phvul.009G079400 | Phvul.009G079400 | PF05254 | PTHR21329 | 0 |
| 54 | | | | | |
| 55 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 56 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 57 | 1 Phvul.003G154400 | Phvul.003G154400 | PF12854,PF14 | PTHR24015,P ⁺ | 0 |
| 58 | 1 Phvul.009G030200 | Phvul.009G030200 | PF08241 | PTHR10108,P ⁺ | 0 |
| 59 | 1 Phvul.004G166100 | Phvul.004G166100 | PF00578 | PTHR10430 KOG0541 | |
| 60 | 1 Phvul.009G160200 | Phvul.009G160200 | PF13414 | PTHR16193 | 0 |

| | | | | | |
|----|--------------------|------------------|--------------|----------------------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.002G119600 | Phvul.002G119600 | PF11443 | PTHR31373,P ⁻ | 0 |
| 3 | 1 Phvul.002G150800 | Phvul.002G150800 | PF00155 | PTHR11751,P ⁻ | 0 |
| 4 | 1 Phvul.002G271400 | Phvul.002G271400 | PF00266 | PTHR11601,P ⁻ | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.011G166200 | Phvul.011G166200 | PF10559,PF00 | PTHR10906 | 0 |
| 7 | 1 Phvul.001G110100 | Phvul.001G110100 | | 0 PTHR11122,P ⁻ | KOG1594 |
| 8 | 1 Phvul.002G037500 | Phvul.002G037500 | | 0 PTHR17130 | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁻ | 0 |
| 11 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁻ | 0 |
| 12 | 1 Phvul.007G022500 | Phvul.007G022500 | PF00111 | PTHR19370,P ⁻ | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P ⁻ | 0 |
| 15 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P ⁻ | 0 |
| 16 | 1 Phvul.006G154900 | Phvul.006G154900 | | 0 PTHR33739,P ⁻ | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.006G047000 | Phvul.006G047000 | PF02922,PF00 | PTHR10357,P ⁻ | 0 |
| 19 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P ⁻ | 0 |
| 20 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 23 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁻ | KOG1383 |
| 24 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁻ | KOG1383 |
| 25 | | | | | |
| 26 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 27 | 1 Phvul.007G106300 | Phvul.007G106300 | PF00067 | PTHR24298,P ⁻ | KOG0156 |
| 28 | 1 Phvul.009G034400 | Phvul.009G034400 | PF16913 | PTHR31376,P ⁻ | 0 |
| 29 | | | | | |
| 30 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 31 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 32 | 1 Phvul.008G070000 | Phvul.008G070000 | PF01988 | PTHR31851,P ⁻ | KOG4473 |
| 33 | 1 Phvul.010G156200 | Phvul.010G156200 | PF00487 | PTHR11351,P ⁻ | KOG1600 |
| 34 | | | | | |
| 35 | 1 Phvul.009G217000 | Phvul.009G217000 | PF04783,PF04 | PTHR21450,P ⁻ | 0 |
| 36 | 1 Phvul.008G043500 | Phvul.008G043500 | PF00847 | PTHR32467,P ⁻ | 0 |
| 37 | 1 Phvul.009G079400 | Phvul.009G079400 | PF05254 | PTHR21329 | 0 |
| 38 | | | | | |
| 39 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 40 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 41 | | | | | |
| 42 | 1 Phvul.003G154400 | Phvul.003G154400 | PF12854,PF14 | PTHR24015,P ⁻ | 0 |
| 43 | 1 Phvul.009G030200 | Phvul.009G030200 | PF08241 | PTHR10108,P ⁻ | 0 |
| 44 | 1 Phvul.004G166100 | Phvul.004G166100 | PF00578 | PTHR10430 | KOG0541 |
| 45 | 1 Phvul.009G160200 | Phvul.009G160200 | PF13414 | PTHR16193 | 0 |
| 46 | | | | | |
| 47 | 1 Phvul.002G119600 | Phvul.002G119600 | PF11443 | PTHR31373,P ⁻ | 0 |
| 48 | 1 Phvul.002G150800 | Phvul.002G150800 | PF00155 | PTHR11751,P ⁻ | 0 |
| 49 | 1 Phvul.002G271400 | Phvul.002G271400 | PF00266 | PTHR11601,P ⁻ | 0 |
| 50 | | | | | |
| 51 | 1 Phvul.011G166200 | Phvul.011G166200 | PF10559,PF00 | PTHR10906 | 0 |
| 52 | 1 Phvul.001G110100 | Phvul.001G110100 | | 0 PTHR11122,P ⁻ | KOG1594 |
| 53 | 1 Phvul.002G037500 | Phvul.002G037500 | | 0 PTHR17130 | 0 |
| 54 | | | | | |
| 55 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁻ | 0 |
| 56 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁻ | 0 |
| 57 | 1 Phvul.007G022500 | Phvul.007G022500 | PF00111 | PTHR19370,P ⁻ | 0 |
| 58 | | | | | |
| 59 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P ⁻ | 0 |
| 60 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P ⁻ | 0 |
| | 1 Phvul.006G154900 | Phvul.006G154900 | | 0 PTHR33739,P ⁻ | 0 |

| | | | | | |
|----|--------------------|------------------|--------------------------------------|------------------------------------|---|
| 1 | | | | | |
| 2 | 1 Phvul.006G047000 | Phvul.006G047000 | PF02922,PF00PTHR10357,P ⁻ | | 0 |
| 3 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P ⁻ | 0 |
| 4 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 7 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁻ KOG1383 | |
| 8 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁻ KOG1383 | |
| 9 | | | | | |
| 10 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 11 | 1 Phvul.007G106300 | Phvul.007G106300 | PF00067 | PTHR24298,P ⁻ KOG0156 | |
| 12 | 1 Phvul.009G034400 | Phvul.009G034400 | PF16913 | PTHR31376,P ⁻ | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 15 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 16 | 1 Phvul.008G070000 | Phvul.008G070000 | PF01988 | PTHR31851,P ⁻ KOG4473 | |
| 17 | 1 Phvul.010G156200 | Phvul.010G156200 | PF00487 | PTHR11351,P ⁻ KOG1600 | |
| 18 | | | | | |
| 19 | 1 Phvul.009G217000 | Phvul.009G217000 | PF04783,PF04PTHR21450,P ⁻ | | 0 |
| 20 | 1 Phvul.008G043500 | Phvul.008G043500 | PF00847 | PTHR32467,P ⁻ | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.009G079400 | Phvul.009G079400 | PF05254 | PTHR21329 | 0 |
| 23 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 24 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.003G154400 | Phvul.003G154400 | PF12854,PF14PTHR24015,P ⁻ | | 0 |
| 27 | 1 Phvul.009G030200 | Phvul.009G030200 | PF08241 | PTHR10108,P ⁻ | 0 |
| 28 | 1 Phvul.004G166100 | Phvul.004G166100 | PF00578 | PTHR10430 KOG0541 | |
| 29 | 1 Phvul.009G160200 | Phvul.009G160200 | PF13414 | PTHR16193 | 0 |
| 30 | | | | | |
| 31 | 1 Phvul.002G119600 | Phvul.002G119600 | PF11443 | PTHR31373,P ⁻ | 0 |
| 32 | 1 Phvul.002G150800 | Phvul.002G150800 | PF00155 | PTHR11751,P ⁻ | 0 |
| 33 | 1 Phvul.002G271400 | Phvul.002G271400 | PF00266 | PTHR11601,P ⁻ | 0 |
| 34 | | | | | |
| 35 | 1 Phvul.011G166200 | Phvul.011G166200 | PF10559,PF00PTHR10906 | | 0 |
| 36 | 1 Phvul.001G110100 | Phvul.001G110100 | | 0 PTHR11122,P ⁻ KOG1594 | |
| 37 | 1 Phvul.002G037500 | Phvul.002G037500 | | 0 PTHR17130 | 0 |
| 38 | | | | | |
| 39 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁻ | 0 |
| 40 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁻ | 0 |
| 41 | 1 Phvul.007G022500 | Phvul.007G022500 | PF00111 | PTHR19370,P ⁻ | 0 |
| 42 | | | | | |
| 43 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12PTHR13950,P ⁻ | | 0 |
| 44 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12PTHR13950,P ⁻ | | 0 |
| 45 | 1 Phvul.006G154900 | Phvul.006G154900 | | 0 PTHR33739,P ⁻ | 0 |
| 46 | | | | | |
| 47 | 1 Phvul.006G047000 | Phvul.006G047000 | PF02922,PF00PTHR10357,P ⁻ | | 0 |
| 48 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P ⁻ | 0 |
| 49 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 50 | | | | | |
| 51 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 52 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁻ KOG1383 | |
| 53 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁻ KOG1383 | |
| 54 | | | | | |
| 55 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 56 | 1 Phvul.007G106300 | Phvul.007G106300 | PF00067 | PTHR24298,P ⁻ KOG0156 | |
| 57 | 1 Phvul.009G034400 | Phvul.009G034400 | PF16913 | PTHR31376,P ⁻ | 0 |
| 58 | | | | | |
| 59 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 60 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| | 1 Phvul.008G070000 | Phvul.008G070000 | PF01988 | PTHR31851,P ⁻ KOG4473 | |

| | | | | | |
|----|--------------------|------------------|--------------|------------------------------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.010G156200 | Phvul.010G156200 | PF00487 | PTHR11351,P ⁻ KOG1600 | |
| 3 | 1 Phvul.009G217000 | Phvul.009G217000 | PF04783,PF04 | PTHR21450,P ⁻ | 0 |
| 4 | 1 Phvul.008G043500 | Phvul.008G043500 | PF00847 | PTHR32467,P ⁻ | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.009G079400 | Phvul.009G079400 | PF05254 | PTHR21329 | 0 |
| 7 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 8 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.003G154400 | Phvul.003G154400 | PF12854,PF14 | PTHR24015,P ⁻ | 0 |
| 11 | 1 Phvul.009G030200 | Phvul.009G030200 | PF08241 | PTHR10108,P ⁻ | 0 |
| 12 | 1 Phvul.004G166100 | Phvul.004G166100 | PF00578 | PTHR10430 | KOG0541 |
| 13 | | | | | |
| 14 | 1 Phvul.009G160200 | Phvul.009G160200 | PF13414 | PTHR16193 | 0 |
| 15 | 1 Phvul.002G119600 | Phvul.002G119600 | PF11443 | PTHR31373,P ⁻ | 0 |
| 16 | 1 Phvul.002G150800 | Phvul.002G150800 | PF00155 | PTHR11751,P ⁻ | 0 |
| 17 | 1 Phvul.002G271400 | Phvul.002G271400 | PF00266 | PTHR11601,P ⁻ | 0 |
| 18 | | | | | |
| 19 | 1 Phvul.011G166200 | Phvul.011G166200 | PF10559,PF00 | PTHR10906 | 0 |
| 20 | 1 Phvul.001G110100 | Phvul.001G110100 | | 0 PTHR11122,P ⁻ KOG1594 | |
| 21 | | | | | |
| 22 | 1 Phvul.002G037500 | Phvul.002G037500 | | 0 PTHR17130 | 0 |
| 23 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁻ | 0 |
| 24 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁻ | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.007G022500 | Phvul.007G022500 | PF00111 | PTHR19370,P ⁻ | 0 |
| 27 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P ⁻ | 0 |
| 28 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P ⁻ | 0 |
| 29 | | | | | |
| 30 | 1 Phvul.006G154900 | Phvul.006G154900 | | 0 PTHR33739,P ⁻ | 0 |
| 31 | 1 Phvul.006G047000 | Phvul.006G047000 | PF02922,PF00 | PTHR10357,P ⁻ | 0 |
| 32 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P ⁻ | 0 |
| 33 | | | | | |
| 34 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 35 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 36 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁻ KOG1383 | |
| 37 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁻ KOG1383 | |
| 38 | | | | | |
| 39 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 40 | 1 Phvul.007G106300 | Phvul.007G106300 | PF00067 | PTHR24298,P ⁻ KOG0156 | |
| 41 | 1 Phvul.009G034400 | Phvul.009G034400 | PF16913 | PTHR31376,P ⁻ | 0 |
| 42 | | | | | |
| 43 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 44 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 45 | | | | | |
| 46 | 1 Phvul.008G070000 | Phvul.008G070000 | PF01988 | PTHR31851,P ⁻ KOG4473 | |
| 47 | 1 Phvul.010G156200 | Phvul.010G156200 | PF00487 | PTHR11351,P ⁻ KOG1600 | |
| 48 | 1 Phvul.009G217000 | Phvul.009G217000 | PF04783,PF04 | PTHR21450,P ⁻ | 0 |
| 49 | 1 Phvul.008G043500 | Phvul.008G043500 | PF00847 | PTHR32467,P ⁻ | 0 |
| 50 | | | | | |
| 51 | 1 Phvul.009G079400 | Phvul.009G079400 | PF05254 | PTHR21329 | 0 |
| 52 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 53 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 54 | | | | | |
| 55 | 1 Phvul.003G154400 | Phvul.003G154400 | PF12854,PF14 | PTHR24015,P ⁻ | 0 |
| 56 | 1 Phvul.009G030200 | Phvul.009G030200 | PF08241 | PTHR10108,P ⁻ | 0 |
| 57 | 1 Phvul.004G166100 | Phvul.004G166100 | PF00578 | PTHR10430 | KOG0541 |
| 58 | | | | | |
| 59 | 1 Phvul.009G160200 | Phvul.009G160200 | PF13414 | PTHR16193 | 0 |
| 60 | 1 Phvul.002G119600 | Phvul.002G119600 | PF11443 | PTHR31373,P ⁻ | 0 |
| | 1 Phvul.002G150800 | Phvul.002G150800 | PF00155 | PTHR11751,P ⁻ | 0 |

| | | | | | |
|----|--------------------|------------------|--------------|------------------------|---|
| 1 | | | | | |
| 2 | 1 Phvul.002G271400 | Phvul.002G271400 | PF00266 | PTHR11601,P' | 0 |
| 3 | 1 Phvul.011G166200 | Phvul.011G166200 | PF10559,PF00 | PTHR10906 | 0 |
| 4 | 1 Phvul.001G110100 | Phvul.001G110100 | | 0 PTHR11122,P' KOG1594 | |
| 5 | | | | | |
| 6 | 1 Phvul.002G037500 | Phvul.002G037500 | | 0 PTHR17130 | 0 |
| 7 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P' | 0 |
| 8 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P' | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.007G022500 | Phvul.007G022500 | PF00111 | PTHR19370,P' | 0 |
| 11 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P' | 0 |
| 12 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P' | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.006G154900 | Phvul.006G154900 | | 0 PTHR33739,P' | 0 |
| 15 | 1 Phvul.006G047000 | Phvul.006G047000 | PF02922,PF00 | PTHR10357,P' | 0 |
| 16 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P' | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 19 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 20 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P' KOG1383 | |
| 21 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P' KOG1383 | |
| 22 | | | | | |
| 23 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 24 | 1 Phvul.007G106300 | Phvul.007G106300 | PF00067 | PTHR24298,P' KOG0156 | |
| 25 | | | | | |
| 26 | 1 Phvul.009G034400 | Phvul.009G034400 | PF16913 | PTHR31376,P' | 0 |
| 27 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 28 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 29 | | | | | |
| 30 | 1 Phvul.008G070000 | Phvul.008G070000 | PF01988 | PTHR31851,P' KOG4473 | |
| 31 | 1 Phvul.010G156200 | Phvul.010G156200 | PF00487 | PTHR11351,P' KOG1600 | |
| 32 | 1 Phvul.009G217000 | Phvul.009G217000 | PF04783,PF04 | PTHR21450,P' | 0 |
| 33 | 1 Phvul.008G043500 | Phvul.008G043500 | PF00847 | PTHR32467,P' | 0 |
| 34 | | | | | |
| 35 | 1 Phvul.009G079400 | Phvul.009G079400 | PF05254 | PTHR21329 | 0 |
| 36 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 37 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 38 | | | | | |
| 39 | 1 Phvul.003G154400 | Phvul.003G154400 | PF12854,PF14 | PTHR24015,P' | 0 |
| 40 | 1 Phvul.009G030200 | Phvul.009G030200 | PF08241 | PTHR10108,P' | 0 |
| 41 | 1 Phvul.004G166100 | Phvul.004G166100 | PF00578 | PTHR10430 KOG0541 | |
| 42 | | | | | |
| 43 | 1 Phvul.009G160200 | Phvul.009G160200 | PF13414 | PTHR16193 | 0 |
| 44 | 1 Phvul.002G119600 | Phvul.002G119600 | PF11443 | PTHR31373,P' | 0 |
| 45 | 1 Phvul.002G150800 | Phvul.002G150800 | PF00155 | PTHR11751,P' | 0 |
| 46 | | | | | |
| 47 | 1 Phvul.002G271400 | Phvul.002G271400 | PF00266 | PTHR11601,P' | 0 |
| 48 | 1 Phvul.011G166200 | Phvul.011G166200 | PF10559,PF00 | PTHR10906 | 0 |
| 49 | 1 Phvul.001G110100 | Phvul.001G110100 | | 0 PTHR11122,P' KOG1594 | |
| 50 | | | | | |
| 51 | 1 Phvul.002G037500 | Phvul.002G037500 | | 0 PTHR17130 | 0 |
| 52 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P' | 0 |
| 53 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P' | 0 |
| 54 | | | | | |
| 55 | 1 Phvul.007G022500 | Phvul.007G022500 | PF00111 | PTHR19370,P' | 0 |
| 56 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P' | 0 |
| 57 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P' | 0 |
| 58 | | | | | |
| 59 | 1 Phvul.006G154900 | Phvul.006G154900 | | 0 PTHR33739,P' | 0 |
| 60 | 1 Phvul.006G047000 | Phvul.006G047000 | PF02922,PF00 | PTHR10357,P' | 0 |
| | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P' | 0 |

| | | | | | |
|----|--------------------|------------------|--------------|--------------------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.003G056900 | Phvul.003G056900 | 0 | PTHR37243 | 0 |
| 3 | 1 Phvul.003G056900 | Phvul.003G056900 | 0 | PTHR37243 | 0 |
| 4 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁻ | KOG1383 |
| 5 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁻ | KOG1383 |
| 6 | 1 Phvul.003G056900 | Phvul.003G056900 | 0 | PTHR37243 | 0 |
| 7 | 1 Phvul.007G106300 | Phvul.007G106300 | PF00067 | PTHR24298,P ⁻ | KOG0156 |
| 8 | 1 Phvul.007G106300 | Phvul.007G106300 | PF00067 | PTHR24298,P ⁻ | KOG0156 |
| 9 | 1 Phvul.009G034400 | Phvul.009G034400 | PF16913 | PTHR31376,P ⁻ | 0 |
| 10 | 1 Phvul.009G034400 | Phvul.009G034400 | PF16913 | PTHR31376,P ⁻ | 0 |
| 11 | 1 Phvul.L002444 | Phvul.L002444 | 0 | PTHR33401 | 0 |
| 12 | 1 Phvul.L002444 | Phvul.L002444 | 0 | PTHR33401 | 0 |
| 13 | 1 Phvul.L002444 | Phvul.L002444 | 0 | PTHR33401 | 0 |
| 14 | 1 Phvul.008G070000 | Phvul.008G070000 | PF01988 | PTHR31851,P ⁻ | KOG4473 |
| 15 | 1 Phvul.010G156200 | Phvul.010G156200 | PF00487 | PTHR11351,P ⁻ | KOG1600 |
| 16 | 1 Phvul.009G217000 | Phvul.009G217000 | PF04783,PF04 | PTHR21450,P ⁻ | 0 |
| 17 | 1 Phvul.008G043500 | Phvul.008G043500 | PF00847 | PTHR32467,P ⁻ | 0 |
| 18 | 1 Phvul.008G043500 | Phvul.008G043500 | PF00847 | PTHR32467,P ⁻ | 0 |
| 19 | 1 Phvul.009G079400 | Phvul.009G079400 | PF05254 | PTHR21329 | 0 |
| 20 | 1 Phvul.001G193000 | Phvul.001G193000 | 0 | PTHR36064 | 0 |
| 21 | 1 Phvul.001G193000 | Phvul.001G193000 | 0 | PTHR36064 | 0 |
| 22 | 1 Phvul.001G193000 | Phvul.001G193000 | 0 | PTHR36064 | 0 |
| 23 | 1 Phvul.003G154400 | Phvul.003G154400 | PF12854,PF14 | PTHR24015,P ⁻ | 0 |
| 24 | 1 Phvul.009G030200 | Phvul.009G030200 | PF08241 | PTHR10108,P ⁻ | 0 |
| 25 | 1 Phvul.004G166100 | Phvul.004G166100 | PF00578 | PTHR10430 | KOG0541 |
| 26 | 1 Phvul.004G166100 | Phvul.004G166100 | PF00578 | PTHR10430 | KOG0541 |
| 27 | 1 Phvul.009G160200 | Phvul.009G160200 | PF13414 | PTHR16193 | 0 |
| 28 | 1 Phvul.002G119600 | Phvul.002G119600 | PF11443 | PTHR31373,P ⁻ | 0 |
| 29 | 1 Phvul.002G119600 | Phvul.002G119600 | PF11443 | PTHR31373,P ⁻ | 0 |
| 30 | 1 Phvul.002G150800 | Phvul.002G150800 | PF00155 | PTHR11751,P ⁻ | 0 |
| 31 | 1 Phvul.002G271400 | Phvul.002G271400 | PF00266 | PTHR11601,P ⁻ | 0 |
| 32 | 1 Phvul.002G271400 | Phvul.002G271400 | PF00266 | PTHR11601,P ⁻ | 0 |
| 33 | 1 Phvul.011G166200 | Phvul.011G166200 | PF10559,PF00 | PTHR10906 | 0 |
| 34 | 1 Phvul.001G110100 | Phvul.001G110100 | 0 | PTHR11122,P ⁻ | KOG1594 |
| 35 | 1 Phvul.002G037500 | Phvul.002G037500 | 0 | PTHR17130 | 0 |
| 36 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁻ | 0 |
| 37 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁻ | 0 |
| 38 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁻ | 0 |
| 39 | 1 Phvul.007G022500 | Phvul.007G022500 | PF00111 | PTHR19370,P ⁻ | 0 |
| 40 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P ⁻ | 0 |
| 41 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P ⁻ | 0 |
| 42 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P ⁻ | 0 |
| 43 | 1 Phvul.006G154900 | Phvul.006G154900 | 0 | PTHR33739,P ⁻ | 0 |
| 44 | 1 Phvul.006G154900 | Phvul.006G154900 | 0 | PTHR33739,P ⁻ | 0 |
| 45 | 1 Phvul.006G047000 | Phvul.006G047000 | PF02922,PF00 | PTHR10357,P ⁻ | 0 |
| 46 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P ⁻ | 0 |
| 47 | 1 Phvul.003G056900 | Phvul.003G056900 | 0 | PTHR37243 | 0 |
| 48 | 1 Phvul.003G056900 | Phvul.003G056900 | 0 | PTHR37243 | 0 |
| 49 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁻ | KOG1383 |
| 50 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁻ | KOG1383 |
| 51 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁻ | KOG1383 |
| 52 | 1 Phvul.003G056900 | Phvul.003G056900 | 0 | PTHR37243 | 0 |
| 53 | 1 Phvul.007G106300 | Phvul.007G106300 | PF00067 | PTHR24298,P ⁻ | KOG0156 |
| 54 | 1 Phvul.007G106300 | Phvul.007G106300 | PF00067 | PTHR24298,P ⁻ | KOG0156 |
| 55 | 1 Phvul.009G034400 | Phvul.009G034400 | PF16913 | PTHR31376,P ⁻ | 0 |
| 56 | 1 Phvul.009G034400 | Phvul.009G034400 | PF16913 | PTHR31376,P ⁻ | 0 |
| 57 | 1 Phvul.L002444 | Phvul.L002444 | 0 | PTHR33401 | 0 |
| 58 | 1 Phvul.L002444 | Phvul.L002444 | 0 | PTHR33401 | 0 |
| 59 | 1 Phvul.008G070000 | Phvul.008G070000 | PF01988 | PTHR31851,P ⁻ | KOG4473 |
| 60 | 1 Phvul.010G156200 | Phvul.010G156200 | PF00487 | PTHR11351,P ⁻ | KOG1600 |
| | 1 Phvul.009G217000 | Phvul.009G217000 | PF04783,PF04 | PTHR21450,P ⁻ | 0 |

| | | | | | |
|----|--------------------|------------------|--------------|------------------------|---|
| 1 | | | | | |
| 2 | 1 Phvul.008G043500 | Phvul.008G043500 | PF00847 | PTHR32467,P' | 0 |
| 3 | 1 Phvul.009G079400 | Phvul.009G079400 | PF05254 | PTHR21329 | 0 |
| 4 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 7 | 1 Phvul.003G154400 | Phvul.003G154400 | PF12854,PF14 | PTHR24015,P' | 0 |
| 8 | 1 Phvul.009G030200 | Phvul.009G030200 | PF08241 | PTHR10108,P' | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.004G166100 | Phvul.004G166100 | PF00578 | PTHR10430 KOG0541 | |
| 11 | 1 Phvul.009G160200 | Phvul.009G160200 | PF13414 | PTHR16193 | 0 |
| 12 | 1 Phvul.002G119600 | Phvul.002G119600 | PF11443 | PTHR31373,P' | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.002G150800 | Phvul.002G150800 | PF00155 | PTHR11751,P' | 0 |
| 15 | 1 Phvul.002G271400 | Phvul.002G271400 | PF00266 | PTHR11601,P' | 0 |
| 16 | 1 Phvul.011G166200 | Phvul.011G166200 | PF10559,PF00 | PTHR10906 | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.001G110100 | Phvul.001G110100 | | 0 PTHR11122,P' KOG1594 | |
| 19 | 1 Phvul.002G037500 | Phvul.002G037500 | | 0 PTHR17130 | 0 |
| 20 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P' | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P' | 0 |
| 23 | 1 Phvul.007G022500 | Phvul.007G022500 | PF00111 | PTHR19370,P' | 0 |
| 24 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P' | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P' | 0 |
| 27 | 1 Phvul.006G154900 | Phvul.006G154900 | | 0 PTHR33739,P' | 0 |
| 28 | 1 Phvul.006G047000 | Phvul.006G047000 | PF02922,PF00 | PTHR10357,P' | 0 |
| 29 | | | | | |
| 30 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P' | 0 |
| 31 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 32 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 33 | | | | | |
| 34 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P' KOG1383 | |
| 35 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P' KOG1383 | |
| 36 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 37 | 1 Phvul.007G106300 | Phvul.007G106300 | PF00067 | PTHR24298,P' KOG0156 | |
| 38 | | | | | |
| 39 | 1 Phvul.009G034400 | Phvul.009G034400 | PF16913 | PTHR31376,P' | 0 |
| 40 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 41 | | | | | |
| 42 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 43 | 1 Phvul.008G070000 | Phvul.008G070000 | PF01988 | PTHR31851,P' KOG4473 | |
| 44 | 1 Phvul.010G156200 | Phvul.010G156200 | PF00487 | PTHR11351,P' KOG1600 | |
| 45 | 1 Phvul.009G217000 | Phvul.009G217000 | PF04783,PF04 | PTHR21450,P' | 0 |
| 46 | | | | | |
| 47 | 1 Phvul.008G043500 | Phvul.008G043500 | PF00847 | PTHR32467,P' | 0 |
| 48 | 1 Phvul.009G079400 | Phvul.009G079400 | PF05254 | PTHR21329 | 0 |
| 49 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 50 | | | | | |
| 51 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 52 | 1 Phvul.003G154400 | Phvul.003G154400 | PF12854,PF14 | PTHR24015,P' | 0 |
| 53 | 1 Phvul.009G030200 | Phvul.009G030200 | PF08241 | PTHR10108,P' | 0 |
| 54 | | | | | |
| 55 | 1 Phvul.004G166100 | Phvul.004G166100 | PF00578 | PTHR10430 KOG0541 | |
| 56 | 1 Phvul.009G160200 | Phvul.009G160200 | PF13414 | PTHR16193 | 0 |
| 57 | 1 Phvul.002G119600 | Phvul.002G119600 | PF11443 | PTHR31373,P' | 0 |
| 58 | | | | | |
| 59 | 1 Phvul.002G150800 | Phvul.002G150800 | PF00155 | PTHR11751,P' | 0 |
| 60 | 1 Phvul.002G271400 | Phvul.002G271400 | PF00266 | PTHR11601,P' | 0 |
| | 1 Phvul.011G166200 | Phvul.011G166200 | PF10559,PF00 | PTHR10906 | 0 |

| | | | | | |
|----|--------------------|------------------|--------------------------------------|------------------------------------|---|
| 1 | | | | | |
| 2 | 1 Phvul.001G110100 | Phvul.001G110100 | | 0 PTHR11122,P ⁻ KOG1594 | |
| 3 | 1 Phvul.002G037500 | Phvul.002G037500 | | 0 PTHR17130 | 0 |
| 4 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁻ | 0 |
| 5 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁻ | 0 |
| 6 | 1 Phvul.007G022500 | Phvul.007G022500 | PF00111 | PTHR19370,P ⁻ | 0 |
| 7 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12PTHR13950,P ⁻ | | 0 |
| 8 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12PTHR13950,P ⁻ | | 0 |
| 9 | 1 Phvul.006G154900 | Phvul.006G154900 | | 0 PTHR33739,P ⁻ | 0 |
| 10 | 1 Phvul.006G047000 | Phvul.006G047000 | PF02922,PF00PTHR10357,P ⁻ | | 0 |
| 11 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P ⁻ | 0 |
| 12 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 13 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 14 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁻ KOG1383 | |
| 15 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁻ KOG1383 | |
| 16 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 17 | 1 Phvul.007G106300 | Phvul.007G106300 | PF00067 | PTHR24298,P ⁻ KOG0156 | |
| 18 | 1 Phvul.009G034400 | Phvul.009G034400 | PF16913 | PTHR31376,P ⁻ | 0 |
| 19 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 20 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 21 | 1 Phvul.008G070000 | Phvul.008G070000 | PF01988 | PTHR31851,P ⁻ KOG4473 | |
| 22 | 1 Phvul.010G156200 | Phvul.010G156200 | PF00487 | PTHR11351,P ⁻ KOG1600 | |
| 23 | 1 Phvul.009G217000 | Phvul.009G217000 | PF04783,PF04PTHR21450,P ⁻ | | 0 |
| 24 | 1 Phvul.008G043500 | Phvul.008G043500 | PF00847 | PTHR32467,P ⁻ | 0 |
| 25 | 1 Phvul.009G079400 | Phvul.009G079400 | PF05254 | PTHR21329 | 0 |
| 26 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 27 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 28 | 1 Phvul.003G154400 | Phvul.003G154400 | PF12854,PF14PTHR24015,P ⁻ | | 0 |
| 29 | 1 Phvul.009G030200 | Phvul.009G030200 | PF08241 | PTHR10108,P ⁻ | 0 |
| 30 | 1 Phvul.004G166100 | Phvul.004G166100 | PF00578 | PTHR10430 KOG0541 | |
| 31 | 1 Phvul.009G160200 | Phvul.009G160200 | PF13414 | PTHR16193 | 0 |
| 32 | 1 Phvul.002G119600 | Phvul.002G119600 | PF11443 | PTHR31373,P ⁻ | 0 |
| 33 | 1 Phvul.002G150800 | Phvul.002G150800 | PF00155 | PTHR11751,P ⁻ | 0 |
| 34 | 1 Phvul.002G271400 | Phvul.002G271400 | PF00266 | PTHR11601,P ⁻ | 0 |
| 35 | 1 Phvul.011G166200 | Phvul.011G166200 | PF10559,PF00PTHR10906 | | 0 |
| 36 | 1 Phvul.001G110100 | Phvul.001G110100 | | 0 PTHR11122,P ⁻ KOG1594 | |
| 37 | 1 Phvul.002G037500 | Phvul.002G037500 | | 0 PTHR17130 | 0 |
| 38 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁻ | 0 |
| 39 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁻ | 0 |
| 40 | 1 Phvul.007G022500 | Phvul.007G022500 | PF00111 | PTHR19370,P ⁻ | 0 |
| 41 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12PTHR13950,P ⁻ | | 0 |
| 42 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12PTHR13950,P ⁻ | | 0 |
| 43 | 1 Phvul.006G154900 | Phvul.006G154900 | | 0 PTHR33739,P ⁻ | 0 |
| 44 | 1 Phvul.006G047000 | Phvul.006G047000 | PF02922,PF00PTHR10357,P ⁻ | | 0 |
| 45 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P ⁻ | 0 |
| 46 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 47 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |

| | | | | | |
|----|--------------------|------------------|--------------|------------------------------------|---|
| 1 | | | | | |
| 2 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁺ KOG1383 | |
| 3 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁺ KOG1383 | |
| 4 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.007G106300 | Phvul.007G106300 | PF00067 | PTHR24298,P ⁺ KOG0156 | |
| 7 | 1 Phvul.009G034400 | Phvul.009G034400 | PF16913 | PTHR31376,P ⁺ | 0 |
| 8 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 11 | 1 Phvul.008G070000 | Phvul.008G070000 | PF01988 | PTHR31851,P ⁺ KOG4473 | |
| 12 | 1 Phvul.010G156200 | Phvul.010G156200 | PF00487 | PTHR11351,P ⁺ KOG1600 | |
| 13 | | | | | |
| 14 | 1 Phvul.009G217000 | Phvul.009G217000 | PF04783,PF04 | PTHR21450,P ⁺ | 0 |
| 15 | 1 Phvul.008G043500 | Phvul.008G043500 | PF00847 | PTHR32467,P ⁺ | 0 |
| 16 | 1 Phvul.009G079400 | Phvul.009G079400 | PF05254 | PTHR21329 | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 19 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 20 | 1 Phvul.003G154400 | Phvul.003G154400 | PF12854,PF14 | PTHR24015,P ⁺ | 0 |
| 21 | 1 Phvul.009G030200 | Phvul.009G030200 | PF08241 | PTHR10108,P ⁺ | 0 |
| 22 | | | | | |
| 23 | 1 Phvul.004G166100 | Phvul.004G166100 | PF00578 | PTHR10430 KOG0541 | |
| 24 | 1 Phvul.009G160200 | Phvul.009G160200 | PF13414 | PTHR16193 | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.002G119600 | Phvul.002G119600 | PF11443 | PTHR31373,P ⁺ | 0 |
| 27 | 1 Phvul.002G150800 | Phvul.002G150800 | PF00155 | PTHR11751,P ⁺ | 0 |
| 28 | 1 Phvul.002G271400 | Phvul.002G271400 | PF00266 | PTHR11601,P ⁺ | 0 |
| 29 | | | | | |
| 30 | 1 Phvul.011G166200 | Phvul.011G166200 | PF10559,PF00 | PTHR10906 | 0 |
| 31 | 1 Phvul.001G110100 | Phvul.001G110100 | | 0 PTHR11122,P ⁺ KOG1594 | |
| 32 | 1 Phvul.002G037500 | Phvul.002G037500 | | 0 PTHR17130 | 0 |
| 33 | | | | | |
| 34 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁺ | 0 |
| 35 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P ⁺ | 0 |
| 36 | 1 Phvul.007G022500 | Phvul.007G022500 | PF00111 | PTHR19370,P ⁺ | 0 |
| 37 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P ⁺ | 0 |
| 38 | | | | | |
| 39 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12 | PTHR13950,P ⁺ | 0 |
| 40 | 1 Phvul.006G154900 | Phvul.006G154900 | | 0 PTHR33739,P ⁺ | 0 |
| 41 | 1 Phvul.006G047000 | Phvul.006G047000 | PF02922,PF00 | PTHR10357,P ⁺ | 0 |
| 42 | | | | | |
| 43 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P ⁺ | 0 |
| 44 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 45 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 46 | | | | | |
| 47 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁺ KOG1383 | |
| 48 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P ⁺ KOG1383 | |
| 49 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 50 | | | | | |
| 51 | 1 Phvul.007G106300 | Phvul.007G106300 | PF00067 | PTHR24298,P ⁺ KOG0156 | |
| 52 | 1 Phvul.009G034400 | Phvul.009G034400 | PF16913 | PTHR31376,P ⁺ | 0 |
| 53 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 54 | | | | | |
| 55 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 56 | 1 Phvul.008G070000 | Phvul.008G070000 | PF01988 | PTHR31851,P ⁺ KOG4473 | |
| 57 | 1 Phvul.010G156200 | Phvul.010G156200 | PF00487 | PTHR11351,P ⁺ KOG1600 | |
| 58 | | | | | |
| 59 | 1 Phvul.009G217000 | Phvul.009G217000 | PF04783,PF04 | PTHR21450,P ⁺ | 0 |
| 60 | 1 Phvul.008G043500 | Phvul.008G043500 | PF00847 | PTHR32467,P ⁺ | 0 |
| | 1 Phvul.009G079400 | Phvul.009G079400 | PF05254 | PTHR21329 | 0 |

| | | | | | |
|----|--------------------|------------------|--------------------------|----------------------|---|
| 1 | | | | | |
| 2 | 1 Phvul.001G193000 | Phvul.001G193000 | 0 PTHR36064 | | 0 |
| 3 | 1 Phvul.001G193000 | Phvul.001G193000 | 0 PTHR36064 | | 0 |
| 4 | 1 Phvul.003G154400 | Phvul.003G154400 | PF12854,PF14PTHR24015,P' | | 0 |
| 5 | 1 Phvul.009G030200 | Phvul.009G030200 | PF08241 | PTHR10108,P' | 0 |
| 6 | 1 Phvul.004G166100 | Phvul.004G166100 | PF00578 | PTHR10430 KOG0541 | |
| 7 | 1 Phvul.009G160200 | Phvul.009G160200 | PF13414 | PTHR16193 | 0 |
| 8 | 1 Phvul.002G119600 | Phvul.002G119600 | PF11443 | PTHR31373,P' | 0 |
| 9 | 1 Phvul.002G150800 | Phvul.002G150800 | PF00155 | PTHR11751,P' | 0 |
| 10 | 1 Phvul.002G271400 | Phvul.002G271400 | PF00266 | PTHR11601,P' | 0 |
| 11 | 1 Phvul.011G166200 | Phvul.011G166200 | PF10559,PF00PTHR10906 | | 0 |
| 12 | 1 Phvul.001G110100 | Phvul.001G110100 | 0 PTHR11122,P' | KOG1594 | |
| 13 | 1 Phvul.002G037500 | Phvul.002G037500 | 0 PTHR17130 | | 0 |
| 14 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P' | 0 |
| 15 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P' | 0 |
| 16 | 1 Phvul.007G022500 | Phvul.007G022500 | PF00111 | PTHR19370,P' | 0 |
| 17 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12PTHR13950,P' | | 0 |
| 18 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12PTHR13950,P' | | 0 |
| 19 | 1 Phvul.006G154900 | Phvul.006G154900 | 0 PTHR33739,P' | | 0 |
| 20 | 1 Phvul.006G047000 | Phvul.006G047000 | PF02922,PF00PTHR10357,P' | | 0 |
| 21 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P' | 0 |
| 22 | 1 Phvul.003G056900 | Phvul.003G056900 | 0 PTHR37243 | | 0 |
| 23 | 1 Phvul.003G056900 | Phvul.003G056900 | 0 PTHR37243 | | 0 |
| 24 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P' KOG1383 | |
| 25 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P' KOG1383 | |
| 26 | 1 Phvul.003G056900 | Phvul.003G056900 | 0 PTHR37243 | | 0 |
| 27 | 1 Phvul.007G106300 | Phvul.007G106300 | PF00067 | PTHR24298,P' KOG0156 | |
| 28 | 1 Phvul.009G034400 | Phvul.009G034400 | PF16913 | PTHR31376,P' | 0 |
| 29 | 1 Phvul.L002444 | Phvul.L002444 | 0 PTHR33401 | | 0 |
| 30 | 1 Phvul.L002444 | Phvul.L002444 | 0 PTHR33401 | | 0 |
| 31 | 1 Phvul.008G070000 | Phvul.008G070000 | PF01988 | PTHR31851,P' KOG4473 | |
| 32 | 1 Phvul.010G156200 | Phvul.010G156200 | PF00487 | PTHR11351,P' KOG1600 | |
| 33 | 1 Phvul.009G217000 | Phvul.009G217000 | PF04783,PF04PTHR21450,P' | | 0 |
| 34 | 1 Phvul.008G043500 | Phvul.008G043500 | PF00847 | PTHR32467,P' | 0 |
| 35 | 1 Phvul.009G079400 | Phvul.009G079400 | PF05254 | PTHR21329 | 0 |
| 36 | 1 Phvul.001G193000 | Phvul.001G193000 | 0 PTHR36064 | | 0 |
| 37 | 1 Phvul.001G193000 | Phvul.001G193000 | 0 PTHR36064 | | 0 |
| 38 | 1 Phvul.003G154400 | Phvul.003G154400 | PF12854,PF14PTHR24015,P' | | 0 |
| 39 | 1 Phvul.009G030200 | Phvul.009G030200 | PF08241 | PTHR10108,P' | 0 |
| 40 | 1 Phvul.004G166100 | Phvul.004G166100 | PF00578 | PTHR10430 KOG0541 | |
| 41 | 1 Phvul.009G160200 | Phvul.009G160200 | PF13414 | PTHR16193 | 0 |
| 42 | 1 Phvul.002G119600 | Phvul.002G119600 | PF11443 | PTHR31373,P' | 0 |
| 43 | 1 Phvul.002G150800 | Phvul.002G150800 | PF00155 | PTHR11751,P' | 0 |
| 44 | 1 Phvul.002G271400 | Phvul.002G271400 | PF00266 | PTHR11601,P' | 0 |
| 45 | 1 Phvul.011G166200 | Phvul.011G166200 | PF10559,PF00PTHR10906 | | 0 |
| 46 | 1 Phvul.001G110100 | Phvul.001G110100 | 0 PTHR11122,P' | KOG1594 | |
| 47 | 1 Phvul.002G037500 | Phvul.002G037500 | 0 PTHR17130 | | 0 |

| | | | | | |
|----|--------------------|------------------|-------------------------|-----------------------|---|
| 1 | | | | | |
| 2 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P | 0 |
| 3 | 1 Phvul.002G017700 | Phvul.002G017700 | PF00069 | PTHR27001,P | 0 |
| 4 | 1 Phvul.007G022500 | Phvul.007G022500 | PF00111 | PTHR19370,P | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12PTHR13950,P | | 0 |
| 7 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12PTHR13950,P | | 0 |
| 8 | 1 Phvul.006G154900 | Phvul.006G154900 | | 0 PTHR33739,P | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.006G047000 | Phvul.006G047000 | PF02922,PF00PTHR10357,P | | 0 |
| 11 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P | 0 |
| 12 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 15 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P KOG1383 | |
| 16 | 1 Phvul.008G017200 | Phvul.008G017200 | PF00282 | PTHR11999,P KOG1383 | |
| 17 | | | | | |
| 18 | 1 Phvul.003G056900 | Phvul.003G056900 | | 0 PTHR37243 | 0 |
| 19 | 1 Phvul.007G106300 | Phvul.007G106300 | PF00067 | PTHR24298,P KOG0156 | |
| 20 | 1 Phvul.009G034400 | Phvul.009G034400 | PF16913 | PTHR31376,P | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 23 | 1 Phvul.L002444 | Phvul.L002444 | | 0 PTHR33401 | 0 |
| 24 | | | | | |
| 25 | 1 Phvul.008G070000 | Phvul.008G070000 | PF01988 | PTHR31851,P KOG4473 | |
| 26 | 1 Phvul.010G156200 | Phvul.010G156200 | PF00487 | PTHR11351,P KOG1600 | |
| 27 | 1 Phvul.009G160200 | Phvul.009G160200 | PF13414 | PTHR16193 | 0 |
| 28 | 1 Phvul.009G217000 | Phvul.009G217000 | PF04783,PF04PTHR21450,P | | 0 |
| 29 | | | | | |
| 30 | 1 Phvul.007G022500 | Phvul.007G022500 | PF00111 | PTHR19370,P | 0 |
| 31 | 1 Phvul.008G043500 | Phvul.008G043500 | PF00847 | PTHR32467,P | 0 |
| 32 | 1 Phvul.009G079400 | Phvul.009G079400 | PF05254 | PTHR21329 | 0 |
| 33 | | | | | |
| 34 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 35 | 1 Phvul.001G193000 | Phvul.001G193000 | | 0 PTHR36064 | 0 |
| 36 | 1 Phvul.009G167700 | Phvul.009G167700 | PF13193,PF00PTHR24096,P | KOG1176 | |
| 37 | 1 Phvul.003G154400 | Phvul.003G154400 | PF12854,PF14PTHR24015,P | | 0 |
| 38 | | | | | |
| 39 | 1 Phvul.L003746 | Phvul.L003746 | PF01823 | PTHR33199,P | 0 |
| 40 | 1 Phvul.L003746 | Phvul.L003746 | PF01823 | PTHR33199,P | 0 |
| 41 | | | | | |
| 42 | 1 Phvul.009G030200 | Phvul.009G030200 | PF08241 | PTHR10108,P | 0 |
| 43 | 1 Phvul.004G166100 | Phvul.004G166100 | PF00578 | PTHR10430 KOG0541 | |
| 44 | 1 Phvul.002G119600 | Phvul.002G119600 | PF11443 | PTHR31373,P | 0 |
| 45 | 1 Phvul.002G150800 | Phvul.002G150800 | PF00155 | PTHR11751,P | 0 |
| 46 | | | | | |
| 47 | 1 Phvul.002G271400 | Phvul.002G271400 | PF00266 | PTHR11601,P | 0 |
| 48 | 1 Phvul.011G166200 | Phvul.011G166200 | PF10559,PF00PTHR10906 | | 0 |
| 49 | 2 Phvul.006G067900 | Phvul.006G067900 | PF01699 | PTHR31503,P KOG1397 | |
| 50 | | | | | |
| 51 | 1 Phvul.001G110100 | Phvul.001G110100 | | 0 PTHR11122,P KOG1594 | |
| 52 | 1 Phvul.002G037500 | Phvul.002G037500 | | 0 PTHR17130 | 0 |
| 53 | | | | | |
| 54 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12PTHR13950,P | | 0 |
| 55 | 1 Phvul.010G115000 | Phvul.010G115000 | PF00400,PF12PTHR13950,P | | 0 |
| 56 | 1 Phvul.002G157000 | Phvul.002G157000 | PF08372,PF00PTHR10024,P | | 0 |
| 57 | 1 Phvul.009G222600 | Phvul.009G222600 | PF04043,PF01PTHR31707,P | | 0 |
| 58 | | | | | |
| 59 | 1 Phvul.002G106900 | Phvul.002G106900 | PF04783,PF04PTHR21450,P | | 0 |
| 60 | 1 Phvul.005G099500 | Phvul.005G099500 | PF02469 | PTHR32077,P | 0 |
| | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P | 0 |

| | | | | | |
|----|--------------------|------------------|--------------------------------------|----------------------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P ⁻ | 0 |
| 3 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P ⁻ | 0 |
| 4 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P ⁻ | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.006G075600 | Phvul.006G075600 | PF00141 | PTHR31388,P ⁻ | 0 |
| 7 | 1 Phvul.008G284900 | Phvul.008G284900 | PF08801 | PTHR13405,P ⁻ | 0 |
| 8 | 1 Phvul.007G163400 | Phvul.007G163400 | PF00632 | PTHR11254,P ⁻ | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.001G266600 | Phvul.001G266600 | PF00464 | PTHR11680,P ⁻ | 0 |
| 11 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P ⁻ | KOG1764 | |
| 12 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P ⁻ | KOG1764 | |
| 13 | | | | | |
| 14 | 1 Phvul.003G037500 | Phvul.003G037500 | PF00454 | PTHR15245,P ⁻ | KOG2381 |
| 15 | 1 Phvul.009G007300 | Phvul.009G007300 | | 0 PTHR35993 | 0 |
| 16 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P ⁻ | | 0 |
| 17 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P ⁻ | | 0 |
| 18 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P ⁻ | | 0 |
| 19 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P ⁻ | | 0 |
| 20 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P ⁻ | | 0 |
| 21 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P ⁻ | | 0 |
| 22 | | | | | |
| 23 | 1 Phvul.007G156200 | Phvul.007G156200 | PF00010 | PTHR12565,P ⁻ | 0 |
| 24 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P ⁻ | KOG4172 |
| 25 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P ⁻ | KOG4172 |
| 26 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P ⁻ | 0 |
| 27 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P ⁻ | KOG4172 |
| 28 | 1 Phvul.008G243700 | Phvul.008G243700 | PF01764 | PTHR21493,P ⁻ | 0 |
| 29 | 1 Phvul.007G201400 | Phvul.007G201400 | PF03789,PF05PTHR11850,P ⁻ | KOG0773 | |
| 30 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 31 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 32 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 33 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 34 | 1 Phvul.003G181600 | Phvul.003G181600 | PF13639 | PTHR22763,P ⁻ | 0 |
| 35 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 36 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 37 | 1 Phvul.006G164800 | Phvul.006G164800 | PF04765 | PTHR12956,P ⁻ | 0 |
| 38 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 39 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 40 | 1 Phvul.005G059700 | Phvul.005G059700 | PF00141 | PTHR31235,P ⁻ | 0 |
| 41 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 42 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 43 | 1 Phvul.005G059500 | Phvul.005G059500 | PF00141 | PTHR31235,P ⁻ | 0 |
| 44 | 1 Phvul.002G116800 | Phvul.002G116800 | PF10181 | PTHR15231,P ⁻ | KOG4551 |
| 45 | 1 Phvul.008G103100 | Phvul.008G103100 | PF00249,PF14PTHR31314,P ⁻ | | 0 |
| 46 | 1 Phvul.008G075300 | Phvul.008G075300 | | 0 PTHR33601,P ⁻ | 0 |
| 47 | 1 Phvul.003G262800 | Phvul.003G262800 | PF02519 | PTHR31374,P ⁻ | 0 |
| 48 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁻ | KOG4658 |
| 49 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁻ | KOG4658 |
| 50 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 51 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |

| | | | | | |
|----|--------------------|------------------|-------------------------|---------|---|
| 1 | | | | | |
| 2 | 1 Phvul.004G088300 | Phvul.004G088300 | 0 PTHR36319,P | | 0 |
| 3 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P | | 0 |
| 4 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P | | 0 |
| 5 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P | | 0 |
| 6 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P | | 0 |
| 7 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P | | 0 |
| 8 | 1 Phvul.004G088300 | Phvul.004G088300 | 0 PTHR36319,P | | 0 |
| 9 | 1 Phvul.009G222600 | Phvul.009G222600 | PF04043,PF01PTHR31707,P | | 0 |
| 10 | 1 Phvul.002G106900 | Phvul.002G106900 | PF04783,PF04PTHR21450,P | | 0 |
| 11 | 1 Phvul.005G099500 | Phvul.005G099500 | PF02469 PTHR32077,P | | 0 |
| 12 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 PTHR12565,P | | 0 |
| 13 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 PTHR12565,P | | 0 |
| 14 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 PTHR11132,P | | 0 |
| 15 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 PTHR11132,P | | 0 |
| 16 | 1 Phvul.006G075600 | Phvul.006G075600 | PF00141 PTHR31388,P | | 0 |
| 17 | 1 Phvul.008G284900 | Phvul.008G284900 | PF08801 PTHR13405,P | | 0 |
| 18 | 1 Phvul.007G163400 | Phvul.007G163400 | PF00632 PTHR11254,P | | 0 |
| 19 | 1 Phvul.001G266600 | Phvul.001G266600 | PF00464 PTHR11680,P | | 0 |
| 20 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P | KOG1764 | |
| 21 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P | KOG1764 | |
| 22 | 1 Phvul.003G037500 | Phvul.003G037500 | PF00454 PTHR15245,P | KOG2381 | |
| 23 | 1 Phvul.009G007300 | Phvul.009G007300 | 0 PTHR35993 | | 0 |
| 24 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P | | 0 |
| 25 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P | | 0 |
| 26 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P | | 0 |
| 27 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P | | 0 |
| 28 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P | | 0 |
| 29 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P | | 0 |
| 30 | 1 Phvul.007G156200 | Phvul.007G156200 | PF00010 PTHR12565,P | | 0 |
| 31 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P | KOG4172 | |
| 32 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P | KOG4172 | |
| 33 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 PTHR13301,P | | 0 |
| 34 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P | KOG4172 | |
| 35 | 1 Phvul.008G243700 | Phvul.008G243700 | PF01764 PTHR21493,P | | 0 |
| 36 | 1 Phvul.007G201400 | Phvul.007G201400 | PF03789,PF05PTHR11850,P | KOG0773 | |
| 37 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 38 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 39 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 40 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 41 | 1 Phvul.003G181600 | Phvul.003G181600 | PF13639 PTHR22763,P | | 0 |
| 42 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 43 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 44 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 45 | 1 Phvul.006G164800 | Phvul.006G164800 | PF04765 PTHR12956,P | | 0 |
| 46 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 47 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 48 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 49 | 1 Phvul.005G059700 | Phvul.005G059700 | PF00141 PTHR31235,P | | 0 |
| 50 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| | | | | | |
|----|---|------------------|------------------|-------------------------|---------|
| 1 | | | | | |
| 2 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | 0 |
| 3 | 1 | Phvul.005G059500 | Phvul.005G059500 | PF00141 PTHR31235,P | 0 |
| 4 | 1 | Phvul.002G116800 | Phvul.002G116800 | PF10181 PTHR15231,P | KOG4551 |
| 5 | | | | | |
| 6 | 1 | Phvul.008G103100 | Phvul.008G103100 | PF00249,PF14PTHR31314,P | 0 |
| 7 | 1 | Phvul.008G075300 | Phvul.008G075300 | 0 PTHR33601,P | 0 |
| 8 | 1 | Phvul.003G262800 | Phvul.003G262800 | PF02519 PTHR31374,P | 0 |
| 9 | | | | | |
| 10 | 1 | Phvul.008G072300 | Phvul.008G072300 | PF00931 PTHR23155,P | KOG4658 |
| 11 | 1 | Phvul.008G072300 | Phvul.008G072300 | PF00931 PTHR23155,P | KOG4658 |
| 12 | 1 | Phvul.004G088300 | Phvul.004G088300 | 0 PTHR36319,P | 0 |
| 13 | | | | | |
| 14 | 1 | Phvul.004G088300 | Phvul.004G088300 | 0 PTHR36319,P | 0 |
| 15 | 1 | Phvul.004G088300 | Phvul.004G088300 | 0 PTHR36319,P | 0 |
| 16 | 1 | Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P | 0 |
| 17 | 1 | Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P | 0 |
| 18 | 1 | Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P | 0 |
| 19 | 1 | Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P | 0 |
| 20 | 1 | Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P | 0 |
| 21 | | | | | |
| 22 | 1 | Phvul.004G088300 | Phvul.004G088300 | 0 PTHR36319,P | 0 |
| 23 | 1 | Phvul.009G222600 | Phvul.009G222600 | PF04043,PF01PTHR31707,P | 0 |
| 24 | 1 | Phvul.002G106900 | Phvul.002G106900 | PF04783,PF04PTHR21450,P | 0 |
| 25 | | | | | |
| 26 | 1 | Phvul.005G099500 | Phvul.005G099500 | PF02469 PTHR32077,P | 0 |
| 27 | 1 | Phvul.003G181900 | Phvul.003G181900 | PF00010 PTHR12565,P | 0 |
| 28 | 1 | Phvul.003G181900 | Phvul.003G181900 | PF00010 PTHR12565,P | 0 |
| 29 | 1 | Phvul.003G121200 | Phvul.003G121200 | PF03151 PTHR11132,P | 0 |
| 30 | 1 | Phvul.003G121200 | Phvul.003G121200 | PF03151 PTHR11132,P | 0 |
| 31 | 1 | Phvul.003G121200 | Phvul.003G121200 | PF03151 PTHR11132,P | 0 |
| 32 | 1 | Phvul.006G075600 | Phvul.006G075600 | PF00141 PTHR31388,P | 0 |
| 33 | 1 | Phvul.008G284900 | Phvul.008G284900 | PF08801 PTHR13405,P | 0 |
| 34 | 1 | Phvul.007G163400 | Phvul.007G163400 | PF00632 PTHR11254,P | 0 |
| 35 | 1 | Phvul.001G266600 | Phvul.001G266600 | PF00464 PTHR11680,P | 0 |
| 36 | 1 | Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P | KOG1764 |
| 37 | | | | | |
| 38 | 1 | Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P | KOG1764 |
| 39 | 1 | Phvul.003G037500 | Phvul.003G037500 | PF00454 PTHR15245,P | KOG2381 |
| 40 | | | | | |
| 41 | 1 | Phvul.009G007300 | Phvul.009G007300 | 0 PTHR35993 | 0 |
| 42 | | | | | |
| 43 | 1 | Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P | 0 |
| 44 | 1 | Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P | 0 |
| 45 | 1 | Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P | 0 |
| 46 | 1 | Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P | 0 |
| 47 | 1 | Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P | 0 |
| 48 | 1 | Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P | 0 |
| 49 | 1 | Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P | 0 |
| 50 | | | | | |
| 51 | 1 | Phvul.007G156200 | Phvul.007G156200 | PF00010 PTHR12565,P | 0 |
| 52 | 1 | Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P | KOG4172 |
| 53 | 1 | Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P | KOG4172 |
| 54 | | | | | |
| 55 | 2 | Phvul.005G001000 | Phvul.005G001000 | PF03552 PTHR13301,P | 0 |
| 56 | 1 | Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P | KOG4172 |
| 57 | 1 | Phvul.008G243700 | Phvul.008G243700 | PF01764 PTHR21493,P | 0 |
| 58 | 1 | Phvul.007G201400 | Phvul.007G201400 | PF03789,PF05PTHR11850,P | KOG0773 |
| 59 | | | | | |
| 60 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | 0 |
| | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | 0 |

| | | | | | |
|----|--------------------|------------------|--------------|----------------------------|---------|
| 1 | | | | | |
| 2 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 3 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 4 | 1 Phvul.003G181600 | Phvul.003G181600 | PF13639 | PTHR22763,P ⁻ | 0 |
| 5 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 6 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 7 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 8 | 1 Phvul.006G164800 | Phvul.006G164800 | PF04765 | PTHR12956,P ⁻ | 0 |
| 9 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 10 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 11 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 12 | 1 Phvul.005G059700 | Phvul.005G059700 | PF00141 | PTHR31235,P ⁻ | 0 |
| 13 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 14 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 15 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 16 | 1 Phvul.005G059500 | Phvul.005G059500 | PF00141 | PTHR31235,P ⁻ | 0 |
| 17 | 1 Phvul.002G116800 | Phvul.002G116800 | PF10181 | PTHR15231,P ⁻ | KOG4551 |
| 18 | 1 Phvul.008G103100 | Phvul.008G103100 | PF00249,PF14 | PTHR31314,P ⁻ | 0 |
| 19 | 1 Phvul.008G075300 | Phvul.008G075300 | | 0 PTHR33601,P ⁻ | 0 |
| 20 | 1 Phvul.008G075300 | Phvul.008G075300 | | 0 PTHR33601,P ⁻ | 0 |
| 21 | 1 Phvul.003G262800 | Phvul.003G262800 | PF02519 | PTHR31374,P ⁻ | 0 |
| 22 | 1 Phvul.003G262800 | Phvul.003G262800 | PF02519 | PTHR31374,P ⁻ | 0 |
| 23 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁻ | KOG4658 |
| 24 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁻ | KOG4658 |
| 25 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁻ | KOG4658 |
| 26 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 27 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 28 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 29 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 30 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12 | PTHR24092,P ⁻ | 0 |
| 31 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02 | PTHR32002,P ⁻ | 0 |
| 32 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02 | PTHR32002,P ⁻ | 0 |
| 33 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02 | PTHR32002,P ⁻ | 0 |
| 34 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12 | PTHR24092,P ⁻ | 0 |
| 35 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12 | PTHR24092,P ⁻ | 0 |
| 36 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 37 | 1 Phvul.009G222600 | Phvul.009G222600 | PF04043,PF01 | PTHR31707,P ⁻ | 0 |
| 38 | 1 Phvul.002G106900 | Phvul.002G106900 | PF04783,PF04 | PTHR21450,P ⁻ | 0 |
| 39 | 1 Phvul.005G099500 | Phvul.005G099500 | PF02469 | PTHR32077,P ⁻ | 0 |
| 40 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P ⁻ | 0 |
| 41 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P ⁻ | 0 |
| 42 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P ⁻ | 0 |
| 43 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P ⁻ | 0 |
| 44 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P ⁻ | 0 |
| 45 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P ⁻ | 0 |
| 46 | 1 Phvul.006G075600 | Phvul.006G075600 | PF00141 | PTHR31388,P ⁻ | 0 |
| 47 | 1 Phvul.008G284900 | Phvul.008G284900 | PF08801 | PTHR13405,P ⁻ | 0 |
| 48 | 1 Phvul.007G163400 | Phvul.007G163400 | PF00632 | PTHR11254,P ⁻ | 0 |
| 49 | 1 Phvul.001G266600 | Phvul.001G266600 | PF00464 | PTHR11680,P ⁻ | 0 |
| 50 | 1 Phvul.001G266600 | Phvul.001G266600 | PF00464 | PTHR11680,P ⁻ | 0 |
| 51 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16 | PTHR13780,P ⁻ | KOG1764 |
| 52 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16 | PTHR13780,P ⁻ | KOG1764 |
| 53 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16 | PTHR13780,P ⁻ | KOG1764 |
| 54 | 1 Phvul.003G037500 | Phvul.003G037500 | PF00454 | PTHR15245,P ⁻ | KOG2381 |
| 55 | 1 Phvul.009G007300 | Phvul.009G007300 | | 0 PTHR35993 | 0 |
| 56 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00 | PTHR10799,P ⁻ | 0 |
| 57 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00 | PTHR10799,P ⁻ | 0 |
| 58 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00 | PTHR10799,P ⁻ | 0 |
| 59 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00 | PTHR23315,P ⁻ | 0 |
| 60 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00 | PTHR23315,P ⁻ | 0 |
| 60 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05 | PTHR11096,P ⁻ | 0 |

| | | | | | |
|----|--------------------|------------------|-------------------------|---------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P | | 0 |
| 3 | 1 Phvul.007G156200 | Phvul.007G156200 | PF00010 | PTHR12565,P | 0 |
| 4 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P | KOG4172 |
| 5 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P | KOG4172 |
| 6 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P | KOG4172 |
| 7 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P | 0 |
| 8 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P | KOG4172 |
| 9 | 1 Phvul.008G243700 | Phvul.008G243700 | PF01764 | PTHR21493,P | 0 |
| 10 | 1 Phvul.007G201400 | Phvul.007G201400 | PF03789,PF05PTHR11850,P | | KOG0773 |
| 11 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 12 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 13 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 14 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 15 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 16 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 17 | 1 Phvul.003G181600 | Phvul.003G181600 | PF13639 | PTHR22763,P | 0 |
| 18 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 19 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 20 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 21 | 1 Phvul.006G164800 | Phvul.006G164800 | PF04765 | PTHR12956,P | 0 |
| 22 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 23 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 24 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 25 | 1 Phvul.005G059700 | Phvul.005G059700 | PF00141 | PTHR31235,P | 0 |
| 26 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 27 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 28 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 29 | 1 Phvul.005G059500 | Phvul.005G059500 | PF00141 | PTHR31235,P | 0 |
| 30 | 1 Phvul.002G116800 | Phvul.002G116800 | PF10181 | PTHR15231,P | KOG4551 |
| 31 | 1 Phvul.008G103100 | Phvul.008G103100 | PF00249,PF14PTHR31314,P | | 0 |
| 32 | 1 Phvul.008G075300 | Phvul.008G075300 | | 0 PTHR33601,P | 0 |
| 33 | 1 Phvul.003G262800 | Phvul.003G262800 | PF02519 | PTHR31374,P | 0 |
| 34 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P | KOG4658 |
| 35 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P | KOG4658 |
| 36 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P | 0 |
| 37 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P | 0 |
| 38 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P | 0 |
| 39 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P | | 0 |
| 40 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P | | 0 |
| 41 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P | | 0 |
| 42 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P | | 0 |
| 43 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P | 0 |
| 44 | 1 Phvul.009G222600 | Phvul.009G222600 | PF04043,PF01PTHR31707,P | | 0 |
| 45 | 1 Phvul.002G106900 | Phvul.002G106900 | PF04783,PF04PTHR21450,P | | 0 |
| 46 | 1 Phvul.005G099500 | Phvul.005G099500 | PF02469 | PTHR32077,P | 0 |
| 47 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P | 0 |
| 48 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P | 0 |
| 49 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P | 0 |
| 50 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P | 0 |
| 51 | 1 Phvul.006G075600 | Phvul.006G075600 | PF00141 | PTHR31388,P | 0 |
| 52 | 1 Phvul.008G284900 | Phvul.008G284900 | PF08801 | PTHR13405,P | 0 |
| 53 | 1 Phvul.007G163400 | Phvul.007G163400 | PF00632 | PTHR11254,P | 0 |

| | | | | | |
|----|--------------------|------------------|-------------------------|---------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.001G266600 | Phvul.001G266600 | PF00464 | PTHR11680,P | 0 |
| 3 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P | KOG1764 | |
| 4 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P | KOG1764 | |
| 5 | | | | | |
| 6 | 1 Phvul.003G037500 | Phvul.003G037500 | PF00454 | PTHR15245,P | KOG2381 |
| 7 | 1 Phvul.009G007300 | Phvul.009G007300 | | 0 PTHR35993 | 0 |
| 8 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P | | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P | | 0 |
| 11 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P | | 0 |
| 12 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P | | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P | | 0 |
| 15 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P | | 0 |
| 16 | 1 Phvul.007G156200 | Phvul.007G156200 | PF00010 | PTHR12565,P | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P | KOG4172 |
| 19 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P | KOG4172 |
| 20 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P | KOG4172 |
| 23 | 1 Phvul.008G243700 | Phvul.008G243700 | PF01764 | PTHR21493,P | 0 |
| 24 | 1 Phvul.007G201400 | Phvul.007G201400 | PF03789,PF05PTHR11850,P | KOG0773 | |
| 25 | | | | | |
| 26 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 27 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 28 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 29 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 30 | | | | | |
| 31 | 1 Phvul.003G181600 | Phvul.003G181600 | PF13639 | PTHR22763,P | 0 |
| 32 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 33 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 34 | | | | | |
| 35 | 1 Phvul.006G164800 | Phvul.006G164800 | PF04765 | PTHR12956,P | 0 |
| 36 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 37 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 38 | | | | | |
| 39 | 1 Phvul.005G059700 | Phvul.005G059700 | PF00141 | PTHR31235,P | 0 |
| 40 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 41 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 42 | | | | | |
| 43 | 1 Phvul.005G059500 | Phvul.005G059500 | PF00141 | PTHR31235,P | 0 |
| 44 | 1 Phvul.002G116800 | Phvul.002G116800 | PF10181 | PTHR15231,P | KOG4551 |
| 45 | 1 Phvul.008G103100 | Phvul.008G103100 | PF00249,PF14PTHR31314,P | | 0 |
| 46 | | | | | |
| 47 | 1 Phvul.008G075300 | Phvul.008G075300 | | 0 PTHR33601,P | 0 |
| 48 | 1 Phvul.003G262800 | Phvul.003G262800 | PF02519 | PTHR31374,P | 0 |
| 49 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P | KOG4658 |
| 50 | | | | | |
| 51 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P | KOG4658 |
| 52 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P | 0 |
| 53 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P | 0 |
| 54 | | | | | |
| 55 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P | 0 |
| 56 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P | | 0 |
| 57 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P | | 0 |
| 58 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P | | 0 |
| 59 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P | | 0 |
| 60 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P | 0 |

| | | | | | |
|----|--------------------|------------------|-------------------------|---------|---|
| 1 | | | | | |
| 2 | 1 Phvul.009G222600 | Phvul.009G222600 | PF04043,PF01PTHR31707,P | | 0 |
| 3 | 1 Phvul.002G106900 | Phvul.002G106900 | PF04783,PF04PTHR21450,P | | 0 |
| 4 | 1 Phvul.005G099500 | Phvul.005G099500 | PF02469 PTHR32077,P | | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 PTHR12565,P | | 0 |
| 7 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 PTHR12565,P | | 0 |
| 8 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 PTHR11132,P | | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 PTHR11132,P | | 0 |
| 11 | 1 Phvul.006G075600 | Phvul.006G075600 | PF00141 PTHR31388,P | | 0 |
| 12 | 1 Phvul.008G284900 | Phvul.008G284900 | PF08801 PTHR13405,P | | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.007G163400 | Phvul.007G163400 | PF00632 PTHR11254,P | | 0 |
| 15 | 1 Phvul.001G266600 | Phvul.001G266600 | PF00464 PTHR11680,P | | 0 |
| 16 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P | KOG1764 | |
| 17 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P | KOG1764 | |
| 18 | 1 Phvul.003G037500 | Phvul.003G037500 | PF00454 PTHR15245,P | KOG2381 | |
| 19 | | | | | |
| 20 | 1 Phvul.009G007300 | Phvul.009G007300 | 0 PTHR35993 | | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P | | 0 |
| 23 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P | | 0 |
| 24 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P | | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P | | 0 |
| 27 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P | | 0 |
| 28 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P | | 0 |
| 29 | | | | | |
| 30 | 1 Phvul.007G156200 | Phvul.007G156200 | PF00010 PTHR12565,P | | 0 |
| 31 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P | KOG4172 | |
| 32 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P | KOG4172 | |
| 33 | | | | | |
| 34 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 PTHR13301,P | | 0 |
| 35 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P | KOG4172 | |
| 36 | 1 Phvul.008G243700 | Phvul.008G243700 | PF01764 PTHR21493,P | | 0 |
| 37 | 1 Phvul.007G201400 | Phvul.007G201400 | PF03789,PF05PTHR11850,P | KOG0773 | |
| 38 | | | | | |
| 39 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 40 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 41 | | | | | |
| 42 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 43 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 44 | 1 Phvul.003G181600 | Phvul.003G181600 | PF13639 PTHR22763,P | | 0 |
| 45 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 46 | | | | | |
| 47 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 48 | 1 Phvul.006G164800 | Phvul.006G164800 | PF04765 PTHR12956,P | | 0 |
| 49 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 50 | | | | | |
| 51 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 52 | 1 Phvul.005G059700 | Phvul.005G059700 | PF00141 PTHR31235,P | | 0 |
| 53 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 54 | | | | | |
| 55 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 56 | 1 Phvul.005G059500 | Phvul.005G059500 | PF00141 PTHR31235,P | | 0 |
| 57 | 1 Phvul.002G116800 | Phvul.002G116800 | PF10181 PTHR15231,P | KOG4551 | |
| 58 | 1 Phvul.008G103100 | Phvul.008G103100 | PF00249,PF14PTHR31314,P | | 0 |
| 59 | 1 Phvul.008G075300 | Phvul.008G075300 | 0 PTHR33601,P | | 0 |
| 60 | 1 Phvul.003G262800 | Phvul.003G262800 | PF02519 PTHR31374,P | | 0 |

| | | | | | |
|----|--------------------|------------------|--------------------------------------|----------------------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁺ | KOG4658 |
| 3 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁺ | KOG4658 |
| 4 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁺ | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁺ | 0 |
| 7 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁺ | 0 |
| 8 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P ⁺ | | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P ⁺ | | 0 |
| 11 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P ⁺ | | 0 |
| 12 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P ⁺ | | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁺ | 0 |
| 15 | 1 Phvul.009G222600 | Phvul.009G222600 | PF04043,PF01PTHR31707,P ⁺ | | 0 |
| 16 | 1 Phvul.002G106900 | Phvul.002G106900 | PF04783,PF04PTHR21450,P ⁺ | | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.005G099500 | Phvul.005G099500 | PF02469 | PTHR32077,P ⁺ | 0 |
| 19 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P ⁺ | 0 |
| 20 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P ⁺ | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P ⁺ | 0 |
| 23 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P ⁺ | 0 |
| 24 | 1 Phvul.006G075600 | Phvul.006G075600 | PF00141 | PTHR31388,P ⁺ | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.008G284900 | Phvul.008G284900 | PF08801 | PTHR13405,P ⁺ | 0 |
| 27 | 1 Phvul.007G163400 | Phvul.007G163400 | PF00632 | PTHR11254,P ⁺ | 0 |
| 28 | 1 Phvul.001G266600 | Phvul.001G266600 | PF00464 | PTHR11680,P ⁺ | 0 |
| 29 | | | | | |
| 30 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P ⁺ | KOG1764 | |
| 31 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P ⁺ | KOG1764 | |
| 32 | 1 Phvul.003G037500 | Phvul.003G037500 | PF00454 | PTHR15245,P ⁺ | KOG2381 |
| 33 | | | | | |
| 34 | 1 Phvul.009G007300 | Phvul.009G007300 | | 0 PTHR35993 | 0 |
| 35 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P ⁺ | | 0 |
| 36 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P ⁺ | | 0 |
| 37 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P ⁺ | | 0 |
| 38 | | | | | |
| 39 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P ⁺ | | 0 |
| 40 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P ⁺ | | 0 |
| 41 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P ⁺ | | 0 |
| 42 | | | | | |
| 43 | 1 Phvul.007G156200 | Phvul.007G156200 | PF00010 | PTHR12565,P ⁺ | 0 |
| 44 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P ⁺ | KOG4172 |
| 45 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P ⁺ | KOG4172 |
| 46 | | | | | |
| 47 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P ⁺ | 0 |
| 48 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P ⁺ | KOG4172 |
| 49 | 1 Phvul.008G243700 | Phvul.008G243700 | PF01764 | PTHR21493,P ⁺ | 0 |
| 50 | | | | | |
| 51 | 1 Phvul.007G201400 | Phvul.007G201400 | PF03789,PF05PTHR11850,P ⁺ | KOG0773 | |
| 52 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁺ | 0 |
| 53 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁺ | 0 |
| 54 | | | | | |
| 55 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁺ | 0 |
| 56 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁺ | 0 |
| 57 | 1 Phvul.003G181600 | Phvul.003G181600 | PF13639 | PTHR22763,P ⁺ | 0 |
| 58 | | | | | |
| 59 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁺ | 0 |
| 60 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁺ | 0 |
| | 1 Phvul.006G164800 | Phvul.006G164800 | PF04765 | PTHR12956,P ⁺ | 0 |

| | | | | | |
|----|---|------------------|------------------|-------------------------|---------|
| 1 | | | | | |
| 2 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | 0 |
| 3 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | 0 |
| 4 | 1 | Phvul.005G059700 | Phvul.005G059700 | PF00141 PTHR31235,P | 0 |
| 5 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | 0 |
| 6 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | 0 |
| 7 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | 0 |
| 8 | 1 | Phvul.005G059500 | Phvul.005G059500 | PF00141 PTHR31235,P | 0 |
| 9 | 1 | Phvul.002G116800 | Phvul.002G116800 | PF10181 PTHR15231,P | KOG4551 |
| 10 | 1 | Phvul.008G103100 | Phvul.008G103100 | PF00249,PF14PTHR31314,P | 0 |
| 11 | 1 | Phvul.008G075300 | Phvul.008G075300 | 0 PTHR33601,P | 0 |
| 12 | 1 | Phvul.003G262800 | Phvul.003G262800 | PF02519 PTHR31374,P | 0 |
| 13 | 1 | Phvul.008G072300 | Phvul.008G072300 | PF00931 PTHR23155,P | KOG4658 |
| 14 | 1 | Phvul.008G072300 | Phvul.008G072300 | PF00931 PTHR23155,P | KOG4658 |
| 15 | 1 | Phvul.004G088300 | Phvul.004G088300 | 0 PTHR36319,P | 0 |
| 16 | 1 | Phvul.004G088300 | Phvul.004G088300 | 0 PTHR36319,P | 0 |
| 17 | 1 | Phvul.004G088300 | Phvul.004G088300 | 0 PTHR36319,P | 0 |
| 18 | 1 | Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P | 0 |
| 19 | 1 | Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P | 0 |
| 20 | 1 | Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P | 0 |
| 21 | 1 | Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P | 0 |
| 22 | 1 | Phvul.004G088300 | Phvul.004G088300 | 0 PTHR36319,P | 0 |
| 23 | 1 | Phvul.009G222600 | Phvul.009G222600 | PF04043,PF01PTHR31707,P | 0 |
| 24 | 1 | Phvul.002G106900 | Phvul.002G106900 | PF04783,PF04PTHR21450,P | 0 |
| 25 | 1 | Phvul.005G099500 | Phvul.005G099500 | PF02469 PTHR32077,P | 0 |
| 26 | 1 | Phvul.003G181900 | Phvul.003G181900 | PF00010 PTHR12565,P | 0 |
| 27 | 1 | Phvul.003G181900 | Phvul.003G181900 | PF00010 PTHR12565,P | 0 |
| 28 | 1 | Phvul.003G121200 | Phvul.003G121200 | PF03151 PTHR11132,P | 0 |
| 29 | 1 | Phvul.003G121200 | Phvul.003G121200 | PF03151 PTHR11132,P | 0 |
| 30 | 1 | Phvul.006G075600 | Phvul.006G075600 | PF00141 PTHR31388,P | 0 |
| 31 | 1 | Phvul.008G284900 | Phvul.008G284900 | PF08801 PTHR13405,P | 0 |
| 32 | 1 | Phvul.007G163400 | Phvul.007G163400 | PF00632 PTHR11254,P | 0 |
| 33 | 1 | Phvul.001G266600 | Phvul.001G266600 | PF00464 PTHR11680,P | 0 |
| 34 | 1 | Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P | KOG1764 |
| 35 | 1 | Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P | KOG1764 |
| 36 | 1 | Phvul.003G037500 | Phvul.003G037500 | PF00454 PTHR15245,P | KOG2381 |
| 37 | 1 | Phvul.009G007300 | Phvul.009G007300 | 0 PTHR35993 | 0 |
| 38 | 1 | Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P | 0 |
| 39 | 1 | Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P | 0 |
| 40 | 1 | Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P | 0 |
| 41 | 1 | Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P | 0 |
| 42 | 1 | Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P | 0 |
| 43 | 1 | Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P | 0 |
| 44 | 1 | Phvul.007G156200 | Phvul.007G156200 | PF00010 PTHR12565,P | 0 |
| 45 | 1 | Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P | KOG4172 |
| 46 | 1 | Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P | KOG4172 |
| 47 | 2 | Phvul.005G001000 | Phvul.005G001000 | PF03552 PTHR13301,P | 0 |
| 48 | 1 | Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P | KOG4172 |

| | | | | | |
|----|--------------------|------------------|--------------------------------------|--------------------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.008G243700 | Phvul.008G243700 | PF01764 | PTHR21493,P ⁻ | 0 |
| 3 | 1 Phvul.007G201400 | Phvul.007G201400 | PF03789,PF05PTHR11850,P ⁻ | KOG0773 | |
| 4 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P ⁻ | 0 |
| 5 | | | | | |
| 6 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P ⁻ | 0 |
| 7 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P ⁻ | 0 |
| 8 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P ⁻ | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.003G181600 | Phvul.003G181600 | PF13639 | PTHR22763,P ⁻ | 0 |
| 11 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P ⁻ | 0 |
| 12 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P ⁻ | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.006G164800 | Phvul.006G164800 | PF04765 | PTHR12956,P ⁻ | 0 |
| 15 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P ⁻ | 0 |
| 16 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P ⁻ | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.005G059700 | Phvul.005G059700 | PF00141 | PTHR31235,P ⁻ | 0 |
| 19 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P ⁻ | 0 |
| 20 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P ⁻ | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.005G059500 | Phvul.005G059500 | PF00141 | PTHR31235,P ⁻ | 0 |
| 23 | 1 Phvul.002G116800 | Phvul.002G116800 | PF10181 | PTHR15231,P ⁻ | KOG4551 |
| 24 | 1 Phvul.008G103100 | Phvul.008G103100 | PF00249,PF14PTHR31314,P ⁻ | | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.008G075300 | Phvul.008G075300 | 0 | PTHR33601,P ⁻ | 0 |
| 27 | 1 Phvul.003G262800 | Phvul.003G262800 | PF02519 | PTHR31374,P ⁻ | 0 |
| 28 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁻ | KOG4658 |
| 29 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁻ | KOG4658 |
| 30 | | | | | |
| 31 | 1 Phvul.004G088300 | Phvul.004G088300 | 0 | PTHR36319,P ⁻ | 0 |
| 32 | 1 Phvul.004G088300 | Phvul.004G088300 | 0 | PTHR36319,P ⁻ | 0 |
| 33 | 1 Phvul.004G088300 | Phvul.004G088300 | 0 | PTHR36319,P ⁻ | 0 |
| 34 | | | | | |
| 35 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P ⁻ | | 0 |
| 36 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P ⁻ | | 0 |
| 37 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P ⁻ | | 0 |
| 38 | | | | | |
| 39 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P ⁻ | | 0 |
| 40 | 1 Phvul.004G088300 | Phvul.004G088300 | 0 | PTHR36319,P ⁻ | 0 |
| 41 | 1 Phvul.009G222600 | Phvul.009G222600 | PF04043,PF01PTHR31707,P ⁻ | | 0 |
| 42 | | | | | |
| 43 | 1 Phvul.002G106900 | Phvul.002G106900 | PF04783,PF04PTHR21450,P ⁻ | | 0 |
| 44 | 1 Phvul.005G099500 | Phvul.005G099500 | PF02469 | PTHR32077,P ⁻ | 0 |
| 45 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P ⁻ | 0 |
| 46 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P ⁻ | 0 |
| 47 | | | | | |
| 48 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P ⁻ | 0 |
| 49 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P ⁻ | 0 |
| 50 | | | | | |
| 51 | 1 Phvul.006G075600 | Phvul.006G075600 | PF00141 | PTHR31388,P ⁻ | 0 |
| 52 | 1 Phvul.008G284900 | Phvul.008G284900 | PF08801 | PTHR13405,P ⁻ | 0 |
| 53 | 1 Phvul.007G163400 | Phvul.007G163400 | PF00632 | PTHR11254,P ⁻ | 0 |
| 54 | | | | | |
| 55 | 1 Phvul.001G266600 | Phvul.001G266600 | PF00464 | PTHR11680,P ⁻ | 0 |
| 56 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P ⁻ | KOG1764 | |
| 57 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P ⁻ | KOG1764 | |
| 58 | | | | | |
| 59 | 1 Phvul.003G037500 | Phvul.003G037500 | PF00454 | PTHR15245,P ⁻ | KOG2381 |
| 60 | 1 Phvul.009G007300 | Phvul.009G007300 | 0 | PTHR35993 | 0 |
| | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P ⁻ | | 0 |

| | | | | | |
|----|---|------------------|------------------|-----------------------------|---------|
| 1 | | | | | |
| 2 | 1 | Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P | 0 |
| 3 | 1 | Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P | 0 |
| 4 | 1 | Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P | 0 |
| 5 | 1 | Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P | 0 |
| 6 | 1 | Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P | 0 |
| 7 | 1 | Phvul.007G156200 | Phvul.007G156200 | PF00010 PTHR12565,P | 0 |
| 8 | 1 | Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P KOG4172 | |
| 9 | 1 | Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P KOG4172 | |
| 10 | 2 | Phvul.005G001000 | Phvul.005G001000 | PF03552 PTHR13301,P | 0 |
| 11 | 1 | Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P KOG4172 | |
| 12 | 1 | Phvul.008G243700 | Phvul.008G243700 | PF01764 PTHR21493,P | 0 |
| 13 | 1 | Phvul.007G201400 | Phvul.007G201400 | PF03789,PF05PTHR11850,P | KOG0773 |
| 14 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | 0 |
| 15 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | 0 |
| 16 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | 0 |
| 17 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | 0 |
| 18 | 1 | Phvul.003G181600 | Phvul.003G181600 | PF13639 PTHR22763,P | 0 |
| 19 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | 0 |
| 20 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | 0 |
| 21 | 1 | Phvul.006G164800 | Phvul.006G164800 | PF04765 PTHR12956,P | 0 |
| 22 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | 0 |
| 23 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | 0 |
| 24 | 1 | Phvul.005G059700 | Phvul.005G059700 | PF00141 PTHR31235,P | 0 |
| 25 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | 0 |
| 26 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | 0 |
| 27 | 1 | Phvul.005G059500 | Phvul.005G059500 | PF00141 PTHR31235,P | 0 |
| 28 | 1 | Phvul.002G116800 | Phvul.002G116800 | PF10181 PTHR15231,P KOG4551 | |
| 29 | 1 | Phvul.008G103100 | Phvul.008G103100 | PF00249,PF14PTHR31314,P | 0 |
| 30 | 1 | Phvul.008G075300 | Phvul.008G075300 | 0 PTHR33601,P | 0 |
| 31 | 1 | Phvul.003G262800 | Phvul.003G262800 | PF02519 PTHR31374,P | 0 |
| 32 | 1 | Phvul.008G072300 | Phvul.008G072300 | PF00931 PTHR23155,P KOG4658 | |
| 33 | 1 | Phvul.008G072300 | Phvul.008G072300 | PF00931 PTHR23155,P KOG4658 | |
| 34 | 1 | Phvul.004G088300 | Phvul.004G088300 | 0 PTHR36319,P | 0 |
| 35 | 1 | Phvul.004G088300 | Phvul.004G088300 | 0 PTHR36319,P | 0 |
| 36 | 1 | Phvul.004G088300 | Phvul.004G088300 | 0 PTHR36319,P | 0 |
| 37 | 1 | Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P | 0 |
| 38 | 1 | Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P | 0 |
| 39 | 1 | Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P | 0 |
| 40 | 1 | Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P | 0 |
| 41 | 1 | Phvul.004G088300 | Phvul.004G088300 | 0 PTHR36319,P | 0 |
| 42 | 1 | Phvul.009G222600 | Phvul.009G222600 | PF04043,PF01PTHR31707,P | 0 |
| 43 | 1 | Phvul.002G106900 | Phvul.002G106900 | PF04783,PF04PTHR21450,P | 0 |
| 44 | 1 | Phvul.005G099500 | Phvul.005G099500 | PF02469 PTHR32077,P | 0 |
| 45 | 1 | Phvul.003G181900 | Phvul.003G181900 | PF00010 PTHR12565,P | 0 |
| 46 | 1 | Phvul.003G181900 | Phvul.003G181900 | PF00010 PTHR12565,P | 0 |
| 47 | 1 | Phvul.003G121200 | Phvul.003G121200 | PF03151 PTHR11132,P | 0 |

| | | | | | |
|----|--------------------|------------------|-------------------------|---------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P | 0 |
| 3 | 1 Phvul.006G075600 | Phvul.006G075600 | PF00141 | PTHR31388,P | 0 |
| 4 | 1 Phvul.008G284900 | Phvul.008G284900 | PF08801 | PTHR13405,P | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.007G163400 | Phvul.007G163400 | PF00632 | PTHR11254,P | 0 |
| 7 | 1 Phvul.001G266600 | Phvul.001G266600 | PF00464 | PTHR11680,P | 0 |
| 8 | | | | | |
| 9 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P | KOG1764 | |
| 10 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P | KOG1764 | |
| 11 | 1 Phvul.003G037500 | Phvul.003G037500 | PF00454 | PTHR15245,P | KOG2381 |
| 12 | 1 Phvul.009G007300 | Phvul.009G007300 | | 0 PTHR35993 | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P | | 0 |
| 15 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P | | 0 |
| 16 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P | | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P | | 0 |
| 19 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P | | 0 |
| 20 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P | | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.007G156200 | Phvul.007G156200 | PF00010 | PTHR12565,P | 0 |
| 23 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P | KOG4172 |
| 24 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P | KOG4172 |
| 25 | | | | | |
| 26 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P | 0 |
| 27 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P | KOG4172 |
| 28 | 1 Phvul.008G243700 | Phvul.008G243700 | PF01764 | PTHR21493,P | 0 |
| 29 | | | | | |
| 30 | 1 Phvul.007G201400 | Phvul.007G201400 | PF03789,PF05PTHR11850,P | KOG0773 | |
| 31 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 32 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 33 | | | | | |
| 34 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 35 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 36 | 1 Phvul.003G181600 | Phvul.003G181600 | PF13639 | PTHR22763,P | 0 |
| 37 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 38 | | | | | |
| 39 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 40 | 1 Phvul.006G164800 | Phvul.006G164800 | PF04765 | PTHR12956,P | 0 |
| 41 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 42 | | | | | |
| 43 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 44 | 1 Phvul.005G059700 | Phvul.005G059700 | PF00141 | PTHR31235,P | 0 |
| 45 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 46 | | | | | |
| 47 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 48 | 1 Phvul.005G059500 | Phvul.005G059500 | PF00141 | PTHR31235,P | 0 |
| 49 | 1 Phvul.002G116800 | Phvul.002G116800 | PF10181 | PTHR15231,P | KOG4551 |
| 50 | | | | | |
| 51 | 1 Phvul.008G103100 | Phvul.008G103100 | PF00249,PF14PTHR31314,P | | 0 |
| 52 | 1 Phvul.008G075300 | Phvul.008G075300 | | 0 PTHR33601,P | 0 |
| 53 | 1 Phvul.003G262800 | Phvul.003G262800 | PF02519 | PTHR31374,P | 0 |
| 54 | | | | | |
| 55 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P | KOG4658 |
| 56 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P | KOG4658 |
| 57 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P | 0 |
| 58 | | | | | |
| 59 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P | 0 |
| 60 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P | 0 |
| | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P | | 0 |

| | | | | | |
|----|--------------------|------------------|-------------------------|---------|---|
| 1 | | | | | |
| 2 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P | | 0 |
| 3 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P | | 0 |
| 4 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P | | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.004G088300 | Phvul.004G088300 | 0 PTHR36319,P | | 0 |
| 7 | 1 Phvul.009G222600 | Phvul.009G222600 | PF04043,PF01PTHR31707,P | | 0 |
| 8 | 1 Phvul.002G106900 | Phvul.002G106900 | PF04783,PF04PTHR21450,P | | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.005G099500 | Phvul.005G099500 | PF02469 PTHR32077,P | | 0 |
| 11 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 PTHR12565,P | | 0 |
| 12 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 PTHR12565,P | | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 PTHR11132,P | | 0 |
| 15 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 PTHR11132,P | | 0 |
| 16 | 1 Phvul.006G075600 | Phvul.006G075600 | PF00141 PTHR31388,P | | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.008G284900 | Phvul.008G284900 | PF08801 PTHR13405,P | | 0 |
| 19 | 1 Phvul.007G163400 | Phvul.007G163400 | PF00632 PTHR11254,P | | 0 |
| 20 | 1 Phvul.001G266600 | Phvul.001G266600 | PF00464 PTHR11680,P | | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P | KOG1764 | |
| 23 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P | KOG1764 | |
| 24 | 1 Phvul.003G037500 | Phvul.003G037500 | PF00454 PTHR15245,P | KOG2381 | |
| 25 | | | | | |
| 26 | 1 Phvul.009G007300 | Phvul.009G007300 | 0 PTHR35993 | | 0 |
| 27 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P | | 0 |
| 28 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P | | 0 |
| 29 | | | | | |
| 30 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P | | 0 |
| 31 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P | | 0 |
| 32 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P | | 0 |
| 33 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P | | 0 |
| 34 | | | | | |
| 35 | 1 Phvul.007G156200 | Phvul.007G156200 | PF00010 PTHR12565,P | | 0 |
| 36 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P | KOG4172 | |
| 37 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P | KOG4172 | |
| 38 | | | | | |
| 39 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 PTHR13301,P | | 0 |
| 40 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P | KOG4172 | |
| 41 | | | | | |
| 42 | 1 Phvul.008G243700 | Phvul.008G243700 | PF01764 PTHR21493,P | | 0 |
| 43 | 1 Phvul.007G201400 | Phvul.007G201400 | PF03789,PF05PTHR11850,P | KOG0773 | |
| 44 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 45 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 46 | | | | | |
| 47 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 48 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 49 | | | | | |
| 50 | 1 Phvul.003G181600 | Phvul.003G181600 | PF13639 PTHR22763,P | | 0 |
| 51 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 52 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 53 | | | | | |
| 54 | 1 Phvul.006G164800 | Phvul.006G164800 | PF04765 PTHR12956,P | | 0 |
| 55 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 56 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 57 | | | | | |
| 58 | 1 Phvul.005G059700 | Phvul.005G059700 | PF00141 PTHR31235,P | | 0 |
| 59 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| 60 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P | | 0 |
| | 1 Phvul.005G059500 | Phvul.005G059500 | PF00141 PTHR31235,P | | 0 |

| | | | | | |
|----|--------------------|------------------|--------------|----------------------------------|---|
| 1 | | | | | |
| 2 | 1 Phvul.002G116800 | Phvul.002G116800 | PF10181 | PTHR15231,P ⁻ KOG4551 | |
| 3 | 1 Phvul.008G103100 | Phvul.008G103100 | PF00249,PF14 | PTHR31314,P ⁻ | 0 |
| 4 | 1 Phvul.008G075300 | Phvul.008G075300 | | 0 PTHR33601,P ⁻ | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.003G262800 | Phvul.003G262800 | PF02519 | PTHR31374,P ⁻ | 0 |
| 7 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁻ KOG4658 | |
| 8 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁻ KOG4658 | |
| 9 | | | | | |
| 10 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 11 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 12 | | | | | |
| 13 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 14 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12 | PTHR24092,P ⁻ | 0 |
| 15 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02 | PTHR32002,P ⁻ | 0 |
| 16 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02 | PTHR32002,P ⁻ | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12 | PTHR24092,P ⁻ | 0 |
| 19 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 20 | 1 Phvul.009G222600 | Phvul.009G222600 | PF04043,PF01 | PTHR31707,P ⁻ | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.002G106900 | Phvul.002G106900 | PF04783,PF04 | PTHR21450,P ⁻ | 0 |
| 23 | 1 Phvul.005G099500 | Phvul.005G099500 | PF02469 | PTHR32077,P ⁻ | 0 |
| 24 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P ⁻ | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P ⁻ | 0 |
| 27 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P ⁻ | 0 |
| 28 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P ⁻ | 0 |
| 29 | | | | | |
| 30 | 1 Phvul.006G075600 | Phvul.006G075600 | PF00141 | PTHR31388,P ⁻ | 0 |
| 31 | 1 Phvul.008G284900 | Phvul.008G284900 | PF08801 | PTHR13405,P ⁻ | 0 |
| 32 | 1 Phvul.007G163400 | Phvul.007G163400 | PF00632 | PTHR11254,P ⁻ | 0 |
| 33 | | | | | |
| 34 | 1 Phvul.001G266600 | Phvul.001G266600 | PF00464 | PTHR11680,P ⁻ | 0 |
| 35 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16 | PTHR13780,P ⁻ KOG1764 | |
| 36 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16 | PTHR13780,P ⁻ KOG1764 | |
| 37 | | | | | |
| 38 | 1 Phvul.003G037500 | Phvul.003G037500 | PF00454 | PTHR15245,P ⁻ KOG2381 | |
| 39 | 1 Phvul.009G007300 | Phvul.009G007300 | | 0 PTHR35993 | 0 |
| 40 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00 | PTHR10799,P ⁻ | 0 |
| 41 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00 | PTHR10799,P ⁻ | 0 |
| 42 | | | | | |
| 43 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00 | PTHR23315,P ⁻ | 0 |
| 44 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00 | PTHR23315,P ⁻ | 0 |
| 45 | | | | | |
| 46 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05 | PTHR11096,P ⁻ | 0 |
| 47 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05 | PTHR11096,P ⁻ | 0 |
| 48 | 1 Phvul.007G156200 | Phvul.007G156200 | PF00010 | PTHR12565,P ⁻ | 0 |
| 49 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P ⁻ KOG4172 | |
| 50 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P ⁻ KOG4172 | |
| 51 | | | | | |
| 52 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P ⁻ | 0 |
| 53 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P ⁻ KOG4172 | |
| 54 | | | | | |
| 55 | 1 Phvul.008G243700 | Phvul.008G243700 | PF01764 | PTHR21493,P ⁻ | 0 |
| 56 | 1 Phvul.007G201400 | Phvul.007G201400 | PF03789,PF05 | PTHR11850,P ⁻ KOG0773 | |
| 57 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 58 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 59 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 60 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |

| | | | | | |
|----|--------------------|------------------|--------------|---------------------|---|
| 1 | | | | | |
| 2 | 1 Phvul.003G181600 | Phvul.003G181600 | PF13639 | PTHR22763,P | 0 |
| 3 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 4 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.006G164800 | Phvul.006G164800 | PF04765 | PTHR12956,P | 0 |
| 7 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 8 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.005G059700 | Phvul.005G059700 | PF00141 | PTHR31235,P | 0 |
| 11 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 12 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.005G059500 | Phvul.005G059500 | PF00141 | PTHR31235,P | 0 |
| 15 | 1 Phvul.002G116800 | Phvul.002G116800 | PF10181 | PTHR15231,P KOG4551 | |
| 16 | 1 Phvul.008G103100 | Phvul.008G103100 | PF00249,PF14 | PTHR31314,P | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.008G075300 | Phvul.008G075300 | | 0 PTHR33601,P | 0 |
| 19 | 1 Phvul.003G262800 | Phvul.003G262800 | PF02519 | PTHR31374,P | 0 |
| 20 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P KOG4658 | |
| 21 | | | | | |
| 22 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P KOG4658 | |
| 23 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P | 0 |
| 24 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P | 0 |
| 27 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12 | PTHR24092,P | 0 |
| 28 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02 | PTHR32002,P | 0 |
| 29 | | | | | |
| 30 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02 | PTHR32002,P | 0 |
| 31 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12 | PTHR24092,P | 0 |
| 32 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P | 0 |
| 33 | | | | | |
| 34 | 1 Phvul.009G222600 | Phvul.009G222600 | PF04043,PF01 | PTHR31707,P | 0 |
| 35 | 1 Phvul.002G106900 | Phvul.002G106900 | PF04783,PF04 | PTHR21450,P | 0 |
| 36 | 1 Phvul.005G099500 | Phvul.005G099500 | PF02469 | PTHR32077,P | 0 |
| 37 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P | 0 |
| 38 | | | | | |
| 39 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P | 0 |
| 40 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P | 0 |
| 41 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P | 0 |
| 42 | | | | | |
| 43 | 1 Phvul.006G075600 | Phvul.006G075600 | PF00141 | PTHR31388,P | 0 |
| 44 | 1 Phvul.008G284900 | Phvul.008G284900 | PF08801 | PTHR13405,P | 0 |
| 45 | 1 Phvul.007G163400 | Phvul.007G163400 | PF00632 | PTHR11254,P | 0 |
| 46 | | | | | |
| 47 | 1 Phvul.001G266600 | Phvul.001G266600 | PF00464 | PTHR11680,P | 0 |
| 48 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16 | PTHR13780,P KOG1764 | |
| 49 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16 | PTHR13780,P KOG1764 | |
| 50 | | | | | |
| 51 | 1 Phvul.003G037500 | Phvul.003G037500 | PF00454 | PTHR15245,P KOG2381 | |
| 52 | 1 Phvul.009G007300 | Phvul.009G007300 | | 0 PTHR35993 | 0 |
| 53 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00 | PTHR10799,P | 0 |
| 54 | | | | | |
| 55 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00 | PTHR10799,P | 0 |
| 56 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00 | PTHR23315,P | 0 |
| 57 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00 | PTHR23315,P | 0 |
| 58 | | | | | |
| 59 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05 | PTHR11096,P | 0 |
| 60 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05 | PTHR11096,P | 0 |
| | 1 Phvul.007G156200 | Phvul.007G156200 | PF00010 | PTHR12565,P | 0 |

| | | | | | |
|----|--------------------|------------------|--------------|----------------------------------|---|
| 1 | | | | | |
| 2 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P ⁻ KOG4172 | |
| 3 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P ⁻ KOG4172 | |
| 4 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P ⁻ | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P ⁻ KOG4172 | |
| 7 | 1 Phvul.008G243700 | Phvul.008G243700 | PF01764 | PTHR21493,P ⁻ | 0 |
| 8 | | | | | |
| 9 | 1 Phvul.007G201400 | Phvul.007G201400 | PF03789,PF05 | PTHR11850,P ⁻ KOG0773 | |
| 10 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 11 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 12 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 13 | | | | | |
| 14 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 15 | 1 Phvul.003G181600 | Phvul.003G181600 | PF13639 | PTHR22763,P ⁻ | 0 |
| 16 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 17 | | | | | |
| 18 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 19 | 1 Phvul.006G164800 | Phvul.006G164800 | PF04765 | PTHR12956,P ⁻ | 0 |
| 20 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 21 | | | | | |
| 22 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 23 | 1 Phvul.005G059700 | Phvul.005G059700 | PF00141 | PTHR31235,P ⁻ | 0 |
| 24 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 25 | | | | | |
| 26 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 27 | 1 Phvul.005G059500 | Phvul.005G059500 | PF00141 | PTHR31235,P ⁻ | 0 |
| 28 | 1 Phvul.002G116800 | Phvul.002G116800 | PF10181 | PTHR15231,P ⁻ KOG4551 | |
| 29 | | | | | |
| 30 | 1 Phvul.008G103100 | Phvul.008G103100 | PF00249,PF14 | PTHR31314,P ⁻ | 0 |
| 31 | 1 Phvul.008G075300 | Phvul.008G075300 | | 0 PTHR33601,P ⁻ | 0 |
| 32 | 1 Phvul.003G262800 | Phvul.003G262800 | PF02519 | PTHR31374,P ⁻ | 0 |
| 33 | | | | | |
| 34 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁻ KOG4658 | |
| 35 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁻ KOG4658 | |
| 36 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 37 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 38 | | | | | |
| 39 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 40 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12 | PTHR24092,P ⁻ | 0 |
| 41 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02 | PTHR32002,P ⁻ | 0 |
| 42 | | | | | |
| 43 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02 | PTHR32002,P ⁻ | 0 |
| 44 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12 | PTHR24092,P ⁻ | 0 |
| 45 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 46 | | | | | |
| 47 | 1 Phvul.009G222600 | Phvul.009G222600 | PF04043,PF01 | PTHR31707,P ⁻ | 0 |
| 48 | 1 Phvul.002G106900 | Phvul.002G106900 | PF04783,PF04 | PTHR21450,P ⁻ | 0 |
| 49 | 1 Phvul.005G099500 | Phvul.005G099500 | PF02469 | PTHR32077,P ⁻ | 0 |
| 50 | | | | | |
| 51 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P ⁻ | 0 |
| 52 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P ⁻ | 0 |
| 53 | | | | | |
| 54 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P ⁻ | 0 |
| 55 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P ⁻ | 0 |
| 56 | 1 Phvul.006G075600 | Phvul.006G075600 | PF00141 | PTHR31388,P ⁻ | 0 |
| 57 | 1 Phvul.008G284900 | Phvul.008G284900 | PF08801 | PTHR13405,P ⁻ | 0 |
| 58 | | | | | |
| 59 | 1 Phvul.007G163400 | Phvul.007G163400 | PF00632 | PTHR11254,P ⁻ | 0 |
| 60 | 1 Phvul.001G266600 | Phvul.001G266600 | PF00464 | PTHR11680,P ⁻ | 0 |
| | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16 | PTHR13780,P ⁻ KOG1764 | |

| | | | | |
|----|--------------------|------------------|-------------------------|---------------------|
| 1 | | | | |
| 2 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P | KOG1764 |
| 3 | 1 Phvul.003G037500 | Phvul.003G037500 | PF00454 | PTHR15245,P KOG2381 |
| 4 | 1 Phvul.009G007300 | Phvul.009G007300 | 0 | PTHR35993 0 |
| 5 | | | | |
| 6 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P | 0 |
| 7 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P | 0 |
| 8 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P | 0 |
| 9 | | | | |
| 10 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P | 0 |
| 11 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P | 0 |
| 12 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P | 0 |
| 13 | | | | |
| 14 | 1 Phvul.007G156200 | Phvul.007G156200 | PF00010 | PTHR12565,P 0 |
| 15 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P KOG4172 |
| 16 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P KOG4172 |
| 17 | | | | |
| 18 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P 0 |
| 19 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P KOG4172 |
| 20 | 1 Phvul.008G243700 | Phvul.008G243700 | PF01764 | PTHR21493,P 0 |
| 21 | | | | |
| 22 | 1 Phvul.007G201400 | Phvul.007G201400 | PF03789,PF05PTHR11850,P | KOG0773 |
| 23 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P 0 |
| 24 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P 0 |
| 25 | | | | |
| 26 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P 0 |
| 27 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P 0 |
| 28 | 1 Phvul.003G181600 | Phvul.003G181600 | PF13639 | PTHR22763,P 0 |
| 29 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P 0 |
| 30 | | | | |
| 31 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P 0 |
| 32 | 1 Phvul.006G164800 | Phvul.006G164800 | PF04765 | PTHR12956,P 0 |
| 33 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P 0 |
| 34 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P 0 |
| 35 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P 0 |
| 36 | 1 Phvul.005G059700 | Phvul.005G059700 | PF00141 | PTHR31235,P 0 |
| 37 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P 0 |
| 38 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P 0 |
| 39 | 2 Phvul.007G157500 | Phvul.007G157500 | 0 | PTHR24320,P 0 |
| 40 | 1 Phvul.005G059500 | Phvul.005G059500 | PF00141 | PTHR31235,P 0 |
| 41 | 1 Phvul.002G116800 | Phvul.002G116800 | PF10181 | PTHR15231,P KOG4551 |
| 42 | | | | |
| 43 | 1 Phvul.008G103100 | Phvul.008G103100 | PF00249,PF14PTHR31314,P | 0 |
| 44 | 1 Phvul.008G075300 | Phvul.008G075300 | 0 | PTHR33601,P 0 |
| 45 | 1 Phvul.003G262800 | Phvul.003G262800 | PF02519 | PTHR31374,P 0 |
| 46 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P KOG4658 |
| 47 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P KOG4658 |
| 48 | | | | |
| 49 | 1 Phvul.004G088300 | Phvul.004G088300 | 0 | PTHR36319,P 0 |
| 50 | 1 Phvul.004G088300 | Phvul.004G088300 | 0 | PTHR36319,P 0 |
| 51 | 1 Phvul.004G088300 | Phvul.004G088300 | 0 | PTHR36319,P 0 |
| 52 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P | 0 |
| 53 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P | 0 |
| 54 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P | 0 |
| 55 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P | 0 |
| 56 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P | 0 |
| 57 | 1 Phvul.004G088300 | Phvul.004G088300 | 0 | PTHR36319,P 0 |
| 58 | 1 Phvul.004G088300 | Phvul.004G088300 | 0 | PTHR36319,P 0 |
| 59 | 1 Phvul.009G222600 | Phvul.009G222600 | PF04043,PF01PTHR31707,P | 0 |
| 60 | 1 Phvul.002G106900 | Phvul.002G106900 | PF04783,PF04PTHR21450,P | 0 |

| | | | | | |
|----|--------------------|------------------|--------------------------------------|----------------------------|---------|
| 1 | | | | | |
| 2 | 1 Phvul.005G099500 | Phvul.005G099500 | PF02469 | PTHR32077,P ⁻ | 0 |
| 3 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P ⁻ | 0 |
| 4 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P ⁻ | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P ⁻ | 0 |
| 7 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P ⁻ | 0 |
| 8 | 1 Phvul.006G075600 | Phvul.006G075600 | PF00141 | PTHR31388,P ⁻ | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.008G284900 | Phvul.008G284900 | PF08801 | PTHR13405,P ⁻ | 0 |
| 11 | 1 Phvul.007G163400 | Phvul.007G163400 | PF00632 | PTHR11254,P ⁻ | 0 |
| 12 | 1 Phvul.001G266600 | Phvul.001G266600 | PF00464 | PTHR11680,P ⁻ | 0 |
| 13 | | | | | |
| 14 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P ⁻ | KOG1764 | |
| 15 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P ⁻ | KOG1764 | |
| 16 | 1 Phvul.003G037500 | Phvul.003G037500 | PF00454 | PTHR15245,P ⁻ | KOG2381 |
| 17 | | | | | |
| 18 | 1 Phvul.009G007300 | Phvul.009G007300 | | 0 PTHR35993 | 0 |
| 19 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P ⁻ | | 0 |
| 20 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P ⁻ | | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P ⁻ | | 0 |
| 23 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P ⁻ | | 0 |
| 24 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P ⁻ | | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P ⁻ | | 0 |
| 27 | 1 Phvul.007G156200 | Phvul.007G156200 | PF00010 | PTHR12565,P ⁻ | 0 |
| 28 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P ⁻ | KOG4172 |
| 29 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P ⁻ | KOG4172 |
| 30 | | | | | |
| 31 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P ⁻ | 0 |
| 32 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P ⁻ | KOG4172 |
| 33 | | | | | |
| 34 | 1 Phvul.008G243700 | Phvul.008G243700 | PF01764 | PTHR21493,P ⁻ | 0 |
| 35 | 1 Phvul.007G201400 | Phvul.007G201400 | PF03789,PF05PTHR11850,P ⁻ | KOG0773 | |
| 36 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 37 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 38 | | | | | |
| 39 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 40 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 41 | | | | | |
| 42 | 1 Phvul.003G181600 | Phvul.003G181600 | PF13639 | PTHR22763,P ⁻ | 0 |
| 43 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 44 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 45 | | | | | |
| 46 | 1 Phvul.006G164800 | Phvul.006G164800 | PF04765 | PTHR12956,P ⁻ | 0 |
| 47 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 48 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 49 | | | | | |
| 50 | 1 Phvul.005G059700 | Phvul.005G059700 | PF00141 | PTHR31235,P ⁻ | 0 |
| 51 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 52 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 53 | | | | | |
| 54 | 1 Phvul.005G059500 | Phvul.005G059500 | PF00141 | PTHR31235,P ⁻ | 0 |
| 55 | 1 Phvul.002G116800 | Phvul.002G116800 | PF10181 | PTHR15231,P ⁻ | KOG4551 |
| 56 | 1 Phvul.008G103100 | Phvul.008G103100 | PF00249,PF14PTHR31314,P ⁻ | | 0 |
| 57 | 1 Phvul.008G075300 | Phvul.008G075300 | | 0 PTHR33601,P ⁻ | 0 |
| 58 | | | | | |
| 59 | 1 Phvul.003G262800 | Phvul.003G262800 | PF02519 | PTHR31374,P ⁻ | 0 |
| 60 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁻ | KOG4658 |
| | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁻ | KOG4658 |

| | | | | | |
|----|---|------------------|------------------|--------------------------------------|---------|
| 1 | | | | | |
| 2 | 1 | Phvul.004G088300 | Phvul.004G088300 | 0 PTHR36319,P ⁻ | 0 |
| 3 | 1 | Phvul.004G088300 | Phvul.004G088300 | 0 PTHR36319,P ⁻ | 0 |
| 4 | 1 | Phvul.004G088300 | Phvul.004G088300 | 0 PTHR36319,P ⁻ | 0 |
| 5 | | | | | |
| 6 | 1 | Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P ⁻ | 0 |
| 7 | 1 | Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P ⁻ | 0 |
| 8 | 1 | Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P ⁻ | 0 |
| 9 | | | | | |
| 10 | 1 | Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P ⁻ | 0 |
| 11 | 1 | Phvul.004G088300 | Phvul.004G088300 | 0 PTHR36319,P ⁻ | 0 |
| 12 | 1 | Phvul.009G222600 | Phvul.009G222600 | PF04043,PF01PTHR31707,P ⁻ | 0 |
| 13 | | | | | |
| 14 | 1 | Phvul.002G106900 | Phvul.002G106900 | PF04783,PF04PTHR21450,P ⁻ | 0 |
| 15 | 1 | Phvul.005G099500 | Phvul.005G099500 | PF02469 PTHR32077,P ⁻ | 0 |
| 16 | 1 | Phvul.003G181900 | Phvul.003G181900 | PF00010 PTHR12565,P ⁻ | 0 |
| 17 | | | | | |
| 18 | 1 | Phvul.003G181900 | Phvul.003G181900 | PF00010 PTHR12565,P ⁻ | 0 |
| 19 | 1 | Phvul.003G121200 | Phvul.003G121200 | PF03151 PTHR11132,P ⁻ | 0 |
| 20 | 1 | Phvul.003G121200 | Phvul.003G121200 | PF03151 PTHR11132,P ⁻ | 0 |
| 21 | | | | | |
| 22 | 1 | Phvul.006G075600 | Phvul.006G075600 | PF00141 PTHR31388,P ⁻ | 0 |
| 23 | 1 | Phvul.008G284900 | Phvul.008G284900 | PF08801 PTHR13405,P ⁻ | 0 |
| 24 | 1 | Phvul.007G163400 | Phvul.007G163400 | PF00632 PTHR11254,P ⁻ | 0 |
| 25 | | | | | |
| 26 | 1 | Phvul.001G266600 | Phvul.001G266600 | PF00464 PTHR11680,P ⁻ | 0 |
| 27 | 1 | Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P ⁻ | KOG1764 |
| 28 | 1 | Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16PTHR13780,P ⁻ | KOG1764 |
| 29 | 1 | Phvul.003G037500 | Phvul.003G037500 | PF00454 PTHR15245,P ⁻ | KOG2381 |
| 30 | | | | | |
| 31 | 1 | Phvul.009G007300 | Phvul.009G007300 | 0 PTHR35993 | 0 |
| 32 | 1 | Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P ⁻ | 0 |
| 33 | 1 | Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00PTHR10799,P ⁻ | 0 |
| 34 | | | | | |
| 35 | 1 | Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P ⁻ | 0 |
| 36 | 1 | Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00PTHR23315,P ⁻ | 0 |
| 37 | | | | | |
| 38 | 1 | Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P ⁻ | 0 |
| 39 | 1 | Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05PTHR11096,P ⁻ | 0 |
| 40 | 1 | Phvul.007G156200 | Phvul.007G156200 | PF00010 PTHR12565,P ⁻ | 0 |
| 41 | 1 | Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P ⁻ | KOG4172 |
| 42 | 1 | Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P ⁻ | KOG4172 |
| 43 | | | | | |
| 44 | 2 | Phvul.005G001000 | Phvul.005G001000 | PF03552 PTHR13301,P ⁻ | 0 |
| 45 | 1 | Phvul.002G006400 | Phvul.002G006400 | PF13920 PTHR10044,P ⁻ | KOG4172 |
| 46 | | | | | |
| 47 | 1 | Phvul.008G243700 | Phvul.008G243700 | PF01764 PTHR21493,P ⁻ | 0 |
| 48 | 1 | Phvul.007G201400 | Phvul.007G201400 | PF03789,PF05PTHR11850,P ⁻ | KOG0773 |
| 49 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P ⁻ | 0 |
| 50 | | | | | |
| 51 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P ⁻ | 0 |
| 52 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P ⁻ | 0 |
| 53 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P ⁻ | 0 |
| 54 | | | | | |
| 55 | 1 | Phvul.003G181600 | Phvul.003G181600 | PF13639 PTHR22763,P ⁻ | 0 |
| 56 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P ⁻ | 0 |
| 57 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P ⁻ | 0 |
| 58 | | | | | |
| 59 | 1 | Phvul.006G164800 | Phvul.006G164800 | PF04765 PTHR12956,P ⁻ | 0 |
| 60 | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P ⁻ | 0 |
| | 2 | Phvul.007G157500 | Phvul.007G157500 | 0 PTHR24320,P ⁻ | 0 |

| | | | | | |
|----|--------------------|------------------|--------------|----------------------------------|---|
| 1 | | | | | |
| 2 | 1 Phvul.005G059700 | Phvul.005G059700 | PF00141 | PTHR31235,P ⁻ | 0 |
| 3 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 4 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 5 | | | | | |
| 6 | 1 Phvul.005G059500 | Phvul.005G059500 | PF00141 | PTHR31235,P ⁻ | 0 |
| 7 | 1 Phvul.002G116800 | Phvul.002G116800 | PF10181 | PTHR15231,P ⁻ KOG4551 | |
| 8 | 1 Phvul.008G103100 | Phvul.008G103100 | PF00249,PF14 | PTHR31314,P ⁻ | 0 |
| 9 | | | | | |
| 10 | 1 Phvul.008G075300 | Phvul.008G075300 | | 0 PTHR33601,P ⁻ | 0 |
| 11 | 1 Phvul.003G262800 | Phvul.003G262800 | PF02519 | PTHR31374,P ⁻ | 0 |
| 12 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁻ KOG4658 | |
| 13 | | | | | |
| 14 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁻ KOG4658 | |
| 15 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 16 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 17 | | | | | |
| 18 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 19 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12 | PTHR24092,P ⁻ | 0 |
| 20 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02 | PTHR32002,P ⁻ | 0 |
| 21 | | | | | |
| 22 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02 | PTHR32002,P ⁻ | 0 |
| 23 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12 | PTHR24092,P ⁻ | 0 |
| 24 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.009G222600 | Phvul.009G222600 | PF04043,PF01 | PTHR31707,P ⁻ | 0 |
| 27 | 1 Phvul.002G106900 | Phvul.002G106900 | PF04783,PF04 | PTHR21450,P ⁻ | 0 |
| 28 | 1 Phvul.005G099500 | Phvul.005G099500 | PF02469 | PTHR32077,P ⁻ | 0 |
| 29 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P ⁻ | 0 |
| 30 | | | | | |
| 31 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P ⁻ | 0 |
| 32 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P ⁻ | 0 |
| 33 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P ⁻ | 0 |
| 34 | | | | | |
| 35 | 1 Phvul.006G075600 | Phvul.006G075600 | PF00141 | PTHR31388,P ⁻ | 0 |
| 36 | 1 Phvul.008G284900 | Phvul.008G284900 | PF08801 | PTHR13405,P ⁻ | 0 |
| 37 | 1 Phvul.007G163400 | Phvul.007G163400 | PF00632 | PTHR11254,P ⁻ | 0 |
| 38 | | | | | |
| 39 | 1 Phvul.001G266600 | Phvul.001G266600 | PF00464 | PTHR11680,P ⁻ | 0 |
| 40 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16 | PTHR13780,P ⁻ KOG1764 | |
| 41 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16 | PTHR13780,P ⁻ KOG1764 | |
| 42 | | | | | |
| 43 | 1 Phvul.003G037500 | Phvul.003G037500 | PF00454 | PTHR15245,P ⁻ KOG2381 | |
| 44 | 1 Phvul.009G007300 | Phvul.009G007300 | | 0 PTHR35993 | 0 |
| 45 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00 | PTHR10799,P ⁻ | 0 |
| 46 | 1 Phvul.003G100200 | Phvul.003G100200 | PF04851,PF00 | PTHR10799,P ⁻ | 0 |
| 47 | | | | | |
| 48 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00 | PTHR23315,P ⁻ | 0 |
| 49 | 1 Phvul.002G262600 | Phvul.002G262600 | PF00168,PF00 | PTHR23315,P ⁻ | 0 |
| 50 | | | | | |
| 51 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05 | PTHR11096,P ⁻ | 0 |
| 52 | 1 Phvul.002G299004 | Phvul.002G299004 | PF01137,PF05 | PTHR11096,P ⁻ | 0 |
| 53 | 1 Phvul.007G156200 | Phvul.007G156200 | PF00010 | PTHR12565,P ⁻ | 0 |
| 54 | | | | | |
| 55 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P ⁻ KOG4172 | |
| 56 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P ⁻ KOG4172 | |
| 57 | | | | | |
| 58 | 2 Phvul.005G001000 | Phvul.005G001000 | PF03552 | PTHR13301,P ⁻ | 0 |
| 59 | 1 Phvul.002G006400 | Phvul.002G006400 | PF13920 | PTHR10044,P ⁻ KOG4172 | |
| 60 | 1 Phvul.008G243700 | Phvul.008G243700 | PF01764 | PTHR21493,P ⁻ | 0 |
| | 1 Phvul.007G201400 | Phvul.007G201400 | PF03789,PF05 | PTHR11850,P ⁻ KOG0773 | |

| | | | | | |
|----|--------------------|------------------|--------------|----------------------------------|---|
| 1 | | | | | |
| 2 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 3 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 4 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 5 | | | | | |
| 6 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 7 | 1 Phvul.003G181600 | Phvul.003G181600 | PF13639 | PTHR22763,P ⁻ | 0 |
| 8 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 9 | | | | | |
| 10 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 11 | 1 Phvul.006G164800 | Phvul.006G164800 | PF04765 | PTHR12956,P ⁻ | 0 |
| 12 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 13 | | | | | |
| 14 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 15 | 1 Phvul.005G059700 | Phvul.005G059700 | PF00141 | PTHR31235,P ⁻ | 0 |
| 16 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 17 | | | | | |
| 18 | 2 Phvul.007G157500 | Phvul.007G157500 | | 0 PTHR24320,P ⁻ | 0 |
| 19 | 1 Phvul.005G059500 | Phvul.005G059500 | PF00141 | PTHR31235,P ⁻ | 0 |
| 20 | 1 Phvul.002G116800 | Phvul.002G116800 | PF10181 | PTHR15231,P ⁻ KOG4551 | |
| 21 | | | | | |
| 22 | 1 Phvul.008G103100 | Phvul.008G103100 | PF00249,PF14 | PTHR31314,P ⁻ | 0 |
| 23 | 1 Phvul.008G075300 | Phvul.008G075300 | | 0 PTHR33601,P ⁻ | 0 |
| 24 | 1 Phvul.003G262800 | Phvul.003G262800 | PF02519 | PTHR31374,P ⁻ | 0 |
| 25 | | | | | |
| 26 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁻ KOG4658 | |
| 27 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁻ KOG4658 | |
| 28 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 29 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 30 | | | | | |
| 31 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 32 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12 | PTHR24092,P ⁻ | 0 |
| 33 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02 | PTHR32002,P ⁻ | 0 |
| 34 | | | | | |
| 35 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02 | PTHR32002,P ⁻ | 0 |
| 36 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12 | PTHR24092,P ⁻ | 0 |
| 37 | 1 Phvul.004G088300 | Phvul.004G088300 | | 0 PTHR36319,P ⁻ | 0 |
| 38 | | | | | |
| 39 | 1 Phvul.006G075600 | Phvul.006G075600 | PF00141 | PTHR31388,P ⁻ | 0 |
| 40 | 1 Phvul.008G284900 | Phvul.008G284900 | PF08801 | PTHR13405,P ⁻ | 0 |
| 41 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16 | PTHR13780,P ⁻ KOG1764 | |
| 42 | | | | | |
| 43 | 1 Phvul.009G222600 | Phvul.009G222600 | PF04043,PF01 | PTHR31707,P ⁻ | 0 |
| 44 | 1 Phvul.006G091100 | Phvul.006G091100 | PF00571,PF16 | PTHR13780,P ⁻ KOG1764 | |
| 45 | 1 Phvul.002G106900 | Phvul.002G106900 | PF04783,PF04 | PTHR21450,P ⁻ | 0 |
| 46 | | | | | |
| 47 | 1 Phvul.005G099500 | Phvul.005G099500 | PF02469 | PTHR32077,P ⁻ | 0 |
| 48 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P ⁻ | 0 |
| 49 | 1 Phvul.003G181900 | Phvul.003G181900 | PF00010 | PTHR12565,P ⁻ | 0 |
| 50 | | | | | |
| 51 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P ⁻ | 0 |
| 52 | 1 Phvul.003G121200 | Phvul.003G121200 | PF03151 | PTHR11132,P ⁻ | 0 |
| 53 | 1 Phvul.005G059700 | Phvul.005G059700 | PF00141 | PTHR31235,P ⁻ | 0 |
| 54 | | | | | |
| 55 | 1 Phvul.005G059500 | Phvul.005G059500 | PF00141 | PTHR31235,P ⁻ | 0 |
| 56 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁻ KOG4658 | |
| 57 | 1 Phvul.008G072300 | Phvul.008G072300 | PF00931 | PTHR23155,P ⁻ KOG4658 | |
| 58 | | | | | |
| 59 | 1 Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12 | PTHR24092,P ⁻ | 0 |
| 60 | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02 | PTHR32002,P ⁻ | 0 |
| | 1 Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02 | PTHR32002,P ⁻ | 0 |

| | | | | | |
|----|---|------------------|------------------|--------------------------------------|---------|
| 1 | | | | | |
| 2 | 1 | Phvul.009G201600 | Phvul.009G201600 | PF00122,PF12PTHR24092,P ⁻ | 0 |
| 3 | 1 | Phvul.005G155100 | Phvul.005G155100 | PF00564,PF02PTHR32002,P ⁻ | 0 |
| 4 | 1 | Phvul.009G114400 | Phvul.009G114400 | PF00069 PTHR27000,P ⁻ | KOG1187 |
| 5 | | | | | |
| 6 | 1 | Phvul.003G240100 | Phvul.003G240100 | PF12710,PF00PTHR24093,P ⁻ | 0 |
| 7 | 1 | Phvul.002G283000 | Phvul.002G283000 | PF12627,PF01PTHR13734,P ⁻ | 0 |
| 8 | 1 | Phvul.002G283000 | Phvul.002G283000 | PF12627,PF01PTHR13734,P ⁻ | 0 |
| 9 | | | | | |
| 10 | 1 | Phvul.002G283000 | Phvul.002G283000 | PF12627,PF01PTHR13734,P ⁻ | 0 |
| 11 | 1 | Phvul.003G170100 | Phvul.003G170100 | PF00862,PF05PTHR12526,P ⁻ | KOG0853 |
| 12 | 1 | Phvul.011G173600 | Phvul.011G173600 | PF01535,PF13PTHR24015,P ⁻ | 0 |
| 13 | | | | | |
| 14 | 1 | Phvul.003G283500 | Phvul.003G283500 | PF07297 PTHR15039,P ⁻ | KOG3488 |
| 15 | 1 | Phvul.007G163400 | Phvul.007G163400 | PF00632 PTHR11254,P ⁻ | 0 |
| 16 | 1 | Phvul.003G037500 | Phvul.003G037500 | PF00454 PTHR15245,P ⁻ | KOG2381 |
| 17 | | | | | |
| 18 | 1 | Phvul.001G266600 | Phvul.001G266600 | PF00464 PTHR11680,P ⁻ | 0 |
| 19 | 1 | Phvul.001G243500 | Phvul.001G243500 | PF00069 PTHR27003,P ⁻ | KOG1187 |
| 20 | 2 | Phvul.006G067900 | Phvul.006G067900 | PF01699 PTHR31503,P ⁻ | KOG1397 |
| 21 | | | | | |
| 22 | 1 | Phvul.008G140600 | Phvul.008G140600 | PF00201 PTHR11926,P ⁻ | 0 |
| 23 | | | | | |
| 24 | | | | | |
| 25 | | | | | |
| 26 | | | | | |
| 27 | | | | | |
| 28 | | | | | |
| 29 | | | | | |
| 30 | | | | | |
| 31 | | | | | |
| 32 | | | | | |
| 33 | | | | | |
| 34 | | | | | |
| 35 | | | | | |
| 36 | | | | | |
| 37 | | | | | |
| 38 | | | | | |
| 39 | | | | | |
| 40 | | | | | |
| 41 | | | | | |
| 42 | | | | | |
| 43 | | | | | |
| 44 | | | | | |
| 45 | | | | | |
| 46 | | | | | |
| 47 | | | | | |
| 48 | | | | | |
| 49 | | | | | |
| 50 | | | | | |
| 51 | | | | | |
| 52 | | | | | |
| 53 | | | | | |
| 54 | | | | | |
| 55 | | | | | |
| 56 | | | | | |
| 57 | | | | | |
| 58 | | | | | |
| 59 | | | | | |
| 60 | | | | | |

| 1 | KEGG | KOG | GO | Best-hit-arabi-arabi-symbol |
|----|------|-----|---|-----------------------------|
| 2 | | | | |
| 3 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 4 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 5 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 6 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 7 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 8 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 9 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 10 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 11 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 12 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 13 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 14 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 15 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 16 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 17 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 18 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 19 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 20 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 21 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 22 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 23 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 24 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 25 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 26 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 27 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 28 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 29 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 30 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 31 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 32 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 33 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 34 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 35 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 36 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 37 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 38 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 39 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 40 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 41 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 42 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 43 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 44 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 45 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 46 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 47 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 48 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 49 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 50 | | 0 | 0 GO:0006355,(AT5G61430.1 ANAC100,ATNAC5,NAC100 | |
| 51 | | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 | |
| 52 | | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 | |
| 53 | | 0 | 0 GO:0006355,(AT1G56010.2 anac021,ANAC022,NAC1 | |
| 54 | | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 | |
| 55 | | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 | |
| 56 | | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 | |
| 57 | | 0 | 0 GO:0006355,(AT1G56010.2 anac021,ANAC022,NAC1 | |
| 58 | | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 | |
| 59 | | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 | |
| 60 | | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 | |
| | | 0 | 0 GO:0006355,(AT1G56010.2 anac021,ANAC022,NAC1 | |

| | | |
|----|---|--|
| 1 | | |
| 2 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 3 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 4 | 0 | 0 GO:0006355,(AT1G56010.2 anac021,ANAC022,NAC1 |
| 5 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 6 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 7 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 8 | 0 | 0 GO:0006355,(AT1G56010.2 anac021,ANAC022,NAC1 |
| 9 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 10 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 11 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 12 | 0 | 0 GO:0006355,(AT1G56010.2 anac021,ANAC022,NAC1 |
| 13 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 14 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 15 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 16 | 0 | 0 GO:0006355,(AT1G56010.2 anac021,ANAC022,NAC1 |
| 17 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 18 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 19 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 20 | 0 | 0 GO:0006355,(AT1G56010.2 anac021,ANAC022,NAC1 |
| 21 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 22 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 23 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 24 | 0 | 0 GO:0006355,(AT1G56010.2 anac021,ANAC022,NAC1 |
| 25 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 26 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 27 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 28 | 0 | 0 GO:0006355,(AT1G56010.2 anac021,ANAC022,NAC1 |
| 29 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 30 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 31 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 32 | 0 | 0 GO:0006355,(AT1G56010.2 anac021,ANAC022,NAC1 |
| 33 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 34 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 35 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 36 | 0 | 0 GO:0006355,(AT1G56010.2 anac021,ANAC022,NAC1 |
| 37 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 38 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 39 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 40 | 0 | 0 GO:0006355,(AT1G56010.2 anac021,ANAC022,NAC1 |
| 41 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 42 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 43 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 44 | 0 | 0 GO:0006355,(AT1G56010.2 anac021,ANAC022,NAC1 |
| 45 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 46 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 47 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 48 | 0 | 0 GO:0006355,(AT1G56010.2 anac021,ANAC022,NAC1 |
| 49 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 50 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 51 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 52 | 0 | 0 GO:0006355,(AT1G56010.2 anac021,ANAC022,NAC1 |
| 53 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 54 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 55 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 56 | 0 | 0 GO:0006355,(AT1G56010.2 anac021,ANAC022,NAC1 |
| 57 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 58 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 59 | 0 | 0 GO:0006355,(AT5G53950.1 ANAC098,ATCUC2,CUC2 |
| 60 | 0 | 0 GO:0006355,(AT1G56010.2 anac021,ANAC022,NAC1 |

| | | | | | |
|----|----------|----------|---|------------------------------|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 AT2G37100.1 | 0 |
| 3 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 4 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 5 | | | | | |
| 6 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 7 | | 0 K00588 | | GO:0008171 AT4G26220.1 | 0 |
| 8 | 3.1.1.3 | | | 0 GO:0016788 AT1G29670.1 | 0 |
| 9 | | | | | |
| 10 | | 0 | 0 | 0 AT2G37100.1 | 0 |
| 11 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 12 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 13 | | | | | |
| 14 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 15 | | 0 K00588 | | GO:0008171 AT4G26220.1 | 0 |
| 16 | 3.1.1.3 | | | 0 GO:0016788 AT1G29670.1 | 0 |
| 17 | | | | | |
| 18 | | 0 | 0 | 0 AT2G37100.1 | 0 |
| 19 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 20 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 21 | | | | | |
| 22 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 23 | | 0 K00588 | | GO:0008171 AT4G26220.1 | 0 |
| 24 | 3.1.1.3 | | | 0 GO:0016788 AT1G29670.1 | 0 |
| 25 | | | | | |
| 26 | | 0 | 0 | 0 AT2G37100.1 | 0 |
| 27 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 28 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 29 | | | | | |
| 30 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 31 | | 0 K00588 | | GO:0008171 AT4G26220.1 | 0 |
| 32 | 3.1.1.3 | | | 0 GO:0016788 AT1G29670.1 | 0 |
| 33 | | | | | |
| 34 | | 0 | 0 | 0 AT2G37100.1 | 0 |
| 35 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 36 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 37 | | | | | |
| 38 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 39 | | 0 K00588 | | GO:0008171 AT4G26220.1 | 0 |
| 40 | 3.1.1.3 | | | 0 GO:0016788 AT1G29670.1 | 0 |
| 41 | | | | | |
| 42 | | 0 | 0 | 0 AT2G37100.1 | 0 |
| 43 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 44 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 45 | | | | | |
| 46 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 47 | | 0 K00588 | | GO:0008171 AT4G26220.1 | 0 |
| 48 | 3.1.1.3 | | | 0 GO:0016788 AT1G29670.1 | 0 |
| 49 | | | | | |
| 50 | | 0 | 0 | 0 AT2G37100.1 | 0 |
| 51 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 52 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 53 | | | | | |
| 54 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 55 | | 0 K00588 | | GO:0008171 AT4G26220.1 | 0 |
| 56 | 3.1.1.3 | | | 0 GO:0016788 AT1G29670.1 | 0 |
| 57 | | | | | |
| 58 | | 0 | 0 | 0 AT2G37100.1 | 0 |
| 59 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| 60 | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |
| | 4.1.1.35 | K08678 | | GO:0055114,(AT2G28760.3 UXS6 | |

| | | | | | |
|----|----------|----------|-------------------------------|--|---|
| 1 | | | | | |
| 2 | | 0 K00588 | GO:0008171 AT4G26220.1 | | 0 |
| 3 | 3.1.1.3 | | 0 GO:0016788 AT1G29670.1 | | 0 |
| 4 | | 0 | 0 0 AT2G37100.1 | | 0 |
| 5 | | | | | |
| 6 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 7 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 8 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 9 | | | | | |
| 10 | | 0 K00588 | GO:0008171 AT4G26220.1 | | 0 |
| 11 | 3.1.1.3 | | 0 GO:0016788 AT1G29670.1 | | 0 |
| 12 | | 0 | 0 0 AT2G37100.1 | | 0 |
| 13 | | | | | |
| 14 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 15 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 16 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 17 | | | | | |
| 18 | | 0 K00588 | GO:0008171 AT4G26220.1 | | 0 |
| 19 | 3.1.1.3 | | 0 GO:0016788 AT1G29670.1 | | 0 |
| 20 | | 0 | 0 0 AT2G37100.1 | | 0 |
| 21 | | | | | |
| 22 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 23 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 24 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 25 | | | | | |
| 26 | | 0 K00588 | GO:0008171 AT4G26220.1 | | 0 |
| 27 | 3.1.1.3 | | 0 GO:0016788 AT1G29670.1 | | 0 |
| 28 | | 0 | 0 0 AT2G37100.1 | | 0 |
| 29 | | | | | |
| 30 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 31 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 32 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 33 | | | | | |
| 34 | | 0 K00588 | GO:0008171 AT4G26220.1 | | 0 |
| 35 | 3.1.1.3 | | 0 GO:0016788 AT1G29670.1 | | 0 |
| 36 | | 0 | 0 0 AT2G37100.1 | | 0 |
| 37 | | | | | |
| 38 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 39 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 40 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 41 | | | | | |
| 42 | | 0 K00588 | GO:0008171 AT4G26220.1 | | 0 |
| 43 | 3.1.1.3 | | 0 GO:0016788 AT1G29670.1 | | 0 |
| 44 | | 0 | 0 0 AT2G37100.1 | | 0 |
| 45 | | | | | |
| 46 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 47 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 48 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 49 | | | | | |
| 50 | | 0 K00588 | GO:0008171 AT4G26220.1 | | 0 |
| 51 | 3.1.1.3 | | 0 GO:0016788 AT1G29670.1 | | 0 |
| 52 | | 0 | 0 0 AT2G37100.1 | | 0 |
| 53 | | | | | |
| 54 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 55 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 56 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |
| 57 | | | | | |
| 58 | | 0 K00588 | GO:0008171 AT4G26220.1 | | 0 |
| 59 | 3.1.1.3 | | 0 GO:0016788 AT1G29670.1 | | 0 |
| 60 | | 0 | 0 0 AT2G37100.1 | | 0 |
| | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | | |

| | | | | |
|----|-----------|----------|---------------------------------------|---|
| 1 | | | | |
| 2 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | |
| 3 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | |
| 4 | | 0 K00588 | GO:0008171 AT4G26220.1 | 0 |
| 5 | | | | |
| 6 | 3.1.1.3 | | 0 GO:0016788 AT1G29670.1 | 0 |
| 7 | | 0 | 0 AT2G37100.1 | 0 |
| 8 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | |
| 9 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | |
| 10 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | |
| 11 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | |
| 12 | | 0 K00588 | GO:0008171 AT4G26220.1 | 0 |
| 13 | | | | |
| 14 | 3.1.1.3 | | 0 GO:0016788 AT1G29670.1 | 0 |
| 15 | | 0 | 0 AT2G37100.1 | 0 |
| 16 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | |
| 17 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | |
| 18 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | |
| 19 | 4.1.1.35 | K08678 | GO:0055114,(CAT2G28760.3 UXS6 | |
| 20 | | 0 K00588 | GO:0008171 AT4G26220.1 | 0 |
| 21 | | 0 | 0 AT2G45680.1 | 0 |
| 22 | | | | |
| 23 | 2.4.1.227 | K02563 | GO:0030259,(AT1G73740.1 | 0 |
| 24 | | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 | |
| 25 | 3.1.1.3 | | 0 GO:0016788 AT1G33811.1 | 0 |
| 26 | | 0 | 0 AT5G40600.1 | 0 |
| 27 | | 0 | 0 AT5G40600.1 | 0 |
| 28 | | 0 | 0 AT5G40600.1 | 0 |
| 29 | | 0 | 0 AT5G40600.1 | 0 |
| 30 | | 0 | 0 0 | 0 |
| 31 | | 0 | 0 0 | 0 |
| 32 | | 0 K13754 | GO:0055085,(AT1G54115.1 ATCCX4,CCX4 | |
| 33 | | 0 | 0 AT2G45680.1 | 0 |
| 34 | | | | |
| 35 | 2.4.1.227 | K02563 | GO:0030259,(AT1G73740.1 | 0 |
| 36 | | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 | |
| 37 | 3.1.1.3 | | 0 GO:0016788 AT1G33811.1 | 0 |
| 38 | | 0 | 0 AT5G40600.1 | 0 |
| 39 | | 0 | 0 AT5G40600.1 | 0 |
| 40 | | 0 | 0 AT5G40600.1 | 0 |
| 41 | | 0 | 0 AT5G40600.1 | 0 |
| 42 | | 0 | 0 0 | 0 |
| 43 | | 0 | 0 0 | 0 |
| 44 | | 0 K13754 | GO:0055085,(AT1G54115.1 ATCCX4,CCX4 | |
| 45 | | 0 | 0 AT2G45680.1 | 0 |
| 46 | | | | |
| 47 | 2.4.1.227 | K02563 | GO:0030259,(AT1G73740.1 | 0 |
| 48 | | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 | |
| 49 | 3.1.1.3 | | 0 GO:0016788 AT1G33811.1 | 0 |
| 50 | | 0 | 0 AT5G40600.1 | 0 |
| 51 | | 0 | 0 AT5G40600.1 | 0 |
| 52 | | 0 | 0 AT5G40600.1 | 0 |
| 53 | | 0 | 0 AT5G40600.1 | 0 |
| 54 | | 0 | 0 0 | 0 |
| 55 | | 0 | 0 0 | 0 |
| 56 | | 0 K13754 | GO:0055085,(AT1G54115.1 ATCCX4,CCX4 | |
| 57 | | 0 | 0 AT2G45680.1 | 0 |
| 58 | | | | |
| 59 | 2.4.1.227 | K02563 | GO:0030259,(AT1G73740.1 | 0 |
| 60 | | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 | |
| | 3.1.1.3 | | 0 GO:0016788 AT1G33811.1 | 0 |

| | | | | |
|----|-----------|----------|-------------------------------------|---------------------------------------|
| 1 | | | | |
| 2 | | 0 | 0 | 0 AT5G40600.1 |
| 3 | | 0 | 0 | 0 AT5G40600.1 |
| 4 | | 0 | 0 | 0 AT5G40600.1 |
| 5 | | 0 | 0 | 0 |
| 6 | | 0 | 0 | 0 |
| 7 | | 0 K13754 | GO:0055085,(AT1G54115.1 ATCCX4,CCX4 | |
| 8 | | 0 | 0 | 0 AT2G45680.1 |
| 9 | | | | |
| 10 | 2.4.1.227 | K02563 | GO:0030259,(AT1G73740.1 | 0 |
| 11 | | 0 | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 |
| 12 | 3.1.1.3 | | 0 GO:0016788 AT1G33811.1 | 0 |
| 13 | | | | |
| 14 | | 0 | 0 | 0 AT5G40600.1 |
| 15 | | 0 | 0 | 0 AT5G40600.1 |
| 16 | | 0 | 0 | 0 AT5G40600.1 |
| 17 | | 0 | 0 | 0 |
| 18 | | 0 | 0 | 0 |
| 19 | | 0 K13754 | GO:0055085,(AT1G54115.1 ATCCX4,CCX4 | |
| 20 | | 0 | 0 | 0 AT2G45680.1 |
| 21 | | | | |
| 22 | 2.4.1.227 | K02563 | GO:0030259,(AT1G73740.1 | 0 |
| 23 | | 0 | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 |
| 24 | 3.1.1.3 | | 0 GO:0016788 AT1G33811.1 | 0 |
| 25 | | | | |
| 26 | | 0 | 0 | 0 AT5G40600.1 |
| 27 | | 0 | 0 | 0 AT5G40600.1 |
| 28 | | 0 | 0 | 0 AT5G40600.1 |
| 29 | | 0 | 0 | 0 |
| 30 | | 0 | 0 | 0 |
| 31 | | 0 K13754 | GO:0055085,(AT1G54115.1 ATCCX4,CCX4 | |
| 32 | | 0 | 0 | 0 AT2G45680.1 |
| 33 | | | | |
| 34 | 2.4.1.227 | K02563 | GO:0030259,(AT1G73740.1 | 0 |
| 35 | | 0 | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 |
| 36 | 3.1.1.3 | | 0 GO:0016788 AT1G33811.1 | 0 |
| 37 | | | | |
| 38 | | 0 | 0 | 0 AT5G40600.1 |
| 39 | | 0 | 0 | 0 AT5G40600.1 |
| 40 | | 0 | 0 | 0 AT5G40600.1 |
| 41 | | 0 | 0 | 0 |
| 42 | | 0 | 0 | 0 |
| 43 | | 0 K13754 | GO:0055085,(AT1G54115.1 ATCCX4,CCX4 | |
| 44 | | 0 | 0 | 0 AT2G45680.1 |
| 45 | | | | |
| 46 | 2.4.1.227 | K02563 | GO:0030259,(AT1G73740.1 | 0 |
| 47 | | 0 | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 |
| 48 | 3.1.1.3 | | 0 GO:0016788 AT1G33811.1 | 0 |
| 49 | | | | |
| 50 | | 0 | 0 | 0 AT5G40600.1 |
| 51 | | 0 | 0 | 0 AT5G40600.1 |
| 52 | | 0 | 0 | 0 AT5G40600.1 |
| 53 | | 0 | 0 | 0 |
| 54 | | 0 | 0 | 0 |
| 55 | | 0 K13754 | GO:0055085,(AT1G54115.1 ATCCX4,CCX4 | |
| 56 | | 0 | 0 | 0 AT2G45680.1 |
| 57 | | | | |
| 58 | 2.4.1.227 | K02563 | GO:0030259,(AT1G73740.1 | 0 |
| 59 | | 0 | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 |
| 60 | 3.1.1.3 | | 0 GO:0016788 AT1G33811.1 | 0 |
| | | 0 | 0 | 0 AT5G40600.1 |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

| | | | | |
|-----------|----------|-------------------------------------|---------------------------------------|---|
| | 0 | 0 | 0 AT5G40600.1 | 0 |
| | 0 | 0 | 0 AT5G40600.1 | 0 |
| | 0 | 0 | 0 0 | 0 |
| | 0 K13754 | GO:0055085,(AT1G54115.1 ATCCX4,CCX4 | | |
| | 0 | 0 | 0 AT2G45680.1 | 0 |
| 2.4.1.227 | K02563 | GO:0030259,(AT1G73740.1 | | 0 |
| | 0 | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 | |
| 3.1.1.3 | | 0 GO:0016788 AT1G33811.1 | | 0 |
| | 0 | 0 | 0 AT5G40600.1 | 0 |
| | 0 | 0 | 0 AT5G40600.1 | 0 |
| | 0 | 0 | 0 AT5G40600.1 | 0 |
| | 0 | 0 | 0 0 | 0 |
| | 0 K13754 | GO:0055085,(AT1G54115.1 ATCCX4,CCX4 | | |
| | 0 | 0 | 0 AT2G45680.1 | 0 |
| 2.4.1.227 | K02563 | GO:0030259,(AT1G73740.1 | | 0 |
| | 0 | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 | |
| 3.1.1.3 | | 0 GO:0016788 AT1G33811.1 | | 0 |
| | 0 | 0 | 0 AT5G40600.1 | 0 |
| | 0 | 0 | 0 AT5G40600.1 | 0 |
| | 0 | 0 | 0 AT5G40600.1 | 0 |
| | 0 | 0 | 0 0 | 0 |
| | 0 K13754 | GO:0055085,(AT1G54115.1 ATCCX4,CCX4 | | |
| | 0 | 0 | 0 AT2G45680.1 | 0 |
| 2.4.1.227 | K02563 | GO:0030259,(AT1G73740.1 | | 0 |
| | 0 | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 | |
| 3.1.1.3 | | 0 GO:0016788 AT1G33811.1 | | 0 |
| | 0 | 0 | 0 AT5G40600.1 | 0 |
| | 0 | 0 | 0 AT5G40600.1 | 0 |
| | 0 | 0 | 0 AT5G40600.1 | 0 |
| | 0 | 0 | 0 0 | 0 |
| | 0 K13754 | GO:0055085,(AT1G54115.1 ATCCX4,CCX4 | | |
| | 0 | 0 | 0 AT2G45680.1 | 0 |
| 2.4.1.227 | K02563 | GO:0030259,(AT1G73740.1 | | 0 |
| | 0 | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 | |
| 3.1.1.3 | | 0 GO:0016788 AT1G33811.1 | | 0 |
| | 0 | 0 | 0 AT5G40600.1 | 0 |
| | 0 | 0 | 0 AT5G40600.1 | 0 |
| | 0 | 0 | 0 AT5G40600.1 | 0 |
| | 0 | 0 | 0 0 | 0 |
| | 0 K13754 | GO:0055085,(AT1G54115.1 ATCCX4,CCX4 | | |
| | 0 | 0 | 0 AT2G45680.1 | 0 |
| 2.4.1.227 | K02563 | GO:0030259,(AT1G73740.1 | | 0 |
| | 0 | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 | |
| 3.1.1.3 | | 0 GO:0016788 AT1G33811.1 | | 0 |
| | 0 | 0 | 0 AT5G40600.1 | 0 |
| | 0 | 0 | 0 AT5G40600.1 | 0 |
| | 0 | 0 | 0 AT5G40600.1 | 0 |
| | 0 | 0 | 0 0 | 0 |
| | 0 K13754 | GO:0055085,(AT1G54115.1 ATCCX4,CCX4 | | |
| | 0 | 0 | 0 AT2G45680.1 | 0 |
| 2.4.1.227 | K02563 | GO:0030259,(AT1G73740.1 | | 0 |
| | 0 | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 | |
| 3.1.1.3 | | 0 GO:0016788 AT1G33811.1 | | 0 |
| | 0 | 0 | 0 AT5G40600.1 | 0 |
| | 0 | 0 | 0 AT5G40600.1 | 0 |

| | | | | | |
|----|-----------|----------|---|--|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 AT5G40600.1 | 0 |
| 3 | | 0 | 0 | 0 | 0 |
| 4 | | 0 K13754 | | GO:0055085,(AT1G54115.1 ATCCX4,CCX4 | |
| 5 | | 0 | 0 | 0 AT2G45680.1 | 0 |
| 6 | | 0 | 0 | 0 AT2G45680.1 | 0 |
| 7 | 2.4.1.227 | K02563 | | GO:0030259,(AT1G73740.1 | 0 |
| 8 | | 0 | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 | |
| 9 | | 0 | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 | |
| 10 | 3.1.1.3 | | | 0 GO:0016788 AT1G33811.1 | 0 |
| 11 | | 0 | 0 | 0 AT5G40600.1 | 0 |
| 12 | | 0 | 0 | 0 AT5G40600.1 | 0 |
| 13 | | 0 | 0 | 0 AT5G40600.1 | 0 |
| 14 | | 0 | 0 | 0 AT5G40600.1 | 0 |
| 15 | | 0 | 0 | 0 | 0 |
| 16 | | 0 K13754 | | GO:0055085,(AT1G54115.1 ATCCX4,CCX4 | |
| 17 | | 0 | 0 | 0 AT2G45680.1 | 0 |
| 18 | | 0 | 0 | 0 AT2G45680.1 | 0 |
| 19 | 2.4.1.227 | K02563 | | GO:0030259,(AT1G73740.1 | 0 |
| 20 | | 0 | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 | |
| 21 | | 0 | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 | |
| 22 | 3.1.1.3 | | | 0 GO:0016788 AT1G33811.1 | 0 |
| 23 | | 0 | 0 | 0 AT5G40600.1 | 0 |
| 24 | | 0 | 0 | 0 AT5G40600.1 | 0 |
| 25 | | 0 | 0 | 0 AT5G40600.1 | 0 |
| 26 | | 0 | 0 | 0 AT5G40600.1 | 0 |
| 27 | | 0 | 0 | 0 | 0 |
| 28 | | 0 K13754 | | GO:0055085,(AT1G54115.1 ATCCX4,CCX4 | |
| 29 | | 0 | 0 | 0 AT2G45680.1 | 0 |
| 30 | | 0 | 0 | 0 AT2G45680.1 | 0 |
| 31 | 2.4.1.227 | K02563 | | GO:0030259,(AT1G73740.1 | 0 |
| 32 | | 0 | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 | |
| 33 | | 0 | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 | |
| 34 | 3.1.1.3 | | | 0 GO:0016788 AT1G33811.1 | 0 |
| 35 | | 0 | 0 | 0 AT5G40600.1 | 0 |
| 36 | | 0 | 0 | 0 AT5G40600.1 | 0 |
| 37 | | 0 | 0 | 0 AT5G40600.1 | 0 |
| 38 | | 0 | 0 | 0 AT5G40600.1 | 0 |
| 39 | | 0 | 0 | 0 | 0 |
| 40 | | 0 K13754 | | GO:0055085,(AT1G54115.1 ATCCX4,CCX4 | |
| 41 | | 0 | 0 | 0 AT2G45680.1 | 0 |
| 42 | | 0 | 0 | 0 AT2G45680.1 | 0 |
| 43 | 2.4.1.227 | K02563 | | GO:0030259,(AT1G73740.1 | 0 |
| 44 | | 0 | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 | |
| 45 | | 0 | 0 | 0 AT3G19180.1 ARC6H,ATCDP1,CDP1,PARC6 | |
| 46 | 3.1.1.3 | | | 0 GO:0016788 AT1G33811.1 | 0 |
| 47 | | 0 | 0 | 0 AT5G40600.1 | 0 |
| 48 | | 0 | 0 | 0 AT5G40600.1 | 0 |
| 49 | | 0 | 0 | 0 AT5G40600.1 | 0 |
| 50 | | 0 | 0 | 0 AT5G40600.1 | 0 |
| 51 | | 0 K12124 | | 0 AT1G22770.1 FB,GI | |
| 52 | | 0 K12124 | | 0 AT1G22770.1 FB,GI | |
| 53 | | 0 K09338 | | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | |
| 54 | | 0 | 0 | 0 AT5G60690.1 IFL,IFL1,REV | |
| 55 | 2.7.11.1 | | | 0 GO:0006468,(AT4G05200.1 CRK25 | |
| 56 | | 0 | 0 | 0 AT4G28100.1 | 0 |
| 57 | | 0 | 0 | 0 AT4G05200.1 CRK25 | |
| 58 | | 0 | 0 | 0 AT4G05200.1 CRK25 | |
| 59 | | 0 | 0 | 0 GO:0055085,(AT1G55620.2 ATCLC-F,CLC-F,CLCF | |
| 60 | 2.3.1.30 | K00640 | | GO:0009001,(AT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M | |
| | | 0 | 0 | 0 | 0 |

| | | | | | |
|----|----------|----------|--|--|---|
| 1 | | | | | |
| 2 | | 0 K13354 | 0 AT2G39970.1 | | 0 |
| 3 | 3.6.4.12 | K11647 | GO:0016787,(AT2G46020.2 ATBRM,BRM,CHA2,CHR2 | | |
| 4 | 5.2.1.8 | K05864 | GO:0005515,(AT2G15790.1 CYP40,SQN | | |
| 5 | | | | | |
| 6 | | 0 | 0 GO:0008168 AT5G64030.1 | | 0 |
| 7 | | 0 | 0 0 0 | | 0 |
| 8 | | | | | |
| 9 | | 0 K09264 | GO:0006355,(AT5G20240.1 PI | | |
| 10 | | 0 | 0 GO:0008168,(AT2G16030.1 | | 0 |
| 11 | | 0 | 0 GO:0005524,(AT1G05910.1 | | 0 |
| 12 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 13 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 14 | | | | | |
| 15 | | 0 K09338 | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | | |
| 16 | 2.7.11.1 | | 0 GO:0006468,(AT4G05200.1 CRK25 | | |
| 17 | | | | | |
| 18 | | 0 | 0 0 AT4G28100.1 | | 0 |
| 19 | | 0 | 0 0 AT4G05200.1 CRK25 | | |
| 20 | | | | | |
| 21 | | 0 | 0 GO:0055085,(AT1G55620.2 ATCLC-F,CLC-F,CLCF | | |
| 22 | 2.3.1.30 | K00640 | GO:0009001,(AT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M | | |
| 23 | | 0 | 0 0 0 | | 0 |
| 24 | | 0 K13354 | 0 AT2G39970.1 | | 0 |
| 25 | | | | | |
| 26 | 3.6.4.12 | K11647 | GO:0016787,(AT2G46020.2 ATBRM,BRM,CHA2,CHR2 | | |
| 27 | 5.2.1.8 | K05864 | GO:0005515,(AT2G15790.1 CYP40,SQN | | |
| 28 | | | | | |
| 29 | | 0 | 0 GO:0008168 AT5G64030.1 | | 0 |
| 30 | | 0 | 0 0 0 | | 0 |
| 31 | | | | | |
| 32 | | 0 K09264 | GO:0006355,(AT5G20240.1 PI | | |
| 33 | | 0 | 0 GO:0008168,(AT2G16030.1 | | 0 |
| 34 | | 0 | 0 GO:0005524,(AT1G05910.1 | | 0 |
| 35 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 36 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 37 | | | | | |
| 38 | | 0 K09338 | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | | |
| 39 | 2.7.11.1 | | 0 GO:0006468,(AT4G05200.1 CRK25 | | |
| 40 | | | | | |
| 41 | | 0 | 0 0 AT4G28100.1 | | 0 |
| 42 | | 0 | 0 0 AT4G05200.1 CRK25 | | |
| 43 | | | | | |
| 44 | | 0 | 0 GO:0055085,(AT1G55620.2 ATCLC-F,CLC-F,CLCF | | |
| 45 | 2.3.1.30 | K00640 | GO:0009001,(AT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M | | |
| 46 | | 0 | 0 0 0 | | 0 |
| 47 | | 0 K13354 | 0 AT2G39970.1 | | 0 |
| 48 | | | | | |
| 49 | 3.6.4.12 | K11647 | GO:0016787,(AT2G46020.2 ATBRM,BRM,CHA2,CHR2 | | |
| 50 | 5.2.1.8 | K05864 | GO:0005515,(AT2G15790.1 CYP40,SQN | | |
| 51 | | | | | |
| 52 | | 0 | 0 GO:0008168 AT5G64030.1 | | 0 |
| 53 | | 0 | 0 0 0 | | 0 |
| 54 | | | | | |
| 55 | | 0 K09264 | GO:0006355,(AT5G20240.1 PI | | |
| 56 | | 0 | 0 GO:0008168,(AT2G16030.1 | | 0 |
| 57 | | 0 | 0 GO:0005524,(AT1G05910.1 | | 0 |
| 58 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 59 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 60 | | | | | |
| | | 0 K09338 | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | | |
| | 2.7.11.1 | | 0 GO:0006468,(AT4G05200.1 CRK25 | | |

| | | | | | |
|----|----------|----------|---|---|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 AT4G28100.1 | 0 |
| 3 | | 0 | 0 | 0 AT4G05200.1 CRK25 | |
| 4 | | 0 | | | |
| 5 | | 0 | | 0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF | |
| 6 | 2.3.1.30 | K00640 | | GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M | |
| 7 | | 0 | 0 | 0 0 | 0 |
| 8 | | 0 K13354 | | 0 AT2G39970.1 | 0 |
| 9 | | | | | |
| 10 | 3.6.4.12 | K11647 | | GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2 | |
| 11 | 5.2.1.8 | K05864 | | GO:0005515,(CAT2G15790.1 CYP40,SQN | |
| 12 | | 0 | 0 | 0 GO:0008168 AT5G64030.1 | 0 |
| 13 | | 0 | 0 | 0 0 | 0 |
| 14 | | 0 K09264 | | GO:0006355,(CAT5G20240.1 PI | |
| 15 | | 0 | 0 | 0 GO:0008168,(CAT2G16030.1 | 0 |
| 16 | | 0 | 0 | 0 GO:0005524,(CAT1G05910.1 | 0 |
| 17 | | 0 K12124 | | 0 AT1G22770.1 FB,GI | |
| 18 | | 0 K12124 | | 0 AT1G22770.1 FB,GI | |
| 19 | | 0 K09338 | | GO:0003677,(CAT5G60690.1 IFL,IFL1,REV | |
| 20 | | | | | |
| 21 | 2.7.11.1 | | | 0 GO:0006468,(CAT4G05200.1 CRK25 | |
| 22 | | 0 | 0 | 0 AT4G28100.1 | 0 |
| 23 | | 0 | 0 | 0 AT4G05200.1 CRK25 | |
| 24 | | 0 | 0 | 0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF | |
| 25 | 2.3.1.30 | K00640 | | GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M | |
| 26 | | 0 | 0 | 0 0 | 0 |
| 27 | | 0 K13354 | | 0 AT2G39970.1 | 0 |
| 28 | 3.6.4.12 | K11647 | | GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2 | |
| 29 | 5.2.1.8 | K05864 | | GO:0005515,(CAT2G15790.1 CYP40,SQN | |
| 30 | | 0 | 0 | 0 GO:0008168 AT5G64030.1 | 0 |
| 31 | | 0 | 0 | 0 0 | 0 |
| 32 | | 0 K09264 | | GO:0006355,(CAT5G20240.1 PI | |
| 33 | | 0 | 0 | 0 GO:0008168,(CAT2G16030.1 | 0 |
| 34 | | 0 | 0 | 0 GO:0005524,(CAT1G05910.1 | 0 |
| 35 | | 0 K12124 | | 0 AT1G22770.1 FB,GI | |
| 36 | | 0 K12124 | | 0 AT1G22770.1 FB,GI | |
| 37 | | 0 K09338 | | GO:0003677,(CAT5G60690.1 IFL,IFL1,REV | |
| 38 | | | | | |
| 39 | 2.7.11.1 | | | 0 GO:0006468,(CAT4G05200.1 CRK25 | |
| 40 | | 0 | 0 | 0 AT4G28100.1 | 0 |
| 41 | | 0 | 0 | 0 AT4G05200.1 CRK25 | |
| 42 | | 0 | 0 | 0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF | |
| 43 | 2.3.1.30 | K00640 | | GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M | |
| 44 | | 0 | 0 | 0 0 | 0 |
| 45 | | 0 K13354 | | 0 AT2G39970.1 | 0 |
| 46 | 3.6.4.12 | K11647 | | GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2 | |
| 47 | 5.2.1.8 | K05864 | | GO:0005515,(CAT2G15790.1 CYP40,SQN | |
| 48 | | 0 | 0 | 0 GO:0008168 AT5G64030.1 | 0 |
| 49 | | 0 | 0 | 0 0 | 0 |
| 50 | | 0 K09264 | | GO:0006355,(CAT5G20240.1 PI | |
| 51 | | 0 | 0 | 0 GO:0008168,(CAT2G16030.1 | 0 |
| 52 | | 0 | 0 | 0 GO:0005524,(CAT1G05910.1 | 0 |
| 53 | | 0 K12124 | | 0 AT1G22770.1 FB,GI | |
| 54 | | 0 K12124 | | 0 AT1G22770.1 FB,GI | |
| 55 | | 0 K09338 | | GO:0003677,(CAT5G60690.1 IFL,IFL1,REV | |
| 56 | | | | | |
| 57 | 2.7.11.1 | | | 0 GO:0006468,(CAT4G05200.1 CRK25 | |
| 58 | | 0 | 0 | 0 AT4G28100.1 | 0 |
| 59 | | 0 | 0 | 0 AT4G05200.1 CRK25 | |
| 60 | | 0 | 0 | 0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF | |
| 61 | 2.3.1.30 | K00640 | | GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M | |
| 62 | | 0 | 0 | 0 0 | 0 |
| 63 | | 0 K13354 | | 0 AT2G39970.1 | 0 |
| 64 | 3.6.4.12 | K11647 | | GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2 | |
| 65 | 5.2.1.8 | K05864 | | GO:0005515,(CAT2G15790.1 CYP40,SQN | |
| 66 | | 0 | 0 | 0 GO:0008168 AT5G64030.1 | 0 |
| 67 | | 0 | 0 | 0 0 | 0 |
| 68 | | 0 K09264 | | GO:0006355,(CAT5G20240.1 PI | |
| 69 | | 0 | 0 | 0 GO:0008168,(CAT2G16030.1 | 0 |

| | | | | | |
|----|----------|----------|---|--|---|
| 1 | | | | | |
| 2 | | 0 | 0 GO:0005524,(CAT1G05910.1 | | 0 |
| 3 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 4 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 5 | | 0 K09338 | GO:0003677,(CAT5G60690.1 IFL,IFL1,REV | | |
| 6 | | | | | |
| 7 | 2.7.11.1 | | 0 GO:0006468,(CAT4G05200.1 CRK25 | | |
| 8 | | 0 | 0 0 AT4G28100.1 | | 0 |
| 9 | | | | | |
| 10 | | 0 | 0 AT4G05200.1 CRK25 | | |
| 11 | | 0 | 0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF | | |
| 12 | 2.3.1.30 | K00640 | GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M | | |
| 13 | | | | | |
| 14 | | 0 | 0 0 0 | | 0 |
| 15 | | 0 K13354 | 0 AT2G39970.1 | | 0 |
| 16 | 3.6.4.12 | K11647 | GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2 | | |
| 17 | 5.2.1.8 | K05864 | GO:0005515,(CAT2G15790.1 CYP40,SQN | | |
| 18 | | | | | |
| 19 | | 0 | 0 GO:0008168 AT5G64030.1 | | 0 |
| 20 | | 0 | 0 0 0 | | 0 |
| 21 | | | | | |
| 22 | | 0 K09264 | GO:0006355,(CAT5G20240.1 PI | | |
| 23 | | 0 | 0 GO:0008168,(CAT2G16030.1 | | 0 |
| 24 | | 0 | 0 GO:0005524,(CAT1G05910.1 | | 0 |
| 25 | | | | | |
| 26 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 27 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 28 | | 0 K09338 | GO:0003677,(CAT5G60690.1 IFL,IFL1,REV | | |
| 29 | | | | | |
| 30 | 2.7.11.1 | | 0 GO:0006468,(CAT4G05200.1 CRK25 | | |
| 31 | | 0 | 0 0 AT4G28100.1 | | 0 |
| 32 | | 0 | 0 AT4G05200.1 CRK25 | | |
| 33 | | | | | |
| 34 | | 0 | 0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF | | |
| 35 | 2.3.1.30 | K00640 | GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M | | |
| 36 | | 0 | 0 0 0 | | 0 |
| 37 | | 0 K13354 | 0 AT2G39970.1 | | 0 |
| 38 | | | | | |
| 39 | 3.6.4.12 | K11647 | GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2 | | |
| 40 | 5.2.1.8 | K05864 | GO:0005515,(CAT2G15790.1 CYP40,SQN | | |
| 41 | | | | | |
| 42 | | 0 | 0 GO:0008168 AT5G64030.1 | | 0 |
| 43 | | 0 | 0 0 0 | | 0 |
| 44 | | 0 K09264 | GO:0006355,(CAT5G20240.1 PI | | |
| 45 | | 0 | 0 GO:0008168,(CAT2G16030.1 | | 0 |
| 46 | | | | | |
| 47 | | 0 | 0 GO:0005524,(CAT1G05910.1 | | 0 |
| 48 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 49 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 50 | | | | | |
| 51 | | 0 K09338 | GO:0003677,(CAT5G60690.1 IFL,IFL1,REV | | |
| 52 | 2.7.11.1 | | 0 GO:0006468,(CAT4G05200.1 CRK25 | | |
| 53 | | 0 | 0 0 AT4G28100.1 | | 0 |
| 54 | | | | | |
| 55 | | 0 | 0 AT4G05200.1 CRK25 | | |
| 56 | | 0 | 0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF | | |
| 57 | 2.3.1.30 | K00640 | GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M | | |
| 58 | | | | | |
| 59 | | 0 | 0 0 0 | | 0 |
| 60 | | 0 K13354 | 0 AT2G39970.1 | | 0 |
| | 3.6.4.12 | K11647 | GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2 | | |

| | | | | | |
|----|----------|----------|---|--|---|
| 1 | | | | | |
| 2 | 5.2.1.8 | K05864 | GO:0005515,(CAT2G15790.1 CYP40,SQN | | |
| 3 | | 0 | 0 GO:0008168 AT5G64030.1 | | 0 |
| 4 | | 0 | 0 0 0 | | 0 |
| 5 | | 0 | | | |
| 6 | | 0 K09264 | GO:0006355,(CAT5G20240.1 PI | | |
| 7 | | 0 | 0 GO:0008168,(CAT2G16030.1 | | 0 |
| 8 | | 0 | 0 GO:0005524,(CAT1G05910.1 | | 0 |
| 9 | | 0 | | | |
| 10 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 11 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 12 | | 0 | | | |
| 13 | | 0 K09338 | GO:0003677,(CAT5G60690.1 IFL,IFL1,REV | | |
| 14 | 2.7.11.1 | | 0 GO:0006468,(CAT4G05200.1 CRK25 | | |
| 15 | | 0 | 0 0 AT4G28100.1 | | 0 |
| 16 | | 0 | 0 0 AT4G05200.1 CRK25 | | |
| 17 | | 0 | | | |
| 18 | | 0 | 0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF | | |
| 19 | 2.3.1.30 | K00640 | GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M | | |
| 20 | | 0 | 0 0 0 | | 0 |
| 21 | | 0 | | | |
| 22 | | 0 K13354 | 0 AT2G39970.1 | | 0 |
| 23 | 3.6.4.12 | K11647 | GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2 | | |
| 24 | 5.2.1.8 | K05864 | GO:0005515,(CAT2G15790.1 CYP40,SQN | | |
| 25 | | 0 | 0 GO:0008168 AT5G64030.1 | | 0 |
| 26 | | 0 | 0 0 0 | | 0 |
| 27 | | 0 | | | |
| 28 | | 0 K09264 | GO:0006355,(CAT5G20240.1 PI | | |
| 29 | | 0 | 0 GO:0008168,(CAT2G16030.1 | | 0 |
| 30 | | 0 | 0 GO:0005524,(CAT1G05910.1 | | 0 |
| 31 | | 0 | | | |
| 32 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 33 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 34 | | 0 | | | |
| 35 | | 0 K09338 | GO:0003677,(CAT5G60690.1 IFL,IFL1,REV | | |
| 36 | 2.7.11.1 | | 0 GO:0006468,(CAT4G05200.1 CRK25 | | |
| 37 | | 0 | 0 0 AT4G28100.1 | | 0 |
| 38 | | 0 | 0 0 AT4G05200.1 CRK25 | | |
| 39 | | 0 | | | |
| 40 | | 0 | 0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF | | |
| 41 | 2.3.1.30 | K00640 | GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M | | |
| 42 | | 0 | 0 0 0 | | 0 |
| 43 | | 0 | | | |
| 44 | | 0 K13354 | 0 AT2G39970.1 | | 0 |
| 45 | 3.6.4.12 | K11647 | GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2 | | |
| 46 | 5.2.1.8 | K05864 | GO:0005515,(CAT2G15790.1 CYP40,SQN | | |
| 47 | | 0 | 0 GO:0008168 AT5G64030.1 | | 0 |
| 48 | | 0 | 0 0 0 | | 0 |
| 49 | | 0 | | | |
| 50 | | 0 K09264 | GO:0006355,(CAT5G20240.1 PI | | |
| 51 | | 0 | 0 GO:0008168,(CAT2G16030.1 | | 0 |
| 52 | | 0 | 0 GO:0005524,(CAT1G05910.1 | | 0 |
| 53 | | 0 | | | |
| 54 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 55 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 56 | | 0 | | | |
| 57 | | 0 K09338 | GO:0003677,(CAT5G60690.1 IFL,IFL1,REV | | |
| 58 | 2.7.11.1 | | 0 GO:0006468,(CAT4G05200.1 CRK25 | | |
| 59 | | 0 | 0 0 AT4G28100.1 | | 0 |
| 60 | | 0 | 0 0 AT4G05200.1 CRK25 | | |

| | | | | | |
|----|----------|----------|---|--|---|
| 1 | | | | | |
| 2 | | 0 | 0 | GO:0055085,(AT1G55620.2 ATCLC-F,CLC-F,CLCF | |
| 3 | 2.3.1.30 | K00640 | | GO:0009001,(AT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M | |
| 4 | | 0 | 0 | 0 | 0 |
| 5 | | 0 | | | |
| 6 | | 0 K13354 | | 0 AT2G39970.1 | 0 |
| 7 | 3.6.4.12 | K11647 | | GO:0016787,(AT2G46020.2 ATBRM,BRM,CHA2,CHR2 | |
| 8 | 5.2.1.8 | K05864 | | GO:0005515,(AT2G15790.1 CYP40,SQN | |
| 9 | | 0 | | | |
| 10 | | 0 | 0 | GO:0008168 AT5G64030.1 | 0 |
| 11 | | 0 | 0 | 0 | 0 |
| 12 | | 0 | | | |
| 13 | | 0 K09264 | | GO:0006355,(AT5G20240.1 PI | |
| 14 | | 0 | | 0 GO:0008168,(AT2G16030.1 | 0 |
| 15 | | 0 | | 0 GO:0005524,(AT1G05910.1 | 0 |
| 16 | | 0 K12124 | | 0 AT1G22770.1 FB,GI | |
| 17 | | 0 K12124 | | 0 AT1G22770.1 FB,GI | |
| 18 | | 0 K09338 | | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | |
| 19 | | 0 | | | |
| 20 | 2.7.11.1 | | | 0 GO:0006468,(AT4G05200.1 CRK25 | |
| 21 | | 0 | | | |
| 22 | | 0 | 0 | 0 AT4G28100.1 | 0 |
| 23 | | 0 | | 0 AT4G05200.1 CRK25 | |
| 24 | | 0 | | 0 GO:0055085,(AT1G55620.2 ATCLC-F,CLC-F,CLCF | |
| 25 | 2.3.1.30 | K00640 | | GO:0009001,(AT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M | |
| 26 | | 0 | 0 | 0 | 0 |
| 27 | | 0 K13354 | | 0 AT2G39970.1 | 0 |
| 28 | | 0 | | | |
| 29 | 3.6.4.12 | K11647 | | GO:0016787,(AT2G46020.2 ATBRM,BRM,CHA2,CHR2 | |
| 30 | 5.2.1.8 | K05864 | | GO:0005515,(AT2G15790.1 CYP40,SQN | |
| 31 | | 0 | | 0 GO:0008168 AT5G64030.1 | 0 |
| 32 | | 0 | 0 | 0 | 0 |
| 33 | | 0 | | | |
| 34 | | 0 K09264 | | GO:0006355,(AT5G20240.1 PI | |
| 35 | | 0 | | 0 GO:0008168,(AT2G16030.1 | 0 |
| 36 | | 0 | | 0 GO:0005524,(AT1G05910.1 | 0 |
| 37 | | 0 | | | |
| 38 | | 0 K12124 | | 0 AT1G22770.1 FB,GI | |
| 39 | | 0 K12124 | | 0 AT1G22770.1 FB,GI | |
| 40 | | 0 K09338 | | GO:0003677,(AT5G60690.1 IFL,IFL1,REV | |
| 41 | | 0 | | | |
| 42 | 2.7.11.1 | | | 0 GO:0006468,(AT4G05200.1 CRK25 | |
| 43 | | 0 | | 0 AT4G28100.1 | 0 |
| 44 | | 0 | | 0 AT4G05200.1 CRK25 | |
| 45 | | 0 | | 0 GO:0055085,(AT1G55620.2 ATCLC-F,CLC-F,CLCF | |
| 46 | 2.3.1.30 | K00640 | | GO:0009001,(AT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M | |
| 47 | | 0 | 0 | 0 | 0 |
| 48 | | 0 K13354 | | 0 AT2G39970.1 | 0 |
| 49 | | 0 | | | |
| 50 | 3.6.4.12 | K11647 | | GO:0016787,(AT2G46020.2 ATBRM,BRM,CHA2,CHR2 | |
| 51 | 5.2.1.8 | K05864 | | GO:0005515,(AT2G15790.1 CYP40,SQN | |
| 52 | | 0 | | 0 GO:0008168 AT5G64030.1 | 0 |
| 53 | | 0 | 0 | 0 | 0 |
| 54 | | 0 | | | |
| 55 | | 0 K09264 | | GO:0006355,(AT5G20240.1 PI | |
| 56 | | 0 | | 0 GO:0008168,(AT2G16030.1 | 0 |
| 57 | | 0 | | 0 GO:0005524,(AT1G05910.1 | 0 |
| 58 | | 0 | | | |
| 59 | | 0 K12124 | | 0 AT1G22770.1 FB,GI | |
| 60 | | 0 | | | |

| | | | | | |
|----|----------|----------|---|---|---|
| 1 | | | | | |
| 2 | | 0 K12124 | | 0 AT1G22770.1 FB,GI | |
| 3 | | 0 K09338 | | GO:0003677,(CAT5G60690.1 IFL,IFL1,REV | |
| 4 | 2.7.11.1 | | | 0 GO:0006468,(CAT4G05200.1 CRK25 | |
| 5 | | | | | |
| 6 | | 0 | 0 | 0 AT4G28100.1 | 0 |
| 7 | | 0 | 0 | 0 AT4G05200.1 CRK25 | |
| 8 | | 0 | | | |
| 9 | | | | 0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF | |
| 10 | 2.3.1.30 | K00640 | | GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M | |
| 11 | | 0 | 0 | 0 0 | 0 |
| 12 | | 0 K13354 | | 0 AT2G39970.1 | 0 |
| 13 | | | | | |
| 14 | 3.6.4.12 | K11647 | | GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2 | |
| 15 | 5.2.1.8 | K05864 | | GO:0005515,(CAT2G15790.1 CYP40,SQN | |
| 16 | | 0 | | 0 GO:0008168 AT5G64030.1 | 0 |
| 17 | | 0 | 0 | 0 0 | 0 |
| 18 | | 0 | | | |
| 19 | | 0 K09264 | | GO:0006355,(CAT5G20240.1 PI | |
| 20 | | 0 | | 0 GO:0008168,(CAT2G16030.1 | 0 |
| 21 | | 0 | | | |
| 22 | | 0 | | 0 GO:0005524,(CAT1G05910.1 | 0 |
| 23 | | 0 K12124 | | 0 AT1G22770.1 FB,GI | |
| 24 | | 0 K12124 | | 0 AT1G22770.1 FB,GI | |
| 25 | | | | | |
| 26 | | 0 K09338 | | GO:0003677,(CAT5G60690.1 IFL,IFL1,REV | |
| 27 | 2.7.11.1 | | | 0 GO:0006468,(CAT4G05200.1 CRK25 | |
| 28 | | 0 | 0 | 0 AT4G28100.1 | 0 |
| 29 | | 0 | 0 | 0 AT4G05200.1 CRK25 | |
| 30 | | | | | |
| 31 | | 0 | | 0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF | |
| 32 | 2.3.1.30 | K00640 | | GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M | |
| 33 | | 0 | 0 | 0 0 | 0 |
| 34 | | 0 K13354 | | 0 AT2G39970.1 | 0 |
| 35 | | | | | |
| 36 | 3.6.4.12 | K11647 | | GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2 | |
| 37 | 5.2.1.8 | K05864 | | GO:0005515,(CAT2G15790.1 CYP40,SQN | |
| 38 | | 0 | | 0 GO:0008168 AT5G64030.1 | 0 |
| 39 | | 0 | 0 | 0 0 | 0 |
| 40 | | 0 | | | |
| 41 | | 0 K09264 | | GO:0006355,(CAT5G20240.1 PI | |
| 42 | | 0 | | 0 GO:0008168,(CAT2G16030.1 | 0 |
| 43 | | 0 | | 0 GO:0005524,(CAT1G05910.1 | 0 |
| 44 | | | | | |
| 45 | | 0 K12124 | | 0 AT1G22770.1 FB,GI | |
| 46 | | 0 K12124 | | 0 AT1G22770.1 FB,GI | |
| 47 | | | | | |
| 48 | | 0 K09338 | | GO:0003677,(CAT5G60690.1 IFL,IFL1,REV | |
| 49 | 2.7.11.1 | | | 0 GO:0006468,(CAT4G05200.1 CRK25 | |
| 50 | | 0 | 0 | 0 AT4G28100.1 | 0 |
| 51 | | 0 | 0 | 0 AT4G05200.1 CRK25 | |
| 52 | | | | | |
| 53 | | 0 | | 0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF | |
| 54 | 2.3.1.30 | K00640 | | GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M | |
| 55 | | 0 | 0 | 0 0 | 0 |
| 56 | | 0 K13354 | | 0 AT2G39970.1 | 0 |
| 57 | | | | | |
| 58 | 3.6.4.12 | K11647 | | GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2 | |
| 59 | 5.2.1.8 | K05864 | | GO:0005515,(CAT2G15790.1 CYP40,SQN | |
| 60 | | 0 | | 0 GO:0008168 AT5G64030.1 | 0 |

| | | | | | |
|----|-----------|----------|---|---|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 | 0 |
| 3 | | 0 K09264 | GO:0006355,(CAT5G20240.1 PI | | |
| 4 | | 0 | 0 GO:0008168,(CAT2G16030.1 | | 0 |
| 5 | | 0 | 0 GO:0005524,(CAT1G05910.1 | | 0 |
| 6 | | 0 | 0 GO:0005524,(CAT1G05910.1 | | 0 |
| 7 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 8 | | 0 K12124 | 0 AT1G22770.1 FB,GI | | |
| 9 | | 0 K09338 | GO:0003677,(CAT5G60690.1 IFL,IFL1,REV | | |
| 10 | | 0 | 0 GO:0005524,(CAT1G05910.1 | | 0 |
| 11 | | 0 | 0 GO:0005524,(CAT1G05910.1 | | 0 |
| 12 | 2.7.11.1 | | 0 GO:0006468,(CAT4G05200.1 CRK25 | | |
| 13 | | | | | |
| 14 | | 0 | 0 0 AT4G28100.1 | | 0 |
| 15 | | 0 | 0 0 AT4G05200.1 CRK25 | | |
| 16 | | 0 | 0 GO:0055085,(CAT1G55620.2 ATCLC-F,CLC-F,CLCF | | |
| 17 | | 0 | 0 GO:0016021,(CAT5G40240.1 | | 0 |
| 18 | | 0 | 0 GO:0016021,(CAT5G40240.1 | | 0 |
| 19 | | 0 | 0 GO:0016021,(CAT5G40240.1 | | 0 |
| 20 | | 0 | 0 GO:0016021,(CAT5G40240.1 | | 0 |
| 21 | | 0 | 0 GO:0016021,(CAT5G40240.1 | | 0 |
| 22 | 2.3.1.30 | K00640 | GO:0009001,(CAT3G13110.1 ATSERAT2;2,SAT-1,SAT-A,SAT-M | | |
| 23 | | 0 | 0 0 0 0 | | 0 |
| 24 | | 0 K13354 | 0 AT2G39970.1 | | 0 |
| 25 | | | | | |
| 26 | 3.6.4.12 | K11647 | GO:0016787,(CAT2G46020.2 ATBRM,BRM,CHA2,CHR2 | | |
| 27 | 5.2.1.8 | K05864 | GO:0005515,(CAT2G15790.1 CYP40,SQN | | |
| 28 | | 0 | 0 GO:0008168 AT5G64030.1 | | 0 |
| 29 | | | | | |
| 30 | 2.7.11.1 | | 0 GO:0005515 AT1G47890.1 AtRLP7,RLP7 | | |
| 31 | | 0 | 0 0 AT1G63470.1 | | 0 |
| 32 | | | | | |
| 33 | 2.4.2.24 | | 0 GO:0016020,(CAT1G27600.2 I9H,IRX9-L | | |
| 34 | | 0 | 0 GO:0055085,(CAT3G18830.1 ATPLT5,ATPMT5,PMT5 | | |
| 35 | 3.1.1.3 | | 0 GO:0016788 AT4G26790.1 | | 0 |
| 36 | 3.4.23.12 | | 0 GO:0006508,(CAT1G03220.1 | | 0 |
| 37 | | | | | |
| 38 | | 0 | 0 0 AT3G63180.1 ATTKL,TKL | | |
| 39 | | 0 K02985 | GO:0003723 AT5G35530.1 | | 0 |
| 40 | 2.7.11.1 | | 0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2 | | |
| 41 | | | | | |
| 42 | 2.7.11.1 | | 0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2 | | |
| 43 | | 0 | 0 0 AT2G37570.1 SLT1 | | |
| 44 | | 0 | 0 0 AT2G37570.1 SLT1 | | |
| 45 | 2.7.4.22 | K09903 | 0 AT3G10030.1 | | 0 |
| 46 | | | | | |
| 47 | | 0 | 0 0 AT3G02250.1 | | 0 |
| 48 | | 0 | 0 GO:0003723 AT3G21740.1 APO4 | | |
| 49 | | 0 | 0 GO:0006355,(CAT2G22840.1 AtGRF1,GRF1 | | |
| 50 | | | | | |
| 51 | 2.1.1.216 | K00555 | GO:0008033,(CAT5G15810.1 | | 0 |
| 52 | 2.1.1.216 | K00555 | GO:0008033,(CAT5G15810.1 | | 0 |
| 53 | | | | | |
| 54 | | 0 K09874 | GO:0016020,(CAT4G10380.1 NIP5;1,NLM6,NLM8 | | |
| 55 | | 0 | 0 0 AT2G16800.1 | | 0 |
| 56 | | 0 | 0 0 AT3G04630.1 WDL1 | | |
| 57 | | 0 | 0 0 AT3G04630.1 WDL1 | | |
| 58 | | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | | |
| 59 | | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | | |
| 60 | | 0 | 0 0 0 0 | | 0 |

| | | | | |
|----|-----------|----------|--|---------------------------------|
| 1 | | | | |
| 2 | | 0 | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I |
| 3 | 3.4.23.12 | | 0 GO:0006508,(AT2G17760.1 | 0 |
| 4 | | 0 | 0 GO:0007165 AT3G29575.3 AFP3 | |
| 5 | | | | |
| 6 | 2.7.11.1 | | 0 GO:0005515,(AT4G20140.1 GSO1 | |
| 7 | 2.7.11.1 | | 0 GO:0005515 AT1G47890.1 AtRLP7,RLP7 | |
| 8 | | 0 | 0 | 0 AT1G63470.1 |
| 9 | | | | |
| 10 | 2.4.2.24 | | 0 GO:0016020,(AT1G27600.2 I9H,IRX9-L | |
| 11 | | 0 | 0 GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5 | |
| 12 | 3.1.1.3 | | 0 GO:0016788 AT4G26790.1 | 0 |
| 13 | | | | |
| 14 | 3.4.23.12 | | 0 GO:0006508,(AT1G03220.1 | 0 |
| 15 | | 0 | 0 | 0 AT3G63180.1 ATTKL,TKL |
| 16 | | 0 K02985 | GO:0003723 AT5G35530.1 | 0 |
| 17 | | | | |
| 18 | 2.7.11.1 | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 19 | 2.7.11.1 | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 20 | | 0 | 0 | 0 AT2G37570.1 SLT1 |
| 21 | | 0 | 0 | 0 AT2G37570.1 SLT1 |
| 22 | | | | |
| 23 | 2.7.4.22 | K09903 | 0 AT3G10030.1 | 0 |
| 24 | | 0 | 0 | 0 AT3G02250.1 |
| 25 | | | | |
| 26 | | 0 | 0 GO:0003723 AT3G21740.1 APO4 | |
| 27 | | 0 | 0 GO:0006355,(AT2G22840.1 AtGRF1,GRF1 | |
| 28 | 2.1.1.216 | K00555 | GO:0008033,(AT5G15810.1 | 0 |
| 29 | 2.1.1.216 | K00555 | GO:0008033,(AT5G15810.1 | 0 |
| 30 | | | | |
| 31 | | 0 K09874 | GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8 | |
| 32 | | 0 | 0 | 0 AT2G16800.1 |
| 33 | | 0 | 0 | 0 AT3G04630.1 WDL1 |
| 34 | | 0 | 0 | 0 AT3G04630.1 WDL1 |
| 35 | | 0 | 0 | 0 AT3G04630.1 WDL1 |
| 36 | | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 37 | | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 38 | | 0 | 0 | 0 |
| 39 | | 0 | 0 | 0 |
| 40 | | 0 | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I |
| 41 | 3.4.23.12 | | 0 GO:0006508,(AT2G17760.1 | 0 |
| 42 | | 0 | 0 GO:0007165 AT3G29575.3 AFP3 | |
| 43 | | | | |
| 44 | 2.7.11.1 | | 0 GO:0005515,(AT4G20140.1 GSO1 | |
| 45 | 2.7.11.1 | | 0 GO:0005515 AT1G47890.1 AtRLP7,RLP7 | |
| 46 | | 0 | 0 | 0 AT1G63470.1 |
| 47 | | | | |
| 48 | 2.4.2.24 | | 0 GO:0016020,(AT1G27600.2 I9H,IRX9-L | |
| 49 | | 0 | 0 GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5 | |
| 50 | | | | |
| 51 | 3.1.1.3 | | 0 GO:0016788 AT4G26790.1 | 0 |
| 52 | 3.4.23.12 | | 0 GO:0006508,(AT1G03220.1 | 0 |
| 53 | | 0 | 0 | 0 AT3G63180.1 ATTKL,TKL |
| 54 | | 0 K02985 | GO:0003723 AT5G35530.1 | 0 |
| 55 | | | | |
| 56 | 2.7.11.1 | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 57 | 2.7.11.1 | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 58 | | 0 | 0 | 0 AT2G37570.1 SLT1 |
| 59 | | 0 | 0 | 0 AT2G37570.1 SLT1 |
| 60 | | | | |
| | 2.7.4.22 | K09903 | 0 AT3G10030.1 | 0 |

| | | | | | |
|----|-----------|----------|---|--|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 AT3G02250.1 | 0 |
| 3 | | 0 | 0 | 0 GO:0003723 AT3G21740.1 APO4 | |
| 4 | | 0 | 0 | 0 GO:0006355,(AT2G22840.1 AtGRF1,GRF1 | |
| 5 | | | | | |
| 6 | 2.1.1.216 | K00555 | | GO:0008033,(AT5G15810.1 | 0 |
| 7 | 2.1.1.216 | K00555 | | GO:0008033,(AT5G15810.1 | 0 |
| 8 | | | | | |
| 9 | | 0 K09874 | | GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8 | |
| 10 | | 0 | 0 | 0 AT2G16800.1 | 0 |
| 11 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 12 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 13 | | | | | |
| 14 | | 0 | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 15 | | 0 | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 16 | | 0 | 0 | 0 0 | 0 |
| 17 | | 0 | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I | |
| 18 | | | | | |
| 19 | 3.4.23.12 | | | 0 GO:0006508,(AT2G17760.1 | 0 |
| 20 | | 0 | 0 | 0 GO:0007165 AT3G29575.3 AFP3 | |
| 21 | | | | | |
| 22 | 2.7.11.1 | | | 0 GO:0005515,(AT4G20140.1 GSO1 | |
| 23 | 2.7.11.1 | | | 0 GO:0005515 AT1G47890.1 AtRLP7,RLP7 | |
| 24 | | 0 | 0 | 0 AT1G63470.1 | 0 |
| 25 | | | | | |
| 26 | 2.4.2.24 | | | 0 GO:0016020,(AT1G27600.2 I9H,IRX9-L | |
| 27 | | 0 | 0 | 0 GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5 | |
| 28 | 3.1.1.3 | | | 0 GO:0016788 AT4G26790.1 | 0 |
| 29 | 3.4.23.12 | | | 0 GO:0006508,(AT1G03220.1 | 0 |
| 30 | | | | | |
| 31 | | 0 | 0 | 0 AT3G63180.1 ATTKL,TKL | |
| 32 | | 0 K02985 | | GO:0003723 AT5G35530.1 | 0 |
| 33 | | | | | |
| 34 | 2.7.11.1 | | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 35 | 2.7.11.1 | | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 36 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 37 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 38 | | | | | |
| 39 | 2.7.4.22 | K09903 | | 0 AT3G10030.1 | 0 |
| 40 | | 0 | 0 | 0 AT3G02250.1 | 0 |
| 41 | | | | | |
| 42 | | 0 | 0 | 0 GO:0003723 AT3G21740.1 APO4 | |
| 43 | | 0 | 0 | 0 GO:0006355,(AT2G22840.1 AtGRF1,GRF1 | |
| 44 | 2.1.1.216 | K00555 | | GO:0008033,(AT5G15810.1 | 0 |
| 45 | 2.1.1.216 | K00555 | | GO:0008033,(AT5G15810.1 | 0 |
| 46 | | | | | |
| 47 | | 0 K09874 | | GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8 | |
| 48 | | 0 | 0 | 0 AT2G16800.1 | 0 |
| 49 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 50 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 51 | | | | | |
| 52 | | 0 | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 53 | | 0 | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 54 | | | | | |
| 55 | | 0 | 0 | 0 0 | 0 |
| 56 | | 0 | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I | |
| 57 | 3.4.23.12 | | | 0 GO:0006508,(AT2G17760.1 | 0 |
| 58 | | 0 | 0 | 0 GO:0007165 AT3G29575.3 AFP3 | |
| 59 | | | | | |
| 60 | 2.7.11.1 | | | 0 GO:0005515,(AT4G20140.1 GSO1 | |
| | 2.7.11.1 | | | 0 GO:0005515 AT1G47890.1 AtRLP7,RLP7 | |

| | | | | | |
|----|-----------|----------|---|--|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 AT1G63470.1 | 0 |
| 3 | 2.4.2.24 | | | 0 GO:0016020,(AT1G27600.2 I9H,IRX9-L | |
| 4 | | 0 | | 0 GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5 | |
| 5 | | | | | |
| 6 | 3.1.1.3 | | | 0 GO:0016788 AT4G26790.1 | 0 |
| 7 | 3.4.23.12 | | | 0 GO:0006508,(AT1G03220.1 | 0 |
| 8 | | 0 | 0 | 0 AT3G63180.1 ATTKL,TKL | |
| 9 | | | | | |
| 10 | | 0 K02985 | | GO:0003723 AT5G35530.1 | 0 |
| 11 | 2.7.11.1 | | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 12 | 2.7.11.1 | | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 13 | | | | | |
| 14 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 15 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 16 | 2.7.4.22 | K09903 | | 0 AT3G10030.1 | 0 |
| 17 | | | | | |
| 18 | | 0 | 0 | 0 AT3G02250.1 | 0 |
| 19 | | | | | |
| 20 | | 0 | | 0 GO:0003723 AT3G21740.1 APO4 | |
| 21 | | | | | |
| 22 | 2.1.1.216 | K00555 | | GO:0008033,(AT5G15810.1 | 0 |
| 23 | 2.1.1.216 | K00555 | | GO:0008033,(AT5G15810.1 | 0 |
| 24 | | | | | |
| 25 | | 0 K09874 | | GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8 | |
| 26 | | 0 | 0 | 0 AT2G16800.1 | 0 |
| 27 | | | | | |
| 28 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 29 | | | | | |
| 30 | | 0 | | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 31 | | | | | |
| 32 | | 0 | 0 | 0 0 | 0 |
| 33 | | | | | |
| 34 | | 0 | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I | |
| 35 | 3.4.23.12 | | | 0 GO:0006508,(AT2G17760.1 | 0 |
| 36 | | 0 | | 0 GO:0007165 AT3G29575.3 AFP3 | |
| 37 | | | | | |
| 38 | 2.7.11.1 | | | 0 GO:0005515,(AT4G20140.1 GSO1 | |
| 39 | 2.7.11.1 | | | 0 GO:0005515 AT1G47890.1 AtRLP7,RLP7 | |
| 40 | | 0 | 0 | 0 AT1G63470.1 | 0 |
| 41 | 2.4.2.24 | | | 0 GO:0016020,(AT1G27600.2 I9H,IRX9-L | |
| 42 | | | | | |
| 43 | | 0 | | 0 GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5 | |
| 44 | 3.1.1.3 | | | 0 GO:0016788 AT4G26790.1 | 0 |
| 45 | 3.4.23.12 | | | 0 GO:0006508,(AT1G03220.1 | 0 |
| 46 | | | | | |
| 47 | | 0 | 0 | 0 AT3G63180.1 ATTKL,TKL | |
| 48 | | 0 K02985 | | GO:0003723 AT5G35530.1 | 0 |
| 49 | 2.7.11.1 | | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 50 | 2.7.11.1 | | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 51 | | | | | |
| 52 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 53 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 54 | | | | | |
| 55 | 2.7.4.22 | K09903 | | 0 AT3G10030.1 | 0 |
| 56 | | 0 | 0 | 0 AT3G02250.1 | 0 |
| 57 | | | | | |
| 58 | | 0 | | 0 GO:0003723 AT3G21740.1 APO4 | |
| 59 | | | | | |
| 60 | | 0 | | 0 GO:0006355,(AT2G22840.1 AtGRF1,GRF1 | |
| | 2.1.1.216 | K00555 | | GO:0008033,(AT5G15810.1 | 0 |
| | 2.1.1.216 | K00555 | | GO:0008033,(AT5G15810.1 | 0 |

| | | | | |
|----|-----------|----------|--|---|
| 1 | | | | |
| 2 | | 0 K09874 | GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8 | |
| 3 | | 0 | 0 AT2G16800.1 | 0 |
| 4 | | 0 | 0 AT3G04630.1 WDL1 | |
| 5 | | 0 | 0 AT3G04630.1 WDL1 | |
| 6 | | 0 | 0 AT3G04630.1 WDL1 | |
| 7 | | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 8 | | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 9 | | 0 | 0 0 0 | 0 |
| 10 | | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I | |
| 11 | | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I | |
| 12 | 3.4.23.12 | | 0 GO:0006508,(AT2G17760.1 | 0 |
| 13 | | | | |
| 14 | | 0 | 0 GO:0007165 AT3G29575.3 AFP3 | |
| 15 | 2.7.11.1 | | 0 GO:0005515,(AT4G20140.1 GSO1 | |
| 16 | 2.7.11.1 | | 0 GO:0005515 AT1G47890.1 AtRLP7,RLP7 | |
| 17 | | | | |
| 18 | | 0 | 0 AT1G63470.1 | 0 |
| 19 | 2.4.2.24 | | 0 GO:0016020,(AT1G27600.2 I9H,IRX9-L | |
| 20 | | | | |
| 21 | | 0 | 0 GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5 | |
| 22 | 3.1.1.3 | | 0 GO:0016788 AT4G26790.1 | 0 |
| 23 | 3.4.23.12 | | 0 GO:0006508,(AT1G03220.1 | 0 |
| 24 | | | | |
| 25 | | 0 | 0 AT3G63180.1 ATTKL,TKL | |
| 26 | | 0 K02985 | GO:0003723 AT5G35530.1 | 0 |
| 27 | 2.7.11.1 | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 28 | 2.7.11.1 | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 29 | | | | |
| 30 | | 0 | 0 AT2G37570.1 SLT1 | |
| 31 | | 0 | 0 AT2G37570.1 SLT1 | |
| 32 | 2.7.4.22 | K09903 | 0 AT3G10030.1 | 0 |
| 33 | | | | |
| 34 | | 0 | 0 AT3G02250.1 | 0 |
| 35 | | | | |
| 36 | | 0 | 0 GO:0003723 AT3G21740.1 APO4 | |
| 37 | | | | |
| 38 | 2.1.1.216 | K00555 | GO:0008033,(AT5G15810.1 | 0 |
| 39 | 2.1.1.216 | K00555 | GO:0008033,(AT5G15810.1 | 0 |
| 40 | | | | |
| 41 | | 0 K09874 | GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8 | |
| 42 | | 0 | 0 AT2G16800.1 | 0 |
| 43 | | 0 | 0 AT3G04630.1 WDL1 | |
| 44 | | 0 | 0 AT3G04630.1 WDL1 | |
| 45 | | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 46 | | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 47 | | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 48 | | 0 | 0 0 0 | 0 |
| 49 | | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I | |
| 50 | | | | |
| 51 | 3.4.23.12 | | 0 GO:0006508,(AT2G17760.1 | 0 |
| 52 | | | | |
| 53 | | 0 | 0 GO:0007165 AT3G29575.3 AFP3 | |
| 54 | 2.7.11.1 | | 0 GO:0005515,(AT4G20140.1 GSO1 | |
| 55 | 2.7.11.1 | | 0 GO:0005515 AT1G47890.1 AtRLP7,RLP7 | |
| 56 | | | | |
| 57 | | 0 | 0 AT1G63470.1 | 0 |
| 58 | 2.4.2.24 | | 0 GO:0016020,(AT1G27600.2 I9H,IRX9-L | |
| 59 | | | | |
| 60 | | 0 | 0 GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5 | |
| | 3.1.1.3 | | 0 GO:0016788 AT4G26790.1 | 0 |
| | 3.4.23.12 | | 0 GO:0006508,(AT1G03220.1 | 0 |

| | | | | |
|----|-----------|----------|----------------|---------------------------------|
| 1 | | | | |
| 2 | | 0 | 0 | 0 AT3G63180.1 ATTKL,TKL |
| 3 | | 0 K02985 | GO:0003723 | AT5G35530.1 0 |
| 4 | 2.7.11.1 | | 0 GO:0005515,(| AT3G02130.1 RPK2,TOAD2 |
| 5 | | | | |
| 6 | 2.7.11.1 | | 0 GO:0005515,(| AT3G02130.1 RPK2,TOAD2 |
| 7 | | 0 | 0 | 0 AT2G37570.1 SLT1 |
| 8 | | 0 | 0 | 0 AT2G37570.1 SLT1 |
| 9 | | | | |
| 10 | 2.7.4.22 | K09903 | | 0 AT3G10030.1 0 |
| 11 | | 0 | 0 | 0 AT3G02250.1 0 |
| 12 | | | | |
| 13 | | 0 | 0 GO:0003723 | AT3G21740.1 APO4 |
| 14 | | 0 | 0 GO:0006355,(| AT2G22840.1 AtGRF1,GRF1 |
| 15 | 2.1.1.216 | K00555 | GO:0008033,(| AT5G15810.1 0 |
| 16 | 2.1.1.216 | K00555 | GO:0008033,(| AT5G15810.1 0 |
| 17 | | | | |
| 18 | | 0 K09874 | GO:0016020,(| AT4G10380.1 NIP5;1,NLM6,NLM8 |
| 19 | | 0 | 0 | 0 AT2G16800.1 0 |
| 20 | | 0 | 0 | 0 AT3G04630.1 WDL1 |
| 21 | | | | |
| 22 | | 0 | 0 | 0 AT3G04630.1 WDL1 |
| 23 | | 0 | 0 GO:0007275 | AT2G45190.1 AFO,FIL,YAB1 |
| 24 | | 0 | 0 GO:0007275 | AT2G45190.1 AFO,FIL,YAB1 |
| 25 | | | | |
| 26 | | 0 | 0 | 0 0 0 |
| 27 | | 0 | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I |
| 28 | 3.4.23.12 | | 0 GO:0006508,(| AT2G17760.1 0 |
| 29 | | 0 | 0 GO:0007165 | AT3G29575.3 AFP3 |
| 30 | | | | |
| 31 | 2.7.11.1 | | 0 GO:0005515,(| AT4G20140.1 GSO1 |
| 32 | 2.7.11.1 | | 0 GO:0005515 | AT1G47890.1 AtRLP7,RLP7 |
| 33 | | | | |
| 34 | | 0 | 0 | 0 AT1G63470.1 0 |
| 35 | 2.4.2.24 | | 0 GO:0016020,(| AT1G27600.2 I9H,IRX9-L |
| 36 | | 0 | 0 GO:0055085,(| AT3G18830.1 ATPLT5,ATPMT5,PMT5 |
| 37 | | | | |
| 38 | 3.1.1.3 | | 0 GO:0016788 | AT4G26790.1 0 |
| 39 | 3.4.23.12 | | 0 GO:0006508,(| AT1G03220.1 0 |
| 40 | | 0 | 0 | 0 AT3G63180.1 ATTKL,TKL |
| 41 | | 0 K02985 | GO:0003723 | AT5G35530.1 0 |
| 42 | | | | |
| 43 | 2.7.11.1 | | 0 GO:0005515,(| AT3G02130.1 RPK2,TOAD2 |
| 44 | 2.7.11.1 | | 0 GO:0005515,(| AT3G02130.1 RPK2,TOAD2 |
| 45 | | 0 | 0 | 0 AT2G37570.1 SLT1 |
| 46 | | 0 | 0 | 0 AT2G37570.1 SLT1 |
| 47 | | | | |
| 48 | 2.7.4.22 | K09903 | | 0 AT3G10030.1 0 |
| 49 | | 0 | 0 | 0 AT3G02250.1 0 |
| 50 | | | | |
| 51 | | 0 | 0 GO:0003723 | AT3G21740.1 APO4 |
| 52 | | 0 | 0 GO:0006355,(| AT2G22840.1 AtGRF1,GRF1 |
| 53 | 2.1.1.216 | K00555 | GO:0008033,(| AT5G15810.1 0 |
| 54 | 2.1.1.216 | K00555 | GO:0008033,(| AT5G15810.1 0 |
| 55 | | | | |
| 56 | | 0 K09874 | GO:0016020,(| AT4G10380.1 NIP5;1,NLM6,NLM8 |
| 57 | | 0 | 0 | 0 AT2G16800.1 0 |
| 58 | | 0 | 0 | 0 AT3G04630.1 WDL1 |
| 59 | | 0 | 0 | 0 AT3G04630.1 WDL1 |
| 60 | | 0 | 0 GO:0007275 | AT2G45190.1 AFO,FIL,YAB1 |

| | | | | | |
|----|-----------|--------|---|---|---|
| 1 | | | | | |
| 2 | | 0 | 0 | GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 3 | | 0 | 0 | 0 | 0 |
| 4 | | 0 | 0 | 0 | 0 |
| 5 | | 0 | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I | |
| 6 | 3.4.23.12 | | 0 | GO:0006508,(AT2G17760.1 | 0 |
| 7 | | 0 | 0 | GO:0007165 AT3G29575.3 AFP3 | |
| 8 | 2.7.11.1 | | 0 | GO:0005515,(AT4G20140.1 GSO1 | |
| 9 | | | | | |
| 10 | 2.7.11.1 | | 0 | GO:0005515 AT1G47890.1 AtRLP7,RLP7 | |
| 11 | | 0 | 0 | 0 AT1G63470.1 | 0 |
| 12 | 2.4.2.24 | | 0 | GO:0016020,(AT1G27600.2 I9H,IRX9-L | |
| 13 | | | | | |
| 14 | | 0 | 0 | GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5 | |
| 15 | 3.1.1.3 | | 0 | GO:0016788 AT4G26790.1 | 0 |
| 16 | 3.4.23.12 | | 0 | GO:0006508,(AT1G03220.1 | 0 |
| 17 | | | | | |
| 18 | | 0 | 0 | 0 AT3G63180.1 ATTKL,TKL | |
| 19 | | 0 | 0 | K02985 GO:0003723 AT5G35530.1 | 0 |
| 20 | 2.7.11.1 | | 0 | GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 21 | | | | | |
| 22 | 2.7.11.1 | | 0 | GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 23 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 24 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 25 | | | | | |
| 26 | 2.7.4.22 | K09903 | 0 | AT3G10030.1 | 0 |
| 27 | | 0 | 0 | 0 AT3G02250.1 | 0 |
| 28 | | 0 | 0 | GO:0003723 AT3G21740.1 APO4 | |
| 29 | | 0 | 0 | GO:0006355,(AT2G22840.1 AtGRF1,GRF1 | |
| 30 | | | | | |
| 31 | 2.1.1.216 | K00555 | 0 | GO:0008033,(AT5G15810.1 | 0 |
| 32 | 2.1.1.216 | K00555 | 0 | GO:0008033,(AT5G15810.1 | 0 |
| 33 | | | | | |
| 34 | | 0 | 0 | K09874 GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8 | |
| 35 | | 0 | 0 | 0 AT2G16800.1 | 0 |
| 36 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 37 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 38 | | | | | |
| 39 | | 0 | 0 | GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 40 | | 0 | 0 | GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 41 | | 0 | 0 | 0 | 0 |
| 42 | | 0 | 0 | 0 | 0 |
| 43 | | 0 | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I | |
| 44 | 3.4.23.12 | | 0 | GO:0006508,(AT2G17760.1 | 0 |
| 45 | | 0 | 0 | GO:0007165 AT3G29575.3 AFP3 | |
| 46 | | | | | |
| 47 | 2.7.11.1 | | 0 | GO:0005515,(AT4G20140.1 GSO1 | |
| 48 | 2.7.11.1 | | 0 | GO:0005515 AT1G47890.1 AtRLP7,RLP7 | |
| 49 | | 0 | 0 | 0 AT1G63470.1 | 0 |
| 50 | | | | | |
| 51 | 2.4.2.24 | | 0 | GO:0016020,(AT1G27600.2 I9H,IRX9-L | |
| 52 | | 0 | 0 | GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5 | |
| 53 | 3.1.1.3 | | 0 | GO:0016788 AT4G26790.1 | 0 |
| 54 | 3.4.23.12 | | 0 | GO:0006508,(AT1G03220.1 | 0 |
| 55 | | | | | |
| 56 | | 0 | 0 | 0 AT3G63180.1 ATTKL,TKL | |
| 57 | | 0 | 0 | K02985 GO:0003723 AT5G35530.1 | 0 |
| 58 | | | | | |
| 59 | 2.7.11.1 | | 0 | GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 60 | 2.7.11.1 | | 0 | GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| | | 0 | 0 | 0 AT2G37570.1 SLT1 | |

| | | | | | |
|----|-----------|----------|---|--|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 3 | 2.7.4.22 | K09903 | | 0 AT3G10030.1 | 0 |
| 4 | | 0 | 0 | 0 AT3G02250.1 | 0 |
| 5 | | 0 | | | |
| 6 | | 0 | 0 | 0 GO:0003723 AT3G21740.1 APO4 | |
| 7 | | 0 | 0 | 0 GO:0006355,(AT2G22840.1 AtGRF1,GRF1 | |
| 8 | 2.1.1.216 | K00555 | | GO:0008033,(AT5G15810.1 | 0 |
| 9 | 2.1.1.216 | K00555 | | GO:0008033,(AT5G15810.1 | 0 |
| 10 | | 0 K09874 | | GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8 | |
| 11 | | 0 | 0 | 0 AT2G16800.1 | 0 |
| 12 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 13 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 14 | | 0 | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 15 | | 0 | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 16 | | 0 | 0 | 0 | 0 |
| 17 | | 0 | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I | |
| 18 | 3.4.23.12 | | | 0 GO:0006508,(AT2G17760.1 | 0 |
| 19 | | 0 | 0 | 0 GO:0007165 AT3G29575.3 AFP3 | |
| 20 | 2.7.11.1 | | | 0 GO:0005515,(AT4G20140.1 GSO1 | |
| 21 | 2.7.11.1 | | | 0 GO:0005515 AT1G47890.1 AtRLP7,RLP7 | |
| 22 | | 0 | 0 | 0 AT1G63470.1 | 0 |
| 23 | 2.4.2.24 | | | 0 GO:0016020,(AT1G27600.2 I9H,IRX9-L | |
| 24 | | 0 | 0 | 0 GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5 | |
| 25 | 3.1.1.3 | | | 0 GO:0016788 AT4G26790.1 | 0 |
| 26 | 3.4.23.12 | | | 0 GO:0006508,(AT1G03220.1 | 0 |
| 27 | | 0 | 0 | 0 AT3G63180.1 ATTKL,TKL | |
| 28 | | 0 K02985 | | GO:0003723 AT5G35530.1 | 0 |
| 29 | 2.7.11.1 | | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 30 | 2.7.11.1 | | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 31 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 32 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 33 | 2.7.4.22 | K09903 | | 0 AT3G10030.1 | 0 |
| 34 | | 0 | 0 | 0 AT3G02250.1 | 0 |
| 35 | | 0 | 0 | 0 GO:0003723 AT3G21740.1 APO4 | |
| 36 | | 0 | 0 | 0 GO:0006355,(AT2G22840.1 AtGRF1,GRF1 | |
| 37 | 2.1.1.216 | K00555 | | GO:0008033,(AT5G15810.1 | 0 |
| 38 | 2.1.1.216 | K00555 | | GO:0008033,(AT5G15810.1 | 0 |
| 39 | | 0 K09874 | | GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8 | |
| 40 | | 0 | 0 | 0 AT2G16800.1 | 0 |
| 41 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 42 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 43 | | 0 | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 44 | | 0 | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 45 | | 0 | 0 | 0 | 0 |
| 46 | | 0 | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I | |
| 47 | 3.4.23.12 | | | 0 GO:0006508,(AT2G17760.1 | 0 |
| 48 | | 0 | 0 | 0 GO:0007165 AT3G29575.3 AFP3 | |

| | | | | |
|----|-----------|----------|---|---|
| 1 | | | | |
| 2 | 2.7.11.1 | | 0 GO:0005515,(CAT4G20140.1 GSO1 | |
| 3 | 2.7.11.1 | | 0 GO:0005515 AT1G47890.1 AtRLP7,RLP7 | |
| 4 | | | | |
| 5 | | 0 | 0 AT1G63470.1 | 0 |
| 6 | 2.4.2.24 | | 0 GO:0016020,(CAT1G27600.2 I9H,IRX9-L | |
| 7 | | 0 | 0 GO:0055085,(CAT3G18830.1 ATPLT5,ATPMT5,PMT5 | |
| 8 | 3.1.1.3 | | 0 GO:0016788 AT4G26790.1 | 0 |
| 9 | | | | |
| 10 | 3.4.23.12 | | 0 GO:0006508,(CAT1G03220.1 | 0 |
| 11 | | 0 | 0 AT3G63180.1 ATTKL,TKL | |
| 12 | | 0 K02985 | GO:0003723 AT5G35530.1 | 0 |
| 13 | | | | |
| 14 | 2.7.11.1 | | 0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2 | |
| 15 | 2.7.11.1 | | 0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2 | |
| 16 | | 0 | 0 AT2G37570.1 SLT1 | |
| 17 | | 0 | 0 AT2G37570.1 SLT1 | |
| 18 | | 0 | 0 AT2G37570.1 SLT1 | |
| 19 | 2.7.4.22 | K09903 | 0 AT3G10030.1 | 0 |
| 20 | | 0 | 0 AT3G02250.1 | 0 |
| 21 | | 0 | 0 GO:0003723 AT3G21740.1 APO4 | |
| 22 | | 0 | 0 GO:0006355,(CAT2G22840.1 AtGRF1,GRF1 | |
| 23 | | 0 | 0 GO:0006355,(CAT2G22840.1 AtGRF1,GRF1 | |
| 24 | 2.1.1.216 | K00555 | GO:0008033,(CAT5G15810.1 | 0 |
| 25 | 2.1.1.216 | K00555 | GO:0008033,(CAT5G15810.1 | 0 |
| 26 | | 0 K09874 | GO:0016020,(CAT4G10380.1 NIP5;1,NLM6,NLM8 | |
| 27 | | 0 | 0 AT2G16800.1 | 0 |
| 28 | | 0 | 0 AT2G16800.1 | 0 |
| 29 | | 0 | 0 AT3G04630.1 WDL1 | |
| 30 | | 0 | 0 AT3G04630.1 WDL1 | |
| 31 | | 0 | 0 AT3G04630.1 WDL1 | |
| 32 | | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 33 | | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 34 | | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 35 | | 0 | 0 0 0 | 0 |
| 36 | | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I | |
| 37 | 3.4.23.12 | | 0 GO:0006508,(CAT2G17760.1 | 0 |
| 38 | | 0 | 0 GO:0007165 AT3G29575.3 AFP3 | |
| 39 | | 0 | 0 GO:0007165 AT3G29575.3 AFP3 | |
| 40 | 2.7.11.1 | | 0 GO:0005515,(CAT4G20140.1 GSO1 | |
| 41 | 2.7.11.1 | | 0 GO:0005515 AT1G47890.1 AtRLP7,RLP7 | |
| 42 | | | | |
| 43 | | 0 | 0 AT1G63470.1 | 0 |
| 44 | 2.4.2.24 | | 0 GO:0016020,(CAT1G27600.2 I9H,IRX9-L | |
| 45 | | 0 | 0 GO:0055085,(CAT3G18830.1 ATPLT5,ATPMT5,PMT5 | |
| 46 | | 0 | 0 GO:0055085,(CAT3G18830.1 ATPLT5,ATPMT5,PMT5 | |
| 47 | 3.1.1.3 | | 0 GO:0016788 AT4G26790.1 | 0 |
| 48 | 3.4.23.12 | | 0 GO:0006508,(CAT1G03220.1 | 0 |
| 49 | | 0 | 0 AT3G63180.1 ATTKL,TKL | |
| 50 | | 0 K02985 | GO:0003723 AT5G35530.1 | 0 |
| 51 | | | | |
| 52 | 2.7.11.1 | | 0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2 | |
| 53 | 2.7.11.1 | | 0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2 | |
| 54 | | 0 | 0 AT2G37570.1 SLT1 | |
| 55 | | 0 | 0 AT2G37570.1 SLT1 | |
| 56 | | 0 | 0 AT2G37570.1 SLT1 | |
| 57 | 2.7.4.22 | K09903 | 0 AT3G10030.1 | 0 |
| 58 | | 0 | 0 AT3G02250.1 | 0 |
| 59 | | 0 | 0 GO:0003723 AT3G21740.1 APO4 | |
| 60 | | 0 | 0 GO:0006355,(CAT2G22840.1 AtGRF1,GRF1 | |

| | | | | | |
|----|-----------|----------|---|---|---|
| 1 | | | | | |
| 2 | 2.1.1.216 | K00555 | GO:0008033,(CAT5G15810.1 | | 0 |
| 3 | 2.1.1.216 | K00555 | GO:0008033,(CAT5G15810.1 | | 0 |
| 4 | | 0 K09874 | GO:0016020,(CAT4G10380.1 NIP5;1,NLM6,NLM8 | | |
| 5 | | 0 | 0 | 0 AT2G16800.1 | 0 |
| 6 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 7 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 8 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 9 | | 0 | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 10 | | 0 | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 11 | | 0 | 0 | 0 | 0 |
| 12 | | 0 | 0 | 0 | 0 |
| 13 | | 0 | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I | |
| 14 | | 0 | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I | |
| 15 | 3.4.23.12 | | 0 GO:0006508,(CAT2G17760.1 | | 0 |
| 16 | | 0 | 0 | 0 GO:0007165 AT3G29575.3 AFP3 | |
| 17 | | 0 | 0 | 0 GO:0005515,(CAT4G20140.1 GSO1 | |
| 18 | 2.7.11.1 | | 0 GO:0005515,(CAT4G20140.1 GSO1 | | |
| 19 | 2.7.11.1 | | 0 GO:0005515 AT1G47890.1 AtRLP7,RLP7 | | |
| 20 | | 0 | 0 | 0 AT1G63470.1 | 0 |
| 21 | | 0 | 0 | 0 AT1G63470.1 | 0 |
| 22 | 2.4.2.24 | | 0 GO:0016020,(CAT1G27600.2 I9H,IRX9-L | | |
| 23 | | 0 | 0 | 0 GO:0055085,(CAT3G18830.1 ATPLT5,ATPMT5,PMT5 | |
| 24 | 3.1.1.3 | | 0 GO:0016788 AT4G26790.1 | | 0 |
| 25 | 3.4.23.12 | | 0 GO:0006508,(CAT1G03220.1 | | 0 |
| 26 | | 0 | 0 | 0 AT3G63180.1 ATTKL,TKL | |
| 27 | | 0 | 0 | 0 AT3G63180.1 ATTKL,TKL | |
| 28 | | 0 K02985 | GO:0003723 AT5G35530.1 | | 0 |
| 29 | | 0 | 0 | 0 AT5G35530.1 | 0 |
| 30 | 2.7.11.1 | | 0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2 | | |
| 31 | 2.7.11.1 | | 0 GO:0005515,(CAT3G02130.1 RPK2,TOAD2 | | |
| 32 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 33 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 34 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 35 | 2.7.4.22 | K09903 | 0 AT3G10030.1 | | 0 |
| 36 | | 0 | 0 | 0 AT3G02250.1 | 0 |
| 37 | | 0 | 0 | 0 AT3G02250.1 | 0 |
| 38 | | 0 | 0 | 0 GO:0003723 AT3G21740.1 APO4 | |
| 39 | | 0 | 0 | 0 GO:0006355,(CAT2G22840.1 AtGRF1,GRF1 | |
| 40 | 2.1.1.216 | K00555 | GO:0008033,(CAT5G15810.1 | | 0 |
| 41 | 2.1.1.216 | K00555 | GO:0008033,(CAT5G15810.1 | | 0 |
| 42 | | 0 K09874 | GO:0016020,(CAT4G10380.1 NIP5;1,NLM6,NLM8 | | |
| 43 | | 0 | 0 | 0 AT2G16800.1 | 0 |
| 44 | | 0 | 0 | 0 AT2G16800.1 | 0 |
| 45 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 46 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 47 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 48 | | 0 | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 49 | | 0 | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 50 | | 0 | 0 | 0 | 0 |
| 51 | | 0 | 0 | 0 | 0 |
| 52 | | 0 | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I | |
| 53 | | 0 | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I | |
| 54 | 3.4.23.12 | | 0 GO:0006508,(CAT2G17760.1 | | 0 |
| 55 | | 0 | 0 | 0 GO:0007165 AT3G29575.3 AFP3 | |
| 56 | 2.7.11.1 | | 0 GO:0005515,(CAT4G20140.1 GSO1 | | |
| 57 | 2.7.11.1 | | 0 GO:0005515 AT1G47890.1 AtRLP7,RLP7 | | |
| 58 | | 0 | 0 | 0 AT1G63470.1 | 0 |
| 59 | | 0 | 0 | 0 AT1G63470.1 | 0 |
| 60 | 2.4.2.24 | | 0 GO:0016020,(CAT1G27600.2 I9H,IRX9-L | | |
| | | 0 | 0 | 0 GO:0055085,(CAT3G18830.1 ATPLT5,ATPMT5,PMT5 | |

| | | | | | |
|----|-----------|----------|--|--|---|
| 1 | | | | | |
| 2 | 3.1.1.3 | | 0 GO:0016788 AT4G26790.1 | | 0 |
| 3 | 3.4.23.12 | | 0 GO:0006508,(AT1G03220.1 | | 0 |
| 4 | | | 0 AT3G63180.1 ATTKL,TKL | | |
| 5 | | 0 | 0 | | |
| 6 | | 0 K02985 | GO:0003723 AT5G35530.1 | | 0 |
| 7 | 2.7.11.1 | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | | |
| 8 | 2.7.11.1 | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | | |
| 9 | | | | | |
| 10 | | 0 | 0 AT2G37570.1 SLT1 | | |
| 11 | | 0 | 0 AT2G37570.1 SLT1 | | |
| 12 | 2.7.4.22 | K09903 | 0 AT3G10030.1 | | 0 |
| 13 | | | | | |
| 14 | | 0 | 0 AT3G02250.1 | | 0 |
| 15 | | 0 | 0 GO:0003723 AT3G21740.1 APO4 | | |
| 16 | | 0 | 0 GO:0006355,(AT2G22840.1 AtGRF1,GRF1 | | |
| 17 | | | | | |
| 18 | 2.1.1.216 | K00555 | GO:0008033,(AT5G15810.1 | | 0 |
| 19 | 2.1.1.216 | K00555 | GO:0008033,(AT5G15810.1 | | 0 |
| 20 | | | | | |
| 21 | | 0 K09874 | GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8 | | |
| 22 | | 0 | 0 AT2G16800.1 | | 0 |
| 23 | | 0 | 0 AT3G04630.1 WDL1 | | |
| 24 | | 0 | 0 AT3G04630.1 WDL1 | | |
| 25 | | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | | |
| 26 | | 0 | 0 GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | | |
| 27 | | 0 | 0 | | |
| 28 | | 0 | 0 | | 0 |
| 29 | | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I | | |
| 30 | | | | | |
| 31 | 3.4.23.12 | | 0 GO:0006508,(AT2G17760.1 | | 0 |
| 32 | | 0 | 0 GO:0007165 AT3G29575.3 AFP3 | | |
| 33 | 2.7.11.1 | | 0 GO:0005515,(AT4G20140.1 GSO1 | | |
| 34 | 2.7.11.1 | | 0 GO:0005515 AT1G47890.1 AtRLP7,RLP7 | | |
| 35 | | | | | |
| 36 | | 0 | 0 AT1G63470.1 | | 0 |
| 37 | 2.4.2.24 | | 0 GO:0016020,(AT1G27600.2 I9H,IRX9-L | | |
| 38 | | | | | |
| 39 | | 0 | 0 GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5 | | |
| 40 | 3.1.1.3 | | 0 GO:0016788 AT4G26790.1 | | 0 |
| 41 | 3.4.23.12 | | 0 GO:0006508,(AT1G03220.1 | | 0 |
| 42 | | | | | |
| 43 | | 0 | 0 AT3G63180.1 ATTKL,TKL | | |
| 44 | | 0 K02985 | GO:0003723 AT5G35530.1 | | 0 |
| 45 | 2.7.11.1 | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | | |
| 46 | 2.7.11.1 | | 0 GO:0005515,(AT3G02130.1 RPK2,TOAD2 | | |
| 47 | | | | | |
| 48 | | 0 | 0 AT2G37570.1 SLT1 | | |
| 49 | | 0 | 0 AT2G37570.1 SLT1 | | |
| 50 | | | | | |
| 51 | 2.7.4.22 | K09903 | 0 AT3G10030.1 | | 0 |
| 52 | | 0 | 0 AT3G02250.1 | | 0 |
| 53 | | 0 | 0 GO:0003723 AT3G21740.1 APO4 | | |
| 54 | | 0 | 0 GO:0006355,(AT2G22840.1 AtGRF1,GRF1 | | |
| 55 | | | | | |
| 56 | 2.1.1.216 | K00555 | GO:0008033,(AT5G15810.1 | | 0 |
| 57 | 2.1.1.216 | K00555 | GO:0008033,(AT5G15810.1 | | 0 |
| 58 | | | | | |
| 59 | | 0 K09874 | GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8 | | |
| 60 | | 0 | 0 AT2G16800.1 | | 0 |
| | | 0 | 0 AT3G04630.1 WDL1 | | |

| | | | | | |
|----|-----------|----------|--|---|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 3 | | 0 | 0 | GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 4 | | 0 | 0 | GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 5 | | 0 | 0 | 0 | 0 |
| 6 | | 0 | 0 | 0 | 0 |
| 7 | | 0 | 0 | 0 AT4G33200.1 ATXI-I,XI-15,XI-I | |
| 8 | 3.4.23.12 | | 0 | GO:0006508,(AT2G17760.1 | 0 |
| 9 | | 0 | 0 | GO:0007165 AT3G29575.3 AFP3 | |
| 10 | | 0 | 0 | GO:0005515,(AT4G20140.1 GSO1 | |
| 11 | 2.7.11.1 | | 0 | GO:0005515,(AT4G20140.1 GSO1 | |
| 12 | 2.7.4.22 | K09903 | 0 | AT3G10030.1 | 0 |
| 13 | | 0 | 0 | GO:0055085,(AT3G18830.1 ATPLT5,ATPMT5,PMT5 | |
| 14 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 15 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 16 | | 0 | 0 | 0 AT3G04630.1 WDL1 | |
| 17 | 3.1.1.3 | | 0 | GO:0016788 AT4G26790.1 | 0 |
| 18 | 2.7.11.1 | | 0 | GO:0005515 AT1G47890.1 AtRLP7,RLP7 | |
| 19 | | 0 | 0 | 0 AT1G63470.1 | 0 |
| 20 | | 0 | 0 | 0 AT1G63470.1 | 0 |
| 21 | 2.4.2.24 | | 0 | GO:0016020,(AT1G27600.2 I9H,IRX9-L | |
| 22 | 3.4.23.12 | | 0 | GO:0006508,(AT1G03220.1 | 0 |
| 23 | | 0 | 0 | 0 AT3G63180.1 ATTKL,TKL | |
| 24 | | 0 | 0 | 0 AT3G63180.1 ATTKL,TKL | |
| 25 | 2.7.11.1 | | 0 | GO:0005515,(AT4G20140.1 GSO1 | |
| 26 | 2.7.1.68 | K00889 | GO:0046488,(AT1G77740.1 PIP5K2 | | |
| 27 | 2.7.1.68 | K00889 | GO:0046488,(AT1G77740.1 PIP5K2 | | |
| 28 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 29 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 30 | | 0 | 0 | 0 AT2G37570.1 SLT1 | |
| 31 | | 0 | 0 | 0 AT3G02250.1 | 0 |
| 32 | | 0 | 0 | 0 AT3G02250.1 | 0 |
| 33 | 0 K02985 | | GO:0003723 AT5G35530.1 | | 0 |
| 34 | | 0 | 0 | 0 AT5G35530.1 | 0 |
| 35 | 2.7.11.1 | | 0 | GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 36 | 2.7.11.1 | | 0 | GO:0005515,(AT3G02130.1 RPK2,TOAD2 | |
| 37 | | 0 | 0 | GO:0003723 AT3G21740.1 APO4 | |
| 38 | | 0 | 0 | GO:0006355,(AT2G22840.1 AtGRF1,GRF1 | |
| 39 | | 0 | 0 | GO:0006355,(AT2G22840.1 AtGRF1,GRF1 | |
| 40 | 2.1.1.216 | K00555 | GO:0008033,(AT5G15810.1 | | 0 |
| 41 | 2.1.1.216 | K00555 | GO:0008033,(AT5G15810.1 | | 0 |
| 42 | | 0 | 0 | 0 AT5G15810.1 | 0 |
| 43 | 3.4.23.12 | | 0 | GO:0006508,(AT2G17760.1 | 0 |
| 44 | | 0 K09874 | GO:0016020,(AT4G10380.1 NIP5;1,NLM6,NLM8 | | |
| 45 | | 0 | 0 | 0 AT2G16800.1 | 0 |
| 46 | | 0 | 0 | 0 AT2G16800.1 | 0 |
| 47 | | 0 | 0 | GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 48 | | 0 | 0 | GO:0007275 AT2G45190.1 AFO,FIL,YAB1 | |
| 49 | | 0 | 0 | 0 | 0 |
| 50 | | 0 | 0 | 0 | 0 |
| 51 | 2.7.11.1 | | 0 | GO:0005515,(AT1G68400.1 | 0 |
| 52 | | 0 K00507 | GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67 | | |
| 53 | | 0 | 0 | 0 AT2G34670.2 | 0 |
| 54 | | 0 | 0 | 0 AT2G34670.2 | 0 |
| 55 | | 0 | 0 | GO:0006355,(AT3G54320.1 ASML1,ATWRI1,WRI,WRI1 | |
| 56 | | 0 K17968 | 0 | AT4G33100.1 | 0 |
| 57 | | 0 | 0 | 0 AT4G33100.1 | 0 |
| 58 | | 0 | 0 | 0 AT5G06240.1 emb2735 | |
| 59 | | 0 | 0 | 0 AT5G06240.1 emb2735 | |
| 60 | | 0 | 0 | 0 AT4G30700.1 | 0 |
| | 2.1.1.163 | | 0 | GO:0008168,(AT1G78140.1 | 0 |

| | | | | |
|----|-----------------------|----------|--|---|
| 1 | | | | |
| 2 | 1.11.1.15 | 0 | GO:0055114,(CAT1G65980.1 TPX1 | |
| 3 | | 0 | 0 AT5G17270.1 | 0 |
| 4 | | 0 | 0 AT5G13210.1 | 0 |
| 5 | | | | |
| 6 | 2.3.2.2,2.6.1.4K14272 | | GO:0030170,(CAT1G70580.2 AOAT2,GGT2 | |
| 7 | 2.8.1.7,4.4.1.1 | 0 | 0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF | |
| 8 | | 0 K10956 | GO:0016020,(CAT2G34250.1 | 0 |
| 9 | | 0 | 0 AT1G64770.1 NDF2,NDH45 | |
| 10 | | 0 | 0 AT5G17170.1 ENH1 | |
| 11 | | | | |
| 12 | 2.7.11.1 | | 0 GO:0006468,(CAT4G02630.1 | 0 |
| 13 | | | | |
| 14 | 2.7.11.1 | | 0 GO:0006468,(CAT4G02630.1 | 0 |
| 15 | | 0 K02639 | GO:0051536,(CAT2G27510.1 ATFD3,FD3 | |
| 16 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 17 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 18 | | 0 | 0 AT3G23590.1 MED33A,RFR1 | |
| 19 | | | | |
| 20 | 2.4.1.18 | K00700 | GO:0005975,(CAT3G20440.2 BE1,EMB2729 | |
| 21 | | | | |
| 22 | 2.4.1.12 | | 0 GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1 | |
| 23 | | 0 | 0 AT4G18470.1 SNI1 | |
| 24 | | 0 | 0 AT4G18470.1 SNI1 | |
| 25 | | | | |
| 26 | 4.1.2.27 | | 0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1 | |
| 27 | 4.1.2.27 | | 0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1 | |
| 28 | | 0 | 0 AT4G18470.1 SNI1 | |
| 29 | | | | |
| 30 | 1.14.13.152 | | 0 GO:0055114,(CAT2G45550.1 CYP76C4 | |
| 31 | | 0 | 0 GO:0016021,(CAT1G28230.1 ATPUP1,PUP1 | |
| 32 | | 0 | 0 AT2G33390.1 | 0 |
| 33 | | 0 | 0 AT2G33390.1 | 0 |
| 34 | | 0 | 0 AT2G01770.1 ATVIT1,VIT1 | |
| 35 | | 0 | 0 AT2G01770.1 ATVIT1,VIT1 | |
| 36 | | 0 K00507 | GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67 | |
| 37 | | 0 | 0 AT2G34670.2 | 0 |
| 38 | | 0 | 0 GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1 | |
| 39 | | 0 | 0 AT4G33100.1 | 0 |
| 40 | | 0 K17968 | 0 AT4G33100.1 | 0 |
| 41 | | 0 | 0 AT5G06240.1 emb2735 | |
| 42 | | 0 | 0 AT5G06240.1 emb2735 | |
| 43 | | 0 | 0 AT4G30700.1 | 0 |
| 44 | | 0 | 0 AT4G30700.1 | 0 |
| 45 | | | | |
| 46 | 2.1.1.163 | | 0 GO:0008168,(CAT1G78140.1 | 0 |
| 47 | 1.11.1.15 | | 0 GO:0055114,(CAT1G65980.1 TPX1 | |
| 48 | | 0 | 0 AT5G17270.1 | 0 |
| 49 | | 0 | 0 AT5G13210.1 | 0 |
| 50 | | | | |
| 51 | 2.3.2.2,2.6.1.4K14272 | | GO:0030170,(CAT1G70580.2 AOAT2,GGT2 | |
| 52 | 2.8.1.7,4.4.1.1 | 0 | 0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF | |
| 53 | | 0 K10956 | GO:0016020,(CAT2G34250.1 | 0 |
| 54 | | 0 | 0 AT1G64770.1 NDF2,NDH45 | |
| 55 | | 0 | 0 AT5G17170.1 ENH1 | |
| 56 | | | | |
| 57 | 2.7.11.1 | | 0 GO:0006468,(CAT4G02630.1 | 0 |
| 58 | | | | |
| 59 | 2.7.11.1 | | 0 GO:0006468,(CAT4G02630.1 | 0 |
| 60 | | 0 K02639 | GO:0051536,(CAT2G27510.1 ATFD3,FD3 | |
| | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |

| | | | | |
|----|-----------------------|----------|---|---|
| 1 | | | | |
| 2 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 3 | | 0 | 0 0 AT3G23590.1 MED33A,RFR1 | |
| 4 | 2.4.1.18 | K00700 | GO:0005975,(AT3G20440.2 BE1,EMB2729 | |
| 5 | | | | |
| 6 | 2.4.1.12 | | 0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 | |
| 7 | | 0 | 0 0 AT4G18470.1 SNI1 | |
| 8 | | 0 | 0 0 AT4G18470.1 SNI1 | |
| 9 | | | | |
| 10 | 4.1.2.27 | | 0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1 | |
| 11 | 4.1.2.27 | | 0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1 | |
| 12 | | 0 | 0 0 AT4G18470.1 SNI1 | |
| 13 | | | | |
| 14 | 1.14.13.152 | | 0 GO:0055114,(AT2G45550.1 CYP76C4 | |
| 15 | | 0 | 0 GO:0016021,(AT1G28230.1 ATPUP1,PUP1 | |
| 16 | | 0 | 0 0 AT2G33390.1 | 0 |
| 17 | | 0 | 0 0 AT2G33390.1 | 0 |
| 18 | | 0 | 0 0 AT2G01770.1 ATVIT1,VIT1 | |
| 19 | | 0 | 0 0 AT2G01770.1 ATVIT1,VIT1 | |
| 20 | | 0 K00507 | GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67 | |
| 21 | | 0 | 0 0 AT2G34670.2 | 0 |
| 22 | | 0 | 0 GO:0006355,(AT3G54320.1 ASML1,ATWRI1,WRI,WRI1 | |
| 23 | | 0 | 0 0 AT4G33100.1 | 0 |
| 24 | | 0 K17968 | 0 AT5G06240.1 emb2735 | |
| 25 | | 0 | 0 AT5G06240.1 emb2735 | |
| 26 | | 0 | 0 AT5G06240.1 emb2735 | |
| 27 | | 0 | 0 AT4G30700.1 | 0 |
| 28 | | 0 | 0 AT4G30700.1 | 0 |
| 29 | | | | |
| 30 | 2.1.1.163 | | 0 GO:0008168,(AT1G78140.1 | 0 |
| 31 | 1.11.1.15 | | 0 GO:0055114,(AT1G65980.1 TPX1 | |
| 32 | | 0 | 0 AT5G17270.1 | 0 |
| 33 | | 0 | 0 AT5G13210.1 | 0 |
| 34 | | | | |
| 35 | 2.3.2.2,2.6.1.4K14272 | | GO:0030170,(AT1G70580.2 AOAT2,GGT2 | |
| 36 | 2.8.1.7,4.4.1.1 | | 0 0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF | |
| 37 | | 0 K10956 | GO:0016020,(AT2G34250.1 | 0 |
| 38 | | 0 | 0 AT1G64770.1 NDF2,NDH45 | |
| 39 | | 0 | 0 AT5G17170.1 ENH1 | |
| 40 | | 0 | 0 AT5G17170.1 ENH1 | |
| 41 | 2.7.11.1 | | 0 GO:0006468,(AT4G02630.1 | 0 |
| 42 | | | | |
| 43 | 2.7.11.1 | | 0 GO:0006468,(AT4G02630.1 | 0 |
| 44 | | 0 K02639 | GO:0051536,(AT2G27510.1 ATFD3,FD3 | |
| 45 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 46 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 47 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 48 | | 0 | 0 0 AT3G23590.1 MED33A,RFR1 | |
| 49 | 2.4.1.18 | K00700 | GO:0005975,(AT3G20440.2 BE1,EMB2729 | |
| 50 | | | | |
| 51 | 2.4.1.12 | | 0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 | |
| 52 | | 0 | 0 0 AT4G18470.1 SNI1 | |
| 53 | | 0 | 0 0 AT4G18470.1 SNI1 | |
| 54 | | | | |
| 55 | 4.1.2.27 | | 0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1 | |
| 56 | 4.1.2.27 | | 0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1 | |
| 57 | | 0 | 0 0 AT4G18470.1 SNI1 | |
| 58 | | | | |
| 59 | 1.14.13.152 | | 0 GO:0055114,(AT2G45550.1 CYP76C4 | |
| 60 | | 0 | 0 GO:0016021,(AT1G28230.1 ATPUP1,PUP1 | |
| | | 0 | 0 0 AT2G33390.1 | 0 |

| | | | | |
|----|-----------------------|----------|-------------------------------------|---|
| 1 | | | | |
| 2 | | 0 | 0 | 0 AT2G33390.1 |
| 3 | | 0 | 0 | 0 AT2G01770.1 ATVIT1,VIT1 |
| 4 | | 0 K00507 | GO:0006629 | AT3G15850.1 ADS3,FAD5,FADB,JB67 |
| 5 | | 0 | 0 | 0 AT2G34670.2 |
| 6 | | 0 | 0 | 0 GO:0006355,(AT3G54320.1 ASML1,ATWRI1,WRI,WRI1 |
| 7 | | 0 K17968 | | 0 AT4G33100.1 |
| 8 | | 0 | 0 | 0 AT5G06240.1 emb2735 |
| 9 | | 0 | 0 | 0 AT5G06240.1 emb2735 |
| 10 | | 0 | 0 | 0 AT4G30700.1 |
| 11 | 2.1.1.163 | | 0 | GO:0008168,(AT1G78140.1 |
| 12 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 |
| 13 | | 0 | 0 | 0 AT5G17270.1 |
| 14 | | 0 | 0 | 0 AT5G13210.1 |
| 15 | 2.3.2.2,2.6.1.4K14272 | | GO:0030170,(AT1G70580.2 AOAT2,GGT2 | |
| 16 | 2.8.1.7,4.4.1.1 | 0 | 0 | AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF |
| 17 | | 0 K10956 | GO:0016020,(AT2G34250.1 | 0 |
| 18 | | 0 | 0 | 0 AT1G64770.1 NDF2,NDH45 |
| 19 | | 0 | 0 | 0 AT5G17170.1 ENH1 |
| 20 | 2.7.11.1 | | 0 | GO:0006468,(AT4G02630.1 |
| 21 | 2.7.11.1 | | 0 | GO:0006468,(AT4G02630.1 |
| 22 | | 0 K02639 | GO:0051536,(AT2G27510.1 ATFD3,FD3 | |
| 23 | | 0 | 0 | 0 GO:0005515 AT2G46560.1 |
| 24 | | 0 | 0 | 0 GO:0005515 AT2G46560.1 |
| 25 | | 0 | 0 | 0 AT3G23590.1 MED33A,RFR1 |
| 26 | 2.4.1.18 | K00700 | GO:0005975,(AT3G20440.2 BE1,EMB2729 | |
| 27 | 2.4.1.12 | | 0 | GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 |
| 28 | | 0 | 0 | 0 AT4G18470.1 SNI1 |
| 29 | | 0 | 0 | 0 AT4G18470.1 SNI1 |
| 30 | 4.1.2.27 | | 0 | GO:0030170,(AT1G27980.1 ATDPL1,DPL1 |
| 31 | 4.1.2.27 | | 0 | GO:0030170,(AT1G27980.1 ATDPL1,DPL1 |
| 32 | | 0 | 0 | 0 AT4G18470.1 SNI1 |
| 33 | 1.14.13.152 | | 0 | GO:0055114,(AT2G45550.1 CYP76C4 |
| 34 | | 0 | 0 | 0 GO:0016021,(AT1G28230.1 ATPUP1,PUP1 |
| 35 | | 0 | 0 | 0 AT2G33390.1 |
| 36 | | 0 | 0 | 0 AT2G33390.1 |
| 37 | | 0 | 0 | 0 AT2G01770.1 ATVIT1,VIT1 |
| 38 | | 0 K00507 | GO:0006629 | AT3G15850.1 ADS3,FAD5,FADB,JB67 |
| 39 | | 0 | 0 | 0 AT2G34670.2 |
| 40 | | 0 | 0 | 0 GO:0006355,(AT3G54320.1 ASML1,ATWRI1,WRI,WRI1 |
| 41 | | 0 K17968 | | 0 AT4G33100.1 |
| 42 | | 0 | 0 | 0 AT5G06240.1 emb2735 |
| 43 | | 0 | 0 | 0 AT5G06240.1 emb2735 |
| 44 | | 0 | 0 | 0 AT4G30700.1 |
| 45 | 2.1.1.163 | | 0 | GO:0008168,(AT1G78140.1 |
| 46 | 1.11.1.15 | | 0 | GO:0055114,(AT1G65980.1 TPX1 |
| 47 | | 0 | 0 | 0 AT5G17270.1 |

| | | | | |
|----|-----------------------|----------|---|--|
| 1 | | | | |
| 2 | | 0 | 0 | 0 AT5G13210.1 |
| 3 | 2.3.2.2,2.6.1.4K14272 | | | GO:0030170,(CAT1G70580.2 AOAT2,GGT2 |
| 4 | 2.8.1.7,4.4.1.1 | | 0 | 0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF |
| 5 | | 0 K10956 | | GO:0016020,(CAT2G34250.1 |
| 6 | | | 0 | |
| 7 | | 0 | | 0 AT1G64770.1 NDF2,NDH45 |
| 8 | | 0 | | 0 AT5G17170.1 ENH1 |
| 9 | | | | |
| 10 | 2.7.11.1 | | 0 | GO:0006468,(CAT4G02630.1 |
| 11 | 2.7.11.1 | | 0 | GO:0006468,(CAT4G02630.1 |
| 12 | | 0 K02639 | | GO:0051536,(CAT2G27510.1 ATFD3,FD3 |
| 13 | | | 0 | |
| 14 | | 0 | | 0 GO:0005515 AT2G46560.1 |
| 15 | | 0 | | 0 GO:0005515 AT2G46560.1 |
| 16 | | 0 | | 0 AT3G23590.1 MED33A,RFR1 |
| 17 | | | | |
| 18 | 2.4.1.18 | K00700 | | GO:0005975,(CAT3G20440.2 BE1,EMB2729 |
| 19 | 2.4.1.12 | | 0 | GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1 |
| 20 | | 0 | | 0 AT4G18470.1 SNI1 |
| 21 | | 0 | | 0 AT4G18470.1 SNI1 |
| 22 | | | | |
| 23 | 4.1.2.27 | | 0 | GO:0030170,(CAT1G27980.1 ATDPL1,DPL1 |
| 24 | 4.1.2.27 | | 0 | GO:0030170,(CAT1G27980.1 ATDPL1,DPL1 |
| 25 | | 0 | | 0 AT4G18470.1 SNI1 |
| 26 | | | | |
| 27 | 1.14.13.152 | | 0 | GO:0055114,(CAT2G45550.1 CYP76C4 |
| 28 | | 0 | | 0 GO:0016021,(CAT1G28230.1 ATPUP1,PUP1 |
| 29 | | 0 | | 0 AT2G33390.1 |
| 30 | | 0 | | 0 AT2G33390.1 |
| 31 | | 0 | | 0 AT2G01770.1 ATVIT1,VIT1 |
| 32 | | 0 | | 0 AT2G01770.1 ATVIT1,VIT1 |
| 33 | | 0 K00507 | | GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67 |
| 34 | | | 0 | |
| 35 | | 0 | | 0 AT2G34670.2 |
| 36 | | 0 | | 0 GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1 |
| 37 | | 0 K17968 | | 0 AT4G33100.1 |
| 38 | | | | |
| 39 | | 0 | | 0 AT5G06240.1 emb2735 |
| 40 | | 0 | | 0 AT5G06240.1 emb2735 |
| 41 | | 0 | | 0 AT4G30700.1 |
| 42 | | | | |
| 43 | 2.1.1.163 | | 0 | GO:0008168,(CAT1G78140.1 |
| 44 | 1.11.1.15 | | 0 | GO:0055114,(CAT1G65980.1 TPX1 |
| 45 | | 0 | | 0 AT5G17270.1 |
| 46 | | 0 | | 0 AT5G13210.1 |
| 47 | | | | |
| 48 | 2.3.2.2,2.6.1.4K14272 | | | GO:0030170,(CAT1G70580.2 AOAT2,GGT2 |
| 49 | 2.8.1.7,4.4.1.1 | | 0 | 0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF |
| 50 | | 0 K10956 | | GO:0016020,(CAT2G34250.1 |
| 51 | | | 0 | |
| 52 | | 0 | | 0 AT1G64770.1 NDF2,NDH45 |
| 53 | | 0 | | 0 AT5G17170.1 ENH1 |
| 54 | | | | |
| 55 | 2.7.11.1 | | 0 | GO:0006468,(CAT4G02630.1 |
| 56 | 2.7.11.1 | | 0 | GO:0006468,(CAT4G02630.1 |
| 57 | | 0 K02639 | | GO:0051536,(CAT2G27510.1 ATFD3,FD3 |
| 58 | | | 0 | |
| 59 | | 0 | | 0 GO:0005515 AT2G46560.1 |
| 60 | | 0 | | 0 GO:0005515 AT2G46560.1 |
| | | 0 | | 0 AT3G23590.1 MED33A,RFR1 |

| | | | | |
|----|-----------------------|----------|---|---|
| 1 | | | | |
| 2 | 2.4.1.18 | K00700 | GO:0005975,(AT3G20440.2 BE1,EMB2729 | |
| 3 | 2.4.1.12 | | 0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 | |
| 4 | | 0 | 0 AT4G18470.1 SNI1 | |
| 5 | | 0 | 0 AT4G18470.1 SNI1 | |
| 6 | | 0 | 0 AT4G18470.1 SNI1 | |
| 7 | 4.1.2.27 | | 0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1 | |
| 8 | 4.1.2.27 | | 0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1 | |
| 9 | | 0 | 0 AT4G18470.1 SNI1 | |
| 10 | | 0 | 0 AT4G18470.1 SNI1 | |
| 11 | 1.14.13.152 | | 0 GO:0055114,(AT2G45550.1 CYP76C4 | |
| 12 | | 0 | 0 GO:0016021,(AT1G28230.1 ATPUP1,PUP1 | |
| 13 | | 0 | 0 AT2G33390.1 | 0 |
| 14 | | 0 | 0 AT2G33390.1 | 0 |
| 15 | | 0 | 0 AT2G01770.1 ATVIT1,VIT1 | |
| 16 | | 0 | 0 AT2G01770.1 ATVIT1,VIT1 | |
| 17 | | 0 K00507 | GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67 | |
| 18 | | 0 | 0 AT2G34670.2 | 0 |
| 19 | | 0 | 0 GO:0006355,(AT3G54320.1 ASML1,ATWRI1,WRI,WRI1 | |
| 20 | | 0 | 0 GO:0006355,(AT3G54320.1 ASML1,ATWRI1,WRI,WRI1 | |
| 21 | | 0 K17968 | 0 AT4G33100.1 | 0 |
| 22 | | 0 | 0 AT4G33100.1 | 0 |
| 23 | | 0 | 0 AT5G06240.1 emb2735 | |
| 24 | | 0 | 0 AT5G06240.1 emb2735 | |
| 25 | | 0 | 0 AT4G30700.1 | 0 |
| 26 | | 0 | 0 AT4G30700.1 | 0 |
| 27 | 2.1.1.163 | | 0 GO:0008168,(AT1G78140.1 | 0 |
| 28 | 1.11.1.15 | | 0 GO:0055114,(AT1G65980.1 TPX1 | |
| 29 | | 0 | 0 AT5G17270.1 | 0 |
| 30 | | 0 | 0 AT5G17270.1 | 0 |
| 31 | | 0 | 0 AT5G13210.1 | 0 |
| 32 | 2.3.2.2,2.6.1.4K14272 | | GO:0030170,(AT1G70580.2 AOAT2,GGT2 | |
| 33 | 2.8.1.7,4.4.1.1 | | 0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF | |
| 34 | | 0 K10956 | GO:0016020,(AT2G34250.1 | 0 |
| 35 | | 0 | 0 AT1G64770.1 NDF2,NDH45 | |
| 36 | | 0 | 0 AT1G64770.1 NDF2,NDH45 | |
| 37 | | 0 | 0 AT5G17170.1 ENH1 | |
| 38 | | 0 | 0 AT5G17170.1 ENH1 | |
| 39 | 2.7.11.1 | | 0 GO:0006468,(AT4G02630.1 | 0 |
| 40 | 2.7.11.1 | | 0 GO:0006468,(AT4G02630.1 | 0 |
| 41 | | 0 K02639 | GO:0051536,(AT2G27510.1 ATFD3,FD3 | |
| 42 | | 0 | 0 GO:0051536,(AT2G27510.1 ATFD3,FD3 | |
| 43 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 44 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 45 | | 0 | 0 AT3G23590.1 MED33A,RFR1 | |
| 46 | | 0 | 0 AT3G23590.1 MED33A,RFR1 | |
| 47 | 2.4.1.18 | K00700 | GO:0005975,(AT3G20440.2 BE1,EMB2729 | |
| 48 | 2.4.1.12 | | 0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 | |
| 49 | | 0 | 0 AT4G18470.1 SNI1 | |
| 50 | | 0 | 0 AT4G18470.1 SNI1 | |
| 51 | | 0 | 0 AT4G18470.1 SNI1 | |
| 52 | 4.1.2.27 | | 0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1 | |
| 53 | 4.1.2.27 | | 0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1 | |
| 54 | | 0 | 0 AT4G18470.1 SNI1 | |
| 55 | | 0 | 0 AT4G18470.1 SNI1 | |
| 56 | 1.14.13.152 | | 0 GO:0055114,(AT2G45550.1 CYP76C4 | |
| 57 | | 0 | 0 GO:0016021,(AT1G28230.1 ATPUP1,PUP1 | |
| 58 | | 0 | 0 AT2G33390.1 | 0 |
| 59 | | 0 | 0 AT2G33390.1 | 0 |
| 60 | | 0 | 0 AT2G01770.1 ATVIT1,VIT1 | |

| | | | | |
|----|-----------------------|----------|---|---|
| 1 | | | | |
| 2 | | 0 K00507 | GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67 | |
| 3 | | 0 | 0 AT2G34670.2 | 0 |
| 4 | | 0 | 0 GO:0006355,(AT3G54320.1 ASML1,ATWRI1,WRI,WRI1 | |
| 5 | | 0 K17968 | 0 AT4G33100.1 | 0 |
| 6 | | 0 | 0 AT5G06240.1 emb2735 | |
| 7 | | 0 | 0 AT5G06240.1 emb2735 | |
| 8 | | 0 | 0 AT4G30700.1 | 0 |
| 9 | | 0 | 0 AT4G30700.1 | 0 |
| 10 | | 0 | 0 AT4G30700.1 | 0 |
| 11 | 2.1.1.163 | | 0 GO:0008168,(AT1G78140.1 | 0 |
| 12 | 1.11.1.15 | | 0 GO:0055114,(AT1G65980.1 TPX1 | |
| 13 | | 0 | 0 AT5G17270.1 | 0 |
| 14 | | 0 | 0 AT5G13210.1 | 0 |
| 15 | | 0 | 0 AT5G13210.1 | 0 |
| 16 | 2.3.2.2,2.6.1.4K14272 | | GO:0030170,(AT1G70580.2 AOAT2,GGT2 | |
| 17 | 2.8.1.7,4.4.1.1 | | 0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF | |
| 18 | | 0 K10956 | GO:0016020,(AT2G34250.1 | 0 |
| 19 | | 0 | 0 AT1G64770.1 NDF2,NDH45 | |
| 20 | | 0 | 0 AT5G17170.1 ENH1 | |
| 21 | | 0 | 0 AT5G17170.1 ENH1 | |
| 22 | | 0 | 0 AT5G17170.1 ENH1 | |
| 23 | 2.7.11.1 | | 0 GO:0006468,(AT4G02630.1 | 0 |
| 24 | 2.7.11.1 | | 0 GO:0006468,(AT4G02630.1 | 0 |
| 25 | | 0 K02639 | GO:0051536,(AT2G27510.1 ATFD3,FD3 | |
| 26 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 27 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 28 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 29 | | 0 | 0 AT3G23590.1 MED33A,RFR1 | |
| 30 | | 0 | 0 AT3G23590.1 MED33A,RFR1 | |
| 31 | 2.4.1.18 | K00700 | GO:0005975,(AT3G20440.2 BE1,EMB2729 | |
| 32 | 2.4.1.12 | | 0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 | |
| 33 | | 0 | 0 AT4G18470.1 SNI1 | |
| 34 | | 0 | 0 AT4G18470.1 SNI1 | |
| 35 | | 0 | 0 AT4G18470.1 SNI1 | |
| 36 | 4.1.2.27 | | 0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1 | |
| 37 | 4.1.2.27 | | 0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1 | |
| 38 | | 0 | 0 AT4G18470.1 SNI1 | |
| 39 | | 0 | 0 AT4G18470.1 SNI1 | |
| 40 | 1.14.13.152 | | 0 GO:0055114,(AT2G45550.1 CYP76C4 | |
| 41 | | 0 | 0 GO:0016021,(AT1G28230.1 ATPUP1,PUP1 | |
| 42 | | 0 | 0 AT2G33390.1 | 0 |
| 43 | | 0 | 0 AT2G33390.1 | 0 |
| 44 | | 0 | 0 AT2G33390.1 | 0 |
| 45 | | 0 | 0 AT2G01770.1 ATVIT1,VIT1 | |
| 46 | | 0 | 0 AT2G01770.1 ATVIT1,VIT1 | |
| 47 | | 0 K00507 | GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67 | |
| 48 | | 0 | 0 AT2G34670.2 | 0 |
| 49 | | 0 | 0 GO:0006355,(AT3G54320.1 ASML1,ATWRI1,WRI,WRI1 | |
| 50 | | 0 K17968 | 0 AT4G33100.1 | 0 |
| 51 | | 0 | 0 AT4G33100.1 | 0 |
| 52 | | 0 | 0 AT5G06240.1 emb2735 | |
| 53 | | 0 | 0 AT5G06240.1 emb2735 | |
| 54 | | 0 | 0 AT5G06240.1 emb2735 | |
| 55 | | 0 | 0 AT4G30700.1 | 0 |
| 56 | 2.1.1.163 | | 0 GO:0008168,(AT1G78140.1 | 0 |
| 57 | 1.11.1.15 | | 0 GO:0055114,(AT1G65980.1 TPX1 | |
| 58 | | 0 | 0 AT5G17270.1 | 0 |
| 59 | | 0 | 0 AT5G17270.1 | 0 |
| 60 | | 0 | 0 AT5G13210.1 | 0 |
| | 2.3.2.2,2.6.1.4K14272 | | GO:0030170,(AT1G70580.2 AOAT2,GGT2 | |

| | | | | |
|----|-----------------------|----------|---|---|
| 1 | | | | |
| 2 | 2.8.1.7,4.4.1.1 | 0 | 0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF | |
| 3 | | 0 K10956 | GO:0016020,(AT2G34250.1 | 0 |
| 4 | | 0 | 0 AT1G64770.1 NDF2,NDH45 | |
| 5 | | 0 | 0 AT5G17170.1 ENH1 | |
| 6 | | 0 | 0 AT5G17170.1 ENH1 | |
| 7 | 2.7.11.1 | | 0 GO:0006468,(AT4G02630.1 | 0 |
| 8 | 2.7.11.1 | | 0 GO:0006468,(AT4G02630.1 | 0 |
| 9 | | | | |
| 10 | | 0 K02639 | GO:0051536,(AT2G27510.1 ATFD3,FD3 | |
| 11 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 12 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 13 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 14 | | 0 | 0 AT3G23590.1 MED33A,RFR1 | |
| 15 | 2.4.1.18 | K00700 | GO:0005975,(AT3G20440.2 BE1,EMB2729 | |
| 16 | 2.4.1.12 | | 0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 | |
| 17 | | | | |
| 18 | | 0 | 0 AT4G18470.1 SNI1 | |
| 19 | | 0 | 0 AT4G18470.1 SNI1 | |
| 20 | 4.1.2.27 | | 0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1 | |
| 21 | | | | |
| 22 | 4.1.2.27 | | 0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1 | |
| 23 | | 0 | 0 AT4G18470.1 SNI1 | |
| 24 | 1.14.13.152 | | 0 GO:0055114,(AT2G45550.1 CYP76C4 | |
| 25 | | | | |
| 26 | | 0 | 0 GO:0016021,(AT1G28230.1 ATPUP1,PUP1 | |
| 27 | | 0 | 0 AT2G33390.1 | 0 |
| 28 | | 0 | 0 AT2G33390.1 | 0 |
| 29 | | 0 | 0 AT2G01770.1 ATVIT1,VIT1 | |
| 30 | | 0 | 0 AT2G01770.1 ATVIT1,VIT1 | |
| 31 | | 0 K00507 | GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67 | |
| 32 | | 0 | 0 AT2G34670.2 | 0 |
| 33 | | 0 | 0 GO:0006355,(AT3G54320.1 ASML1,ATWRI1,WRI,WRI1 | |
| 34 | | | | |
| 35 | | 0 K17968 | 0 AT4G33100.1 | 0 |
| 36 | | 0 | 0 AT5G06240.1 emb2735 | |
| 37 | | 0 | 0 AT5G06240.1 emb2735 | |
| 38 | | 0 | 0 AT5G06240.1 emb2735 | |
| 39 | | 0 | 0 AT4G30700.1 | 0 |
| 40 | 2.1.1.163 | | 0 GO:0008168,(AT1G78140.1 | 0 |
| 41 | 1.11.1.15 | | 0 GO:0055114,(AT1G65980.1 TPX1 | |
| 42 | | | | |
| 43 | | 0 | 0 AT5G17270.1 | 0 |
| 44 | | 0 | 0 AT5G13210.1 | 0 |
| 45 | 2.3.2.2,2.6.1.4K14272 | | GO:0030170,(AT1G70580.2 AOAT2,GGT2 | |
| 46 | | | | |
| 47 | 2.8.1.7,4.4.1.1 | 0 | 0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF | |
| 48 | | 0 K10956 | GO:0016020,(AT2G34250.1 | 0 |
| 49 | | 0 | 0 AT1G64770.1 NDF2,NDH45 | |
| 50 | | 0 | 0 AT5G17170.1 ENH1 | |
| 51 | | 0 | 0 AT5G17170.1 ENH1 | |
| 52 | 2.7.11.1 | | 0 GO:0006468,(AT4G02630.1 | 0 |
| 53 | 2.7.11.1 | | 0 GO:0006468,(AT4G02630.1 | 0 |
| 54 | | | | |
| 55 | | 0 K02639 | GO:0051536,(AT2G27510.1 ATFD3,FD3 | |
| 56 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 57 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 58 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 59 | | 0 | 0 AT3G23590.1 MED33A,RFR1 | |
| 60 | 2.4.1.18 | K00700 | GO:0005975,(AT3G20440.2 BE1,EMB2729 | |
| | 2.4.1.12 | | 0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 | |

| | | | | | |
|----|-----------------------|----------|---|--|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 AT4G18470.1 SNI1 | |
| 3 | | 0 | 0 | 0 AT4G18470.1 SNI1 | |
| 4 | 4.1.2.27 | | | 0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1 | |
| 5 | | | | | |
| 6 | 4.1.2.27 | | | 0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1 | |
| 7 | | 0 | 0 | 0 AT4G18470.1 SNI1 | |
| 8 | 1.14.13.152 | | | 0 GO:0055114,(CAT2G45550.1 CYP76C4 | |
| 9 | | | | | |
| 10 | | 0 | | 0 GO:0016021,(CAT1G28230.1 ATPUP1,PUP1 | |
| 11 | | 0 | 0 | 0 AT2G33390.1 | 0 |
| 12 | | 0 | 0 | 0 AT2G33390.1 | 0 |
| 13 | | 0 | 0 | 0 AT2G01770.1 ATVIT1,VIT1 | |
| 14 | | 0 | 0 | 0 AT2G01770.1 ATVIT1,VIT1 | |
| 15 | | 0 K00507 | | GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67 | |
| 16 | | 0 | 0 | 0 AT2G34670.2 | 0 |
| 17 | | 0 | | | |
| 18 | | 0 | | 0 GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1 | |
| 19 | | 0 K17968 | | 0 AT4G33100.1 | 0 |
| 20 | | 0 | 0 | 0 AT5G06240.1 emb2735 | |
| 21 | | 0 | 0 | 0 AT5G06240.1 emb2735 | |
| 22 | | 0 | 0 | 0 AT5G06240.1 emb2735 | |
| 23 | | 0 | 0 | 0 AT4G30700.1 | 0 |
| 24 | 2.1.1.163 | | | 0 GO:0008168,(CAT1G78140.1 | 0 |
| 25 | | | | | |
| 26 | 1.11.1.15 | | | 0 GO:0055114,(CAT1G65980.1 TPX1 | |
| 27 | | 0 | 0 | 0 AT5G17270.1 | 0 |
| 28 | | 0 | 0 | 0 AT5G13210.1 | 0 |
| 29 | | | | | |
| 30 | 2.3.2.2,2.6.1.4K14272 | | | GO:0030170,(CAT1G70580.2 AOAT2,GGT2 | |
| 31 | 2.8.1.7,4.4.1.1 | | 0 | 0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF | |
| 32 | | 0 K10956 | | GO:0016020,(CAT2G34250.1 | 0 |
| 33 | | 0 | 0 | 0 AT1G64770.1 NDF2,NDH45 | |
| 34 | | 0 | 0 | 0 AT1G64770.1 NDF2,NDH45 | |
| 35 | | 0 | 0 | 0 AT5G17170.1 ENH1 | |
| 36 | 2.7.11.1 | | | 0 GO:0006468,(CAT4G02630.1 | 0 |
| 37 | | | | | |
| 38 | 2.7.11.1 | | | 0 GO:0006468,(CAT4G02630.1 | 0 |
| 39 | | 0 K02639 | | GO:0051536,(CAT2G27510.1 ATFD3,FD3 | |
| 40 | | 0 | | 0 GO:0005515 AT2G46560.1 | 0 |
| 41 | | 0 | | 0 GO:0005515 AT2G46560.1 | 0 |
| 42 | | 0 | | 0 GO:0005515 AT2G46560.1 | 0 |
| 43 | | 0 | 0 | 0 AT3G23590.1 MED33A,RFR1 | |
| 44 | 2.4.1.18 | K00700 | | GO:0005975,(CAT3G20440.2 BE1,EMB2729 | |
| 45 | 2.4.1.12 | | | 0 GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1 | |
| 46 | | | | | |
| 47 | | 0 | 0 | 0 AT4G18470.1 SNI1 | |
| 48 | | 0 | 0 | 0 AT4G18470.1 SNI1 | |
| 49 | 4.1.2.27 | | | 0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1 | |
| 50 | | | | | |
| 51 | 4.1.2.27 | | | 0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1 | |
| 52 | | 0 | 0 | 0 AT4G18470.1 SNI1 | |
| 53 | 1.14.13.152 | | | 0 GO:0055114,(CAT2G45550.1 CYP76C4 | |
| 54 | | | | | |
| 55 | | 0 | | 0 GO:0016021,(CAT1G28230.1 ATPUP1,PUP1 | |
| 56 | | 0 | 0 | 0 AT2G33390.1 | 0 |
| 57 | | 0 | 0 | 0 AT2G33390.1 | 0 |
| 58 | | 0 | 0 | 0 AT2G01770.1 ATVIT1,VIT1 | |
| 59 | | 0 | 0 | 0 AT2G01770.1 ATVIT1,VIT1 | |
| 60 | | 0 K00507 | | GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67 | |
| | | 0 | 0 | 0 AT2G34670.2 | 0 |

| | | | | |
|----|-----------------------|----------|--|---|
| 1 | | | | |
| 2 | | 0 | 0 GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1 | |
| 3 | | 0 K17968 | 0 AT4G33100.1 | 0 |
| 4 | | 0 | 0 AT5G06240.1 emb2735 | |
| 5 | | 0 | 0 AT5G06240.1 emb2735 | |
| 6 | | 0 | 0 AT4G30700.1 | 0 |
| 7 | | 0 | 0 AT4G30700.1 | 0 |
| 8 | 2.1.1.163 | | 0 GO:0008168,(CAT1G78140.1 | 0 |
| 9 | | | | |
| 10 | 1.11.1.15 | | 0 GO:0055114,(CAT1G65980.1 TPX1 | |
| 11 | | 0 | 0 AT5G17270.1 | 0 |
| 12 | | 0 | 0 AT5G13210.1 | 0 |
| 13 | | | | |
| 14 | 2.3.2.2,2.6.1.4K14272 | | GO:0030170,(CAT1G70580.2 AOAT2,GGT2 | |
| 15 | 2.8.1.7,4.4.1.1 | | 0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF | |
| 16 | | 0 K10956 | GO:0016020,(CAT2G34250.1 | 0 |
| 17 | | 0 | 0 AT1G64770.1 NDF2,NDH45 | |
| 18 | | 0 | 0 AT5G17170.1 ENH1 | |
| 19 | | 0 | 0 AT5G17170.1 ENH1 | |
| 20 | 2.7.11.1 | | 0 GO:0006468,(CAT4G02630.1 | 0 |
| 21 | | | | |
| 22 | 2.7.11.1 | | 0 GO:0006468,(CAT4G02630.1 | 0 |
| 23 | | 0 K02639 | GO:0051536,(CAT2G27510.1 ATFD3,FD3 | |
| 24 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 25 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 26 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 27 | | 0 | 0 AT3G23590.1 MED33A,RFR1 | |
| 28 | 2.4.1.18 | K00700 | GO:0005975,(CAT3G20440.2 BE1,EMB2729 | |
| 29 | | | | |
| 30 | 2.4.1.12 | | 0 GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1 | |
| 31 | | 0 | 0 AT4G18470.1 SNI1 | |
| 32 | | 0 | 0 AT4G18470.1 SNI1 | |
| 33 | | | | |
| 34 | 4.1.2.27 | | 0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1 | |
| 35 | 4.1.2.27 | | 0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1 | |
| 36 | | 0 | 0 AT4G18470.1 SNI1 | |
| 37 | | | | |
| 38 | 1.14.13.152 | | 0 GO:0055114,(CAT2G45550.1 CYP76C4 | |
| 39 | | 0 | 0 GO:0016021,(CAT1G28230.1 ATPUP1,PUP1 | |
| 40 | | 0 | 0 AT2G33390.1 | 0 |
| 41 | | 0 | 0 AT2G33390.1 | 0 |
| 42 | | 0 | 0 AT2G33390.1 | 0 |
| 43 | | 0 | 0 AT2G01770.1 ATVIT1,VIT1 | |
| 44 | | 0 K00507 | GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67 | |
| 45 | | 0 | 0 AT2G34670.2 | 0 |
| 46 | | 0 | 0 AT2G34670.2 | 0 |
| 47 | | 0 | 0 GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1 | |
| 48 | | 0 K17968 | 0 AT4G33100.1 | 0 |
| 49 | | 0 | 0 AT5G06240.1 emb2735 | |
| 50 | | 0 | 0 AT5G06240.1 emb2735 | |
| 51 | | 0 | 0 AT5G06240.1 emb2735 | |
| 52 | | 0 | 0 AT4G30700.1 | 0 |
| 53 | | | | |
| 53 | 2.1.1.163 | | 0 GO:0008168,(CAT1G78140.1 | 0 |
| 54 | | | | |
| 55 | 1.11.1.15 | | 0 GO:0055114,(CAT1G65980.1 TPX1 | |
| 56 | | 0 | 0 AT5G17270.1 | 0 |
| 57 | | 0 | 0 AT5G13210.1 | 0 |
| 58 | | | | |
| 59 | 2.3.2.2,2.6.1.4K14272 | | GO:0030170,(CAT1G70580.2 AOAT2,GGT2 | |
| 60 | 2.8.1.7,4.4.1.1 | | 0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF | |
| | | 0 K10956 | GO:0016020,(CAT2G34250.1 | 0 |

| | | | | |
|----|-----------------|---|--------|---|
| 1 | | | | |
| 2 | | 0 | 0 | 0 AT1G64770.1 NDF2,NDH45 |
| 3 | | 0 | 0 | 0 AT5G17170.1 ENH1 |
| 4 | 2.7.11.1 | | 0 | GO:0006468,(AT4G02630.1 |
| 5 | | | | 0 |
| 6 | 2.7.11.1 | | 0 | GO:0006468,(AT4G02630.1 |
| 7 | | 0 | K02639 | GO:0051536,(AT2G27510.1 ATFD3,FD3 |
| 8 | | 0 | | 0 GO:0005515 AT2G46560.1 |
| 9 | | | | 0 |
| 10 | | 0 | | 0 GO:0005515 AT2G46560.1 |
| 11 | | | | 0 |
| 12 | 2.4.1.18 | | K00700 | GO:0005975,(AT3G20440.2 BE1,EMB2729 |
| 13 | | | | |
| 14 | 2.4.1.12 | | | 0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 |
| 15 | | 0 | | 0 AT4G18470.1 SNI1 |
| 16 | | 0 | | 0 AT4G18470.1 SNI1 |
| 17 | | | | |
| 18 | 4.1.2.27 | | | 0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1 |
| 19 | 4.1.2.27 | | | 0 GO:0030170,(AT1G27980.1 ATDPL1,DPL1 |
| 20 | | 0 | | 0 AT4G18470.1 SNI1 |
| 21 | | | | |
| 22 | 1.14.13.152 | | | 0 GO:0055114,(AT2G45550.1 CYP76C4 |
| 23 | | 0 | | 0 GO:0016021,(AT1G28230.1 ATPUP1,PUP1 |
| 24 | | 0 | | 0 AT2G33390.1 |
| 25 | | | | 0 |
| 26 | | 0 | | 0 AT2G33390.1 |
| 27 | | 0 | | 0 AT2G01770.1 ATVIT1,VIT1 |
| 28 | | 0 | K00507 | GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67 |
| 29 | | 0 | | 0 AT2G34670.2 |
| 30 | | | | 0 |
| 31 | | 0 | | 0 GO:0006355,(AT3G54320.1 ASML1,ATWRI1,WRI,WRI1 |
| 32 | | 0 | K17968 | 0 AT4G33100.1 |
| 33 | | | | 0 |
| 34 | | 0 | | 0 AT5G06240.1 emb2735 |
| 35 | | 0 | | 0 AT5G06240.1 emb2735 |
| 36 | | 0 | | 0 AT4G30700.1 |
| 37 | | | | 0 |
| 38 | 2.1.1.163 | | | 0 GO:0008168,(AT1G78140.1 |
| 39 | 1.11.1.15 | | | 0 GO:0055114,(AT1G65980.1 TPX1 |
| 40 | | 0 | | 0 AT5G17270.1 |
| 41 | | 0 | | 0 AT5G13210.1 |
| 42 | | | | 0 |
| 43 | 2.3.2.2,2.6.1.4 | | K14272 | GO:0030170,(AT1G70580.2 AOAT2,GGT2 |
| 44 | 2.8.1.7,4.4.1.1 | | | 0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF |
| 45 | | 0 | K10956 | GO:0016020,(AT2G34250.1 |
| 46 | | | | 0 |
| 47 | | 0 | | 0 AT1G64770.1 NDF2,NDH45 |
| 48 | | 0 | | 0 AT5G17170.1 ENH1 |
| 49 | 2.7.11.1 | | | 0 GO:0006468,(AT4G02630.1 |
| 50 | | | | 0 |
| 51 | 2.7.11.1 | | | 0 GO:0006468,(AT4G02630.1 |
| 52 | | 0 | K02639 | GO:0051536,(AT2G27510.1 ATFD3,FD3 |
| 53 | | 0 | | 0 GO:0005515 AT2G46560.1 |
| 54 | | | | 0 |
| 55 | | 0 | | 0 GO:0005515 AT2G46560.1 |
| 56 | | 0 | | 0 AT3G23590.1 MED33A,RFR1 |
| 57 | 2.4.1.18 | | K00700 | GO:0005975,(AT3G20440.2 BE1,EMB2729 |
| 58 | | | | |
| 59 | 2.4.1.12 | | | 0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 |
| 60 | | 0 | | 0 AT4G18470.1 SNI1 |
| | | 0 | | 0 AT4G18470.1 SNI1 |

| | | | | |
|----|-----------------------|--|--|---|
| 1 | | | | |
| 2 | 4.1.2.27 | 0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1 | | |
| 3 | 4.1.2.27 | 0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1 | | |
| 4 | | 0 | 0 AT4G18470.1 SNI1 | |
| 5 | | 0 | | |
| 6 | 1.14.13.152 | 0 GO:0055114,(CAT2G45550.1 CYP76C4 | | |
| 7 | | 0 GO:0016021,(CAT1G28230.1 ATPUP1,PUP1 | | |
| 8 | | 0 | 0 AT2G33390.1 | 0 |
| 9 | | 0 | 0 AT2G33390.1 | 0 |
| 10 | | 0 | 0 AT2G33390.1 | 0 |
| 11 | | 0 | 0 AT2G01770.1 ATVIT1,VIT1 | |
| 12 | | 0 K00507 | GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67 | |
| 13 | | 0 | 0 AT2G34670.2 | 0 |
| 14 | | 0 | 0 AT2G34670.2 | 0 |
| 15 | | 0 GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1 | | |
| 16 | | 0 K17968 | 0 AT4G33100.1 | 0 |
| 17 | | 0 | 0 AT4G33100.1 | 0 |
| 18 | | 0 | 0 AT5G06240.1 emb2735 | |
| 19 | | 0 | 0 AT5G06240.1 emb2735 | |
| 20 | | 0 | 0 AT5G06240.1 emb2735 | |
| 21 | | 0 | 0 AT4G30700.1 | 0 |
| 22 | 2.1.1.163 | 0 GO:0008168,(CAT1G78140.1 | | 0 |
| 23 | 1.11.1.15 | 0 GO:0055114,(CAT1G65980.1 TPX1 | | |
| 24 | | 0 | 0 AT5G17270.1 | 0 |
| 25 | | 0 | 0 AT5G17270.1 | 0 |
| 26 | | 0 | 0 AT5G13210.1 | 0 |
| 27 | 2.3.2.2,2.6.1.4K14272 | GO:0030170,(CAT1G70580.2 AOAT2,GGT2 | | |
| 28 | 2.8.1.7,4.4.1.1 | 0 | 0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF | |
| 29 | | 0 K10956 | GO:0016020,(CAT2G34250.1 | 0 |
| 30 | | 0 | 0 AT2G34250.1 | 0 |
| 31 | | 0 | 0 AT1G64770.1 NDF2,NDH45 | |
| 32 | | 0 | 0 AT1G64770.1 NDF2,NDH45 | |
| 33 | | 0 | 0 AT5G17170.1 ENH1 | |
| 34 | 2.7.11.1 | 0 GO:0006468,(CAT4G02630.1 | | 0 |
| 35 | 2.7.11.1 | 0 GO:0006468,(CAT4G02630.1 | | 0 |
| 36 | | 0 K02639 | GO:0051536,(CAT2G27510.1 ATFD3,FD3 | |
| 37 | | 0 | 0 AT2G27510.1 ATFD3,FD3 | |
| 38 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 39 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 40 | | 0 | 0 AT3G23590.1 MED33A,RFR1 | |
| 41 | 2.4.1.18 | K00700 | GO:0005975,(CAT3G20440.2 BE1,EMB2729 | |
| 42 | | | 0 BE1,EMB2729 | |
| 43 | 2.4.1.12 | 0 GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1 | | |
| 44 | | 0 | 0 AT4G18470.1 SNI1 | |
| 45 | | 0 | 0 AT4G18470.1 SNI1 | |
| 46 | | 0 | 0 AT4G18470.1 SNI1 | |
| 47 | 4.1.2.27 | 0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1 | | |
| 48 | 4.1.2.27 | 0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1 | | |
| 49 | | 0 | 0 AT4G18470.1 SNI1 | |
| 50 | | 0 | 0 AT4G18470.1 SNI1 | |
| 51 | 1.14.13.152 | 0 GO:0055114,(CAT2G45550.1 CYP76C4 | | |
| 52 | | 0 GO:0016021,(CAT1G28230.1 ATPUP1,PUP1 | | |
| 53 | | 0 | 0 AT2G33390.1 | 0 |
| 54 | | 0 | 0 AT2G33390.1 | 0 |
| 55 | | 0 | 0 AT2G33390.1 | 0 |
| 56 | | 0 | 0 AT2G01770.1 ATVIT1,VIT1 | |
| 57 | | 0 K00507 | GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67 | |
| 58 | | 0 | 0 AT2G34670.2 | 0 |
| 59 | | 0 | 0 AT2G34670.2 | 0 |
| 60 | | 0 GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1 | | |
| | | 0 K17968 | 0 AT4G33100.1 | 0 |

| | | | | |
|----|-----------------------|----------|-------------------------------------|--|
| 1 | | | | |
| 2 | | 0 | 0 | 0 AT5G06240.1 emb2735 |
| 3 | | 0 | 0 | 0 AT5G06240.1 emb2735 |
| 4 | | 0 | 0 | 0 AT4G30700.1 |
| 5 | | 0 | 0 | 0 AT4G30700.1 |
| 6 | 2.1.1.163 | | 0 | GO:0008168,(CAT1G78140.1 |
| 7 | 1.11.1.15 | | 0 | GO:0055114,(CAT1G65980.1 TPX1 |
| 8 | | 0 | 0 | 0 AT5G17270.1 |
| 9 | | 0 | 0 | 0 AT5G13210.1 |
| 10 | | 0 | 0 | 0 AT5G13210.1 |
| 11 | 2.3.2.2,2.6.1.4K14272 | | GO:0030170,(CAT1G70580.2 AOAT2,GGT2 | |
| 12 | 2.8.1.7,4.4.1.1 | | 0 | 0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF |
| 13 | | | | |
| 14 | | 0 K10956 | | GO:0016020,(CAT2G34250.1 |
| 15 | | 0 | 0 | 0 AT1G64770.1 NDF2,NDH45 |
| 16 | | 0 | 0 | 0 AT5G17170.1 ENH1 |
| 17 | | | | |
| 18 | 2.7.11.1 | | 0 | GO:0006468,(CAT4G02630.1 |
| 19 | 2.7.11.1 | | 0 | GO:0006468,(CAT4G02630.1 |
| 20 | | 0 K02639 | | GO:0051536,(CAT2G27510.1 ATFD3,FD3 |
| 21 | | 0 | 0 | GO:0005515 AT2G46560.1 |
| 22 | | 0 | 0 | GO:0005515 AT2G46560.1 |
| 23 | | 0 | 0 | GO:0005515 AT2G46560.1 |
| 24 | | 0 | 0 | 0 AT3G23590.1 MED33A,RFR1 |
| 25 | | | | |
| 26 | 2.4.1.18 | K00700 | | GO:0005975,(CAT3G20440.2 BE1,EMB2729 |
| 27 | 2.4.1.12 | | 0 | GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1 |
| 28 | | 0 | 0 | 0 AT4G18470.1 SNI1 |
| 29 | | 0 | 0 | 0 AT4G18470.1 SNI1 |
| 30 | | | | |
| 31 | 4.1.2.27 | | 0 | GO:0030170,(CAT1G27980.1 ATDPL1,DPL1 |
| 32 | 4.1.2.27 | | 0 | GO:0030170,(CAT1G27980.1 ATDPL1,DPL1 |
| 33 | | 0 | 0 | 0 AT4G18470.1 SNI1 |
| 34 | | | | |
| 35 | 1.14.13.152 | | 0 | GO:0055114,(CAT2G45550.1 CYP76C4 |
| 36 | | 0 | 0 | GO:0016021,(CAT1G28230.1 ATPUP1,PUP1 |
| 37 | | 0 | 0 | 0 AT2G33390.1 |
| 38 | | 0 | 0 | 0 AT2G33390.1 |
| 39 | | 0 | 0 | 0 AT2G33390.1 |
| 40 | | 0 | 0 | 0 AT2G01770.1 ATVIT1,VIT1 |
| 41 | | | | |
| 42 | | 0 K00507 | | GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67 |
| 43 | | 0 | 0 | 0 AT2G34670.2 |
| 44 | | 0 | 0 | GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1 |
| 45 | | 0 K17968 | | 0 AT4G33100.1 |
| 46 | | 0 | 0 | 0 AT5G06240.1 emb2735 |
| 47 | | 0 | 0 | 0 AT5G06240.1 emb2735 |
| 48 | | 0 | 0 | 0 AT5G06240.1 emb2735 |
| 49 | | 0 | 0 | 0 AT4G30700.1 |
| 50 | | | | |
| 51 | 2.1.1.163 | | 0 | GO:0008168,(CAT1G78140.1 |
| 52 | 1.11.1.15 | | 0 | GO:0055114,(CAT1G65980.1 TPX1 |
| 53 | | 0 | 0 | 0 AT5G17270.1 |
| 54 | | 0 | 0 | 0 AT5G13210.1 |
| 55 | | 0 | 0 | 0 AT5G13210.1 |
| 56 | 2.3.2.2,2.6.1.4K14272 | | GO:0030170,(CAT1G70580.2 AOAT2,GGT2 | |
| 57 | 2.8.1.7,4.4.1.1 | | 0 | 0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF |
| 58 | | | | |
| 59 | | 0 K10956 | | GO:0016020,(CAT2G34250.1 |
| 60 | | 0 | 0 | 0 AT1G64770.1 NDF2,NDH45 |
| | | 0 | 0 | 0 AT5G17170.1 ENH1 |

| | | | | |
|----|-----------------|--------|--|---|
| 1 | | | | |
| 2 | 2.7.11.1 | 0 | GO:0006468,(CAT4G02630.1 | 0 |
| 3 | 2.7.11.1 | 0 | GO:0006468,(CAT4G02630.1 | 0 |
| 4 | | 0 | K02639 GO:0051536,(AT2G27510.1 ATFD3,FD3 | |
| 5 | | 0 | | |
| 6 | | 0 | GO:0005515 AT2G46560.1 | 0 |
| 7 | | 0 | GO:0005515 AT2G46560.1 | 0 |
| 8 | | 0 | | |
| 9 | | 0 | 0 AT3G23590.1 MED33A,RFR1 | |
| 10 | 2.4.1.18 | K00700 | GO:0005975,(CAT3G20440.2 BE1,EMB2729 | |
| 11 | 2.4.1.12 | | 0 GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1 | |
| 12 | | 0 | 0 AT4G18470.1 SNI1 | |
| 13 | | 0 | 0 AT4G18470.1 SNI1 | |
| 14 | | 0 | 0 AT4G18470.1 SNI1 | |
| 15 | 4.1.2.27 | | 0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1 | |
| 16 | 4.1.2.27 | | 0 GO:0030170,(CAT1G27980.1 ATDPL1,DPL1 | |
| 17 | | 0 | 0 AT4G18470.1 SNI1 | |
| 18 | | 0 | 0 AT4G18470.1 SNI1 | |
| 19 | 1.14.13.152 | | 0 GO:0055114,(CAT2G45550.1 CYP76C4 | |
| 20 | | 0 | 0 GO:0016021,(CAT1G28230.1 ATPUP1,PUP1 | |
| 21 | | 0 | 0 AT2G33390.1 | 0 |
| 22 | | 0 | 0 AT2G33390.1 | 0 |
| 23 | | 0 | 0 AT2G01770.1 ATVIT1,VIT1 | |
| 24 | | 0 | 0 AT2G01770.1 ATVIT1,VIT1 | |
| 25 | | 0 | 0 AT2G01770.1 ATVIT1,VIT1 | |
| 26 | | 0 | K00507 GO:0006629 AT3G15850.1 ADS3,FAD5,FADB,JB67 | |
| 27 | | 0 | 0 AT5G17270.1 | 0 |
| 28 | | 0 | 0 AT2G34670.2 | 0 |
| 29 | | 0 | 0 K02639 GO:0051536,(CAT2G27510.1 ATFD3,FD3 | |
| 30 | | 0 | 0 GO:0006355,(CAT3G54320.1 ASML1,ATWRI1,WRI,WRI1 | |
| 31 | | 0 | 0 K17968 0 AT4G33100.1 | 0 |
| 32 | | 0 | 0 AT5G06240.1 emb2735 | |
| 33 | | 0 | 0 AT5G06240.1 emb2735 | |
| 34 | | 0 | 0 AT5G06240.1 emb2735 | |
| 35 | | 0 | 0 AT5G06240.1 emb2735 | |
| 36 | | 0 | 0 GO:0008152,(CAT5G63380.1 | 0 |
| 37 | | 0 | 0 AT4G30700.1 | 0 |
| 38 | | 0 | 0 AT4G30700.1 | 0 |
| 39 | | 0 | 0 AT1G14780.1 | 0 |
| 40 | | 0 | 0 AT1G14780.1 | 0 |
| 41 | | 0 | 0 AT1G14780.1 | 0 |
| 42 | 2.1.1.163 | | 0 GO:0008168,(CAT1G78140.1 | 0 |
| 43 | 1.11.1.15 | | 0 GO:0055114,(CAT1G65980.1 TPX1 | |
| 44 | | 0 | 0 AT5G13210.1 | 0 |
| 45 | 2.3.2.2,2.6.1.4 | K14272 | GO:0030170,(CAT1G70580.2 AOAT2,GGT2 | |
| 46 | 2.8.1.7,4.4.1.1 | | 0 AT1G08490.1 ATCPNIFS,ATNFS2,ATSUFS,CPNIF | |
| 47 | | 0 | 0 K10956 GO:0016020,(CAT2G34250.1 | 0 |
| 48 | | 0 | 0 K07300 GO:0055085,(CAT2G38170.3 ATCAX1,CAX1,RCI4 | |
| 49 | | 0 | 0 AT1G64770.1 NDF2,NDH45 | |
| 50 | | 0 | 0 AT1G64770.1 NDF2,NDH45 | |
| 51 | | 0 | 0 AT5G17170.1 ENH1 | |
| 52 | | 0 | 0 AT5G17170.1 ENH1 | |
| 53 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 54 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 55 | | 0 | 0 GO:0005515 AT2G46560.1 | 0 |
| 56 | | 0 | 0 GO:0005515 AT4G11610.1 | 0 |
| 57 | 3.1.1.11 | K01051 | GO:0004857,(CAT4G33230.1 | 0 |
| 58 | | 0 | 0 AT3G51290.2 | 0 |
| 59 | | 0 | 0 AT1G03870.1 FLA9 | |
| 60 | | 0 | 0 AT1G03870.1 FLA9 | |
| | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | |

| | | | | |
|----|-----------|----------|---|---|
| 1 | | | | |
| 2 | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | |
| 3 | | 0 | 0 0 AT3G17430.1 | 0 |
| 4 | | 0 | 0 0 AT3G17430.1 | 0 |
| 5 | | 0 | 0 0 AT3G17430.1 | 0 |
| 6 | 1.11.1.7 | K00430 | GO:0055114,(AT5G05340.1 | 0 |
| 7 | | 0 K14300 | 0 AT2G05120.1 | 0 |
| 8 | 6.3.2.19 | K10590 | GO:0004842 AT5G02880.1 UPL4 | |
| 9 | 2.1.2.1 | K00600 | GO:0016740 AT4G13930.1 SHM4 | |
| 10 | | 0 | 0 0 AT1G09020.1 ATSNF4,SNF4 | |
| 11 | | 0 | 0 0 AT1G09020.1 ATSNF4,SNF4 | |
| 12 | | 0 | 0 0 AT1G09020.1 ATSNF4,SNF4 | |
| 13 | 2.7.1.67 | | 0 GO:0016773 AT1G26270.1 | 0 |
| 14 | | 0 | 0 0 AT1G76405.2 | 0 |
| 15 | | 0 | 0 0 AT1G76405.2 | 0 |
| 16 | 3.6.4.12 | | 0 GO:0016787,(AT2G28290.1 CHR3,SYD | |
| 17 | 3.6.4.12 | | 0 GO:0016787,(AT2G28290.1 CHR3,SYD | |
| 18 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | |
| 19 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | |
| 20 | 6.5.1.4 | | 0 GO:0006396 AT5G22100.1 | 0 |
| 21 | 6.5.1.4 | | 0 GO:0006396 AT5G22100.1 | 0 |
| 22 | | 0 | 0 GO:0046983 AT2G20180.2 PIF1,PIL5 | |
| 23 | | 0 | 0 0 AT2G35330.1 | 0 |
| 24 | | 0 | 0 0 AT2G35330.1 | 0 |
| 25 | | 0 | 0 0 AT2G35330.1 | 0 |
| 26 | 2.4.1.12 | | 0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 | |
| 27 | | 0 | 0 0 AT2G35330.1 | 0 |
| 28 | | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 29 | | 0 | 0 GO:0003677,(AT1G70510.1 ATK1,KNAT2 | |
| 30 | 1.1.1.330 | | 0 0 AT5G02540.1 | 0 |
| 31 | 1.1.1.330 | | 0 0 AT5G02540.1 | 0 |
| 32 | 1.1.1.330 | | 0 0 AT5G02540.1 | 0 |
| 33 | 1.1.1.330 | | 0 0 AT5G02540.1 | 0 |
| 34 | 6.3.2.19 | | 0 GO:0008270,(AT5G60820.1 | 0 |
| 35 | 1.1.1.330 | | 0 0 AT5G02540.1 | 0 |
| 36 | 1.1.1.330 | | 0 0 AT5G02540.1 | 0 |
| 37 | 1.1.1.330 | | 0 0 AT5G02540.1 | 0 |
| 38 | | 0 | 0 0 AT5G46220.1 | 0 |
| 39 | 1.1.1.330 | | 0 0 AT5G02540.1 | 0 |
| 40 | 1.1.1.330 | | 0 0 AT5G02540.1 | 0 |
| 41 | | 0 | 0 0 AT5G46220.1 | 0 |
| 42 | 1.1.1.330 | | 0 0 AT5G02540.1 | 0 |
| 43 | 1.11.1.7 | K00430 | GO:0055114,(AT4G33870.1 | 0 |
| 44 | 1.1.1.330 | | 0 0 AT5G02540.1 | 0 |
| 45 | 1.1.1.330 | | 0 0 AT5G02540.1 | 0 |
| 46 | 1.11.1.7 | K00430 | GO:0055114,(AT4G33870.1 | 0 |
| 47 | 2.4.1.198 | K03858 | GO:0017176 AT4G35530.1 | 0 |
| 48 | | 0 | 0 0 AT2G01060.1 | 0 |
| 49 | | 0 | 0 0 AT3G60890.2 ZPR2 | |
| 50 | | 0 K14488 | GO:0009733 AT4G34760.1 | 0 |
| 51 | | 0 | 0 GO:0043531 AT1G63350.1 | 0 |
| 52 | | 0 | 0 GO:0043531 AT1G63350.1 | 0 |
| 53 | | 0 | 0 0 AT1G22770.1 FB,GI | |
| 54 | | 0 | 0 0 AT1G22770.1 FB,GI | |
| 55 | | 0 | 0 0 AT1G22770.1 FB,GI | |
| 56 | | 0 | 0 0 AT1G22770.1 FB,GI | |
| 57 | | 0 | 0 0 AT1G22770.1 FB,GI | |
| 58 | | 0 | 0 0 AT1G22770.1 FB,GI | |
| 59 | | 0 | 0 0 AT1G22770.1 FB,GI | |
| 60 | | 0 | 0 0 AT1G22770.1 FB,GI | |

| | | | | | |
|----|-----------|----------|---|--|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 3 | 3.6.3.1 | | 0 | GO:0046872,(CAT1G68710.1 | 0 |
| 4 | | 0 | 0 | GO:0005515 AT2G43500.1 | 0 |
| 5 | | 0 | 0 | GO:0005515 AT2G43500.1 | 0 |
| 6 | | 0 | 0 | GO:0005515 AT2G43500.1 | 0 |
| 7 | 3.6.3.1 | | 0 | GO:0046872,(CAT1G68710.1 | 0 |
| 8 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 9 | | | | | |
| 10 | 3.1.1.11 | K01051 | | GO:0004857,(CAT4G33230.1 | 0 |
| 11 | | 0 | 0 | 0 AT3G51290.2 | 0 |
| 12 | | 0 | 0 | 0 AT1G03870.1 FLA9 | |
| 13 | | 0 | 0 | GO:0046983 AT5G08130.5 BIM1 | |
| 14 | | 0 | 0 | GO:0046983 AT5G08130.5 BIM1 | |
| 15 | | 0 | 0 | 0 AT3G17430.1 | 0 |
| 16 | | 0 | 0 | 0 AT3G17430.1 | 0 |
| 17 | | 0 | 0 | 0 AT3G17430.1 | 0 |
| 18 | | 0 | 0 | 0 AT3G17430.1 | 0 |
| 19 | 1.11.1.7 | K00430 | | GO:0055114,(CAT5G05340.1 | 0 |
| 20 | | 0 K14300 | | 0 AT2G05120.1 | 0 |
| 21 | | | | | |
| 22 | 6.3.2.19 | K10590 | | GO:0004842 AT5G02880.1 UPL4 | |
| 23 | 2.1.2.1 | K00600 | | GO:0016740 AT4G13930.1 SHM4 | |
| 24 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 25 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 26 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 27 | 2.7.1.67 | | | 0 GO:0016773 AT1G26270.1 | 0 |
| 28 | | 0 | 0 | 0 AT1G76405.2 | 0 |
| 29 | | | | | |
| 30 | 3.6.4.12 | | | 0 GO:0016787,(CAT2G28290.1 CHR3,SYD | |
| 31 | 3.6.4.12 | | | 0 GO:0016787,(CAT2G28290.1 CHR3,SYD | |
| 32 | | 0 | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | |
| 33 | | 0 | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | |
| 34 | | | | | |
| 35 | 6.5.1.4 | | | 0 GO:0006396 AT5G22100.1 | 0 |
| 36 | 6.5.1.4 | | | 0 GO:0006396 AT5G22100.1 | 0 |
| 37 | | | | | |
| 38 | | 0 | 0 | 0 GO:0046983 AT2G20180.2 PIF1,PIL5 | |
| 39 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 40 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 41 | | | | | |
| 42 | 2.4.1.12 | | | 0 GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1 | |
| 43 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 44 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 45 | | 0 | 0 | 0 GO:0003677,(CAT1G70510.1 ATK1,KNAT2 | |
| 46 | | | | | |
| 47 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 48 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 49 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 50 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 51 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 52 | 6.3.2.19 | | | 0 GO:0008270,(CAT5G60820.1 | 0 |
| 53 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 54 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 55 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 56 | | 0 | 0 | 0 AT5G46220.1 | 0 |
| 57 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 58 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 59 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 60 | 1.11.1.7 | K00430 | | GO:0055114,(CAT4G33870.1 | 0 |
| | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |

| | | | | | |
|----|-----------|----------|---|---------------------------------------|---|
| 1 | | | | | |
| 2 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 3 | 1.11.1.7 | K00430 | | GO:0055114,(AT4G33870.1 | 0 |
| 4 | 2.4.1.198 | K03858 | | GO:0017176 AT4G35530.1 | 0 |
| 5 | | | | | |
| 6 | | 0 | 0 | 0 AT2G01060.1 | 0 |
| 7 | | 0 | 0 | 0 AT3G60890.2 ZPR2 | |
| 8 | | 0 K14488 | | GO:0009733 AT4G34760.1 | 0 |
| 9 | | | | | |
| 10 | | 0 | 0 | GO:0043531 AT1G63350.1 | 0 |
| 11 | | 0 | 0 | GO:0043531 AT1G63350.1 | 0 |
| 12 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 13 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 14 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 15 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 16 | 3.6.3.1 | | 0 | GO:0046872,(AT1G68710.1 | 0 |
| 17 | | | | | |
| 18 | | 0 | 0 | GO:0005515 AT2G43500.1 | 0 |
| 19 | | 0 | 0 | GO:0005515 AT2G43500.1 | 0 |
| 20 | 3.6.3.1 | | 0 | GO:0046872,(AT1G68710.1 | 0 |
| 21 | | | | | |
| 22 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 23 | 3.1.1.11 | K01051 | | GO:0004857,(AT4G33230.1 | 0 |
| 24 | | 0 | 0 | 0 AT3G51290.2 | 0 |
| 25 | | 0 | 0 | 0 AT1G03870.1 FLA9 | |
| 26 | | 0 | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | |
| 27 | | 0 | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | |
| 28 | | 0 | 0 | 0 AT3G17430.1 | 0 |
| 29 | | 0 | 0 | 0 AT3G17430.1 | 0 |
| 30 | | 0 | 0 | 0 AT3G17430.1 | 0 |
| 31 | | 0 | 0 | 0 AT3G17430.1 | 0 |
| 32 | 1.11.1.7 | K00430 | | GO:0055114,(AT5G05340.1 | 0 |
| 33 | | 0 K14300 | | 0 AT2G05120.1 | 0 |
| 34 | | | | | |
| 35 | 6.3.2.19 | K10590 | | GO:0004842 AT5G02880.1 UPL4 | |
| 36 | 2.1.2.1 | K00600 | | GO:0016740 AT4G13930.1 SHM4 | |
| 37 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 38 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 39 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 40 | 2.7.1.67 | | 0 | GO:0016773 AT1G26270.1 | 0 |
| 41 | | 0 | 0 | 0 AT1G76405.2 | 0 |
| 42 | | | | | |
| 43 | 3.6.4.12 | | 0 | GO:0016787,(AT2G28290.1 CHR3,SYD | |
| 44 | 3.6.4.12 | | 0 | GO:0016787,(AT2G28290.1 CHR3,SYD | |
| 45 | | 0 | 0 | GO:0005515 AT2G22125.1 CSI1 | |
| 46 | | 0 | 0 | GO:0005515 AT2G22125.1 CSI1 | |
| 47 | | 0 | 0 | GO:0005515 AT2G22125.1 CSI1 | |
| 48 | 6.5.1.4 | | 0 | GO:0006396 AT5G22100.1 | 0 |
| 49 | 6.5.1.4 | | 0 | GO:0006396 AT5G22100.1 | 0 |
| 50 | | 0 | 0 | GO:0046983 AT2G20180.2 PIF1,PIL5 | |
| 51 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 52 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 53 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 54 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 55 | 2.4.1.12 | | 0 | GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 | |
| 56 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 57 | | 0 | 0 | GO:0006629 AT4G16070.1 | 0 |
| 58 | | 0 | 0 | GO:0003677,(AT1G70510.1 ATK1,KNAT2 | |
| 59 | | 0 | 0 | GO:0003677,(AT1G70510.1 ATK1,KNAT2 | |
| 60 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |

| | | | | | | |
|----|-----------|--------|--------------|-------------------|-------------------------|------------------|
| 1 | | | | | | |
| 2 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 3 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 4 | 6.3.2.19 | 0 | GO:0008270,(| AT5G60820.1 | 0 | |
| 5 | | | | | | |
| 6 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 7 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 8 | | | | | | |
| 9 | 0 | 0 | 0 | AT5G46220.1 | 0 | |
| 10 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 11 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 12 | 1.11.1.7 | K00430 | GO:0055114,(| AT4G33870.1 | 0 | |
| 13 | | | | | | |
| 14 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 15 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 16 | 1.11.1.7 | K00430 | GO:0055114,(| AT4G33870.1 | 0 | |
| 17 | | | | | | |
| 18 | 2.4.1.198 | K03858 | GO:0017176 | AT4G35530.1 | 0 | |
| 19 | | | | | | |
| 20 | 0 | 0 | 0 | AT2G01060.1 | 0 | |
| 21 | 0 | 0 | 0 | AT3G60890.2 ZPR2 | | |
| 22 | 0 | K14488 | GO:0009733 | AT4G34760.1 | 0 | |
| 23 | 0 | 0 | GO:0043531 | AT1G63350.1 | 0 | |
| 24 | 0 | 0 | GO:0043531 | AT1G63350.1 | 0 | |
| 25 | 0 | 0 | 0 | AT1G22770.1 FB,GI | | |
| 26 | 0 | 0 | 0 | AT1G22770.1 FB,GI | | |
| 27 | 0 | 0 | 0 | AT1G22770.1 FB,GI | | |
| 28 | 0 | 0 | 0 | AT1G22770.1 FB,GI | | |
| 29 | | | | | | |
| 30 | 3.6.3.1 | | 0 | GO:0046872,(| AT1G68710.1 | 0 |
| 31 | | | 0 | GO:0005515 | AT2G43500.1 | 0 |
| 32 | | | 0 | GO:0005515 | AT2G43500.1 | 0 |
| 33 | | | | | | |
| 34 | 3.6.3.1 | | 0 | GO:0046872,(| AT1G68710.1 | 0 |
| 35 | | | 0 | 0 | AT1G22770.1 FB,GI | |
| 36 | 3.1.1.11 | K01051 | GO:0004857,(| AT4G33230.1 | 0 | |
| 37 | | | 0 | 0 | AT3G51290.2 | 0 |
| 38 | | | 0 | 0 | AT1G03870.1 FLA9 | |
| 39 | | | 0 | 0 | GO:0046983 | AT5G08130.5 BIM1 |
| 40 | | | 0 | 0 | GO:0046983 | AT5G08130.5 BIM1 |
| 41 | | | 0 | 0 | 0 | AT3G17430.1 |
| 42 | | | 0 | 0 | 0 | AT3G17430.1 |
| 43 | | | | | | |
| 44 | | | | | | |
| 45 | 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 | |
| 46 | | | 0 | 0 | AT2G05120.1 | 0 |
| 47 | | | | | | |
| 48 | 6.3.2.19 | K10590 | GO:0004842 | AT5G02880.1 UPL4 | | |
| 49 | 2.1.2.1 | K00600 | GO:0016740 | AT4G13930.1 SHM4 | | |
| 50 | | | | | | |
| 51 | | | 0 | 0 | AT1G09020.1 ATSNF4,SNF4 | |
| 52 | | | 0 | 0 | AT1G09020.1 ATSNF4,SNF4 | |
| 53 | 2.7.1.67 | | 0 | GO:0016773 | AT1G26270.1 | 0 |
| 54 | | | 0 | 0 | 0 | AT1G76405.2 |
| 55 | | | | | | |
| 56 | 3.6.4.12 | | 0 | GO:0016787,(| AT2G28290.1 CHR3,SYD | |
| 57 | 3.6.4.12 | | 0 | GO:0016787,(| AT2G28290.1 CHR3,SYD | |
| 58 | | | 0 | GO:0005515 | AT2G22125.1 CSI1 | |
| 59 | | | 0 | GO:0005515 | AT2G22125.1 CSI1 | |
| 60 | | | | | | |
| | 6.5.1.4 | | 0 | GO:0006396 | AT5G22100.1 | 0 |

| | | | | |
|----|-----------|----------|---|---|
| 1 | | | | |
| 2 | 6.5.1.4 | | 0 GO:0006396 AT5G22100.1 | 0 |
| 3 | | 0 | 0 GO:0046983 AT2G20180.2 PIF1,PIL5 | |
| 4 | | 0 | 0 AT2G35330.1 | 0 |
| 5 | | 0 | 0 AT2G35330.1 | 0 |
| 6 | | 0 | 0 AT2G35330.1 | 0 |
| 7 | 2.4.1.12 | | 0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 | |
| 8 | | 0 | 0 AT2G35330.1 | 0 |
| 9 | | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 10 | | 0 | 0 GO:0003677,(AT1G70510.1 ATK1,KNAT2 | |
| 11 | | 0 | 0 AT5G02540.1 | 0 |
| 12 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 13 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 14 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 15 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 16 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 17 | 6.3.2.19 | | 0 GO:0008270,(AT5G60820.1 | 0 |
| 18 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 19 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 20 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 21 | | 0 | 0 AT5G46220.1 | 0 |
| 22 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 23 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 24 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 25 | 1.11.1.7 | K00430 | GO:0055114,(AT4G33870.1 | 0 |
| 26 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 27 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 28 | 1.11.1.7 | K00430 | GO:0055114,(AT4G33870.1 | 0 |
| 29 | 2.4.1.198 | K03858 | GO:0017176 AT4G35530.1 | 0 |
| 30 | | 0 | 0 AT2G01060.1 | 0 |
| 31 | | 0 | 0 AT3G60890.2 ZPR2 | |
| 32 | | 0 K14488 | GO:0009733 AT4G34760.1 | 0 |
| 33 | | 0 | 0 GO:0043531 AT1G63350.1 | 0 |
| 34 | | 0 | 0 GO:0043531 AT1G63350.1 | 0 |
| 35 | | 0 | 0 AT1G22770.1 FB,GI | |
| 36 | | 0 | 0 AT1G22770.1 FB,GI | |
| 37 | | 0 | 0 AT1G22770.1 FB,GI | |
| 38 | 3.6.3.1 | | 0 GO:0046872,(AT1G68710.1 | 0 |
| 39 | | 0 | 0 GO:0005515 AT2G43500.1 | 0 |
| 40 | | 0 | 0 GO:0005515 AT2G43500.1 | 0 |
| 41 | 3.6.3.1 | | 0 GO:0046872,(AT1G68710.1 | 0 |
| 42 | | 0 | 0 AT1G22770.1 FB,GI | |
| 43 | 3.1.1.11 | K01051 | GO:0004857,(AT4G33230.1 | 0 |
| 44 | | 0 | 0 AT3G51290.2 | 0 |
| 45 | | 0 | 0 AT1G03870.1 FLA9 | |
| 46 | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | |
| 47 | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | |
| 48 | | 0 | 0 AT3G17430.1 | 0 |
| 49 | | 0 | 0 AT3G17430.1 | 0 |
| 50 | 1.11.1.7 | K00430 | GO:0055114,(AT5G05340.1 | 0 |
| 51 | | 0 K14300 | 0 AT2G05120.1 | 0 |
| 52 | 6.3.2.19 | K10590 | GO:0004842 AT5G02880.1 UPL4 | |

| | | | | | |
|----|-----------|----------|----------------------------|---------------------------|---|
| 1 | | | | | |
| 2 | 2.1.2.1 | K00600 | GO:0016740 | AT4G13930.1 SHM4 | |
| 3 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 4 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 5 | | | | | |
| 6 | 2.7.1.67 | | 0 GO:0016773 | AT1G26270.1 | 0 |
| 7 | | 0 | 0 | 0 AT1G76405.2 | 0 |
| 8 | 3.6.4.12 | | 0 GO:0016787,(CAT2G28290.1 | CHR3,SYD | |
| 9 | 3.6.4.12 | | 0 GO:0016787,(CAT2G28290.1 | CHR3,SYD | |
| 10 | | | | | |
| 11 | | 0 | 0 GO:0005515 | AT2G22125.1 CSI1 | |
| 12 | | 0 | 0 GO:0005515 | AT2G22125.1 CSI1 | |
| 13 | | | | | |
| 14 | 6.5.1.4 | | 0 GO:0006396 | AT5G22100.1 | 0 |
| 15 | 6.5.1.4 | | 0 GO:0006396 | AT5G22100.1 | 0 |
| 16 | | | | | |
| 17 | | 0 | 0 GO:0046983 | AT2G20180.2 PIF1,PIL5 | |
| 18 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 19 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 20 | 2.4.1.12 | | 0 GO:0030244,(CAT4G24010.1 | ATCSLG1,CSLG1 | |
| 21 | | | | | |
| 22 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 23 | | 0 | 0 GO:0006629 | AT4G16070.1 | 0 |
| 24 | | 0 | 0 GO:0003677,(CAT1G70510.1 | ATK1,KNAT2 | |
| 25 | | | | | |
| 26 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 27 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 28 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 29 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 30 | | | | | |
| 31 | 6.3.2.19 | | 0 GO:0008270,(CAT5G60820.1 | | 0 |
| 32 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 33 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 34 | | | | | |
| 35 | | 0 | 0 | 0 AT5G46220.1 | 0 |
| 36 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 37 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 38 | | | | | |
| 39 | 1.11.1.7 | K00430 | GO:0055114,(CAT4G33870.1 | | 0 |
| 40 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 41 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 42 | | | | | |
| 43 | 1.11.1.7 | K00430 | GO:0055114,(CAT4G33870.1 | | 0 |
| 44 | 2.4.1.198 | K03858 | GO:0017176 | AT4G35530.1 | 0 |
| 45 | | | | | |
| 46 | | 0 | 0 | 0 AT2G01060.1 | 0 |
| 47 | | 0 | 0 | 0 AT3G60890.2 ZPR2 | |
| 48 | | 0 K14488 | GO:0009733 | AT4G34760.1 | 0 |
| 49 | | 0 | 0 GO:0043531 | AT1G63350.1 | 0 |
| 50 | | 0 | 0 GO:0043531 | AT1G63350.1 | 0 |
| 51 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 52 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 53 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 54 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 55 | | | | | |
| 56 | 3.6.3.1 | | 0 GO:0046872,(CAT1G68710.1 | | 0 |
| 57 | | 0 | 0 GO:0005515 | AT2G43500.1 | 0 |
| 58 | | 0 | 0 GO:0005515 | AT2G43500.1 | 0 |
| 59 | | | | | |
| 60 | 3.6.3.1 | | 0 GO:0046872,(CAT1G68710.1 | | 0 |
| | | 0 | 0 | 0 AT1G22770.1 FB,GI | |

| | | | | | |
|----|-----------|----------|--|---------------------------------------|---|
| 1 | | | | | |
| 2 | 3.1.1.11 | K01051 | GO:0004857,(CAT4G33230.1 | | 0 |
| 3 | | 0 | 0 | 0 AT3G51290.2 | 0 |
| 4 | | 0 | 0 | 0 AT1G03870.1 FLA9 | |
| 5 | | 0 | 0 | GO:0046983 AT5G08130.5 BIM1 | |
| 6 | | 0 | 0 | GO:0046983 AT5G08130.5 BIM1 | |
| 7 | | 0 | 0 | 0 AT3G17430.1 | 0 |
| 8 | | 0 | 0 | 0 AT3G17430.1 | 0 |
| 9 | | 0 | 0 | 0 AT3G17430.1 | 0 |
| 10 | | 0 | 0 | 0 AT3G17430.1 | 0 |
| 11 | 1.11.1.7 | K00430 | GO:0055114,(CAT5G05340.1 | | 0 |
| 12 | | 0 K14300 | 0 AT2G05120.1 | | 0 |
| 13 | 6.3.2.19 | K10590 | GO:0004842 AT5G02880.1 UPL4 | | |
| 14 | 2.1.2.1 | K00600 | GO:0016740 AT4G13930.1 SHM4 | | |
| 15 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 16 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 17 | 2.7.1.67 | | 0 GO:0016773 AT1G26270.1 | | 0 |
| 18 | | 0 | 0 | 0 AT1G76405.2 | 0 |
| 19 | 3.6.4.12 | | 0 GO:0016787,(CAT2G28290.1 CHR3,SYD | | |
| 20 | 3.6.4.12 | | 0 GO:0016787,(CAT2G28290.1 CHR3,SYD | | |
| 21 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | | |
| 22 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | | |
| 23 | 6.5.1.4 | | 0 GO:0006396 AT5G22100.1 | | 0 |
| 24 | 6.5.1.4 | | 0 GO:0006396 AT5G22100.1 | | 0 |
| 25 | | 0 | 0 GO:0046983 AT2G20180.2 PIF1,PIL5 | | |
| 26 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 27 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 28 | 2.4.1.12 | | 0 GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1 | | |
| 29 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 30 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 31 | | 0 | 0 | 0 GO:0003677,(CAT1G70510.1 ATK1,KNAT2 | |
| 32 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 33 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 34 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 35 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 36 | 6.3.2.19 | | 0 GO:0008270,(CAT5G60820.1 | | 0 |
| 37 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 38 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 39 | | 0 | 0 | 0 AT5G46220.1 | 0 |
| 40 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 41 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 42 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 43 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 44 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 45 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 46 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 47 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 48 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 49 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 50 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 51 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 52 | 1.11.1.7 | K00430 | GO:0055114,(CAT4G33870.1 | | 0 |
| 53 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 54 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 55 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 56 | 1.11.1.7 | K00430 | GO:0055114,(CAT4G33870.1 | | 0 |
| 57 | 2.4.1.198 | K03858 | GO:0017176 AT4G35530.1 | | 0 |
| 58 | | 0 | 0 | 0 AT2G01060.1 | 0 |
| 59 | | 0 | 0 | 0 AT3G60890.2 ZPR2 | 0 |
| 60 | | 0 K14488 | GO:0009733 AT4G34760.1 | | 0 |

| | | | | |
|----|-----------|----------|---|---|
| 1 | | | | |
| 2 | | 0 | 0 GO:0043531 AT1G63350.1 | 0 |
| 3 | | 0 | 0 GO:0043531 AT1G63350.1 | 0 |
| 4 | | 0 | 0 AT1G22770.1 FB,GI | |
| 5 | | 0 | 0 AT1G22770.1 FB,GI | |
| 6 | | 0 | 0 AT1G22770.1 FB,GI | |
| 7 | | 0 | 0 AT1G22770.1 FB,GI | |
| 8 | 3.6.3.1 | | 0 GO:0046872,(AT1G68710.1 | 0 |
| 9 | | 0 | 0 GO:0005515 AT2G43500.1 | 0 |
| 10 | | 0 | 0 GO:0005515 AT2G43500.1 | 0 |
| 11 | | 0 | 0 GO:0005515 AT2G43500.1 | 0 |
| 12 | 3.6.3.1 | | 0 GO:0046872,(AT1G68710.1 | 0 |
| 13 | | 0 | 0 AT1G22770.1 FB,GI | |
| 14 | | 0 | 0 AT1G22770.1 FB,GI | |
| 15 | 3.1.1.11 | K01051 | GO:0004857,(AT4G33230.1 | 0 |
| 16 | | 0 | 0 AT3G51290.2 | 0 |
| 17 | | 0 | 0 AT1G03870.1 FLA9 | |
| 18 | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | |
| 19 | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | |
| 20 | | 0 | 0 AT3G17430.1 | 0 |
| 21 | | 0 | 0 AT3G17430.1 | 0 |
| 22 | | 0 | 0 AT3G17430.1 | 0 |
| 23 | | 0 | 0 AT3G17430.1 | 0 |
| 24 | 1.11.1.7 | K00430 | GO:0055114,(AT5G05340.1 | 0 |
| 25 | | 0 K14300 | 0 AT2G05120.1 | 0 |
| 26 | | 0 | 0 AT2G05120.1 | 0 |
| 27 | 6.3.2.19 | K10590 | GO:0004842 AT5G02880.1 UPL4 | |
| 28 | 2.1.2.1 | K00600 | GO:0016740 AT4G13930.1 SHM4 | |
| 29 | | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 30 | | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 31 | | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 32 | 2.7.1.67 | | 0 GO:0016773 AT1G26270.1 | 0 |
| 33 | | 0 | 0 AT1G76405.2 | 0 |
| 34 | | 0 | 0 AT1G76405.2 | 0 |
| 35 | 3.6.4.12 | | 0 GO:0016787,(AT2G28290.1 CHR3,SYD | |
| 36 | 3.6.4.12 | | 0 GO:0016787,(AT2G28290.1 CHR3,SYD | |
| 37 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | |
| 38 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | |
| 39 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | |
| 40 | 6.5.1.4 | | 0 GO:0006396 AT5G22100.1 | 0 |
| 41 | 6.5.1.4 | | 0 GO:0006396 AT5G22100.1 | 0 |
| 42 | | 0 | 0 GO:0006396 AT5G22100.1 | 0 |
| 43 | | 0 | 0 GO:0046983 AT2G20180.2 PIF1,PIL5 | |
| 44 | | 0 | 0 AT2G35330.1 | 0 |
| 45 | | 0 | 0 AT2G35330.1 | 0 |
| 46 | | 0 | 0 AT2G35330.1 | 0 |
| 47 | 2.4.1.12 | | 0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 | |
| 48 | | 0 | 0 AT2G35330.1 | 0 |
| 49 | | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 50 | | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 51 | | 0 | 0 GO:0003677,(AT1G70510.1 ATK1,KNAT2 | |
| 52 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 53 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 54 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 55 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 56 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 57 | 6.3.2.19 | | 0 GO:0008270,(AT5G60820.1 | 0 |
| 58 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 59 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 60 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| | | 0 | 0 AT5G46220.1 | 0 |

| | | | | | |
|----|-----------|----------|---|---------------------------------------|---|
| 1 | | | | | |
| 2 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 3 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 4 | 1.11.1.7 | K00430 | | GO:0055114,(AT4G33870.1 | 0 |
| 5 | | | | | |
| 6 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 7 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 8 | 1.11.1.7 | K00430 | | GO:0055114,(AT4G33870.1 | 0 |
| 9 | | | | | |
| 10 | 2.4.1.198 | K03858 | | GO:0017176 AT4G35530.1 | 0 |
| 11 | | 0 | 0 | 0 AT2G01060.1 | 0 |
| 12 | | 0 | 0 | 0 AT3G60890.2 ZPR2 | |
| 13 | | | | | |
| 14 | | 0 K14488 | | GO:0009733 AT4G34760.1 | 0 |
| 15 | | 0 | 0 | GO:0043531 AT1G63350.1 | 0 |
| 16 | | 0 | 0 | GO:0043531 AT1G63350.1 | 0 |
| 17 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 18 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 19 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 20 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 21 | | | | | |
| 22 | 3.6.3.1 | | 0 | GO:0046872,(AT1G68710.1 | 0 |
| 23 | | 0 | 0 | GO:0005515 AT2G43500.1 | 0 |
| 24 | | 0 | 0 | GO:0005515 AT2G43500.1 | 0 |
| 25 | 3.6.3.1 | | 0 | GO:0046872,(AT1G68710.1 | 0 |
| 26 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 27 | | | | | |
| 28 | 3.1.1.11 | K01051 | | GO:0004857,(AT4G33230.1 | 0 |
| 29 | | 0 | 0 | 0 AT3G51290.2 | 0 |
| 30 | | 0 | 0 | 0 AT1G03870.1 FLA9 | |
| 31 | | 0 | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | |
| 32 | | 0 | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | |
| 33 | | 0 | 0 | 0 AT3G17430.1 | 0 |
| 34 | | 0 | 0 | 0 AT3G17430.1 | 0 |
| 35 | | | | | |
| 36 | | | | | |
| 37 | 1.11.1.7 | K00430 | | GO:0055114,(AT5G05340.1 | 0 |
| 38 | | 0 K14300 | | 0 AT2G05120.1 | 0 |
| 39 | | | | | |
| 40 | 6.3.2.19 | K10590 | | GO:0004842 AT5G02880.1 UPL4 | |
| 41 | 2.1.2.1 | K00600 | | GO:0016740 AT4G13930.1 SHM4 | |
| 42 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 43 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 44 | | | | | |
| 45 | 2.7.1.67 | | 0 | GO:0016773 AT1G26270.1 | 0 |
| 46 | | 0 | 0 | 0 AT1G76405.2 | 0 |
| 47 | | | | | |
| 48 | 3.6.4.12 | | 0 | GO:0016787,(AT2G28290.1 CHR3,SYD | |
| 49 | 3.6.4.12 | | 0 | GO:0016787,(AT2G28290.1 CHR3,SYD | |
| 50 | | 0 | 0 | GO:0005515 AT2G22125.1 CSI1 | |
| 51 | | 0 | 0 | GO:0005515 AT2G22125.1 CSI1 | |
| 52 | | | | | |
| 53 | 6.5.1.4 | | 0 | GO:0006396 AT5G22100.1 | 0 |
| 54 | 6.5.1.4 | | 0 | GO:0006396 AT5G22100.1 | 0 |
| 55 | | 0 | 0 | GO:0046983 AT2G20180.2 PIF1,PIL5 | |
| 56 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 57 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 58 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 59 | | | | | |
| 60 | 2.4.1.12 | | 0 | GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 | |
| | | 0 | 0 | 0 AT2G35330.1 | 0 |

| | | | | |
|----|-----------|----------|--------------------------------------|---|
| 1 | | | | |
| 2 | | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 3 | | 0 | 0 GO:0003677,(AT1G70510.1 ATK1,KNAT2 | |
| 4 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 5 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 6 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 7 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 8 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 9 | | | | |
| 10 | 6.3.2.19 | | 0 GO:0008270,(AT5G60820.1 | 0 |
| 11 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 12 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 13 | | | | |
| 14 | | 0 | 0 AT5G46220.1 | 0 |
| 15 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 16 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 17 | | | | |
| 18 | 1.11.1.7 | K00430 | GO:0055114,(AT4G33870.1 | 0 |
| 19 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 20 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 21 | | | | |
| 22 | 1.11.1.7 | K00430 | GO:0055114,(AT4G33870.1 | 0 |
| 23 | 2.4.1.198 | K03858 | GO:0017176 AT4G35530.1 | 0 |
| 24 | | 0 | 0 AT2G01060.1 | 0 |
| 25 | | 0 | 0 AT3G60890.2 ZPR2 | |
| 26 | | | | |
| 27 | | 0 K14488 | GO:0009733 AT4G34760.1 | 0 |
| 28 | | 0 | 0 GO:0043531 AT1G63350.1 | 0 |
| 29 | | 0 | 0 GO:0043531 AT1G63350.1 | 0 |
| 30 | | 0 | 0 AT1G22770.1 FB,GI | |
| 31 | | 0 | 0 AT1G22770.1 FB,GI | |
| 32 | | 0 | 0 AT1G22770.1 FB,GI | |
| 33 | | 0 | 0 AT1G22770.1 FB,GI | |
| 34 | | | | |
| 35 | 3.6.3.1 | | 0 GO:0046872,(AT1G68710.1 | 0 |
| 36 | | 0 | 0 GO:0005515 AT2G43500.1 | 0 |
| 37 | | 0 | 0 GO:0005515 AT2G43500.1 | 0 |
| 38 | | | | |
| 39 | 3.6.3.1 | | 0 GO:0046872,(AT1G68710.1 | 0 |
| 40 | | 0 | 0 AT1G22770.1 FB,GI | |
| 41 | 3.1.1.11 | K01051 | GO:0004857,(AT4G33230.1 | 0 |
| 42 | | 0 | 0 AT3G51290.2 | 0 |
| 43 | | 0 | 0 AT1G03870.1 FLA9 | |
| 44 | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | |
| 45 | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | |
| 46 | | 0 | 0 AT3G17430.1 | 0 |
| 47 | | 0 | 0 AT3G17430.1 | 0 |
| 48 | | | | |
| 49 | | | | |
| 50 | | | | |
| 51 | 1.11.1.7 | K00430 | GO:0055114,(AT5G05340.1 | 0 |
| 52 | | 0 K14300 | 0 AT2G05120.1 | 0 |
| 53 | 6.3.2.19 | K10590 | GO:0004842 AT5G02880.1 UPL4 | |
| 54 | 2.1.2.1 | K00600 | GO:0016740 AT4G13930.1 SHM4 | |
| 55 | | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 56 | | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 57 | | | | |
| 58 | 2.7.1.67 | | 0 GO:0016773 AT1G26270.1 | 0 |
| 59 | | 0 | 0 AT1G76405.2 | 0 |
| 60 | | | | |
| | 3.6.4.12 | | 0 GO:0016787,(AT2G28290.1 CHR3,SYD | |

| | | | | |
|----|-----------|----------|--|---|
| 1 | | | | |
| 2 | 3.6.4.12 | | 0 GO:0016787,(CAT2G28290.1 CHR3,SYD | |
| 3 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | |
| 4 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | |
| 5 | | | | |
| 6 | 6.5.1.4 | | 0 GO:0006396 AT5G22100.1 | 0 |
| 7 | 6.5.1.4 | | 0 GO:0006396 AT5G22100.1 | 0 |
| 8 | | 0 | 0 GO:0046983 AT2G20180.2 PIF1,PIL5 | |
| 9 | | | | |
| 10 | | 0 | 0 AT2G35330.1 | 0 |
| 11 | | 0 | 0 AT2G35330.1 | 0 |
| 12 | 2.4.1.12 | | 0 GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1 | |
| 13 | | | | |
| 14 | | 0 | 0 AT2G35330.1 | 0 |
| 15 | | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 16 | | 0 | 0 GO:0003677,(CAT1G70510.1 ATK1,KNAT2 | |
| 17 | | | | |
| 18 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 19 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 20 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 21 | | | | |
| 22 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 23 | 6.3.2.19 | | 0 GO:0008270,(CAT5G60820.1 | 0 |
| 24 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 25 | | | | |
| 26 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 27 | | 0 | 0 AT5G46220.1 | 0 |
| 28 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 29 | | | | |
| 30 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 31 | 1.11.1.7 | K00430 | GO:0055114,(CAT4G33870.1 | 0 |
| 32 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 33 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 34 | | | | |
| 35 | 1.11.1.7 | K00430 | GO:0055114,(CAT4G33870.1 | 0 |
| 36 | 2.4.1.198 | K03858 | GO:0017176 AT4G35530.1 | 0 |
| 37 | | | | |
| 38 | | 0 | 0 AT2G01060.1 | 0 |
| 39 | | 0 | 0 AT3G60890.2 ZPR2 | |
| 40 | | 0 K14488 | GO:0009733 AT4G34760.1 | 0 |
| 41 | | | | |
| 42 | | 0 | 0 GO:0043531 AT1G63350.1 | 0 |
| 43 | | 0 | 0 GO:0043531 AT1G63350.1 | 0 |
| 44 | | 0 | 0 AT1G22770.1 FB,GI | |
| 45 | | 0 | 0 AT1G22770.1 FB,GI | |
| 46 | | 0 | 0 AT1G22770.1 FB,GI | |
| 47 | | 0 | 0 AT1G22770.1 FB,GI | |
| 48 | 3.6.3.1 | | 0 GO:0046872,(CAT1G68710.1 | 0 |
| 49 | | 0 | 0 GO:0005515 AT2G43500.1 | 0 |
| 50 | | | | |
| 51 | | 0 | 0 GO:0005515 AT2G43500.1 | 0 |
| 52 | 3.6.3.1 | | 0 GO:0046872,(CAT1G68710.1 | 0 |
| 53 | | 0 | 0 AT1G22770.1 FB,GI | |
| 54 | | | | |
| 55 | 3.1.1.11 | K01051 | GO:0004857,(CAT4G33230.1 | 0 |
| 56 | | 0 | 0 AT3G51290.2 | 0 |
| 57 | | 0 | 0 AT1G03870.1 FLA9 | |
| 58 | | | | |
| 59 | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | |
| 60 | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | |
| | | 0 | 0 AT3G17430.1 | 0 |

| | | | | | |
|----|-----------|----------|---|---|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 AT3G17430.1 | 0 |
| 3 | 1.11.1.7 | K00430 | | GO:0055114,(AT5G05340.1 | 0 |
| 4 | | 0 K14300 | | 0 AT2G05120.1 | 0 |
| 5 | | | | | |
| 6 | 6.3.2.19 | K10590 | | GO:0004842 AT5G02880.1 UPL4 | |
| 7 | 2.1.2.1 | K00600 | | GO:0016740 AT4G13930.1 SHM4 | |
| 8 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 9 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 10 | | | | | |
| 11 | 2.7.1.67 | | | 0 GO:0016773 AT1G26270.1 | 0 |
| 12 | | 0 | 0 | 0 AT1G76405.2 | 0 |
| 13 | | | | | |
| 14 | 3.6.4.12 | | | 0 GO:0016787,(AT2G28290.1 CHR3,SYD | |
| 15 | 3.6.4.12 | | | 0 GO:0016787,(AT2G28290.1 CHR3,SYD | |
| 16 | | 0 | | 0 GO:0005515 AT2G22125.1 CSI1 | |
| 17 | | 0 | | 0 GO:0005515 AT2G22125.1 CSI1 | |
| 18 | | | | | |
| 19 | 6.5.1.4 | | | 0 GO:0006396 AT5G22100.1 | 0 |
| 20 | 6.5.1.4 | | | 0 GO:0006396 AT5G22100.1 | 0 |
| 21 | | | | | |
| 22 | | 0 | | 0 GO:0046983 AT2G20180.2 PIF1,PIL5 | |
| 23 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 24 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 25 | | | | | |
| 26 | 2.4.1.12 | | | 0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 | |
| 27 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 28 | | 0 | | 0 GO:0006629 AT4G16070.1 | 0 |
| 29 | | 0 | | 0 GO:0003677,(AT1G70510.1 ATK1,KNAT2 | |
| 30 | | | | | |
| 31 | 1.1.1.330 | | | 0 AT5G02540.1 | 0 |
| 32 | 1.1.1.330 | | | 0 AT5G02540.1 | 0 |
| 33 | 1.1.1.330 | | | 0 AT5G02540.1 | 0 |
| 34 | 1.1.1.330 | | | 0 AT5G02540.1 | 0 |
| 35 | 1.1.1.330 | | | 0 AT5G02540.1 | 0 |
| 36 | 6.3.2.19 | | | 0 GO:0008270,(AT5G60820.1 | 0 |
| 37 | 1.1.1.330 | | | 0 AT5G02540.1 | 0 |
| 38 | 1.1.1.330 | | | 0 AT5G02540.1 | 0 |
| 39 | 1.1.1.330 | | | 0 AT5G02540.1 | 0 |
| 40 | | 0 | | 0 AT5G46220.1 | 0 |
| 41 | 1.1.1.330 | | | 0 AT5G02540.1 | 0 |
| 42 | 1.1.1.330 | | | 0 AT5G02540.1 | 0 |
| 43 | 1.1.1.330 | | | 0 AT5G02540.1 | 0 |
| 44 | 1.11.1.7 | K00430 | | GO:0055114,(AT4G33870.1 | 0 |
| 45 | 1.1.1.330 | | | 0 AT5G02540.1 | 0 |
| 46 | 1.1.1.330 | | | 0 AT5G02540.1 | 0 |
| 47 | 1.1.1.330 | | | 0 AT5G02540.1 | 0 |
| 48 | 1.11.1.7 | K00430 | | GO:0055114,(AT4G33870.1 | 0 |
| 49 | 2.4.1.198 | K03858 | | GO:0017176 AT4G35530.1 | 0 |
| 50 | | | | | |
| 51 | | 0 | 0 | 0 AT2G01060.1 | 0 |
| 52 | | 0 | 0 | 0 AT3G60890.2 ZPR2 | |
| 53 | | 0 K14488 | | GO:0009733 AT4G34760.1 | 0 |
| 54 | | | | | |
| 55 | | 0 | | 0 GO:0043531 AT1G63350.1 | 0 |
| 56 | | 0 | | 0 GO:0043531 AT1G63350.1 | 0 |
| 57 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 58 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 59 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 60 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| | 3.6.3.1 | | | 0 GO:0046872,(AT1G68710.1 | 0 |

| | | | | |
|----|-----------|----------|---|---|
| 1 | | | | |
| 2 | | 0 | 0 GO:0005515 AT2G43500.1 | 0 |
| 3 | | 0 | 0 GO:0005515 AT2G43500.1 | 0 |
| 4 | 3.6.3.1 | | 0 GO:0046872,(AT1G68710.1 | 0 |
| 5 | | | | |
| 6 | | 0 | 0 AT1G22770.1 FB,GI | |
| 7 | 3.1.1.11 | K01051 | GO:0004857,(AT4G33230.1 | 0 |
| 8 | | 0 | 0 AT3G51290.2 | 0 |
| 9 | | | | |
| 10 | | 0 | 0 AT1G03870.1 FLA9 | |
| 11 | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | |
| 12 | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | |
| 13 | | | | |
| 14 | | 0 | 0 AT3G17430.1 | 0 |
| 15 | | 0 | 0 AT3G17430.1 | 0 |
| 16 | 1.11.1.7 | K00430 | GO:0055114,(AT5G05340.1 | 0 |
| 17 | | 0 K14300 | 0 AT2G05120.1 | 0 |
| 18 | | | | |
| 19 | 6.3.2.19 | K10590 | GO:0004842 AT5G02880.1 UPL4 | |
| 20 | 2.1.2.1 | K00600 | GO:0016740 AT4G13930.1 SHM4 | |
| 21 | | | | |
| 22 | | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 23 | | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 24 | 2.7.1.67 | | 0 GO:0016773 AT1G26270.1 | 0 |
| 25 | | 0 | 0 AT1G76405.2 | 0 |
| 26 | | | | |
| 27 | 3.6.4.12 | | 0 GO:0016787,(AT2G28290.1 CHR3,SYD | |
| 28 | 3.6.4.12 | | 0 GO:0016787,(AT2G28290.1 CHR3,SYD | |
| 29 | | | | |
| 30 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | |
| 31 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | |
| 32 | 6.5.1.4 | | 0 GO:0006396 AT5G22100.1 | 0 |
| 33 | 6.5.1.4 | | 0 GO:0006396 AT5G22100.1 | 0 |
| 34 | | | | |
| 35 | | 0 | 0 GO:0046983 AT2G20180.2 PIF1,PIL5 | |
| 36 | | 0 | 0 AT2G35330.1 | 0 |
| 37 | | 0 | 0 AT2G35330.1 | 0 |
| 38 | | | | |
| 39 | 2.4.1.12 | | 0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 | |
| 40 | | 0 | 0 AT2G35330.1 | 0 |
| 41 | | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 42 | | | | |
| 43 | | 0 | 0 GO:0003677,(AT1G70510.1 ATK1,KNAT2 | |
| 44 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 45 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 46 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 47 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 48 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 49 | 6.3.2.19 | | 0 GO:0008270,(AT5G60820.1 | 0 |
| 50 | | | | |
| 51 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 52 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 53 | | 0 | 0 AT5G46220.1 | 0 |
| 54 | | | | |
| 55 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 56 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 57 | 1.11.1.7 | K00430 | GO:0055114,(AT4G33870.1 | 0 |
| 58 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 59 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 60 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| | 1.11.1.7 | K00430 | GO:0055114,(AT4G33870.1 | 0 |

| | | | | | |
|----|-----------|----------|-------------------------|---------------------------------------|---|
| 1 | | | | | |
| 2 | 2.4.1.198 | K03858 | GO:0017176 | AT4G35530.1 | 0 |
| 3 | | 0 | 0 | 0 AT2G01060.1 | 0 |
| 4 | | 0 | 0 | 0 AT3G60890.2 ZPR2 | |
| 5 | | | | | |
| 6 | | 0 K14488 | GO:0009733 | AT4G34760.1 | 0 |
| 7 | | 0 | 0 | GO:0043531 AT1G63350.1 | 0 |
| 8 | | 0 | 0 | GO:0043531 AT1G63350.1 | 0 |
| 9 | | | | | |
| 10 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 11 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 12 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 13 | | | | | |
| 14 | 3.6.3.1 | | 0 | GO:0046872,(AT1G68710.1 | 0 |
| 15 | | 0 | 0 | GO:0005515 AT2G43500.1 | 0 |
| 16 | | 0 | 0 | GO:0005515 AT2G43500.1 | 0 |
| 17 | | | | | |
| 18 | 3.6.3.1 | | 0 | GO:0046872,(AT1G68710.1 | 0 |
| 19 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 20 | 3.1.1.11 | K01051 | GO:0004857,(AT4G33230.1 | | 0 |
| 21 | | 0 | 0 | 0 AT3G51290.2 | 0 |
| 22 | | 0 | 0 | 0 AT1G03870.1 FLA9 | |
| 23 | | | | | |
| 24 | | 0 | 0 | GO:0046983 AT5G08130.5 BIM1 | |
| 25 | | 0 | 0 | GO:0046983 AT5G08130.5 BIM1 | |
| 26 | | | | | |
| 27 | | 0 | 0 | 0 AT3G17430.1 | 0 |
| 28 | | 0 | 0 | 0 AT3G17430.1 | 0 |
| 29 | | | | | |
| 30 | 1.11.1.7 | K00430 | GO:0055114,(AT5G05340.1 | | 0 |
| 31 | | 0 K14300 | 0 | AT2G05120.1 | 0 |
| 32 | 6.3.2.19 | K10590 | GO:0004842 | AT5G02880.1 UPL4 | |
| 33 | 2.1.2.1 | K00600 | GO:0016740 | AT4G13930.1 SHM4 | |
| 34 | | | | | |
| 35 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 36 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 37 | 2.7.1.67 | | 0 | GO:0016773 AT1G26270.1 | 0 |
| 38 | | 0 | 0 | 0 AT1G76405.2 | 0 |
| 39 | | | | | |
| 40 | 3.6.4.12 | | 0 | GO:0016787,(AT2G28290.1 CHR3,SYD | |
| 41 | 3.6.4.12 | | 0 | GO:0016787,(AT2G28290.1 CHR3,SYD | |
| 42 | | | | | |
| 43 | | 0 | 0 | GO:0005515 AT2G22125.1 CSI1 | |
| 44 | | 0 | 0 | GO:0005515 AT2G22125.1 CSI1 | |
| 45 | 6.5.1.4 | | 0 | GO:0006396 AT5G22100.1 | 0 |
| 46 | 6.5.1.4 | | 0 | GO:0006396 AT5G22100.1 | 0 |
| 47 | | | | | |
| 48 | | 0 | 0 | GO:0046983 AT2G20180.2 PIF1,PIL5 | |
| 49 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 50 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 51 | | | | | |
| 52 | 2.4.1.12 | | 0 | GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 | |
| 53 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 54 | | | | | |
| 55 | | 0 | 0 | GO:0006629 AT4G16070.1 | 0 |
| 56 | | 0 | 0 | GO:0003677,(AT1G70510.1 ATK1,KNAT2 | |
| 57 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 58 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 59 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 60 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |

| | | | | | |
|----|-----------|----------|-------------------------------------|--|---|
| 1 | | | | | |
| 2 | 6.3.2.19 | | 0 GO:0008270,(CAT5G60820.1 | | 0 |
| 3 | 1.1.1.330 | | 0 0 AT5G02540.1 | | 0 |
| 4 | 1.1.1.330 | | 0 0 AT5G02540.1 | | 0 |
| 5 | | | | | |
| 6 | | 0 | 0 0 AT5G46220.1 | | 0 |
| 7 | 1.1.1.330 | | 0 0 AT5G02540.1 | | 0 |
| 8 | 1.1.1.330 | | 0 0 AT5G02540.1 | | 0 |
| 9 | | | | | |
| 10 | 1.11.1.7 | K00430 | GO:0055114,(CAT4G33870.1 | | 0 |
| 11 | 1.1.1.330 | | 0 0 AT5G02540.1 | | 0 |
| 12 | 1.1.1.330 | | 0 0 AT5G02540.1 | | 0 |
| 13 | | | | | |
| 14 | 1.11.1.7 | K00430 | GO:0055114,(CAT4G33870.1 | | 0 |
| 15 | 2.4.1.198 | K03858 | GO:0017176 AT4G35530.1 | | 0 |
| 16 | | 0 | 0 0 AT2G01060.1 | | 0 |
| 17 | | 0 | 0 0 AT3G60890.2 ZPR2 | | |
| 18 | | 0 | 0 0 AT3G60890.2 ZPR2 | | |
| 19 | | 0 K14488 | GO:0009733 AT4G34760.1 | | 0 |
| 20 | | 0 | 0 GO:0043531 AT1G63350.1 | | 0 |
| 21 | | 0 | 0 GO:0043531 AT1G63350.1 | | 0 |
| 22 | | 0 | 0 GO:0043531 AT1G63350.1 | | 0 |
| 23 | | 0 | 0 0 AT1G22770.1 FB,GI | | |
| 24 | | 0 | 0 0 AT1G22770.1 FB,GI | | |
| 25 | | 0 | 0 0 AT1G22770.1 FB,GI | | |
| 26 | | 0 | 0 0 AT1G22770.1 FB,GI | | |
| 27 | 3.6.3.1 | | 0 GO:0046872,(CAT1G68710.1 | | 0 |
| 28 | | 0 | 0 GO:0005515 AT2G43500.1 | | 0 |
| 29 | | 0 | 0 GO:0005515 AT2G43500.1 | | 0 |
| 30 | | 0 | 0 GO:0005515 AT2G43500.1 | | 0 |
| 31 | 3.6.3.1 | | 0 GO:0046872,(CAT1G68710.1 | | 0 |
| 32 | | 0 | 0 0 AT1G22770.1 FB,GI | | |
| 33 | 3.1.1.11 | K01051 | GO:0004857,(CAT4G33230.1 | | 0 |
| 34 | | 0 | 0 0 AT3G51290.2 | | 0 |
| 35 | | 0 | 0 0 AT3G51290.2 | | 0 |
| 36 | | 0 | 0 0 AT1G03870.1 FLA9 | | |
| 37 | | 0 | 0 0 AT1G03870.1 FLA9 | | |
| 38 | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | | |
| 39 | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | | |
| 40 | | 0 | 0 0 AT3G17430.1 | | 0 |
| 41 | | 0 | 0 0 AT3G17430.1 | | 0 |
| 42 | | 0 | 0 0 AT3G17430.1 | | 0 |
| 43 | 1.11.1.7 | K00430 | GO:0055114,(CAT5G05340.1 | | 0 |
| 44 | | 0 K14300 | 0 AT2G05120.1 | | 0 |
| 45 | 6.3.2.19 | K10590 | GO:0004842 AT5G02880.1 UPL4 | | |
| 46 | 2.1.2.1 | K00600 | GO:0016740 AT4G13930.1 SHM4 | | |
| 47 | | 0 | 0 0 AT1G09020.1 ATSNF4,SNF4 | | |
| 48 | | 0 | 0 0 AT1G09020.1 ATSNF4,SNF4 | | |
| 49 | | 0 | 0 0 AT1G09020.1 ATSNF4,SNF4 | | |
| 50 | | 0 | 0 0 AT1G09020.1 ATSNF4,SNF4 | | |
| 51 | 2.7.1.67 | | 0 GO:0016773 AT1G26270.1 | | 0 |
| 52 | | 0 | 0 0 AT1G76405.2 | | 0 |
| 53 | 3.6.4.12 | | 0 GO:0016787,(CAT2G28290.1 CHR3,SYD | | |
| 54 | 3.6.4.12 | | 0 GO:0016787,(CAT2G28290.1 CHR3,SYD | | |
| 55 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | | |
| 56 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | | |
| 57 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | | |
| 58 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | | |
| 59 | 6.5.1.4 | | 0 GO:0006396 AT5G22100.1 | | 0 |
| 60 | 6.5.1.4 | | 0 GO:0006396 AT5G22100.1 | | 0 |
| | | 0 | 0 GO:0046983 AT2G20180.2 PIF1,PIL5 | | |

| | | | | |
|----|-----------|----------|---|---|
| 1 | | | | |
| 2 | | 0 | 0 | 0 AT2G35330.1 |
| 3 | | 0 | 0 | 0 AT2G35330.1 |
| 4 | 2.4.1.12 | | | 0 GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 |
| 5 | | | | |
| 6 | | 0 | 0 | 0 AT2G35330.1 |
| 7 | | 0 | 0 | 0 GO:0006629 AT4G16070.1 |
| 8 | | 0 | 0 | 0 GO:0003677,(AT1G70510.1 ATK1,KNAT2 |
| 9 | | | | |
| 10 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 11 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 12 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 13 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 14 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 15 | 6.3.2.19 | | 0 | 0 GO:0008270,(AT5G60820.1 |
| 16 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 17 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 18 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 19 | | 0 | 0 | 0 AT5G46220.1 |
| 20 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 21 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 22 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 23 | 1.11.1.7 | K00430 | | GO:0055114,(AT4G33870.1 |
| 24 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 25 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 26 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 27 | 1.11.1.7 | K00430 | | GO:0055114,(AT4G33870.1 |
| 28 | 2.4.1.198 | K03858 | | GO:0017176 AT4G35530.1 |
| 29 | | | | |
| 30 | | 0 | 0 | 0 AT2G01060.1 |
| 31 | | 0 | 0 | 0 AT3G60890.2 ZPR2 |
| 32 | | 0 K14488 | | GO:0009733 AT4G34760.1 |
| 33 | | 0 | 0 | 0 GO:0043531 AT1G63350.1 |
| 34 | | 0 | 0 | 0 GO:0043531 AT1G63350.1 |
| 35 | | 0 | 0 | 0 GO:0043531 AT1G63350.1 |
| 36 | | 0 | 0 | 0 AT1G22770.1 FB,GI |
| 37 | | 0 | 0 | 0 AT1G22770.1 FB,GI |
| 38 | | 0 | 0 | 0 AT1G22770.1 FB,GI |
| 39 | | 0 | 0 | 0 AT1G22770.1 FB,GI |
| 40 | 3.6.3.1 | | | 0 GO:0046872,(AT1G68710.1 |
| 41 | | 0 | 0 | 0 GO:0005515 AT2G43500.1 |
| 42 | | 0 | 0 | 0 GO:0005515 AT2G43500.1 |
| 43 | | 0 | 0 | 0 GO:0005515 AT2G43500.1 |
| 44 | 3.6.3.1 | | | 0 GO:0046872,(AT1G68710.1 |
| 45 | | 0 | 0 | 0 AT1G22770.1 FB,GI |
| 46 | | 0 | 0 | 0 AT1G22770.1 FB,GI |
| 47 | 3.1.1.11 | K01051 | | GO:0004857,(AT4G33230.1 |
| 48 | | 0 | 0 | 0 AT3G51290.2 |
| 49 | | 0 | 0 | 0 AT1G03870.1 FLA9 |
| 50 | | 0 | 0 | 0 GO:0046983 AT5G08130.5 BIM1 |
| 51 | | 0 | 0 | 0 GO:0046983 AT5G08130.5 BIM1 |
| 52 | | 0 | 0 | 0 GO:0046983 AT5G08130.5 BIM1 |
| 53 | | 0 | 0 | 0 AT3G17430.1 |
| 54 | | 0 | 0 | 0 AT3G17430.1 |
| 55 | | 0 | 0 | 0 AT3G17430.1 |
| 56 | 1.11.1.7 | K00430 | | GO:0055114,(AT5G05340.1 |
| 57 | | 0 K14300 | | 0 AT2G05120.1 |
| 58 | | | | |
| 59 | 6.3.2.19 | K10590 | | GO:0004842 AT5G02880.1 UPL4 |
| 60 | 2.1.2.1 | K00600 | | GO:0016740 AT4G13930.1 SHM4 |
| | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |

| | | | | | |
|----|-----------|----------|---|---------------------------------------|---|
| 1 | | | | | |
| 2 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 3 | 2.7.1.67 | | 0 | GO:0016773 AT1G26270.1 | 0 |
| 4 | | 0 | 0 | 0 AT1G76405.2 | 0 |
| 5 | | | | | |
| 6 | 3.6.4.12 | | 0 | GO:0016787,(AT2G28290.1 CHR3,SYD | |
| 7 | 3.6.4.12 | | 0 | GO:0016787,(AT2G28290.1 CHR3,SYD | |
| 8 | | 0 | 0 | GO:0005515 AT2G22125.1 CSI1 | |
| 9 | | 0 | 0 | GO:0005515 AT2G22125.1 CSI1 | |
| 10 | | | | | |
| 11 | 6.5.1.4 | | 0 | GO:0006396 AT5G22100.1 | 0 |
| 12 | 6.5.1.4 | | 0 | GO:0006396 AT5G22100.1 | 0 |
| 13 | | | | | |
| 14 | | 0 | 0 | GO:0046983 AT2G20180.2 PIF1,PIL5 | |
| 15 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 16 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 17 | | | | | |
| 18 | 2.4.1.12 | | 0 | GO:0030244,(AT4G24010.1 ATCSLG1,CSLG1 | |
| 19 | | 0 | 0 | 0 AT2G35330.1 | 0 |
| 20 | | 0 | 0 | GO:0006629 AT4G16070.1 | 0 |
| 21 | | | | | |
| 22 | | 0 | 0 | GO:0003677,(AT1G70510.1 ATK1,KNAT2 | |
| 23 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 24 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 25 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 26 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 27 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 28 | 6.3.2.19 | | 0 | GO:0008270,(AT5G60820.1 | 0 |
| 29 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 30 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 31 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 32 | | 0 | 0 | 0 AT5G46220.1 | 0 |
| 33 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 34 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 35 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 36 | 1.11.1.7 | K00430 | 0 | GO:0055114,(AT4G33870.1 | 0 |
| 37 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 38 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 39 | 1.1.1.330 | | 0 | 0 AT5G02540.1 | 0 |
| 40 | 1.11.1.7 | K00430 | 0 | GO:0055114,(AT4G33870.1 | 0 |
| 41 | 2.4.1.198 | K03858 | 0 | GO:0017176 AT4G35530.1 | 0 |
| 42 | | | | | |
| 43 | | 0 | 0 | 0 AT2G01060.1 | 0 |
| 44 | | 0 | 0 | 0 AT3G60890.2 ZPR2 | |
| 45 | | 0 K14488 | 0 | GO:0009733 AT4G34760.1 | 0 |
| 46 | | | 0 | GO:0043531 AT1G63350.1 | 0 |
| 47 | | | 0 | GO:0043531 AT1G63350.1 | 0 |
| 48 | | | 0 | 0 AT1G22770.1 FB,GI | |
| 49 | | | 0 | 0 AT1G22770.1 FB,GI | |
| 50 | | | 0 | 0 AT1G22770.1 FB,GI | |
| 51 | | | 0 | 0 AT1G22770.1 FB,GI | |
| 52 | | | 0 | 0 AT1G22770.1 FB,GI | |
| 53 | 3.6.3.1 | | 0 | GO:0046872,(AT1G68710.1 | 0 |
| 54 | | 0 | 0 | GO:0005515 AT2G43500.1 | 0 |
| 55 | | 0 | 0 | GO:0005515 AT2G43500.1 | 0 |
| 56 | | | | | |
| 57 | 3.6.3.1 | | 0 | GO:0046872,(AT1G68710.1 | 0 |
| 58 | | 0 | 0 | 0 AT1G22770.1 FB,GI | |
| 59 | 3.1.1.11 | K01051 | 0 | GO:0004857,(AT4G33230.1 | 0 |
| 60 | | 0 | 0 | 0 AT3G51290.2 | 0 |

| | | | | |
|----|-----------|----------|----------------|-----------------------------|
| 1 | | | | |
| 2 | | 0 | 0 | 0 AT1G03870.1 FLA9 |
| 3 | | 0 | 0 | GO:0046983 AT5G08130.5 BIM1 |
| 4 | | 0 | 0 | GO:0046983 AT5G08130.5 BIM1 |
| 5 | | 0 | 0 | 0 AT3G17430.1 |
| 6 | | 0 | 0 | 0 AT3G17430.1 |
| 7 | | 0 | 0 | 0 AT3G17430.1 |
| 8 | 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 |
| 9 | | 0 K14300 | | 0 AT2G05120.1 |
| 10 | | 0 K14300 | | 0 AT2G05120.1 |
| 11 | 6.3.2.19 | K10590 | GO:0004842 | AT5G02880.1 UPL4 |
| 12 | 2.1.2.1 | K00600 | GO:0016740 | AT4G13930.1 SHM4 |
| 13 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 14 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 15 | | 0 | 0 | 0 AT1G09020.1 ATSNF4,SNF4 |
| 16 | 2.7.1.67 | | 0 GO:0016773 | AT1G26270.1 |
| 17 | | 0 | 0 | 0 AT1G76405.2 |
| 18 | | 0 | 0 | 0 AT1G76405.2 |
| 19 | 3.6.4.12 | | 0 GO:0016787,(| AT2G28290.1 CHR3,SYD |
| 20 | 3.6.4.12 | | 0 GO:0016787,(| AT2G28290.1 CHR3,SYD |
| 21 | | 0 | 0 GO:0005515 | AT2G22125.1 CSI1 |
| 22 | | 0 | 0 GO:0005515 | AT2G22125.1 CSI1 |
| 23 | | 0 | 0 GO:0005515 | AT2G22125.1 CSI1 |
| 24 | 6.5.1.4 | | 0 GO:0006396 | AT5G22100.1 |
| 25 | 6.5.1.4 | | 0 GO:0006396 | AT5G22100.1 |
| 26 | | 0 | 0 GO:0046983 | AT2G20180.2 PIF1,PIL5 |
| 27 | | 0 | 0 | 0 AT2G35330.1 |
| 28 | | 0 | 0 | 0 AT2G35330.1 |
| 29 | | 0 | 0 | 0 AT2G35330.1 |
| 30 | | 0 | 0 | 0 AT2G35330.1 |
| 31 | 2.4.1.12 | | 0 GO:0030244,(| AT4G24010.1 ATCSLG1,CSLG1 |
| 32 | | 0 | 0 | 0 AT2G35330.1 |
| 33 | | 0 | 0 GO:0006629 | AT4G16070.1 |
| 34 | | 0 | 0 GO:0003677,(| AT1G70510.1 ATK1,KNAT2 |
| 35 | | 0 | 0 GO:0003677,(| AT1G70510.1 ATK1,KNAT2 |
| 36 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 37 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 38 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 39 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 40 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 41 | 6.3.2.19 | | 0 GO:0008270,(| AT5G60820.1 |
| 42 | | 0 | 0 | 0 AT5G02540.1 |
| 43 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 44 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 45 | | 0 | 0 | 0 AT5G46220.1 |
| 46 | | 0 | 0 | 0 AT5G46220.1 |
| 47 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 48 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 49 | 1.11.1.7 | K00430 | GO:0055114,(| AT4G33870.1 |
| 50 | | 0 | 0 | 0 AT5G02540.1 |
| 51 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 52 | 1.1.1.330 | | 0 | 0 AT5G02540.1 |
| 53 | 1.11.1.7 | K00430 | GO:0055114,(| AT4G33870.1 |
| 54 | | 0 | 0 | 0 AT5G02540.1 |
| 55 | 2.4.1.198 | K03858 | GO:0017176 | AT4G35530.1 |
| 56 | | 0 | 0 | 0 AT2G01060.1 |
| 57 | | 0 | 0 | 0 AT3G60890.2 ZPR2 |
| 58 | | 0 K14488 | GO:0009733 | AT4G34760.1 |
| 59 | | 0 | 0 GO:0043531 | AT1G63350.1 |
| 60 | | 0 | 0 GO:0043531 | AT1G63350.1 |

| | | | | |
|----|-----------|----------|--|---------------------|
| 1 | | | | |
| 2 | | 0 | 0 | 0 AT1G22770.1 FB,GI |
| 3 | | 0 | 0 | 0 AT1G22770.1 FB,GI |
| 4 | | 0 | 0 | 0 AT1G22770.1 FB,GI |
| 5 | | 0 | 0 | 0 AT1G22770.1 FB,GI |
| 6 | 3.6.3.1 | | 0 GO:0046872,(CAT1G68710.1 | 0 |
| 7 | | 0 | 0 GO:0005515 AT2G43500.1 | 0 |
| 8 | | 0 | 0 GO:0005515 AT2G43500.1 | 0 |
| 9 | | 0 | 0 GO:0005515 AT2G43500.1 | 0 |
| 10 | 3.6.3.1 | | 0 GO:0046872,(CAT1G68710.1 | 0 |
| 11 | | 0 | 0 AT1G22770.1 FB,GI | |
| 12 | 3.1.1.11 | K01051 | GO:0004857,(CAT4G33230.1 | 0 |
| 13 | | 0 | 0 AT3G51290.2 | 0 |
| 14 | | 0 | 0 AT3G51290.2 | 0 |
| 15 | | 0 | 0 AT1G03870.1 FLA9 | |
| 16 | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | |
| 17 | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | |
| 18 | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | |
| 19 | | 0 | 0 AT3G17430.1 | 0 |
| 20 | | 0 | 0 AT3G17430.1 | 0 |
| 21 | | 0 | 0 AT3G17430.1 | 0 |
| 22 | 1.11.1.7 | K00430 | GO:0055114,(CAT5G05340.1 | 0 |
| 23 | | 0 K14300 | 0 AT2G05120.1 | 0 |
| 24 | 6.3.2.19 | K10590 | GO:0004842 AT5G02880.1 UPL4 | |
| 25 | 2.1.2.1 | K00600 | GO:0016740 AT4G13930.1 SHM4 | |
| 26 | | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 27 | | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 28 | | 0 | 0 AT1G09020.1 ATSNF4,SNF4 | |
| 29 | 2.7.1.67 | | 0 GO:0016773 AT1G26270.1 | 0 |
| 30 | | 0 | 0 AT1G76405.2 | 0 |
| 31 | | 0 | 0 AT1G76405.2 | 0 |
| 32 | 3.6.4.12 | | 0 GO:0016787,(CAT2G28290.1 CHR3,SYD | |
| 33 | 3.6.4.12 | | 0 GO:0016787,(CAT2G28290.1 CHR3,SYD | |
| 34 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | |
| 35 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | |
| 36 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | |
| 37 | 6.5.1.4 | | 0 GO:0006396 AT5G22100.1 | 0 |
| 38 | 6.5.1.4 | | 0 GO:0006396 AT5G22100.1 | 0 |
| 39 | | 0 | 0 GO:0006396 AT5G22100.1 | 0 |
| 40 | | 0 | 0 GO:0046983 AT2G20180.2 PIF1,PIL5 | |
| 41 | | 0 | 0 AT2G35330.1 | 0 |
| 42 | | 0 | 0 AT2G35330.1 | 0 |
| 43 | | 0 | 0 AT2G35330.1 | 0 |
| 44 | 2.4.1.12 | | 0 GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1 | |
| 45 | | 0 | 0 AT2G35330.1 | 0 |
| 46 | | 0 | 0 AT2G35330.1 | 0 |
| 47 | | 0 | 0 GO:0006629 AT4G16070.1 | 0 |
| 48 | | 0 | 0 GO:0003677,(CAT1G70510.1 ATK1,KNAT2 | |
| 49 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 50 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 51 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 52 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 53 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 54 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 55 | 6.3.2.19 | | 0 GO:0008270,(CAT5G60820.1 | 0 |
| 56 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 57 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 58 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| 59 | | 0 | 0 AT5G46220.1 | 0 |
| 60 | 1.1.1.330 | | 0 AT5G02540.1 | 0 |
| | 1.1.1.330 | | 0 AT5G02540.1 | 0 |

| | | | | | |
|----|-----------|----------|--|--|---|
| 1 | | | | | |
| 2 | 1.11.1.7 | K00430 | GO:0055114,(CAT4G33870.1 | | 0 |
| 3 | 1.1.1.330 | | 0 0 AT5G02540.1 | | 0 |
| 4 | 1.1.1.330 | | 0 0 AT5G02540.1 | | 0 |
| 5 | 1.11.1.7 | K00430 | GO:0055114,(CAT4G33870.1 | | 0 |
| 6 | 2.4.1.198 | K03858 | GO:0017176 AT4G35530.1 | | 0 |
| 7 | | | | | |
| 8 | | 0 | 0 0 AT2G01060.1 | | 0 |
| 9 | | | | | |
| 10 | | 0 | 0 0 AT3G60890.2 ZPR2 | | |
| 11 | | 0 K14488 | GO:0009733 AT4G34760.1 | | 0 |
| 12 | | 0 | 0 GO:0043531 AT1G63350.1 | | 0 |
| 13 | | 0 | 0 GO:0043531 AT1G63350.1 | | 0 |
| 14 | | 0 | 0 GO:0043531 AT1G63350.1 | | 0 |
| 15 | | 0 | 0 0 AT1G22770.1 FB,GI | | |
| 16 | | 0 | 0 0 AT1G22770.1 FB,GI | | |
| 17 | | 0 | 0 0 AT1G22770.1 FB,GI | | |
| 18 | | 0 | 0 0 AT1G22770.1 FB,GI | | |
| 19 | 3.6.3.1 | | 0 GO:0046872,(CAT1G68710.1 | | 0 |
| 20 | | 0 | 0 GO:0005515 AT2G43500.1 | | 0 |
| 21 | | 0 | 0 GO:0005515 AT2G43500.1 | | 0 |
| 22 | | 0 | 0 GO:0005515 AT2G43500.1 | | 0 |
| 23 | 3.6.3.1 | | 0 GO:0046872,(CAT1G68710.1 | | 0 |
| 24 | | 0 | 0 0 AT1G22770.1 FB,GI | | |
| 25 | 3.1.1.11 | K01051 | GO:0004857,(CAT4G33230.1 | | 0 |
| 26 | | 0 | 0 0 AT3G51290.2 | | 0 |
| 27 | | 0 | 0 0 AT1G03870.1 FLA9 | | |
| 28 | | 0 | 0 0 AT1G03870.1 FLA9 | | |
| 29 | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | | |
| 30 | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | | |
| 31 | | 0 | 0 GO:0046983 AT5G08130.5 BIM1 | | |
| 32 | | 0 | 0 0 AT3G17430.1 | | 0 |
| 33 | | 0 | 0 0 AT3G17430.1 | | 0 |
| 34 | | 0 | 0 0 AT3G17430.1 | | 0 |
| 35 | 1.11.1.7 | K00430 | GO:0055114,(CAT5G05340.1 | | 0 |
| 36 | | 0 K14300 | 0 AT2G05120.1 | | 0 |
| 37 | 6.3.2.19 | K10590 | GO:0004842 AT5G02880.1 UPL4 | | |
| 38 | 2.1.2.1 | K00600 | GO:0016740 AT4G13930.1 SHM4 | | |
| 39 | | | | | |
| 40 | | 0 | 0 0 AT1G09020.1 ATSNF4,SNF4 | | |
| 41 | | 0 | 0 0 AT1G09020.1 ATSNF4,SNF4 | | |
| 42 | | 0 | 0 0 AT1G09020.1 ATSNF4,SNF4 | | |
| 43 | 2.7.1.67 | | 0 GO:0016773 AT1G26270.1 | | 0 |
| 44 | | 0 | 0 0 AT1G76405.2 | | 0 |
| 45 | 3.6.4.12 | | 0 GO:0016787,(CAT2G28290.1 CHR3,SYD | | |
| 46 | 3.6.4.12 | | 0 GO:0016787,(CAT2G28290.1 CHR3,SYD | | |
| 47 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | | |
| 48 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | | |
| 49 | | 0 | 0 GO:0005515 AT2G22125.1 CSI1 | | |
| 50 | 6.5.1.4 | | 0 GO:0006396 AT5G22100.1 | | 0 |
| 51 | 6.5.1.4 | | 0 GO:0006396 AT5G22100.1 | | 0 |
| 52 | | 0 | 0 GO:0046983 AT2G20180.2 PIF1,PIL5 | | |
| 53 | | 0 | 0 0 AT2G35330.1 | | 0 |
| 54 | | 0 | 0 0 AT2G35330.1 | | 0 |
| 55 | | 0 | 0 0 AT2G35330.1 | | 0 |
| 56 | 2.4.1.12 | | 0 GO:0030244,(CAT4G24010.1 ATCSLG1,CSLG1 | | |
| 57 | | 0 | 0 0 AT2G35330.1 | | 0 |
| 58 | | 0 | 0 GO:0006629 AT4G16070.1 | | 0 |
| 59 | | 0 | 0 GO:0006629 AT4G16070.1 | | 0 |
| 60 | | 0 | 0 GO:0003677,(CAT1G70510.1 ATK1,KNAT2 | | |

| | | | | | | |
|----|-----------|--------|--------------|------------------|------------------|---|
| 1 | | | | | | |
| 2 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 3 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 4 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 5 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 6 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 7 | 6.3.2.19 | 0 | GO:0008270,(| AT5G60820.1 | 0 | |
| 8 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 9 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 10 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 11 | 0 | 0 | 0 | AT5G46220.1 | 0 | |
| 12 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 13 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 14 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 15 | 1.11.1.7 | K00430 | GO:0055114,(| AT4G33870.1 | 0 | |
| 16 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 17 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 18 | 1.1.1.330 | 0 | 0 | AT5G02540.1 | 0 | |
| 19 | 1.11.1.7 | K00430 | GO:0055114,(| AT4G33870.1 | 0 | |
| 20 | 2.4.1.198 | K03858 | GO:0017176 | AT4G35530.1 | 0 | |
| 21 | | | | | | |
| 22 | 0 | 0 | 0 | AT2G01060.1 | 0 | |
| 23 | 0 | 0 | 0 | AT3G60890.2 ZPR2 | | |
| 24 | 0 | K14488 | GO:0009733 | AT4G34760.1 | 0 | |
| 25 | 0 | | 0 | GO:0043531 | AT1G63350.1 | 0 |
| 26 | 0 | | 0 | GO:0043531 | AT1G63350.1 | 0 |
| 27 | 0 | | 0 | GO:0043531 | AT1G63350.1 | 0 |
| 28 | 0 | | 0 | AT1G22770.1 | FB,GI | |
| 29 | 0 | | 0 | AT1G22770.1 | FB,GI | |
| 30 | 0 | | 0 | AT1G22770.1 | FB,GI | |
| 31 | 0 | | 0 | AT1G22770.1 | FB,GI | |
| 32 | 3.6.3.1 | | 0 | GO:0046872,(| AT1G68710.1 | 0 |
| 33 | 0 | | 0 | GO:0005515 | AT2G43500.1 | 0 |
| 34 | 0 | | 0 | GO:0005515 | AT2G43500.1 | 0 |
| 35 | 0 | | 0 | GO:0005515 | AT2G43500.1 | 0 |
| 36 | 3.6.3.1 | | 0 | GO:0046872,(| AT1G68710.1 | 0 |
| 37 | 0 | | 0 | AT1G22770.1 | FB,GI | |
| 38 | 0 | | 0 | AT1G22770.1 | FB,GI | |
| 39 | 1.11.1.7 | K00430 | GO:0055114,(| AT5G05340.1 | 0 | |
| 40 | 0 | K14300 | | AT2G05120.1 | 0 | |
| 41 | 0 | | 0 | AT1G09020.1 | ATSNF4,SNF4 | |
| 42 | 0 | | 0 | AT1G09020.1 | ATSNF4,SNF4 | |
| 43 | 3.1.1.11 | K01051 | GO:0004857,(| AT4G33230.1 | 0 | |
| 44 | 0 | | 0 | AT1G09020.1 | ATSNF4,SNF4 | |
| 45 | 0 | | 0 | AT3G51290.2 | 0 | |
| 46 | 0 | | 0 | AT1G03870.1 | FLA9 | |
| 47 | 0 | | 0 | AT1G03870.1 | FLA9 | |
| 48 | 0 | | 0 | GO:0046983 | AT5G08130.5 BIM1 | |
| 49 | 0 | | 0 | GO:0046983 | AT5G08130.5 BIM1 | |
| 50 | 0 | | 0 | AT3G17430.1 | 0 | |
| 51 | 0 | | 0 | AT3G17430.1 | 0 | |
| 52 | 0 | | 0 | AT3G17430.1 | 0 | |
| 53 | 1.11.1.7 | K00430 | GO:0055114,(| AT4G33870.1 | 0 | |
| 54 | 1.11.1.7 | K00430 | GO:0055114,(| AT4G33870.1 | 0 | |
| 55 | 0 | | 0 | GO:0043531 | AT1G63350.1 | 0 |
| 56 | 0 | | 0 | GO:0043531 | AT1G63350.1 | 0 |
| 57 | 0 | | 0 | GO:0043531 | AT1G63350.1 | 0 |
| 58 | 0 | | 0 | GO:0043531 | AT1G63350.1 | 0 |
| 59 | 3.6.3.1 | | 0 | GO:0046872,(| AT1G68710.1 | 0 |
| 60 | 0 | | 0 | GO:0005515 | AT2G43500.1 | 0 |
| | 0 | | 0 | GO:0005515 | AT2G43500.1 | 0 |

| | | | | |
|----|-----------|----------|---|---|
| 1 | | | | |
| 2 | 3.6.3.1 | | 0 GO:0046872,(CAT1G68710.1 | 0 |
| 3 | | 0 | 0 GO:0005515 AT2G43500.1 | 0 |
| 4 | 2.7.11.1 | | 0 GO:0006468,(CAT5G49660.1 | 0 |
| 5 | | | | |
| 6 | | 0 | 0 GO:0046872,(CAT4G37270.1 ATHMA1,HMA1 | |
| 7 | 2.7.7.19 | | 0 GO:0016779,(CAT5G23690.1 | 0 |
| 8 | 2.7.7.19 | | 0 GO:0016779,(CAT5G23690.1 | 0 |
| 9 | 2.7.7.19 | | 0 GO:0016779,(CAT5G23690.1 | 0 |
| 10 | 2.7.7.19 | | 0 GO:0016779,(CAT5G23690.1 | 0 |
| 11 | 2.4.1.14 | K00696 | GO:0016157,(CAT5G20280.1 ATSPS1F,SPS1F | |
| 12 | | 0 | 0 AT2G40720.1 | 0 |
| 13 | | | | |
| 14 | 2.4.1.83 | K09658 | GO:0030176,(CAT1G74340.1 | 0 |
| 15 | 6.3.2.19 | K10590 | GO:0004842 AT5G02880.1 UPL4 | |
| 16 | 2.7.1.67 | | 0 GO:0016773 AT1G26270.1 | 0 |
| 17 | | | | |
| 18 | 2.1.2.1 | K00600 | GO:0016740 AT4G13930.1 SHM4 | |
| 19 | 2.7.11.1 | | 0 GO:0006468,(CAT3G55950.1 ATCRR3,CCR3 | |
| 20 | | 0 K07300 | GO:0055085,(CAT2G38170.3 ATCAX1,CAX1,RCI4 | |
| 21 | | | | |
| 22 | 2.4.1.218 | K08237 | GO:0016758,(CAT4G01070.1 GT72B1,UGT72B1 | |
| 23 | | | | |
| 24 | | | | |
| 25 | | | | |
| 26 | | | | |
| 27 | | | | |
| 28 | | | | |
| 29 | | | | |
| 30 | | | | |
| 31 | | | | |
| 32 | | | | |
| 33 | | | | |
| 34 | | | | |
| 35 | | | | |
| 36 | | | | |
| 37 | | | | |
| 38 | | | | |
| 39 | | | | |
| 40 | | | | |
| 41 | | | | |
| 42 | | | | |
| 43 | | | | |
| 44 | | | | |
| 45 | | | | |
| 46 | | | | |
| 47 | | | | |
| 48 | | | | |
| 49 | | | | |
| 50 | | | | |
| 51 | | | | |
| 52 | | | | |
| 53 | | | | |
| 54 | | | | |
| 55 | | | | |
| 56 | | | | |
| 57 | | | | |
| 58 | | | | |
| 59 | | | | |
| 60 | | | | |

not distribute

1
2 NAC (No Apical Meristem) domain transcriptional regulPhvul.005G07PTHR31744:SFPhvul.005G07
3 NAC (No Apical Meristem) domain transcriptional regulPhvul.011G16PTHR31744:SFPhvul.011G16
4 NAC domain containing protein 1 Phvul.005G05PTHR31744:SFPhvul.005G05
5
6 NAC (No Apical Meristem) domain transcriptional regulPhvul.005G07PTHR31744:SFPhvul.005G07
7 NAC (No Apical Meristem) domain transcriptional regulPhvul.011G16PTHR31744:SFPhvul.011G16
8 NAC domain containing protein 1 Phvul.005G05PTHR31744:SFPhvul.005G05
9
10 NAC (No Apical Meristem) domain transcriptional regulPhvul.005G07PTHR31744:SFPhvul.005G07
11 NAC (No Apical Meristem) domain transcriptional regulPhvul.011G16PTHR31744:SFPhvul.011G16
12 NAC domain containing protein 1 Phvul.005G05PTHR31744:SFPhvul.005G05
13
14 NAC (No Apical Meristem) domain transcriptional regulPhvul.005G07PTHR31744:SFPhvul.005G07
15 NAC (No Apical Meristem) domain transcriptional regulPhvul.011G16PTHR31744:SFPhvul.011G16
16 NAC domain containing protein 1 Phvul.005G05PTHR31744:SFPhvul.005G05
17
18 NAC (No Apical Meristem) domain transcriptional regulPhvul.005G07PTHR31744:SFPhvul.005G07
19 NAC (No Apical Meristem) domain transcriptional regulPhvul.011G16PTHR31744:SFPhvul.011G16
20 NAC domain containing protein 1 Phvul.005G05PTHR31744:SFPhvul.005G05
21
22 NAC (No Apical Meristem) domain transcriptional regulPhvul.005G07PTHR31744:SFPhvul.005G07
23 NAC (No Apical Meristem) domain transcriptional regulPhvul.011G16PTHR31744:SFPhvul.011G16
24 NAC domain containing protein 1 Phvul.005G05PTHR31744:SFPhvul.005G05
25
26 NAC (No Apical Meristem) domain transcriptional regulPhvul.005G07PTHR31744:SFPhvul.005G07
27 NAC (No Apical Meristem) domain transcriptional regulPhvul.011G16PTHR31744:SFPhvul.011G16
28 NAC domain containing protein 1 Phvul.005G05PTHR31744:SFPhvul.005G05
29
30 NAC (No Apical Meristem) domain transcriptional regulPhvul.005G07PTHR31744:SFPhvul.005G07
31 NAC (No Apical Meristem) domain transcriptional regulPhvul.011G16PTHR31744:SFPhvul.011G16
32 NAC domain containing protein 1 Phvul.005G05PTHR31744:SFPhvul.005G05
33
34 NAC (No Apical Meristem) domain transcriptional regulPhvul.005G07PTHR31744:SFPhvul.005G07
35 NAC (No Apical Meristem) domain transcriptional regulPhvul.011G16PTHR31744:SFPhvul.011G16
36 NAC domain containing protein 1 Phvul.005G05PTHR31744:SFPhvul.005G05
37
38 NAC (No Apical Meristem) domain transcriptional regulPhvul.005G07PTHR31744:SFPhvul.005G07
39 NAC (No Apical Meristem) domain transcriptional regulPhvul.011G16PTHR31744:SFPhvul.011G16
40 NAC domain containing protein 1 Phvul.005G05PTHR31744:SFPhvul.005G05
41
42 NAC (No Apical Meristem) domain transcriptional regulPhvul.005G07PTHR31744:SFPhvul.005G07
43 NAC (No Apical Meristem) domain transcriptional regulPhvul.011G16PTHR31744:SFPhvul.011G16
44 NAC domain containing protein 1 Phvul.005G05PTHR31744:SFPhvul.005G05
45
46 NAC (No Apical Meristem) domain transcriptional regulPhvul.005G07PTHR31744:SFPhvul.005G07
47 NAC (No Apical Meristem) domain transcriptional regulPhvul.011G16PTHR31744:SFPhvul.011G16
48 NAC domain containing protein 1 Phvul.005G05PTHR31744:SFPhvul.005G05
49
50 NAC (No Apical Meristem) domain transcriptional regulPhvul.005G07PTHR31744:SFPhvul.005G07
51 NAC (No Apical Meristem) domain transcriptional regulPhvul.011G16PTHR31744:SFPhvul.011G16
52 NAC domain containing protein 1 Phvul.005G05PTHR31744:SFPhvul.005G05
53
54 NAC (No Apical Meristem) domain transcriptional regulPhvul.005G07PTHR31744:SFPhvul.005G07
55 NAC (No Apical Meristem) domain transcriptional regulPhvul.011G16PTHR31744:SFPhvul.011G16
56 NAC domain containing protein 1 Phvul.005G05PTHR31744:SFPhvul.005G05
57
58 NAC (No Apical Meristem) domain transcriptional regulPhvul.005G07PTHR31744:SFPhvul.005G07
59 NAC (No Apical Meristem) domain transcriptional regulPhvul.011G16PTHR31744:SFPhvul.011G16
60 NAC domain containing protein 1 Phvul.005G05PTHR31744:SFPhvul.005G05
GDSL-like Lipase/Acylhydrolase superfamily protein Phvul.006G16PTHR22835//IPhvul.006G16

| | | |
|----|---|--------------------------------------|
| 1 | | |
| 2 | protamine P1 family protein | Phvul.007G16PTHR33448:SFPhvul.007G16 |
| 3 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 4 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 5 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 6 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 7 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.004G17PTHR10509//IPhvul.004G17 |
| 8 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G16PTHR22835//IPhvul.006G16 |
| 9 | | |
| 10 | protamine P1 family protein | Phvul.007G16PTHR33448:SFPhvul.007G16 |
| 11 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 12 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 13 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 14 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 15 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.004G17PTHR10509//IPhvul.004G17 |
| 16 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G16PTHR22835//IPhvul.006G16 |
| 17 | | |
| 18 | protamine P1 family protein | Phvul.007G16PTHR33448:SFPhvul.007G16 |
| 19 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 20 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 21 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 22 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 23 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.004G17PTHR10509//IPhvul.004G17 |
| 24 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G16PTHR22835//IPhvul.006G16 |
| 25 | | |
| 26 | protamine P1 family protein | Phvul.007G16PTHR33448:SFPhvul.007G16 |
| 27 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 28 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 29 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 30 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 31 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.004G17PTHR10509//IPhvul.004G17 |
| 32 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G16PTHR22835//IPhvul.006G16 |
| 33 | | |
| 34 | protamine P1 family protein | Phvul.007G16PTHR33448:SFPhvul.007G16 |
| 35 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 36 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 37 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 38 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 39 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.004G17PTHR10509//IPhvul.004G17 |
| 40 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G16PTHR22835//IPhvul.006G16 |
| 41 | | |
| 42 | protamine P1 family protein | Phvul.007G16PTHR33448:SFPhvul.007G16 |
| 43 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 44 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 45 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 46 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 47 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.004G17PTHR10509//IPhvul.004G17 |
| 48 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G16PTHR22835//IPhvul.006G16 |
| 49 | | |
| 50 | protamine P1 family protein | Phvul.007G16PTHR33448:SFPhvul.007G16 |
| 51 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 52 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 53 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 54 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 55 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.004G17PTHR10509//IPhvul.004G17 |
| 56 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G16PTHR22835//IPhvul.006G16 |
| 57 | | |
| 58 | protamine P1 family protein | Phvul.007G16PTHR33448:SFPhvul.007G16 |
| 59 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 60 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |

| | | |
|----|---|-------------------------------------|
| 1 | | |
| 2 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.004G17PTHR10509//IPhvu.004G17 |
| 3 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G16PTHR22835//IPhvu.006G16 |
| 4 | protamine P1 family protein | Phvul.007G16PTHR33448:SFPhvu.007G16 |
| 5 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 6 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 7 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 8 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 9 | | |
| 10 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.004G17PTHR10509//IPhvu.004G17 |
| 11 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G16PTHR22835//IPhvu.006G16 |
| 12 | protamine P1 family protein | Phvul.007G16PTHR33448:SFPhvu.007G16 |
| 13 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 14 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 15 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 16 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 17 | | |
| 18 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.004G17PTHR10509//IPhvu.004G17 |
| 19 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G16PTHR22835//IPhvu.006G16 |
| 20 | protamine P1 family protein | Phvul.007G16PTHR33448:SFPhvu.007G16 |
| 21 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 22 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 23 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 24 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 25 | | |
| 26 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.004G17PTHR10509//IPhvu.004G17 |
| 27 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G16PTHR22835//IPhvu.006G16 |
| 28 | protamine P1 family protein | Phvul.007G16PTHR33448:SFPhvu.007G16 |
| 29 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 30 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 31 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 32 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 33 | | |
| 34 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.004G17PTHR10509//IPhvu.004G17 |
| 35 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G16PTHR22835//IPhvu.006G16 |
| 36 | protamine P1 family protein | Phvul.007G16PTHR33448:SFPhvu.007G16 |
| 37 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 38 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 39 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 40 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 41 | | |
| 42 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.004G17PTHR10509//IPhvu.004G17 |
| 43 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G16PTHR22835//IPhvu.006G16 |
| 44 | protamine P1 family protein | Phvul.007G16PTHR33448:SFPhvu.007G16 |
| 45 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 46 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 47 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 48 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 49 | | |
| 50 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.004G17PTHR10509//IPhvu.004G17 |
| 51 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G16PTHR22835//IPhvu.006G16 |
| 52 | protamine P1 family protein | Phvul.007G16PTHR33448:SFPhvu.007G16 |
| 53 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 54 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 55 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 56 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |
| 57 | | |
| 58 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.004G17PTHR10509//IPhvu.004G17 |
| 59 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G16PTHR22835//IPhvu.006G16 |
| 60 | protamine P1 family protein | Phvul.007G16PTHR33448:SFPhvu.007G16 |
| | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvu.011G06 |

| | | |
|----|---|---|
| 1 | | |
| 2 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 3 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 4 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.004G17PTHR10509//IPhvul.004G17 |
| 5 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G16PTHR22835//IPhvul.006G16 |
| 6 | protamine P1 family protein | Phvul.007G16PTHR33448:SFPhvul.007G16 |
| 7 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 8 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 9 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 10 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 11 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 12 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.004G17PTHR10509//IPhvul.004G17 |
| 13 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G16PTHR22835//IPhvul.006G16 |
| 14 | protamine P1 family protein | Phvul.007G16PTHR33448:SFPhvul.007G16 |
| 15 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 16 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 17 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 18 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 19 | UDP-XYL synthase 6 | Phvul.011G06PTHR10366//IPhvul.011G06 |
| 20 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.004G17PTHR10509//IPhvul.004G17 |
| 21 | TCP family transcription factor | Phvul.010G08PTHR31072:SFPhvul.010G08 |
| 22 | UDP-Glycosyltransferase superfamily protein | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 23 | paralog of ARC6 | Phvul.004G13PTHR33925:SFPhvul.004G13 |
| 24 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.005G00PTHR22835//IPhvul.005G00 |
| 25 | | 0 Phvul.008G14PF17035 - BroPhvul.008G14 |
| 26 | | 0 Phvul.008G14PF17035 - BroPhvul.008G14 |
| 27 | | 0 Phvul.008G14PF17035 - BroPhvul.008G14 |
| 28 | | 0 Phvul.008G14PF17035 - BroPhvul.008G14 |
| 29 | | 0 Phvul.008G14PF17035 - BroPhvul.008G14 |
| 30 | | 0 Phvul.008G14PF17035 - BroPhvul.008G14 |
| 31 | | 0 0 0 Phvul.006G08 |
| 32 | cation calcium exchanger 4 | Phvul.010G12PTHR12266:SFPhvul.010G12 |
| 33 | TCP family transcription factor | Phvul.010G08PTHR31072:SFPhvul.010G08 |
| 34 | UDP-Glycosyltransferase superfamily protein | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 35 | paralog of ARC6 | Phvul.004G13PTHR33925:SFPhvul.004G13 |
| 36 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.005G00PTHR22835//IPhvul.005G00 |
| 37 | | 0 Phvul.008G14PF17035 - BroPhvul.008G14 |
| 38 | | 0 Phvul.008G14PF17035 - BroPhvul.008G14 |
| 39 | | 0 Phvul.008G14PF17035 - BroPhvul.008G14 |
| 40 | | 0 Phvul.008G14PF17035 - BroPhvul.008G14 |
| 41 | | 0 Phvul.008G14PF17035 - BroPhvul.008G14 |
| 42 | | 0 Phvul.008G14PF17035 - BroPhvul.008G14 |
| 43 | | 0 0 0 Phvul.006G08 |
| 44 | cation calcium exchanger 4 | Phvul.010G12PTHR12266:SFPhvul.010G12 |
| 45 | TCP family transcription factor | Phvul.010G08PTHR31072:SFPhvul.010G08 |
| 46 | UDP-Glycosyltransferase superfamily protein | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 47 | paralog of ARC6 | Phvul.004G13PTHR33925:SFPhvul.004G13 |
| 48 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.005G00PTHR22835//IPhvul.005G00 |
| 49 | | 0 Phvul.008G14PF17035 - BroPhvul.008G14 |
| 50 | | 0 Phvul.008G14PF17035 - BroPhvul.008G14 |
| 51 | | 0 Phvul.008G14PF17035 - BroPhvul.008G14 |
| 52 | | 0 Phvul.008G14PF17035 - BroPhvul.008G14 |
| 53 | | 0 Phvul.008G14PF17035 - BroPhvul.008G14 |
| 54 | | 0 Phvul.008G14PF17035 - BroPhvul.008G14 |
| 55 | | 0 0 0 Phvul.006G08 |
| 56 | cation calcium exchanger 4 | Phvul.010G12PTHR12266:SFPhvul.010G12 |
| 57 | TCP family transcription factor | Phvul.010G08PTHR31072:SFPhvul.010G08 |
| 58 | UDP-Glycosyltransferase superfamily protein | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 59 | paralog of ARC6 | Phvul.004G13PTHR33925:SFPhvul.004G13 |
| 60 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.005G00PTHR22835//IPhvul.005G00 |

| | | | |
|----|--|---|--|
| 1 | | | |
| 2 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 3 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 4 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 5 | | | |
| 6 | | 0 | 0 Phvul.006G08 |
| 7 | cation calcium exchanger 4 | | Phvul.010G12PTHR12266:SfPhvul.010G12 |
| 8 | TCP family transcription factor | | Phvul.010G08PTHR31072:SfPhvul.010G08 |
| 9 | UDP-Glycosyltransferase superfamily protein | | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 10 | paralog of ARC6 | | Phvul.004G13PTHR33925:SfPhvul.004G13 |
| 11 | GDSL-like Lipase/Acylhydrolase superfamily protein | | Phvul.005G00PTHR22835//IPhvul.005G00 |
| 12 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 13 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 14 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 15 | | | |
| 16 | | 0 | 0 Phvul.006G08 |
| 17 | cation calcium exchanger 4 | | Phvul.010G12PTHR12266:SfPhvul.010G12 |
| 18 | TCP family transcription factor | | Phvul.010G08PTHR31072:SfPhvul.010G08 |
| 19 | UDP-Glycosyltransferase superfamily protein | | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 20 | paralog of ARC6 | | Phvul.004G13PTHR33925:SfPhvul.004G13 |
| 21 | GDSL-like Lipase/Acylhydrolase superfamily protein | | Phvul.005G00PTHR22835//IPhvul.005G00 |
| 22 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 23 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 24 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 25 | | | |
| 26 | | 0 | 0 Phvul.006G08 |
| 27 | cation calcium exchanger 4 | | Phvul.010G12PTHR12266:SfPhvul.010G12 |
| 28 | TCP family transcription factor | | Phvul.010G08PTHR31072:SfPhvul.010G08 |
| 29 | UDP-Glycosyltransferase superfamily protein | | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 30 | paralog of ARC6 | | Phvul.004G13PTHR33925:SfPhvul.004G13 |
| 31 | GDSL-like Lipase/Acylhydrolase superfamily protein | | Phvul.005G00PTHR22835//IPhvul.005G00 |
| 32 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 33 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 34 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 35 | | | |
| 36 | | 0 | 0 Phvul.006G08 |
| 37 | cation calcium exchanger 4 | | Phvul.010G12PTHR12266:SfPhvul.010G12 |
| 38 | TCP family transcription factor | | Phvul.010G08PTHR31072:SfPhvul.010G08 |
| 39 | UDP-Glycosyltransferase superfamily protein | | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 40 | paralog of ARC6 | | Phvul.004G13PTHR33925:SfPhvul.004G13 |
| 41 | GDSL-like Lipase/Acylhydrolase superfamily protein | | Phvul.005G00PTHR22835//IPhvul.005G00 |
| 42 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 43 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 44 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 45 | | | |
| 46 | | 0 | 0 Phvul.006G08 |
| 47 | cation calcium exchanger 4 | | Phvul.010G12PTHR12266:SfPhvul.010G12 |
| 48 | TCP family transcription factor | | Phvul.010G08PTHR31072:SfPhvul.010G08 |
| 49 | UDP-Glycosyltransferase superfamily protein | | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 50 | paralog of ARC6 | | Phvul.004G13PTHR33925:SfPhvul.004G13 |
| 51 | GDSL-like Lipase/Acylhydrolase superfamily protein | | Phvul.005G00PTHR22835//IPhvul.005G00 |
| 52 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 53 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 54 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 55 | | | |
| 56 | | 0 | 0 Phvul.006G08 |
| 57 | cation calcium exchanger 4 | | Phvul.010G12PTHR12266:SfPhvul.010G12 |
| 58 | TCP family transcription factor | | Phvul.010G08PTHR31072:SfPhvul.010G08 |
| 59 | UDP-Glycosyltransferase superfamily protein | | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 60 | paralog of ARC6 | | Phvul.004G13PTHR33925:SfPhvul.004G13 |
| 61 | GDSL-like Lipase/Acylhydrolase superfamily protein | | Phvul.005G00PTHR22835//IPhvul.005G00 |
| 62 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |

| | | | |
|----|--|---|--|
| 1 | | | |
| 2 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 3 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 4 | | 0 | 0 |
| 5 | | 0 | 0 Phvul.006G08 |
| 6 | cation calcium exchanger 4 | | Phvul.010G12PTHR12266:SfPhvul.010G12 |
| 7 | TCP family transcription factor | | Phvul.010G08PTHR31072:SfPhvul.010G08 |
| 8 | UDP-Glycosyltransferase superfamily protein | | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 9 | paralog of ARC6 | | Phvul.004G13PTHR33925:SfPhvul.004G13 |
| 10 | GDSL-like Lipase/Acylhydrolase superfamily protein | | Phvul.005G00PTHR22835//IPhvul.005G00 |
| 11 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 12 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 13 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 14 | | 0 | 0 |
| 15 | | 0 | 0 Phvul.006G08 |
| 16 | | 0 | 0 |
| 17 | cation calcium exchanger 4 | | Phvul.010G12PTHR12266:SfPhvul.010G12 |
| 18 | TCP family transcription factor | | Phvul.010G08PTHR31072:SfPhvul.010G08 |
| 19 | UDP-Glycosyltransferase superfamily protein | | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 20 | paralog of ARC6 | | Phvul.004G13PTHR33925:SfPhvul.004G13 |
| 21 | GDSL-like Lipase/Acylhydrolase superfamily protein | | Phvul.005G00PTHR22835//IPhvul.005G00 |
| 22 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 23 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 24 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 25 | | 0 | 0 |
| 26 | | 0 | 0 Phvul.006G08 |
| 27 | | 0 | 0 |
| 28 | cation calcium exchanger 4 | | Phvul.010G12PTHR12266:SfPhvul.010G12 |
| 29 | TCP family transcription factor | | Phvul.010G08PTHR31072:SfPhvul.010G08 |
| 30 | UDP-Glycosyltransferase superfamily protein | | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 31 | paralog of ARC6 | | Phvul.004G13PTHR33925:SfPhvul.004G13 |
| 32 | GDSL-like Lipase/Acylhydrolase superfamily protein | | Phvul.005G00PTHR22835//IPhvul.005G00 |
| 33 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 34 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 35 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 36 | | 0 | 0 |
| 37 | | 0 | 0 Phvul.006G08 |
| 38 | | 0 | 0 |
| 39 | cation calcium exchanger 4 | | Phvul.010G12PTHR12266:SfPhvul.010G12 |
| 40 | TCP family transcription factor | | Phvul.010G08PTHR31072:SfPhvul.010G08 |
| 41 | UDP-Glycosyltransferase superfamily protein | | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 42 | paralog of ARC6 | | Phvul.004G13PTHR33925:SfPhvul.004G13 |
| 43 | GDSL-like Lipase/Acylhydrolase superfamily protein | | Phvul.005G00PTHR22835//IPhvul.005G00 |
| 44 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 45 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 46 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 47 | | 0 | 0 |
| 48 | | 0 | 0 Phvul.006G08 |
| 49 | | 0 | 0 |
| 50 | cation calcium exchanger 4 | | Phvul.010G12PTHR12266:SfPhvul.010G12 |
| 51 | TCP family transcription factor | | Phvul.010G08PTHR31072:SfPhvul.010G08 |
| 52 | UDP-Glycosyltransferase superfamily protein | | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 53 | paralog of ARC6 | | Phvul.004G13PTHR33925:SfPhvul.004G13 |
| 54 | GDSL-like Lipase/Acylhydrolase superfamily protein | | Phvul.005G00PTHR22835//IPhvul.005G00 |
| 55 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 56 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 57 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 58 | | 0 | 0 |
| 59 | | 0 | 0 Phvul.006G08 |
| 60 | | 0 | 0 |

| | | | |
|----|--|---|--|
| 1 | | | |
| 2 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 3 | | 0 | 0 0 Phvul.006G08 |
| 4 | cation calcium exchanger 4 | | Phvul.010G12PTHR12266:SfPhvul.010G12 |
| 5 | TCP family transcription factor | | Phvul.010G08PTHR31072:SfPhvul.010G08 |
| 6 | UDP-Glycosyltransferase superfamily protein | | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 7 | paralog of ARC6 | | Phvul.004G13PTHR33925:SfPhvul.004G13 |
| 8 | GDSL-like Lipase/Acylhydrolase superfamily protein | | Phvul.005G00PTHR22835//IPhvul.005G00 |
| 9 | | | |
| 10 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 11 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 12 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 13 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 14 | | 0 | 0 0 Phvul.006G08 |
| 15 | cation calcium exchanger 4 | | Phvul.010G12PTHR12266:SfPhvul.010G12 |
| 16 | TCP family transcription factor | | Phvul.010G08PTHR31072:SfPhvul.010G08 |
| 17 | UDP-Glycosyltransferase superfamily protein | | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 18 | paralog of ARC6 | | Phvul.004G13PTHR33925:SfPhvul.004G13 |
| 19 | GDSL-like Lipase/Acylhydrolase superfamily protein | | Phvul.005G00PTHR22835//IPhvul.005G00 |
| 20 | | | |
| 21 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 22 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 23 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 24 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 25 | | 0 | 0 0 Phvul.006G08 |
| 26 | cation calcium exchanger 4 | | Phvul.010G12PTHR12266:SfPhvul.010G12 |
| 27 | TCP family transcription factor | | Phvul.010G08PTHR31072:SfPhvul.010G08 |
| 28 | UDP-Glycosyltransferase superfamily protein | | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 29 | paralog of ARC6 | | Phvul.004G13PTHR33925:SfPhvul.004G13 |
| 30 | GDSL-like Lipase/Acylhydrolase superfamily protein | | Phvul.005G00PTHR22835//IPhvul.005G00 |
| 31 | | | |
| 32 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 33 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 34 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 35 | | 0 | 0 0 Phvul.006G08 |
| 36 | cation calcium exchanger 4 | | Phvul.010G12PTHR12266:SfPhvul.010G12 |
| 37 | TCP family transcription factor | | Phvul.010G08PTHR31072:SfPhvul.010G08 |
| 38 | UDP-Glycosyltransferase superfamily protein | | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 39 | paralog of ARC6 | | Phvul.004G13PTHR33925:SfPhvul.004G13 |
| 40 | GDSL-like Lipase/Acylhydrolase superfamily protein | | Phvul.005G00PTHR22835//IPhvul.005G00 |
| 41 | | | |
| 42 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 43 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 44 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 45 | | 0 | 0 0 Phvul.006G08 |
| 46 | cation calcium exchanger 4 | | Phvul.010G12PTHR12266:SfPhvul.010G12 |
| 47 | TCP family transcription factor | | Phvul.010G08PTHR31072:SfPhvul.010G08 |
| 48 | UDP-Glycosyltransferase superfamily protein | | Phvul.002G322.4.1.227 - UnPhvul.002G32 |
| 49 | paralog of ARC6 | | Phvul.004G13PTHR33925:SfPhvul.004G13 |
| 50 | GDSL-like Lipase/Acylhydrolase superfamily protein | | Phvul.005G00PTHR22835//IPhvul.005G00 |
| 51 | | | |
| 52 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 53 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 54 | | 0 | Phvul.008G14PF17035 - BroPhvul.008G14 |
| 55 | gigantea protein (GI) | | Phvul.007G08K12124 - GIG/Phvul.007G08 |
| 56 | gigantea protein (GI) | | Phvul.007G08K12124 - GIG/Phvul.007G08 |
| 57 | Homeobox-leucine zipper family protein / lipid-binding | | Phvul.011G07PF08670 - ME Phvul.011G07 |
| 58 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | | Phvul.008G07PF01657//PF0Phvul.008G07 |
| 59 | | 0 | 0 0 Phvul.011G11 |
| 60 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | | Phvul.008G07PTHR32099 - (Phvul.008G07 |
| 61 | chloride channel F | | Phvul.005G00PTHR11689:SfPhvul.005G00 |
| 62 | serine acetyltransferase 2;2 | | Phvul.008G27PTHR23416:SfPhvul.008G27 |
| 63 | | 0 | 0 0 Phvul.003G06 |

| | | | |
|----|---|----------------------------|---------------|
| 1 | | | |
| 2 | Mitochondrial substrate carrier family protein | Phvul.001G24K13354 - solut | Phvul.001G24 |
| 3 | transcription regulatory protein SNF2, putative | Phvul.008G06K11647 - SWI/ | Phvul.008G06 |
| 4 | peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF | Phvul.003G24K05864 - pept | Phvul.003G24 |
| 5 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.009G13PTHR10108:SF | Phvul.009G13 |
| 6 | | 0 | 0 |
| 7 | | 0 | 0 |
| 8 | K-box region and MADS-box transcription factor family | Phvul.009G13PTHR11945:SF | Phvul.009G13 |
| 9 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.011G10PTHR10108//I | Phvul.011G10 |
| 10 | cell division cycle protein 48-related / CDC48-related | Phvul.011G05PTHR23069 - | Phvul.011G05 |
| 11 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 12 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 13 | Homeobox-leucine zipper family protein / lipid-binding | Phvul.011G07PF08670 - ME | Phvul.011G07 |
| 14 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PF01657//PF0 | Phvul.008G07 |
| 15 | | 0 | 0 |
| 16 | | 0 | 0 |
| 17 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PTHR32099 - | (Phvul.008G07 |
| 18 | chloride channel F | Phvul.005G00PTHR11689:SF | Phvul.005G00 |
| 19 | serine acetyltransferase 2;2 | Phvul.008G27PTHR23416:SF | Phvul.008G27 |
| 20 | | 0 | 0 |
| 21 | | 0 | 0 |
| 22 | Mitochondrial substrate carrier family protein | Phvul.001G24K13354 - solut | Phvul.001G24 |
| 23 | transcription regulatory protein SNF2, putative | Phvul.008G06K11647 - SWI/ | Phvul.008G06 |
| 24 | peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF | Phvul.003G24K05864 - pept | Phvul.003G24 |
| 25 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.009G13PTHR10108:SF | Phvul.009G13 |
| 26 | | 0 | 0 |
| 27 | | 0 | 0 |
| 28 | K-box region and MADS-box transcription factor family | Phvul.009G13PTHR11945:SF | Phvul.009G13 |
| 29 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.011G10PTHR10108//I | Phvul.011G10 |
| 30 | cell division cycle protein 48-related / CDC48-related | Phvul.011G05PTHR23069 - | Phvul.011G05 |
| 31 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 32 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 33 | Homeobox-leucine zipper family protein / lipid-binding | Phvul.011G07PF08670 - ME | Phvul.011G07 |
| 34 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PF01657//PF0 | Phvul.008G07 |
| 35 | | 0 | 0 |
| 36 | | 0 | 0 |
| 37 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PTHR32099 - | (Phvul.008G07 |
| 38 | chloride channel F | Phvul.005G00PTHR11689:SF | Phvul.005G00 |
| 39 | serine acetyltransferase 2;2 | Phvul.008G27PTHR23416:SF | Phvul.008G27 |
| 40 | | 0 | 0 |
| 41 | | 0 | 0 |
| 42 | Mitochondrial substrate carrier family protein | Phvul.001G24K13354 - solut | Phvul.001G24 |
| 43 | transcription regulatory protein SNF2, putative | Phvul.008G06K11647 - SWI/ | Phvul.008G06 |
| 44 | peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF | Phvul.003G24K05864 - pept | Phvul.003G24 |
| 45 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.009G13PTHR10108:SF | Phvul.009G13 |
| 46 | | 0 | 0 |
| 47 | | 0 | 0 |
| 48 | K-box region and MADS-box transcription factor family | Phvul.009G13PTHR11945:SF | Phvul.009G13 |
| 49 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.011G10PTHR10108//I | Phvul.011G10 |
| 50 | cell division cycle protein 48-related / CDC48-related | Phvul.011G05PTHR23069 - | Phvul.011G05 |
| 51 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 52 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 53 | Homeobox-leucine zipper family protein / lipid-binding | Phvul.011G07PF08670 - ME | Phvul.011G07 |
| 54 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PF01657//PF0 | Phvul.008G07 |
| 55 | | 0 | 0 |
| 56 | | 0 | 0 |
| 57 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PTHR32099 - | (Phvul.008G07 |
| 58 | chloride channel F | Phvul.005G00PTHR11689:SF | Phvul.005G00 |
| 59 | serine acetyltransferase 2;2 | Phvul.008G27PTHR23416:SF | Phvul.008G27 |
| 60 | | 0 | 0 |
| 61 | | 0 | 0 |
| 62 | Mitochondrial substrate carrier family protein | Phvul.001G24K13354 - solut | Phvul.001G24 |
| 63 | transcription regulatory protein SNF2, putative | Phvul.008G06K11647 - SWI/ | Phvul.008G06 |
| 64 | peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF | Phvul.003G24K05864 - pept | Phvul.003G24 |
| 65 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.009G13PTHR10108:SF | Phvul.009G13 |
| 66 | | 0 | 0 |
| 67 | | 0 | 0 |
| 68 | K-box region and MADS-box transcription factor family | Phvul.009G13PTHR11945:SF | Phvul.009G13 |
| 69 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.011G10PTHR10108//I | Phvul.011G10 |
| 70 | cell division cycle protein 48-related / CDC48-related | Phvul.011G05PTHR23069 - | Phvul.011G05 |
| 71 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 72 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 73 | Homeobox-leucine zipper family protein / lipid-binding | Phvul.011G07PF08670 - ME | Phvul.011G07 |
| 74 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PF01657//PF0 | Phvul.008G07 |

| | | | |
|---|--|---|----------------|
| | 0 | 0 | 0 Phvul.011G11 |
| cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PTHR32099 - (Phvul.008G07 | | |
| chloride channel F | Phvul.005G00PTHR11689:SfPhvul.005G00 | | |
| serine acetyltransferase 2;2 | Phvul.008G27PTHR23416:SfPhvul.008G27 | | |
| | 0 | 0 | 0 Phvul.003G06 |
| Mitochondrial substrate carrier family protein | Phvul.001G24K13354 - solutPhvul.001G24 | | |
| transcription regulatory protein SNF2, putative | Phvul.008G06K11647 - SWI/Phvul.008G06 | | |
| peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF | Phvul.003G24K05864 - peptPhvul.003G24 | | |
| S-adenosyl-L-methionine-dependent methyltransferas | Phvul.009G13PTHR10108:SfPhvul.009G13 | | |
| | 0 | 0 | 0 Phvul.005G08 |
| K-box region and MADS-box transcription factor family | Phvul.009G13PTHR11945:SfPhvul.009G13 | | |
| S-adenosyl-L-methionine-dependent methyltransferas | Phvul.011G10PTHR10108//IPhvul.011G10 | | |
| cell division cycle protein 48-related / CDC48-related | Phvul.011G05PTHR23069 - Phvul.011G05 | | |
| gigantea protein (GI) | Phvul.007G08K12124 - GIG/Phvul.007G08 | | |
| gigantea protein (GI) | Phvul.007G08K12124 - GIG/Phvul.007G08 | | |
| Homeobox-leucine zipper family protein / lipid-binding | Phvul.011G07PF08670 - ME Phvul.011G07 | | |
| cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PF01657//PF0Phvul.008G07 | | |
| | 0 | 0 | 0 Phvul.011G11 |
| cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PTHR32099 - (Phvul.008G07 | | |
| chloride channel F | Phvul.005G00PTHR11689:SfPhvul.005G00 | | |
| serine acetyltransferase 2;2 | Phvul.008G27PTHR23416:SfPhvul.008G27 | | |
| | 0 | 0 | 0 Phvul.003G06 |
| Mitochondrial substrate carrier family protein | Phvul.001G24K13354 - solutPhvul.001G24 | | |
| transcription regulatory protein SNF2, putative | Phvul.008G06K11647 - SWI/Phvul.008G06 | | |
| peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF | Phvul.003G24K05864 - peptPhvul.003G24 | | |
| S-adenosyl-L-methionine-dependent methyltransferas | Phvul.009G13PTHR10108:SfPhvul.009G13 | | |
| | 0 | 0 | 0 Phvul.005G08 |
| K-box region and MADS-box transcription factor family | Phvul.009G13PTHR11945:SfPhvul.009G13 | | |
| S-adenosyl-L-methionine-dependent methyltransferas | Phvul.011G10PTHR10108//IPhvul.011G10 | | |
| cell division cycle protein 48-related / CDC48-related | Phvul.011G05PTHR23069 - Phvul.011G05 | | |
| gigantea protein (GI) | Phvul.007G08K12124 - GIG/Phvul.007G08 | | |
| gigantea protein (GI) | Phvul.007G08K12124 - GIG/Phvul.007G08 | | |
| Homeobox-leucine zipper family protein / lipid-binding | Phvul.011G07PF08670 - ME Phvul.011G07 | | |
| cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PF01657//PF0Phvul.008G07 | | |
| | 0 | 0 | 0 Phvul.011G11 |
| cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PTHR32099 - (Phvul.008G07 | | |
| chloride channel F | Phvul.005G00PTHR11689:SfPhvul.005G00 | | |
| serine acetyltransferase 2;2 | Phvul.008G27PTHR23416:SfPhvul.008G27 | | |
| | 0 | 0 | 0 Phvul.003G06 |
| Mitochondrial substrate carrier family protein | Phvul.001G24K13354 - solutPhvul.001G24 | | |
| transcription regulatory protein SNF2, putative | Phvul.008G06K11647 - SWI/Phvul.008G06 | | |
| peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF | Phvul.003G24K05864 - peptPhvul.003G24 | | |
| S-adenosyl-L-methionine-dependent methyltransferas | Phvul.009G13PTHR10108:SfPhvul.009G13 | | |
| | 0 | 0 | 0 Phvul.005G08 |
| K-box region and MADS-box transcription factor family | Phvul.009G13PTHR11945:SfPhvul.009G13 | | |
| S-adenosyl-L-methionine-dependent methyltransferas | Phvul.011G10PTHR10108//IPhvul.011G10 | | |

| | | | |
|----|---|----------------------------|----------------|
| 1 | | | |
| 2 | cell division cycle protein 48-related / CDC48-related | Phvul.011G05 PTHR23069 - | Phvul.011G05 |
| 3 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 4 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 5 | | | |
| 6 | Homeobox-leucine zipper family protein / lipid-binding | Phvul.011G07 PF08670 - ME | Phvul.011G07 |
| 7 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07 PF01657//PF0 | Phvul.008G07 |
| 8 | | 0 | 0 Phvul.011G11 |
| 9 | | | |
| 10 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07 PTHR32099 - (| Phvul.008G07 |
| 11 | chloride channel F | Phvul.005G00 PTHR11689:Sf | Phvul.005G00 |
| 12 | serine acetyltransferase 2;2 | Phvul.008G27 PTHR23416:Sf | Phvul.008G27 |
| 13 | | | |
| 14 | | 0 | 0 Phvul.003G06 |
| 15 | Mitochondrial substrate carrier family protein | Phvul.001G24K13354 - solut | Phvul.001G24 |
| 16 | transcription regulatory protein SNF2, putative | Phvul.008G06K11647 - SWI/ | Phvul.008G06 |
| 17 | | | |
| 18 | peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF | Phvul.003G24K05864 - pept | Phvul.003G24 |
| 19 | S-adenosyl-L-methionine-dependent methyltransferas | Phvul.009G13 PTHR10108:Sf | Phvul.009G13 |
| 20 | | 0 | 0 Phvul.005G08 |
| 21 | | | |
| 22 | K-box region and MADS-box transcription factor family | Phvul.009G13 PTHR11945:Sf | Phvul.009G13 |
| 23 | S-adenosyl-L-methionine-dependent methyltransferas | Phvul.011G10 PTHR10108//I | Phvul.011G10 |
| 24 | cell division cycle protein 48-related / CDC48-related | Phvul.011G05 PTHR23069 - | Phvul.011G05 |
| 25 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 26 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 27 | | | |
| 28 | Homeobox-leucine zipper family protein / lipid-binding | Phvul.011G07 PF08670 - ME | Phvul.011G07 |
| 29 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07 PF01657//PF0 | Phvul.008G07 |
| 30 | | 0 | 0 Phvul.011G11 |
| 31 | | | |
| 32 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07 PTHR32099 - (| Phvul.008G07 |
| 33 | chloride channel F | Phvul.005G00 PTHR11689:Sf | Phvul.005G00 |
| 34 | serine acetyltransferase 2;2 | Phvul.008G27 PTHR23416:Sf | Phvul.008G27 |
| 35 | | | |
| 36 | | 0 | 0 Phvul.003G06 |
| 37 | Mitochondrial substrate carrier family protein | Phvul.001G24K13354 - solut | Phvul.001G24 |
| 38 | transcription regulatory protein SNF2, putative | Phvul.008G06K11647 - SWI/ | Phvul.008G06 |
| 39 | | | |
| 40 | peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF | Phvul.003G24K05864 - pept | Phvul.003G24 |
| 41 | S-adenosyl-L-methionine-dependent methyltransferas | Phvul.009G13 PTHR10108:Sf | Phvul.009G13 |
| 42 | | 0 | 0 Phvul.005G08 |
| 43 | | | |
| 44 | K-box region and MADS-box transcription factor family | Phvul.009G13 PTHR11945:Sf | Phvul.009G13 |
| 45 | S-adenosyl-L-methionine-dependent methyltransferas | Phvul.011G10 PTHR10108//I | Phvul.011G10 |
| 46 | cell division cycle protein 48-related / CDC48-related | Phvul.011G05 PTHR23069 - | Phvul.011G05 |
| 47 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 48 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 49 | | | |
| 50 | Homeobox-leucine zipper family protein / lipid-binding | Phvul.011G07 PF08670 - ME | Phvul.011G07 |
| 51 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07 PF01657//PF0 | Phvul.008G07 |
| 52 | | 0 | 0 Phvul.011G11 |
| 53 | | | |
| 54 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07 PTHR32099 - (| Phvul.008G07 |
| 55 | chloride channel F | Phvul.005G00 PTHR11689:Sf | Phvul.005G00 |
| 56 | serine acetyltransferase 2;2 | Phvul.008G27 PTHR23416:Sf | Phvul.008G27 |
| 57 | | | |
| 58 | | 0 | 0 Phvul.003G06 |
| 59 | Mitochondrial substrate carrier family protein | Phvul.001G24K13354 - solut | Phvul.001G24 |
| 60 | transcription regulatory protein SNF2, putative | Phvul.008G06K11647 - SWI/ | Phvul.008G06 |

1 peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYFPhvul.003G24K05864 - peptPhvul.003G24
2 S-adenosyl-L-methionine-dependent methyltransferase Phvul.009G13 PTHR10108:SFPhvul.009G13
3
4 0 0 0 Phvul.005G08
5
6 K-box region and MADS-box transcription factor family Phvul.009G13 PTHR11945:SFPhvul.009G13
7 S-adenosyl-L-methionine-dependent methyltransferase Phvul.011G10 PTHR10108//IPhvul.011G10
8 cell division cycle protein 48-related / CDC48-related Phvul.011G05 PTHR23069 - Phvul.011G05
9 gigantea protein (GI) Phvul.007G08K12124 - GIG/Phvul.007G08
10 gigantea protein (GI) Phvul.007G08K12124 - GIG/Phvul.007G08
11 Homeobox-leucine zipper family protein / lipid-binding Phvul.011G07 PF08670 - ME Phvul.011G07
12 cysteine-rich RLK (RECEPTOR-like protein kinase) 25 Phvul.008G07 PF01657//PF0Phvul.008G07
13
14 0 0 0 Phvul.011G11
15
16 cysteine-rich RLK (RECEPTOR-like protein kinase) 25 Phvul.008G07 PTHR32099 - (Phvul.008G07
17 chloride channel F Phvul.005G00 PTHR11689:SFPhvul.005G00
18 serine acetyltransferase 2;2 Phvul.008G27 PTHR23416:SFPhvul.008G27
19
20 0 0 0 Phvul.003G06
21
22 Mitochondrial substrate carrier family protein Phvul.001G24K13354 - solutPhvul.001G24
23 transcription regulatory protein SNF2, putative Phvul.008G06K11647 - SWI/Phvul.008G06
24 peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYFPhvul.003G24K05864 - peptPhvul.003G24
25 S-adenosyl-L-methionine-dependent methyltransferase Phvul.009G13 PTHR10108:SFPhvul.009G13
26
27 0 0 0 Phvul.005G08
28
29 K-box region and MADS-box transcription factor family Phvul.009G13 PTHR11945:SFPhvul.009G13
30 S-adenosyl-L-methionine-dependent methyltransferase Phvul.011G10 PTHR10108//IPhvul.011G10
31 cell division cycle protein 48-related / CDC48-related Phvul.011G05 PTHR23069 - Phvul.011G05
32 gigantea protein (GI) Phvul.007G08K12124 - GIG/Phvul.007G08
33 gigantea protein (GI) Phvul.007G08K12124 - GIG/Phvul.007G08
34 Homeobox-leucine zipper family protein / lipid-binding Phvul.011G07 PF08670 - ME Phvul.011G07
35 cysteine-rich RLK (RECEPTOR-like protein kinase) 25 Phvul.008G07 PF01657//PF0Phvul.008G07
36
37 0 0 0 Phvul.011G11
38
39 cysteine-rich RLK (RECEPTOR-like protein kinase) 25 Phvul.008G07 PTHR32099 - (Phvul.008G07
40 chloride channel F Phvul.005G00 PTHR11689:SFPhvul.005G00
41 serine acetyltransferase 2;2 Phvul.008G27 PTHR23416:SFPhvul.008G27
42
43 0 0 0 Phvul.003G06
44
45 Mitochondrial substrate carrier family protein Phvul.001G24K13354 - solutPhvul.001G24
46 transcription regulatory protein SNF2, putative Phvul.008G06K11647 - SWI/Phvul.008G06
47 peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYFPhvul.003G24K05864 - peptPhvul.003G24
48 S-adenosyl-L-methionine-dependent methyltransferase Phvul.009G13 PTHR10108:SFPhvul.009G13
49
50 0 0 0 Phvul.005G08
51
52 K-box region and MADS-box transcription factor family Phvul.009G13 PTHR11945:SFPhvul.009G13
53 S-adenosyl-L-methionine-dependent methyltransferase Phvul.011G10 PTHR10108//IPhvul.011G10
54 cell division cycle protein 48-related / CDC48-related Phvul.011G05 PTHR23069 - Phvul.011G05
55 gigantea protein (GI) Phvul.007G08K12124 - GIG/Phvul.007G08
56 gigantea protein (GI) Phvul.007G08K12124 - GIG/Phvul.007G08
57 Homeobox-leucine zipper family protein / lipid-binding Phvul.011G07 PF08670 - ME Phvul.011G07
58 cysteine-rich RLK (RECEPTOR-like protein kinase) 25 Phvul.008G07 PF01657//PF0Phvul.008G07
59
60 0 0 0 Phvul.011G11
cysteine-rich RLK (RECEPTOR-like protein kinase) 25 Phvul.008G07 PTHR32099 - (Phvul.008G07

| | | | |
|----|---|----------------------------|----------------|
| 1 | | | |
| 2 | chloride channel F | Phvul.005G00PTHR11689:SF | Phvul.005G00 |
| 3 | serine acetyltransferase 2;2 | Phvul.008G27PTHR23416:SF | Phvul.008G27 |
| 4 | | 0 | 0 Phvul.003G06 |
| 5 | | | |
| 6 | Mitochondrial substrate carrier family protein | Phvul.001G24K13354 - solut | Phvul.001G24 |
| 7 | transcription regulatory protein SNF2, putative | Phvul.008G06K11647 - SWI/ | Phvul.008G06 |
| 8 | peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF | Phvul.003G24K05864 - pept | Phvul.003G24 |
| 9 | S-adenosyl-L-methionine-dependent methyltransferas | Phvul.009G13PTHR10108:SF | Phvul.009G13 |
| 10 | | 0 | 0 Phvul.005G08 |
| 11 | | | |
| 12 | K-box region and MADS-box transcription factor family | Phvul.009G13PTHR11945:SF | Phvul.009G13 |
| 13 | S-adenosyl-L-methionine-dependent methyltransferas | Phvul.011G10PTHR10108//I | Phvul.011G10 |
| 14 | cell division cycle protein 48-related / CDC48-related | Phvul.011G05PTHR23069 - | Phvul.011G05 |
| 15 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 16 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 17 | Homeobox-leucine zipper family protein / lipid-binding | Phvul.011G07PF08670 - ME | Phvul.011G07 |
| 18 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PF01657//PF0 | Phvul.008G07 |
| 19 | | 0 | 0 Phvul.011G11 |
| 20 | | | |
| 21 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PTHR32099 - | (Phvul.008G07 |
| 22 | chloride channel F | Phvul.005G00PTHR11689:SF | Phvul.005G00 |
| 23 | serine acetyltransferase 2;2 | Phvul.008G27PTHR23416:SF | Phvul.008G27 |
| 24 | | 0 | 0 Phvul.003G06 |
| 25 | | | |
| 26 | Mitochondrial substrate carrier family protein | Phvul.001G24K13354 - solut | Phvul.001G24 |
| 27 | transcription regulatory protein SNF2, putative | Phvul.008G06K11647 - SWI/ | Phvul.008G06 |
| 28 | peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF | Phvul.003G24K05864 - pept | Phvul.003G24 |
| 29 | S-adenosyl-L-methionine-dependent methyltransferas | Phvul.009G13PTHR10108:SF | Phvul.009G13 |
| 30 | | 0 | 0 Phvul.005G08 |
| 31 | | | |
| 32 | K-box region and MADS-box transcription factor family | Phvul.009G13PTHR11945:SF | Phvul.009G13 |
| 33 | S-adenosyl-L-methionine-dependent methyltransferas | Phvul.011G10PTHR10108//I | Phvul.011G10 |
| 34 | cell division cycle protein 48-related / CDC48-related | Phvul.011G05PTHR23069 - | Phvul.011G05 |
| 35 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 36 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 37 | Homeobox-leucine zipper family protein / lipid-binding | Phvul.011G07PF08670 - ME | Phvul.011G07 |
| 38 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PF01657//PF0 | Phvul.008G07 |
| 39 | | 0 | 0 Phvul.011G11 |
| 40 | | | |
| 41 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PTHR32099 - | (Phvul.008G07 |
| 42 | chloride channel F | Phvul.005G00PTHR11689:SF | Phvul.005G00 |
| 43 | serine acetyltransferase 2;2 | Phvul.008G27PTHR23416:SF | Phvul.008G27 |
| 44 | | 0 | 0 Phvul.003G06 |
| 45 | | | |
| 46 | Mitochondrial substrate carrier family protein | Phvul.001G24K13354 - solut | Phvul.001G24 |
| 47 | transcription regulatory protein SNF2, putative | Phvul.008G06K11647 - SWI/ | Phvul.008G06 |
| 48 | peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF | Phvul.003G24K05864 - pept | Phvul.003G24 |
| 49 | S-adenosyl-L-methionine-dependent methyltransferas | Phvul.009G13PTHR10108:SF | Phvul.009G13 |
| 50 | | 0 | 0 Phvul.005G08 |
| 51 | | | |
| 52 | K-box region and MADS-box transcription factor family | Phvul.009G13PTHR11945:SF | Phvul.009G13 |
| 53 | S-adenosyl-L-methionine-dependent methyltransferas | Phvul.011G10PTHR10108//I | Phvul.011G10 |
| 54 | cell division cycle protein 48-related / CDC48-related | Phvul.011G05PTHR23069 - | Phvul.011G05 |
| 55 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 56 | | | |
| 57 | | | |
| 58 | | | |
| 59 | | | |
| 60 | | | |

| | | | |
|----|---|----------------------------|----------------|
| 1 | | | |
| 2 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 3 | Homeobox-leucine zipper family protein / lipid-binding | Phvul.011G07PF08670 - ME | Phvul.011G07 |
| 4 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PF01657//PF0 | Phvul.008G07 |
| 5 | | | |
| 6 | | 0 | 0 Phvul.011G11 |
| 7 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PTHR32099 - (| Phvul.008G07 |
| 8 | chloride channel F | Phvul.005G00PTHR11689:Sf | Phvul.005G00 |
| 9 | | | |
| 10 | serine acetyltransferase 2;2 | Phvul.008G27PTHR23416:Sf | Phvul.008G27 |
| 11 | | 0 | 0 Phvul.003G06 |
| 12 | Mitochondrial substrate carrier family protein | Phvul.001G24K13354 - solut | Phvul.001G24 |
| 13 | transcription regulatory protein SNF2, putative | Phvul.008G06K11647 - SWI/ | Phvul.008G06 |
| 14 | peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF | Phvul.003G24K05864 - pept | Phvul.003G24 |
| 15 | S-adenosyl-L-methionine-dependent methyltransferas | Phvul.009G13PTHR10108:Sf | Phvul.009G13 |
| 16 | | | |
| 17 | | 0 | 0 Phvul.005G08 |
| 18 | | | |
| 19 | K-box region and MADS-box transcription factor family | Phvul.009G13PTHR11945:Sf | Phvul.009G13 |
| 20 | S-adenosyl-L-methionine-dependent methyltransferas | Phvul.011G10PTHR10108//I | Phvul.011G10 |
| 21 | | | |
| 22 | cell division cycle protein 48-related / CDC48-related | Phvul.011G05PTHR23069 - | Phvul.011G05 |
| 23 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 24 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 25 | Homeobox-leucine zipper family protein / lipid-binding | Phvul.011G07PF08670 - ME | Phvul.011G07 |
| 26 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PF01657//PF0 | Phvul.008G07 |
| 27 | | | |
| 28 | | 0 | 0 Phvul.011G11 |
| 29 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PTHR32099 - (| Phvul.008G07 |
| 30 | chloride channel F | Phvul.005G00PTHR11689:Sf | Phvul.005G00 |
| 31 | | | |
| 32 | serine acetyltransferase 2;2 | Phvul.008G27PTHR23416:Sf | Phvul.008G27 |
| 33 | | 0 | 0 Phvul.003G06 |
| 34 | | | |
| 35 | Mitochondrial substrate carrier family protein | Phvul.001G24K13354 - solut | Phvul.001G24 |
| 36 | transcription regulatory protein SNF2, putative | Phvul.008G06K11647 - SWI/ | Phvul.008G06 |
| 37 | peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF | Phvul.003G24K05864 - pept | Phvul.003G24 |
| 38 | S-adenosyl-L-methionine-dependent methyltransferas | Phvul.009G13PTHR10108:Sf | Phvul.009G13 |
| 39 | | | |
| 40 | | 0 | 0 Phvul.005G08 |
| 41 | | | |
| 42 | K-box region and MADS-box transcription factor family | Phvul.009G13PTHR11945:Sf | Phvul.009G13 |
| 43 | S-adenosyl-L-methionine-dependent methyltransferas | Phvul.011G10PTHR10108//I | Phvul.011G10 |
| 44 | cell division cycle protein 48-related / CDC48-related | Phvul.011G05PTHR23069 - | Phvul.011G05 |
| 45 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 46 | gigantea protein (GI) | Phvul.007G08K12124 - GIG/ | Phvul.007G08 |
| 47 | Homeobox-leucine zipper family protein / lipid-binding | Phvul.011G07PF08670 - ME | Phvul.011G07 |
| 48 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PF01657//PF0 | Phvul.008G07 |
| 49 | | | |
| 50 | | 0 | 0 Phvul.011G11 |
| 51 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07PTHR32099 - (| Phvul.008G07 |
| 52 | chloride channel F | Phvul.005G00PTHR11689:Sf | Phvul.005G00 |
| 53 | | | |
| 54 | serine acetyltransferase 2;2 | Phvul.008G27PTHR23416:Sf | Phvul.008G27 |
| 55 | | 0 | 0 Phvul.003G06 |
| 56 | | | |
| 57 | Mitochondrial substrate carrier family protein | Phvul.001G24K13354 - solut | Phvul.001G24 |
| 58 | transcription regulatory protein SNF2, putative | Phvul.008G06K11647 - SWI/ | Phvul.008G06 |
| 59 | peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF | Phvul.003G24K05864 - pept | Phvul.003G24 |
| 60 | S-adenosyl-L-methionine-dependent methyltransferas | Phvul.009G13PTHR10108:Sf | Phvul.009G13 |

| | | | | |
|----|---|--------------|----------------|----------------|
| 1 | | | | |
| 2 | | 0 | 0 | 0 Phvul.005G08 |
| 3 | K-box region and MADS-box transcription factor family | Phvul.009G13 | PTHR11945:SF | Phvul.009G13 |
| 4 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.011G10 | PTHR10108://I | Phvul.011G10 |
| 5 | cell division cycle protein 48-related / CDC48-related | Phvul.011G05 | PTHR23069 - T | Phvul.011G05 |
| 6 | gigantea protein (GI) | Phvul.007G08 | K12124 - GIG | Phvul.007G08 |
| 7 | gigantea protein (GI) | Phvul.007G08 | K12124 - GIG | Phvul.007G08 |
| 8 | Homeobox-leucine zipper family protein / lipid-binding | Phvul.011G07 | PF08670 - ME | Phvul.011G07 |
| 9 | cell division cycle protein 48-related / CDC48-related | Phvul.011G05 | PTHR23069 - T | Phvul.011G05 |
| 10 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07 | PF01657//PF0 | Phvul.008G07 |
| 11 | | 0 | 0 | 0 Phvul.011G11 |
| 12 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 | Phvul.008G07 | PTHR32099 - (| Phvul.008G07 |
| 13 | chloride channel F | Phvul.005G00 | PTHR11689:SF | Phvul.005G00 |
| 14 | nodulin MtN21 /EamA-like transporter family protein | Phvul.002G07 | KOG4510 - Pe | Phvul.002G07 |
| 15 | nodulin MtN21 /EamA-like transporter family protein | Phvul.002G07 | KOG4510 - Pe | Phvul.002G07 |
| 16 | nodulin MtN21 /EamA-like transporter family protein | Phvul.002G07 | KOG4510 - Pe | Phvul.002G07 |
| 17 | serine acetyltransferase 2;2 | Phvul.008G27 | PTHR23416:SF | Phvul.008G27 |
| 18 | | 0 | 0 | 0 Phvul.003G06 |
| 19 | Mitochondrial substrate carrier family protein | Phvul.001G24 | K13354 - solut | Phvul.001G24 |
| 20 | transcription regulatory protein SNF2, putative | Phvul.008G06 | K11647 - SWI | Phvul.008G06 |
| 21 | peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYF | Phvul.003G24 | K05864 - pept | Phvul.003G24 |
| 22 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.009G13 | PTHR10108:SF | Phvul.009G13 |
| 23 | receptor like protein 7 | Phvul.004G09 | PF00560//PF0 | Phvul.004G09 |
| 24 | AT hook motif DNA-binding family protein | Phvul.002G15 | PTHR31500:SF | Phvul.002G15 |
| 25 | Nucleotide-diphospho-sugar transferases superfamily | Phvul.009G14 | PTHR10896:SF | Phvul.009G14 |
| 26 | polyol/monosaccharide transporter 5 | Phvul.011G04 | PTHR23500:SF | Phvul.011G04 |
| 27 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G02 | PTHR22835://I | Phvul.006G02 |
| 28 | Eukaryotic aspartyl protease family protein | Phvul.006G09 | PTHR13683:SF | Phvul.006G09 |
| 29 | TIC-like | Phvul.001G15 | PTHR34798:SF | Phvul.001G15 |
| 30 | Ribosomal protein S3 family protein | Phvul.007G23 | K02985 - smal | Phvul.007G23 |
| 31 | receptor-like protein kinase 2 | Phvul.004G03 | PTHR27000:SF | Phvul.004G03 |
| 32 | receptor-like protein kinase 2 | Phvul.004G03 | PTHR27000:SF | Phvul.004G03 |
| 33 | HSP20-like chaperones superfamily protein | Phvul.007G15 | PTHR33981:SF | Phvul.007G15 |
| 34 | HSP20-like chaperones superfamily protein | Phvul.007G15 | PTHR33981:SF | Phvul.007G15 |
| 35 | aspartate/glutamate/uridylate kinase family protein | Phvul.007G10 | PTHR21499//I | Phvul.007G10 |
| 36 | O-fucosyltransferase family protein | Phvul.008G15 | PF10250 - GD | Phvul.008G15 |
| 37 | Arabidopsis thaliana protein of unknown function (DUF | Phvul.005G11 | PTHR10388:SF | Phvul.005G11 |
| 38 | growth-regulating factor 1 | Phvul.001G03 | PTHR31602:SF | Phvul.001G03 |
| 39 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 | 2.1.1.216 - tR | Phvul.004G04 |
| 40 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 | 2.1.1.216 - tR | Phvul.004G04 |
| 41 | NOD26-like intrinsic protein 5;1 | Phvul.007G08 | PTHR19139:SF | Phvul.007G08 |
| 42 | high-affinity nickel-transport family protein | Phvul.009G11 | PTHR33876:SF | Phvul.009G11 |
| 43 | WVD2-like 1 | Phvul.006G10 | PTHR31358:SF | Phvul.006G10 |
| 44 | WVD2-like 1 | Phvul.006G10 | PTHR31358:SF | Phvul.006G10 |
| 45 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 | PTHR31675:SF | Phvul.010G07 |
| 46 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 | PTHR31675:SF | Phvul.010G07 |
| 47 | | 0 | 0 | 0 Phvul.008G12 |

| | | |
|----|--|--|
| 1 | | |
| 2 | myosin, putative | Phvul.001G03 PTHR13140:SFPhvul.001G03 |
| 3 | Eukaryotic aspartyl protease family protein | Phvul.002G10 PTHR13683:SFPhvul.002G10 |
| 4 | ABI five binding protein 3 | Phvul.008G03 PTHR31413:SFPhvul.008G03 |
| 5 | Leucine-rich repeat transmembrane protein kinase | Phvul.009G24 PF00069//PF0Phvul.009G24 |
| 6 | receptor like protein 7 | Phvul.004G09 PF00560//PF0Phvul.004G09 |
| 7 | AT hook motif DNA-binding family protein | Phvul.002G15 PTHR31500:SFPhvul.002G15 |
| 8 | Nucleotide-diphospho-sugar transferases superfamily | Phvul.009G14 PTHR10896:SFPhvul.009G14 |
| 9 | polyol/monosaccharide transporter 5 | Phvul.011G04 PTHR23500:SFPhvul.011G04 |
| 10 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G02 PTHR22835//IPhvul.006G02 |
| 11 | Eukaryotic aspartyl protease family protein | Phvul.006G09 PTHR13683:SFPhvul.006G09 |
| 12 | TIC-like | Phvul.001G15 PTHR34798:SFPhvul.001G15 |
| 13 | Ribosomal protein S3 family protein | Phvul.007G23 K02985 - smalPhvul.007G23 |
| 14 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SFPhvul.004G03 |
| 15 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SFPhvul.004G03 |
| 16 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SFPhvul.007G15 |
| 17 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SFPhvul.007G15 |
| 18 | aspartate/glutamate/uridylate kinase family protein | Phvul.007G10 PTHR21499//IPhvul.007G10 |
| 19 | O-fucosyltransferase family protein | Phvul.008G15 PF10250 - GDIPhvul.008G15 |
| 20 | Arabidopsis thaliana protein of unknown function (DUF | Phvul.005G11 PTHR10388:SFPhvul.005G11 |
| 21 | growth-regulating factor 1 | Phvul.001G03 PTHR31602:SFPhvul.001G03 |
| 22 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvul.004G04 |
| 23 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvul.004G04 |
| 24 | NOD26-like intrinsic protein 5;1 | Phvul.007G08 PTHR19139:SFPhvul.007G08 |
| 25 | high-affinity nickel-transport family protein | Phvul.009G11 PTHR33876:SFPhvul.009G11 |
| 26 | WVD2-like 1 | Phvul.006G10 PTHR31358:SFPhvul.006G10 |
| 27 | WVD2-like 1 | Phvul.006G10 PTHR31358:SFPhvul.006G10 |
| 28 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 PTHR31675:SFPhvul.010G07 |
| 29 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 PTHR31675:SFPhvul.010G07 |
| 30 | | 0 0 0 Phvul.008G12 |
| 31 | myosin, putative | Phvul.001G03 PTHR13140:SFPhvul.001G03 |
| 32 | Eukaryotic aspartyl protease family protein | Phvul.002G10 PTHR13683:SFPhvul.002G10 |
| 33 | ABI five binding protein 3 | Phvul.008G03 PTHR31413:SFPhvul.008G03 |
| 34 | Leucine-rich repeat transmembrane protein kinase | Phvul.009G24 PF00069//PF0Phvul.009G24 |
| 35 | receptor like protein 7 | Phvul.004G09 PF00560//PF0Phvul.004G09 |
| 36 | AT hook motif DNA-binding family protein | Phvul.002G15 PTHR31500:SFPhvul.002G15 |
| 37 | Nucleotide-diphospho-sugar transferases superfamily | Phvul.009G14 PTHR10896:SFPhvul.009G14 |
| 38 | polyol/monosaccharide transporter 5 | Phvul.011G04 PTHR23500:SFPhvul.011G04 |
| 39 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G02 PTHR22835//IPhvul.006G02 |
| 40 | Eukaryotic aspartyl protease family protein | Phvul.006G09 PTHR13683:SFPhvul.006G09 |
| 41 | TIC-like | Phvul.001G15 PTHR34798:SFPhvul.001G15 |
| 42 | Ribosomal protein S3 family protein | Phvul.007G23 K02985 - smalPhvul.007G23 |
| 43 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SFPhvul.004G03 |
| 44 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SFPhvul.004G03 |
| 45 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SFPhvul.007G15 |
| 46 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SFPhvul.007G15 |
| 47 | aspartate/glutamate/uridylate kinase family protein | Phvul.007G10 PTHR21499//IPhvul.007G10 |

| | | |
|----|--|--|
| 1 | | |
| 2 | O-fucosyltransferase family protein | Phvul.008G15 PF10250 - GDIPhvul.008G15 |
| 3 | Arabidopsis thaliana protein of unknown function (DUFPhvul.005G11 PTHR10388:SFPhvul.005G11 | |
| 4 | growth-regulating factor 1 | Phvul.001G03 PTHR31602:SFPhvul.001G03 |
| 5 | | |
| 6 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvul.004G04 |
| 7 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvul.004G04 |
| 8 | NOD26-like intrinsic protein 5;1 | Phvul.007G08 PTHR19139:SFPhvul.007G08 |
| 9 | | |
| 10 | high-affinity nickel-transport family protein | Phvul.009G11 PTHR33876:SFPhvul.009G11 |
| 11 | WVD2-like 1 | Phvul.006G10 PTHR31358:SFPhvul.006G10 |
| 12 | WVD2-like 1 | Phvul.006G10 PTHR31358:SFPhvul.006G10 |
| 13 | | |
| 14 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 PTHR31675:SFPhvul.010G07 |
| 15 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 PTHR31675:SFPhvul.010G07 |
| 16 | | 0 0 0 Phvul.008G12 |
| 17 | | |
| 18 | myosin, putative | Phvul.001G03 PTHR13140:SFPhvul.001G03 |
| 19 | Eukaryotic aspartyl protease family protein | Phvul.002G10 PTHR13683:SFPhvul.002G10 |
| 20 | ABI five binding protein 3 | Phvul.008G03 PTHR31413:SFPhvul.008G03 |
| 21 | | |
| 22 | Leucine-rich repeat transmembrane protein kinase | Phvul.009G24 PF00069//PF0Phvul.009G24 |
| 23 | receptor like protein 7 | Phvul.004G09 PF00560//PF0Phvul.004G09 |
| 24 | AT hook motif DNA-binding family protein | Phvul.002G15 PTHR31500:SFPhvul.002G15 |
| 25 | | |
| 26 | Nucleotide-diphospho-sugar transferases superfamily r | Phvul.009G14 PTHR10896:SFPhvul.009G14 |
| 27 | polyol/monosaccharide transporter 5 | Phvul.011G04 PTHR23500:SFPhvul.011G04 |
| 28 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G02 PTHR22835//IPhvul.006G02 |
| 29 | Eukaryotic aspartyl protease family protein | Phvul.006G09 PTHR13683:SFPhvul.006G09 |
| 30 | TIC-like | Phvul.001G15 PTHR34798:SFPhvul.001G15 |
| 31 | | |
| 32 | Ribosomal protein S3 family protein | Phvul.007G23 K02985 - smalPhvul.007G23 |
| 33 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SFPhvul.004G03 |
| 34 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SFPhvul.004G03 |
| 35 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SFPhvul.007G15 |
| 36 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SFPhvul.007G15 |
| 37 | aspartate/glutamate/uridylate kinase family protein | Phvul.007G10 PTHR21499//IPhvul.007G10 |
| 38 | | |
| 39 | O-fucosyltransferase family protein | Phvul.008G15 PF10250 - GDIPhvul.008G15 |
| 40 | Arabidopsis thaliana protein of unknown function (DUFPhvul.005G11 PTHR10388:SFPhvul.005G11 | |
| 41 | growth-regulating factor 1 | Phvul.001G03 PTHR31602:SFPhvul.001G03 |
| 42 | | |
| 43 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvul.004G04 |
| 44 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvul.004G04 |
| 45 | NOD26-like intrinsic protein 5;1 | Phvul.007G08 PTHR19139:SFPhvul.007G08 |
| 46 | | |
| 47 | high-affinity nickel-transport family protein | Phvul.009G11 PTHR33876:SFPhvul.009G11 |
| 48 | WVD2-like 1 | Phvul.006G10 PTHR31358:SFPhvul.006G10 |
| 49 | WVD2-like 1 | Phvul.006G10 PTHR31358:SFPhvul.006G10 |
| 50 | | |
| 51 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 PTHR31675:SFPhvul.010G07 |
| 52 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 PTHR31675:SFPhvul.010G07 |
| 53 | | 0 0 0 Phvul.008G12 |
| 54 | | |
| 55 | myosin, putative | Phvul.001G03 PTHR13140:SFPhvul.001G03 |
| 56 | Eukaryotic aspartyl protease family protein | Phvul.002G10 PTHR13683:SFPhvul.002G10 |
| 57 | ABI five binding protein 3 | Phvul.008G03 PTHR31413:SFPhvul.008G03 |
| 58 | | |
| 59 | Leucine-rich repeat transmembrane protein kinase | Phvul.009G24 PF00069//PF0Phvul.009G24 |
| 60 | receptor like protein 7 | Phvul.004G09 PF00560//PF0Phvul.004G09 |

| | | |
|----|--|--|
| 1 | | |
| 2 | AT hook motif DNA-binding family protein | Phvul.002G15 PTHR31500:SFPhvul.002G15 |
| 3 | Nucleotide-diphospho-sugar transferases superfamily | Phvul.009G14 PTHR10896:SFPhvul.009G14 |
| 4 | polyol/monosaccharide transporter 5 | Phvul.011G04 PTHR23500:SFPhvul.011G04 |
| 5 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G02 PTHR22835//IPhvul.006G02 |
| 6 | Eukaryotic aspartyl protease family protein | Phvul.006G09 PTHR13683:SFPhvul.006G09 |
| 7 | TIC-like | Phvul.001G15 PTHR34798:SFPhvul.001G15 |
| 8 | | |
| 9 | Ribosomal protein S3 family protein | Phvul.007G23 K02985 - smalPhvul.007G23 |
| 10 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SFPhvul.004G03 |
| 11 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SFPhvul.004G03 |
| 12 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SFPhvul.007G15 |
| 13 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SFPhvul.007G15 |
| 14 | aspartate/glutamate/uridylate kinase family protein | Phvul.007G10 PTHR21499//IPhvul.007G10 |
| 15 | O-fucosyltransferase family protein | Phvul.008G15 PF10250 - GDIPhvul.008G15 |
| 16 | Arabidopsis thaliana protein of unknown function (DUF | Phvul.005G11 PTHR10388:SFPhvul.005G11 |
| 17 | growth-regulating factor 1 | Phvul.001G03 PTHR31602:SFPhvul.001G03 |
| 18 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvul.004G04 |
| 19 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvul.004G04 |
| 20 | NOD26-like intrinsic protein 5;1 | Phvul.007G08 PTHR19139:SFPhvul.007G08 |
| 21 | high-affinity nickel-transport family protein | Phvul.009G11 PTHR33876:SFPhvul.009G11 |
| 22 | WVD2-like 1 | Phvul.006G10 PTHR31358:SFPhvul.006G10 |
| 23 | WVD2-like 1 | Phvul.006G10 PTHR31358:SFPhvul.006G10 |
| 24 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 PTHR31675:SFPhvul.010G07 |
| 25 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 PTHR31675:SFPhvul.010G07 |
| 26 | | 0 0 0 Phvul.008G12 |
| 27 | myosin, putative | Phvul.001G03 PTHR13140:SFPhvul.001G03 |
| 28 | Eukaryotic aspartyl protease family protein | Phvul.002G10 PTHR13683:SFPhvul.002G10 |
| 29 | ABI five binding protein 3 | Phvul.008G03 PTHR31413:SFPhvul.008G03 |
| 30 | Leucine-rich repeat transmembrane protein kinase | Phvul.009G24 PF00069//PF0Phvul.009G24 |
| 31 | receptor like protein 7 | Phvul.004G09 PF00560//PF0Phvul.004G09 |
| 32 | AT hook motif DNA-binding family protein | Phvul.002G15 PTHR31500:SFPhvul.002G15 |
| 33 | Nucleotide-diphospho-sugar transferases superfamily | Phvul.009G14 PTHR10896:SFPhvul.009G14 |
| 34 | polyol/monosaccharide transporter 5 | Phvul.011G04 PTHR23500:SFPhvul.011G04 |
| 35 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G02 PTHR22835//IPhvul.006G02 |
| 36 | Eukaryotic aspartyl protease family protein | Phvul.006G09 PTHR13683:SFPhvul.006G09 |
| 37 | TIC-like | Phvul.001G15 PTHR34798:SFPhvul.001G15 |
| 38 | Ribosomal protein S3 family protein | Phvul.007G23 K02985 - smalPhvul.007G23 |
| 39 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SFPhvul.004G03 |
| 40 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SFPhvul.004G03 |
| 41 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SFPhvul.007G15 |
| 42 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SFPhvul.007G15 |
| 43 | aspartate/glutamate/uridylate kinase family protein | Phvul.007G10 PTHR21499//IPhvul.007G10 |
| 44 | O-fucosyltransferase family protein | Phvul.008G15 PF10250 - GDIPhvul.008G15 |
| 45 | Arabidopsis thaliana protein of unknown function (DUF | Phvul.005G11 PTHR10388:SFPhvul.005G11 |
| 46 | growth-regulating factor 1 | Phvul.001G03 PTHR31602:SFPhvul.001G03 |
| 47 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvul.004G04 |
| 48 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvul.004G04 |

| | | | | |
|----|--|---|---|--|
| 1 | | | | |
| 2 | NOD26-like intrinsic protein 5;1 | | | Phvul.007G08 PTHR19139:SfPhvul.007G08 |
| 3 | high-affinity nickel-transport family protein | | | Phvul.009G11 PTHR33876:SfPhvul.009G11 |
| 4 | WVD2-like 1 | | | Phvul.006G10 PTHR31358:SfPhvul.006G10 |
| 5 | WVD2-like 1 | | | Phvul.006G10 PTHR31358:SfPhvul.006G10 |
| 6 | WVD2-like 1 | | | Phvul.006G10 PTHR31358:SfPhvul.006G10 |
| 7 | Plant-specific transcription factor YABBY family protein | | | Phvul.010G07 PTHR31675:SfPhvul.010G07 |
| 8 | Plant-specific transcription factor YABBY family protein | | | Phvul.010G07 PTHR31675:SfPhvul.010G07 |
| 9 | | | | |
| 10 | | 0 | 0 | 0 Phvul.008G12 |
| 11 | myosin, putative | | | Phvul.001G03 PTHR13140:SfPhvul.001G03 |
| 12 | Eukaryotic aspartyl protease family protein | | | Phvul.002G10 PTHR13683:SfPhvul.002G10 |
| 13 | ABI five binding protein 3 | | | Phvul.008G03 PTHR31413:SfPhvul.008G03 |
| 14 | ABI five binding protein 3 | | | Phvul.008G03 PTHR31413:SfPhvul.008G03 |
| 15 | Leucine-rich repeat transmembrane protein kinase | | | Phvul.009G24 PF00069//PF0Phvul.009G24 |
| 16 | receptor like protein 7 | | | Phvul.004G09 PF00560//PF0Phvul.004G09 |
| 17 | receptor like protein 7 | | | Phvul.004G09 PF00560//PF0Phvul.004G09 |
| 18 | AT hook motif DNA-binding family protein | | | Phvul.002G15 PTHR31500:SfPhvul.002G15 |
| 19 | Nucleotide-diphospho-sugar transferases superfamily | | | Phvul.009G14 PTHR10896:SfPhvul.009G14 |
| 20 | polyol/monosaccharide transporter 5 | | | Phvul.011G04 PTHR23500:SfPhvul.011G04 |
| 21 | polyol/monosaccharide transporter 5 | | | Phvul.011G04 PTHR23500:SfPhvul.011G04 |
| 22 | GDSL-like Lipase/Acylhydrolase superfamily protein | | | Phvul.006G02 PTHR22835//IPhvul.006G02 |
| 23 | Eukaryotic aspartyl protease family protein | | | Phvul.006G09 PTHR13683:SfPhvul.006G09 |
| 24 | TIC-like | | | Phvul.001G15 PTHR34798:SfPhvul.001G15 |
| 25 | TIC-like | | | Phvul.001G15 PTHR34798:SfPhvul.001G15 |
| 26 | Ribosomal protein S3 family protein | | | Phvul.007G23 K02985 - smalPhvul.007G23 |
| 27 | receptor-like protein kinase 2 | | | Phvul.004G03 PTHR27000:SfPhvul.004G03 |
| 28 | receptor-like protein kinase 2 | | | Phvul.004G03 PTHR27000:SfPhvul.004G03 |
| 29 | receptor-like protein kinase 2 | | | Phvul.004G03 PTHR27000:SfPhvul.004G03 |
| 30 | HSP20-like chaperones superfamily protein | | | Phvul.007G15 PTHR33981:SfPhvul.007G15 |
| 31 | HSP20-like chaperones superfamily protein | | | Phvul.007G15 PTHR33981:SfPhvul.007G15 |
| 32 | HSP20-like chaperones superfamily protein | | | Phvul.007G15 PTHR33981:SfPhvul.007G15 |
| 33 | aspartate/glutamate/uridylate kinase family protein | | | Phvul.007G10 PTHR21499//IPhvul.007G10 |
| 34 | O-fucosyltransferase family protein | | | Phvul.008G15 PF10250 - GDIPhvul.008G15 |
| 35 | Arabidopsis thaliana protein of unknown function (DUF | | | Phvul.005G11 PTHR10388:SfPhvul.005G11 |
| 36 | growth-regulating factor 1 | | | Phvul.001G03 PTHR31602:SfPhvul.001G03 |
| 37 | growth-regulating factor 1 | | | Phvul.001G03 PTHR31602:SfPhvul.001G03 |
| 38 | N2,N2-dimethylguanosine tRNA methyltransferase | | | Phvul.004G04 2.1.1.216 - tRIPhvul.004G04 |
| 39 | N2,N2-dimethylguanosine tRNA methyltransferase | | | Phvul.004G04 2.1.1.216 - tRIPhvul.004G04 |
| 40 | N2,N2-dimethylguanosine tRNA methyltransferase | | | Phvul.004G04 2.1.1.216 - tRIPhvul.004G04 |
| 41 | NOD26-like intrinsic protein 5;1 | | | Phvul.007G08 PTHR19139:SfPhvul.007G08 |
| 42 | high-affinity nickel-transport family protein | | | Phvul.009G11 PTHR33876:SfPhvul.009G11 |
| 43 | WVD2-like 1 | | | Phvul.006G10 PTHR31358:SfPhvul.006G10 |
| 44 | WVD2-like 1 | | | Phvul.006G10 PTHR31358:SfPhvul.006G10 |
| 45 | WVD2-like 1 | | | Phvul.006G10 PTHR31358:SfPhvul.006G10 |
| 46 | Plant-specific transcription factor YABBY family protein | | | Phvul.010G07 PTHR31675:SfPhvul.010G07 |
| 47 | Plant-specific transcription factor YABBY family protein | | | Phvul.010G07 PTHR31675:SfPhvul.010G07 |
| 48 | | | | |
| 49 | | 0 | 0 | 0 Phvul.008G12 |
| 50 | myosin, putative | | | Phvul.001G03 PTHR13140:SfPhvul.001G03 |
| 51 | myosin, putative | | | Phvul.001G03 PTHR13140:SfPhvul.001G03 |
| 52 | Eukaryotic aspartyl protease family protein | | | Phvul.002G10 PTHR13683:SfPhvul.002G10 |
| 53 | Eukaryotic aspartyl protease family protein | | | Phvul.002G10 PTHR13683:SfPhvul.002G10 |
| 54 | ABI five binding protein 3 | | | Phvul.008G03 PTHR31413:SfPhvul.008G03 |
| 55 | ABI five binding protein 3 | | | Phvul.008G03 PTHR31413:SfPhvul.008G03 |
| 56 | Leucine-rich repeat transmembrane protein kinase | | | Phvul.009G24 PF00069//PF0Phvul.009G24 |
| 57 | receptor like protein 7 | | | Phvul.004G09 PF00560//PF0Phvul.004G09 |
| 58 | receptor like protein 7 | | | Phvul.004G09 PF00560//PF0Phvul.004G09 |
| 59 | AT hook motif DNA-binding family protein | | | Phvul.002G15 PTHR31500:SfPhvul.002G15 |
| 60 | AT hook motif DNA-binding family protein | | | Phvul.002G15 PTHR31500:SfPhvul.002G15 |
| 61 | Nucleotide-diphospho-sugar transferases superfamily | | | Phvul.009G14 PTHR10896:SfPhvul.009G14 |
| 62 | polyol/monosaccharide transporter 5 | | | Phvul.011G04 PTHR23500:SfPhvul.011G04 |
| 63 | polyol/monosaccharide transporter 5 | | | Phvul.011G04 PTHR23500:SfPhvul.011G04 |
| 64 | GDSL-like Lipase/Acylhydrolase superfamily protein | | | Phvul.006G02 PTHR22835//IPhvul.006G02 |
| 65 | Eukaryotic aspartyl protease family protein | | | Phvul.006G09 PTHR13683:SfPhvul.006G09 |

| | | |
|----|--|--|
| 1 | | |
| 2 | TIC-like | Phvul.001G15 PTHR34798:SfPhvul.001G15 |
| 3 | Ribosomal protein S3 family protein | Phvul.007G23 K02985 - smalPhvul.007G23 |
| 4 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SfPhvul.004G03 |
| 5 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SfPhvul.004G03 |
| 6 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SfPhvul.007G15 |
| 7 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SfPhvul.007G15 |
| 8 | aspartate/glutamate/uridylate kinase family protein | Phvul.007G10 PTHR21499//IPhvul.007G10 |
| 9 | O-fucosyltransferase family protein | Phvul.008G15 PF10250 - GDIPhvul.008G15 |
| 10 | Arabidopsis thaliana protein of unknown function (DUF | Phvul.005G11 PTHR10388:SfPhvul.005G11 |
| 11 | growth-regulating factor 1 | Phvul.001G03 PTHR31602:SfPhvul.001G03 |
| 12 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvul.004G04 |
| 13 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvul.004G04 |
| 14 | NOD26-like intrinsic protein 5;1 | Phvul.007G08 PTHR19139:SfPhvul.007G08 |
| 15 | high-affinity nickel-transport family protein | Phvul.009G11 PTHR33876:SfPhvul.009G11 |
| 16 | WVD2-like 1 | Phvul.006G10 PTHR31358:SfPhvul.006G10 |
| 17 | WVD2-like 1 | Phvul.006G10 PTHR31358:SfPhvul.006G10 |
| 18 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 PTHR31675:SfPhvul.010G07 |
| 19 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 PTHR31675:SfPhvul.010G07 |
| 20 | | 0 0 0 Phvul.008G12 |
| 21 | myosin, putative | Phvul.001G03 PTHR13140:SfPhvul.001G03 |
| 22 | Eukaryotic aspartyl protease family protein | Phvul.002G10 PTHR13683:SfPhvul.002G10 |
| 23 | ABI five binding protein 3 | Phvul.008G03 PTHR31413:SfPhvul.008G03 |
| 24 | Leucine-rich repeat transmembrane protein kinase | Phvul.009G24 PF00069//PF0Phvul.009G24 |
| 25 | receptor like protein 7 | Phvul.004G09 PF00560//PF0Phvul.004G09 |
| 26 | AT hook motif DNA-binding family protein | Phvul.002G15 PTHR31500:SfPhvul.002G15 |
| 27 | Nucleotide-diphospho-sugar transferases superfamily p | Phvul.009G14 PTHR10896:SfPhvul.009G14 |
| 28 | polyol/monosaccharide transporter 5 | Phvul.011G04 PTHR23500:SfPhvul.011G04 |
| 29 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G02 PTHR22835//IPhvul.006G02 |
| 30 | Eukaryotic aspartyl protease family protein | Phvul.006G09 PTHR13683:SfPhvul.006G09 |
| 31 | TIC-like | Phvul.001G15 PTHR34798:SfPhvul.001G15 |
| 32 | Ribosomal protein S3 family protein | Phvul.007G23 K02985 - smalPhvul.007G23 |
| 33 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SfPhvul.004G03 |
| 34 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SfPhvul.004G03 |
| 35 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SfPhvul.007G15 |
| 36 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SfPhvul.007G15 |
| 37 | aspartate/glutamate/uridylate kinase family protein | Phvul.007G10 PTHR21499//IPhvul.007G10 |
| 38 | O-fucosyltransferase family protein | Phvul.008G15 PF10250 - GDIPhvul.008G15 |
| 39 | Arabidopsis thaliana protein of unknown function (DUF | Phvul.005G11 PTHR10388:SfPhvul.005G11 |
| 40 | growth-regulating factor 1 | Phvul.001G03 PTHR31602:SfPhvul.001G03 |
| 41 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvul.004G04 |
| 42 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvul.004G04 |
| 43 | NOD26-like intrinsic protein 5;1 | Phvul.007G08 PTHR19139:SfPhvul.007G08 |
| 44 | high-affinity nickel-transport family protein | Phvul.009G11 PTHR33876:SfPhvul.009G11 |
| 45 | WVD2-like 1 | Phvul.006G10 PTHR31358:SfPhvul.006G10 |
| 46 | WVD2-like 1 | Phvul.006G10 PTHR31358:SfPhvul.006G10 |
| 47 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 PTHR31675:SfPhvul.010G07 |
| 48 | | |
| 49 | | |
| 50 | | |
| 51 | | |
| 52 | | |
| 53 | | |
| 54 | | |
| 55 | | |
| 56 | | |
| 57 | | |
| 58 | | |
| 59 | | |
| 60 | | |

| | | | | |
|----|--|--------------|----------------|----------------|
| 1 | | | | |
| 2 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 | PTHR31675:SF | Phvul.010G07 |
| 3 | | 0 | 0 | 0 Phvul.008G12 |
| 4 | myosin, putative | Phvul.001G03 | PTHR13140:SF | Phvul.001G03 |
| 5 | Eukaryotic aspartyl protease family protein | Phvul.002G10 | PTHR13683:SF | Phvul.002G10 |
| 6 | ABI five binding protein 3 | Phvul.008G03 | PTHR31413:SF | Phvul.008G03 |
| 7 | Leucine-rich repeat transmembrane protein kinase | Phvul.009G24 | PF00069//PF0 | Phvul.009G24 |
| 8 | receptor like protein 7 | Phvul.004G09 | PF00560//PF0 | Phvul.004G09 |
| 9 | AT hook motif DNA-binding family protein | Phvul.002G15 | PTHR31500:SF | Phvul.002G15 |
| 10 | Nucleotide-diphospho-sugar transferases superfamily γ | Phvul.009G14 | PTHR10896:SF | Phvul.009G14 |
| 11 | polyol/monosaccharide transporter 5 | Phvul.011G04 | PTHR23500:SF | Phvul.011G04 |
| 12 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G02 | PTHR22835//I | Phvul.006G02 |
| 13 | Eukaryotic aspartyl protease family protein | Phvul.006G09 | PTHR13683:SF | Phvul.006G09 |
| 14 | TIC-like | Phvul.001G15 | PTHR34798:SF | Phvul.001G15 |
| 15 | Ribosomal protein S3 family protein | Phvul.007G23 | K02985 - smal | Phvul.007G23 |
| 16 | receptor-like protein kinase 2 | Phvul.004G03 | PTHR27000:SF | Phvul.004G03 |
| 17 | receptor-like protein kinase 2 | Phvul.004G03 | PTHR27000:SF | Phvul.004G03 |
| 18 | HSP20-like chaperones superfamily protein | Phvul.007G15 | PTHR33981:SF | Phvul.007G15 |
| 19 | HSP20-like chaperones superfamily protein | Phvul.007G15 | PTHR33981:SF | Phvul.007G15 |
| 20 | aspartate/glutamate/uridylate kinase family protein | Phvul.007G10 | PTHR21499//I | Phvul.007G10 |
| 21 | O-fucosyltransferase family protein | Phvul.008G15 | PF10250 - GD | Phvul.008G15 |
| 22 | Arabidopsis thaliana protein of unknown function (DUF | Phvul.005G11 | PTHR10388:SF | Phvul.005G11 |
| 23 | growth-regulating factor 1 | Phvul.001G03 | PTHR31602:SF | Phvul.001G03 |
| 24 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 | 2.1.1.216 - tR | Phvul.004G04 |
| 25 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 | 2.1.1.216 - tR | Phvul.004G04 |
| 26 | NOD26-like intrinsic protein 5;1 | Phvul.007G08 | PTHR19139:SF | Phvul.007G08 |
| 27 | high-affinity nickel-transport family protein | Phvul.009G11 | PTHR33876:SF | Phvul.009G11 |
| 28 | WVD2-like 1 | Phvul.006G10 | PTHR31358:SF | Phvul.006G10 |
| 29 | WVD2-like 1 | Phvul.006G10 | PTHR31358:SF | Phvul.006G10 |
| 30 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 | PTHR31675:SF | Phvul.010G07 |
| 31 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 | PTHR31675:SF | Phvul.010G07 |
| 32 | | 0 | 0 | 0 Phvul.008G12 |
| 33 | myosin, putative | Phvul.001G03 | PTHR13140:SF | Phvul.001G03 |
| 34 | Eukaryotic aspartyl protease family protein | Phvul.002G10 | PTHR13683:SF | Phvul.002G10 |
| 35 | ABI five binding protein 3 | Phvul.008G03 | PTHR31413:SF | Phvul.008G03 |
| 36 | Leucine-rich repeat transmembrane protein kinase | Phvul.009G24 | PF00069//PF0 | Phvul.009G24 |
| 37 | receptor like protein 7 | Phvul.004G09 | PF00560//PF0 | Phvul.004G09 |
| 38 | AT hook motif DNA-binding family protein | Phvul.002G15 | PTHR31500:SF | Phvul.002G15 |
| 39 | Nucleotide-diphospho-sugar transferases superfamily γ | Phvul.009G14 | PTHR10896:SF | Phvul.009G14 |
| 40 | polyol/monosaccharide transporter 5 | Phvul.011G04 | PTHR23500:SF | Phvul.011G04 |
| 41 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G02 | PTHR22835//I | Phvul.006G02 |
| 42 | Eukaryotic aspartyl protease family protein | Phvul.006G09 | PTHR13683:SF | Phvul.006G09 |
| 43 | TIC-like | Phvul.001G15 | PTHR34798:SF | Phvul.001G15 |
| 44 | Ribosomal protein S3 family protein | Phvul.007G23 | K02985 - smal | Phvul.007G23 |
| 45 | receptor-like protein kinase 2 | Phvul.004G03 | PTHR27000:SF | Phvul.004G03 |
| 46 | receptor-like protein kinase 2 | Phvul.004G03 | PTHR27000:SF | Phvul.004G03 |
| 47 | HSP20-like chaperones superfamily protein | Phvul.007G15 | PTHR33981:SF | Phvul.007G15 |

| | | | |
|----|--|--------------|-----------------------------|
| 1 | | | |
| 2 | HSP20-like chaperones superfamily protein | Phvul.007G15 | PTHR33981:SfPhvul.007G15 |
| 3 | aspartate/glutamate/uridylate kinase family protein | Phvul.007G10 | PTHR21499//IPhvul.007G10 |
| 4 | O-fucosyltransferase family protein | Phvul.008G15 | PF10250 - GDIPhvul.008G15 |
| 5 | | | |
| 6 | Arabidopsis thaliana protein of unknown function (DUF | Phvul.005G11 | PTHR10388:SfPhvul.005G11 |
| 7 | growth-regulating factor 1 | Phvul.001G03 | PTHR31602:SfPhvul.001G03 |
| 8 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 | 2.1.1.216 - tRIPhvul.004G04 |
| 9 | | | |
| 10 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 | 2.1.1.216 - tRIPhvul.004G04 |
| 11 | NOD26-like intrinsic protein 5;1 | Phvul.007G08 | PTHR19139:SfPhvul.007G08 |
| 12 | high-affinity nickel-transport family protein | Phvul.009G11 | PTHR33876:SfPhvul.009G11 |
| 13 | | | |
| 14 | WVD2-like 1 | Phvul.006G10 | PTHR31358:SfPhvul.006G10 |
| 15 | WVD2-like 1 | Phvul.006G10 | PTHR31358:SfPhvul.006G10 |
| 16 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 | PTHR31675:SfPhvul.010G07 |
| 17 | | | |
| 18 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 | PTHR31675:SfPhvul.010G07 |
| 19 | | 0 | 0 0 Phvul.008G12 |
| 20 | | | |
| 21 | myosin, putative | Phvul.001G03 | PTHR13140:SfPhvul.001G03 |
| 22 | Eukaryotic aspartyl protease family protein | Phvul.002G10 | PTHR13683:SfPhvul.002G10 |
| 23 | ABI five binding protein 3 | Phvul.008G03 | PTHR31413:SfPhvul.008G03 |
| 24 | Leucine-rich repeat transmembrane protein kinase | Phvul.009G24 | PF00069//PF0Phvul.009G24 |
| 25 | | | |
| 26 | receptor like protein 7 | Phvul.004G09 | PF00560//PF0Phvul.004G09 |
| 27 | AT hook motif DNA-binding family protein | Phvul.002G15 | PTHR31500:SfPhvul.002G15 |
| 28 | Nucleotide-diphospho-sugar transferases superfamily | Phvul.009G14 | PTHR10896:SfPhvul.009G14 |
| 29 | | | |
| 30 | polyol/monosaccharide transporter 5 | Phvul.011G04 | PTHR23500:SfPhvul.011G04 |
| 31 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G02 | PTHR22835//IPhvul.006G02 |
| 32 | Eukaryotic aspartyl protease family protein | Phvul.006G09 | PTHR13683:SfPhvul.006G09 |
| 33 | TIC-like | Phvul.001G15 | PTHR34798:SfPhvul.001G15 |
| 34 | | | |
| 35 | Ribosomal protein S3 family protein | Phvul.007G23 | K02985 - smalPhvul.007G23 |
| 36 | receptor-like protein kinase 2 | Phvul.004G03 | PTHR27000:SfPhvul.004G03 |
| 37 | | | |
| 38 | receptor-like protein kinase 2 | Phvul.004G03 | PTHR27000:SfPhvul.004G03 |
| 39 | HSP20-like chaperones superfamily protein | Phvul.007G15 | PTHR33981:SfPhvul.007G15 |
| 40 | HSP20-like chaperones superfamily protein | Phvul.007G15 | PTHR33981:SfPhvul.007G15 |
| 41 | aspartate/glutamate/uridylate kinase family protein | Phvul.007G10 | PTHR21499//IPhvul.007G10 |
| 42 | | | |
| 43 | O-fucosyltransferase family protein | Phvul.008G15 | PF10250 - GDIPhvul.008G15 |
| 44 | Arabidopsis thaliana protein of unknown function (DUF | Phvul.005G11 | PTHR10388:SfPhvul.005G11 |
| 45 | growth-regulating factor 1 | Phvul.001G03 | PTHR31602:SfPhvul.001G03 |
| 46 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 | 2.1.1.216 - tRIPhvul.004G04 |
| 47 | | | |
| 48 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 | 2.1.1.216 - tRIPhvul.004G04 |
| 49 | NOD26-like intrinsic protein 5;1 | Phvul.007G08 | PTHR19139:SfPhvul.007G08 |
| 50 | high-affinity nickel-transport family protein | Phvul.009G11 | PTHR33876:SfPhvul.009G11 |
| 51 | | | |
| 52 | WVD2-like 1 | Phvul.006G10 | PTHR31358:SfPhvul.006G10 |
| 53 | WVD2-like 1 | Phvul.006G10 | PTHR31358:SfPhvul.006G10 |
| 54 | | | |
| 55 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 | PTHR31675:SfPhvul.010G07 |
| 56 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 | PTHR31675:SfPhvul.010G07 |
| 57 | | 0 | 0 0 Phvul.008G12 |
| 58 | | | |
| 59 | myosin, putative | Phvul.001G03 | PTHR13140:SfPhvul.001G03 |
| 60 | Eukaryotic aspartyl protease family protein | Phvul.002G10 | PTHR13683:SfPhvul.002G10 |
| | ABI five binding protein 3 | Phvul.008G03 | PTHR31413:SfPhvul.008G03 |

| | | |
|----|--|--|
| 1 | | |
| 2 | Leucine-rich repeat transmembrane protein kinase | Phvul.009G24 PF00069//PF0Phvul.009G24 |
| 3 | receptor like protein 7 | Phvul.004G09 PF00560//PF0Phvul.004G09 |
| 4 | AT hook motif DNA-binding family protein | Phvul.002G15 PTHR31500:SfPhvul.002G15 |
| 5 | Nucleotide-diphospho-sugar transferases superfamily | Phvul.009G14 PTHR10896:SfPhvul.009G14 |
| 6 | polyol/monosaccharide transporter 5 | Phvul.011G04 PTHR23500:SfPhvul.011G04 |
| 7 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G02 PTHR22835//IPhvul.006G02 |
| 8 | Eukaryotic aspartyl protease family protein | Phvul.006G09 PTHR13683:SfPhvul.006G09 |
| 9 | TIC-like | Phvul.001G15 PTHR34798:SfPhvul.001G15 |
| 10 | Ribosomal protein S3 family protein | Phvul.007G23 K02985 - smalPhvul.007G23 |
| 11 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SfPhvul.004G03 |
| 12 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SfPhvul.004G03 |
| 13 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SfPhvul.007G15 |
| 14 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SfPhvul.007G15 |
| 15 | aspartate/glutamate/uridylate kinase family protein | Phvul.007G10 PTHR21499//IPhvul.007G10 |
| 16 | O-fucosyltransferase family protein | Phvul.008G15 PF10250 - GDIPhvul.008G15 |
| 17 | Arabidopsis thaliana protein of unknown function (DUF | Phvul.005G11 PTHR10388:SfPhvul.005G11 |
| 18 | growth-regulating factor 1 | Phvul.001G03 PTHR31602:SfPhvul.001G03 |
| 19 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvul.004G04 |
| 20 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvul.004G04 |
| 21 | NOD26-like intrinsic protein 5;1 | Phvul.007G08 PTHR19139:SfPhvul.007G08 |
| 22 | high-affinity nickel-transport family protein | Phvul.009G11 PTHR33876:SfPhvul.009G11 |
| 23 | WVD2-like 1 | Phvul.006G10 PTHR31358:SfPhvul.006G10 |
| 24 | WVD2-like 1 | Phvul.006G10 PTHR31358:SfPhvul.006G10 |
| 25 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 PTHR31675:SfPhvul.010G07 |
| 26 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 PTHR31675:SfPhvul.010G07 |
| 27 | | 0 0 0 Phvul.008G12 |
| 28 | myosin, putative | Phvul.001G03 PTHR13140:SfPhvul.001G03 |
| 29 | Eukaryotic aspartyl protease family protein | Phvul.002G10 PTHR13683:SfPhvul.002G10 |
| 30 | ABI five binding protein 3 | Phvul.008G03 PTHR31413:SfPhvul.008G03 |
| 31 | Leucine-rich repeat transmembrane protein kinase | Phvul.009G24 PF00069//PF0Phvul.009G24 |
| 32 | receptor like protein 7 | Phvul.004G09 PF00560//PF0Phvul.004G09 |
| 33 | AT hook motif DNA-binding family protein | Phvul.002G15 PTHR31500:SfPhvul.002G15 |
| 34 | Nucleotide-diphospho-sugar transferases superfamily | Phvul.009G14 PTHR10896:SfPhvul.009G14 |
| 35 | polyol/monosaccharide transporter 5 | Phvul.011G04 PTHR23500:SfPhvul.011G04 |
| 36 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G02 PTHR22835//IPhvul.006G02 |
| 37 | Eukaryotic aspartyl protease family protein | Phvul.006G09 PTHR13683:SfPhvul.006G09 |
| 38 | TIC-like | Phvul.001G15 PTHR34798:SfPhvul.001G15 |
| 39 | Ribosomal protein S3 family protein | Phvul.007G23 K02985 - smalPhvul.007G23 |
| 40 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SfPhvul.004G03 |
| 41 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SfPhvul.004G03 |
| 42 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SfPhvul.007G15 |
| 43 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SfPhvul.007G15 |
| 44 | aspartate/glutamate/uridylate kinase family protein | Phvul.007G10 PTHR21499//IPhvul.007G10 |
| 45 | O-fucosyltransferase family protein | Phvul.008G15 PF10250 - GDIPhvul.008G15 |
| 46 | Arabidopsis thaliana protein of unknown function (DUF | Phvul.005G11 PTHR10388:SfPhvul.005G11 |
| 47 | growth-regulating factor 1 | Phvul.001G03 PTHR31602:SfPhvul.001G03 |

| | | | | |
|----|--|--------------|-----------|-------------------|
| 1 | | | | |
| 2 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 | 2.1.1.216 | - tRIPhvu.004G04 |
| 3 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 | 2.1.1.216 | - tRIPhvu.004G04 |
| 4 | NOD26-like intrinsic protein 5;1 | Phvul.007G08 | PTHR19139 | :SfPhvu.007G08 |
| 5 | high-affinity nickel-transport family protein | Phvul.009G11 | PTHR33876 | :SfPhvu.009G11 |
| 6 | WVD2-like 1 | Phvul.006G10 | PTHR31358 | :SfPhvu.006G10 |
| 7 | WVD2-like 1 | Phvul.006G10 | PTHR31358 | :SfPhvu.006G10 |
| 8 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 | PTHR31675 | :SfPhvu.010G07 |
| 9 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 | PTHR31675 | :SfPhvu.010G07 |
| 10 | | 0 | 0 | 0 Phvu.008G12 |
| 11 | myosin, putative | Phvul.001G03 | PTHR13140 | :SfPhvu.001G03 |
| 12 | Eukaryotic aspartyl protease family protein | Phvul.002G10 | PTHR13683 | :SfPhvu.002G10 |
| 13 | ABI five binding protein 3 | Phvul.008G03 | PTHR31413 | :SfPhvu.008G03 |
| 14 | Leucine-rich repeat transmembrane protein kinase | Phvul.009G24 | PF00069 | //PF0Phvu.009G24 |
| 15 | receptor like protein 7 | Phvul.004G09 | PF00560 | //PF0Phvu.004G09 |
| 16 | AT hook motif DNA-binding family protein | Phvul.002G15 | PTHR31500 | :SfPhvu.002G15 |
| 17 | Nucleotide-diphospho-sugar transferases superfamily γ | Phvul.009G14 | PTHR10896 | :SfPhvu.009G14 |
| 18 | polyol/monosaccharide transporter 5 | Phvul.011G04 | PTHR23500 | :SfPhvu.011G04 |
| 19 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G02 | PTHR22835 | //IPhvu.006G02 |
| 20 | Eukaryotic aspartyl protease family protein | Phvul.006G09 | PTHR13683 | :SfPhvu.006G09 |
| 21 | TIC-like | Phvul.001G15 | PTHR34798 | :SfPhvu.001G15 |
| 22 | Ribosomal protein S3 family protein | Phvul.007G23 | K02985 | - smalPhvu.007G23 |
| 23 | receptor-like protein kinase 2 | Phvul.004G03 | PTHR27000 | :SfPhvu.004G03 |
| 24 | receptor-like protein kinase 2 | Phvul.004G03 | PTHR27000 | :SfPhvu.004G03 |
| 25 | HSP20-like chaperones superfamily protein | Phvul.007G15 | PTHR33981 | :SfPhvu.007G15 |
| 26 | HSP20-like chaperones superfamily protein | Phvul.007G15 | PTHR33981 | :SfPhvu.007G15 |
| 27 | aspartate/glutamate/uridylate kinase family protein | Phvul.007G10 | PTHR21499 | //IPhvu.007G10 |
| 28 | O-fucosyltransferase family protein | Phvul.008G15 | PF10250 | - GDIPhvu.008G15 |
| 29 | Arabidopsis thaliana protein of unknown function (DUF | Phvul.005G11 | PTHR10388 | :SfPhvu.005G11 |
| 30 | growth-regulating factor 1 | Phvul.001G03 | PTHR31602 | :SfPhvu.001G03 |
| 31 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 | 2.1.1.216 | - tRIPhvu.004G04 |
| 32 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 | 2.1.1.216 | - tRIPhvu.004G04 |
| 33 | NOD26-like intrinsic protein 5;1 | Phvul.007G08 | PTHR19139 | :SfPhvu.007G08 |
| 34 | high-affinity nickel-transport family protein | Phvul.009G11 | PTHR33876 | :SfPhvu.009G11 |
| 35 | WVD2-like 1 | Phvul.006G10 | PTHR31358 | :SfPhvu.006G10 |
| 36 | WVD2-like 1 | Phvul.006G10 | PTHR31358 | :SfPhvu.006G10 |
| 37 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 | PTHR31675 | :SfPhvu.010G07 |
| 38 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 | PTHR31675 | :SfPhvu.010G07 |
| 39 | | 0 | 0 | 0 Phvu.008G12 |
| 40 | myosin, putative | Phvul.001G03 | PTHR13140 | :SfPhvu.001G03 |
| 41 | Eukaryotic aspartyl protease family protein | Phvul.002G10 | PTHR13683 | :SfPhvu.002G10 |
| 42 | ABI five binding protein 3 | Phvul.008G03 | PTHR31413 | :SfPhvu.008G03 |
| 43 | Leucine-rich repeat transmembrane protein kinase | Phvul.009G24 | PF00069 | //PF0Phvu.009G24 |
| 44 | receptor like protein 7 | Phvul.004G09 | PF00560 | //PF0Phvu.004G09 |
| 45 | AT hook motif DNA-binding family protein | Phvul.002G15 | PTHR31500 | :SfPhvu.002G15 |
| 46 | Nucleotide-diphospho-sugar transferases superfamily γ | Phvul.009G14 | PTHR10896 | :SfPhvu.009G14 |
| 47 | polyol/monosaccharide transporter 5 | Phvul.011G04 | PTHR23500 | :SfPhvu.011G04 |

| | | |
|----|--|---|
| 1 | | |
| 2 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G02 PTHR22835//IPhvu.006G02 |
| 3 | Eukaryotic aspartyl protease family protein | Phvul.006G09 PTHR13683:SfPhvu.006G09 |
| 4 | TIC-like | Phvul.001G15 PTHR34798:SfPhvu.001G15 |
| 5 | | |
| 6 | Ribosomal protein S3 family protein | Phvul.007G23 K02985 - smalPhvu.007G23 |
| 7 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SfPhvu.004G03 |
| 8 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SfPhvu.004G03 |
| 9 | | |
| 10 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SfPhvu.007G15 |
| 11 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SfPhvu.007G15 |
| 12 | aspartate/glutamate/uridylate kinase family protein | Phvul.007G10 PTHR21499//IPhvu.007G10 |
| 13 | | |
| 14 | O-fucosyltransferase family protein | Phvul.008G15 PF10250 - GDIPhvu.008G15 |
| 15 | Arabidopsis thaliana protein of unknown function (DUF | Phvul.005G11 PTHR10388:SfPhvu.005G11 |
| 16 | growth-regulating factor 1 | Phvul.001G03 PTHR31602:SfPhvu.001G03 |
| 17 | | |
| 18 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvu.004G04 |
| 19 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvu.004G04 |
| 20 | NOD26-like intrinsic protein 5;1 | Phvul.007G08 PTHR19139:SfPhvu.007G08 |
| 21 | | |
| 22 | high-affinity nickel-transport family protein | Phvul.009G11 PTHR33876:SfPhvu.009G11 |
| 23 | WVD2-like 1 | Phvul.006G10 PTHR31358:SfPhvu.006G10 |
| 24 | WVD2-like 1 | Phvul.006G10 PTHR31358:SfPhvu.006G10 |
| 25 | | |
| 26 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 PTHR31675:SfPhvu.010G07 |
| 27 | Plant-specific transcription factor YABBY family protein | Phvul.010G07 PTHR31675:SfPhvu.010G07 |
| 28 | | 0 0 0 Phvu.008G12 |
| 29 | | |
| 30 | myosin, putative | Phvul.001G03 PTHR13140:SfPhvu.001G03 |
| 31 | Eukaryotic aspartyl protease family protein | Phvul.002G10 PTHR13683:SfPhvu.002G10 |
| 32 | ABI five binding protein 3 | Phvul.008G03 PTHR31413:SfPhvu.008G03 |
| 33 | | |
| 34 | Leucine-rich repeat transmembrane protein kinase | Phvul.009G24 PF00069//PF0Phvu.009G24 |
| 35 | receptor like protein 7 | Phvul.004G09 PF00560//PF0Phvu.004G09 |
| 36 | AT hook motif DNA-binding family protein | Phvul.002G15 PTHR31500:SfPhvu.002G15 |
| 37 | | |
| 38 | Nucleotide-diphospho-sugar transferases superfamily | Phvul.009G14 PTHR10896:SfPhvu.009G14 |
| 39 | polyol/monosaccharide transporter 5 | Phvul.011G04 PTHR23500:SfPhvu.011G04 |
| 40 | GDSL-like Lipase/Acylhydrolase superfamily protein | Phvul.006G02 PTHR22835//IPhvu.006G02 |
| 41 | Eukaryotic aspartyl protease family protein | Phvul.006G09 PTHR13683:SfPhvu.006G09 |
| 42 | | |
| 43 | TIC-like | Phvul.001G15 PTHR34798:SfPhvu.001G15 |
| 44 | Ribosomal protein S3 family protein | Phvul.007G23 K02985 - smalPhvu.007G23 |
| 45 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SfPhvu.004G03 |
| 46 | receptor-like protein kinase 2 | Phvul.004G03 PTHR27000:SfPhvu.004G03 |
| 47 | | |
| 48 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SfPhvu.007G15 |
| 49 | HSP20-like chaperones superfamily protein | Phvul.007G15 PTHR33981:SfPhvu.007G15 |
| 50 | | |
| 51 | aspartate/glutamate/uridylate kinase family protein | Phvul.007G10 PTHR21499//IPhvu.007G10 |
| 52 | O-fucosyltransferase family protein | Phvul.008G15 PF10250 - GDIPhvu.008G15 |
| 53 | | |
| 54 | Arabidopsis thaliana protein of unknown function (DUF | Phvul.005G11 PTHR10388:SfPhvu.005G11 |
| 55 | growth-regulating factor 1 | Phvul.001G03 PTHR31602:SfPhvu.001G03 |
| 56 | | |
| 57 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvu.004G04 |
| 58 | N2,N2-dimethylguanosine tRNA methyltransferase | Phvul.004G04 2.1.1.216 - tRIPhvu.004G04 |
| 59 | NOD26-like intrinsic protein 5;1 | Phvul.007G08 PTHR19139:SfPhvu.007G08 |
| 60 | high-affinity nickel-transport family protein | Phvul.009G11 PTHR33876:SfPhvu.009G11 |
| | WVD2-like 1 | Phvul.006G10 PTHR31358:SfPhvu.006G10 |

| | | | | |
|----|--|---|---|---|
| 1 | | | | |
| 2 | WVD2-like 1 | | | Phvul.006G10PTHR31358:SfPhvul.006G10 |
| 3 | Plant-specific transcription factor YABBY family protein | | | Phvul.010G07PTHR31675:SfPhvul.010G07 |
| 4 | Plant-specific transcription factor YABBY family protein | | | Phvul.010G07PTHR31675:SfPhvul.010G07 |
| 5 | | | | |
| 6 | | 0 | 0 | 0 Phvul.008G12 |
| 7 | myosin, putative | | | Phvul.001G03PTHR13140:SfPhvul.001G03 |
| 8 | Eukaryotic aspartyl protease family protein | | | Phvul.002G10PTHR13683:SfPhvul.002G10 |
| 9 | ABI five binding protein 3 | | | Phvul.008G03PTHR31413:SfPhvul.008G03 |
| 10 | Leucine-rich repeat transmembrane protein kinase | | | Phvul.009G24PF00069//PF0Phvul.009G24 |
| 11 | aspartate/glutamate/uridylate kinase family protein | | | Phvul.007G10PTHR21499//IPhvul.007G10 |
| 12 | polyol/monosaccharide transporter 5 | | | Phvul.011G04PTHR23500:SfPhvul.011G04 |
| 13 | WVD2-like 1 | | | Phvul.006G10PTHR31358:SfPhvul.006G10 |
| 14 | WVD2-like 1 | | | Phvul.006G10PTHR31358:SfPhvul.006G10 |
| 15 | GDSL-like Lipase/Acylhydrolase superfamily protein | | | Phvul.006G02PTHR22835//IPhvul.006G02 |
| 16 | receptor like protein 7 | | | Phvul.004G09PF00560//PF0Phvul.004G09 |
| 17 | AT hook motif DNA-binding family protein | | | Phvul.002G15PTHR31500:SfPhvul.002G15 |
| 18 | Nucleotide-diphospho-sugar transferases superfamily p | | | Phvul.009G14PTHR10896:SfPhvul.009G14 |
| 19 | Eukaryotic aspartyl protease family protein | | | Phvul.006G09PTHR13683:SfPhvul.006G09 |
| 20 | TIC-like | | | Phvul.001G15PTHR34798:SfPhvul.001G15 |
| 21 | Leucine-rich repeat transmembrane protein kinase | | | Phvul.009G24PF00069//PF0Phvul.009G24 |
| 22 | phosphatidylinositol-4-phosphate 5-kinase 2 | | | Phvul.009G12PTHR23086:SfPhvul.009G12 |
| 23 | phosphatidylinositol-4-phosphate 5-kinase 2 | | | Phvul.009G12PTHR23086:SfPhvul.009G12 |
| 24 | HSP20-like chaperones superfamily protein | | | Phvul.007G15PTHR33981:SfPhvul.007G15 |
| 25 | HSP20-like chaperones superfamily protein | | | Phvul.007G15PTHR33981:SfPhvul.007G15 |
| 26 | O-fucosyltransferase family protein | | | Phvul.008G15PF10250 - GDIPhvul.008G15 |
| 27 | Ribosomal protein S3 family protein | | | Phvul.007G23K02985 - smalPhvul.007G23 |
| 28 | receptor-like protein kinase 2 | | | Phvul.004G03PTHR27000:SfPhvul.004G03 |
| 29 | receptor-like protein kinase 2 | | | Phvul.004G03PTHR27000:SfPhvul.004G03 |
| 30 | Arabidopsis thaliana protein of unknown function (DUF | | | Phvul.005G11PTHR10388:SfPhvul.005G11 |
| 31 | growth-regulating factor 1 | | | Phvul.001G03PTHR31602:SfPhvul.001G03 |
| 32 | N2,N2-dimethylguanosine tRNA methyltransferase | | | Phvul.004G042.1.1.216 - tRIPhvul.004G04 |
| 33 | N2,N2-dimethylguanosine tRNA methyltransferase | | | Phvul.004G042.1.1.216 - tRIPhvul.004G04 |
| 34 | Eukaryotic aspartyl protease family protein | | | Phvul.002G10PTHR13683:SfPhvul.002G10 |
| 35 | NOD26-like intrinsic protein 5;1 | | | Phvul.007G08PTHR19139:SfPhvul.007G08 |
| 36 | high-affinity nickel-transport family protein | | | Phvul.009G11PTHR33876:SfPhvul.009G11 |
| 37 | Plant-specific transcription factor YABBY family protein | | | Phvul.010G07PTHR31675:SfPhvul.010G07 |
| 38 | Plant-specific transcription factor YABBY family protein | | | Phvul.010G07PTHR31675:SfPhvul.010G07 |
| 39 | | 0 | 0 | 0 Phvul.008G12 |
| 40 | leucine-rich repeat transmembrane protein kinase fam | | | Phvul.007G02PF00560//PF0Phvul.007G02 |
| 41 | fatty acid desaturase 5 | | | Phvul.010G15K00507 - steaIPhvul.010G15 |
| 42 | Protein of unknown function (DUF630 and DUF632) | | | Phvul.009G21PF04782 - ProPhvul.009G21 |
| 43 | Integrase-type DNA-binding superfamily protein | | | Phvul.008G04PF00847 - AP2Phvul.008G04 |
| 44 | | 0 | | 0 Phvul.009G07K17968 - TRIAPhvul.009G07 |
| 45 | embryo defective 2735 | | 0 | 0 Phvul.001G19 |
| 46 | embryo defective 2735 | | 0 | 0 Phvul.001G19 |
| 47 | Pentatricopeptide repeat (PPR) superfamily protein | | | Phvul.003G15PF01535//PF1Phvul.003G15 |
| 48 | S-adenosyl-L-methionine-dependent methyltransferase | | | Phvul.009G03PTHR10108//IPhvul.009G03 |

| | | | |
|----|---|---|---|
| 1 | | | |
| 2 | thioredoxin-dependent peroxidase 1 | | Phvul.004G16PTHR10430 - IPhvul.004G16 |
| 3 | Protein prenyltransferase superfamily protein | | Phvul.009G16PF13414 - TPRPhvul.009G16 |
| 4 | Uncharacterised conserved protein UCP015417, vWA | | Phvul.002G11PTHR31373:SfPhvul.002G11 |
| 5 | alanine-2-oxoglutarate aminotransferase 2 | | Phvul.002G152.6.1.4 - GlyciPhvul.002G15 |
| 6 | chloroplastic NIFS-like cysteine desulfurase | | Phvul.002G274.4.1.16 - SelePhvul.002G27 |
| 7 | SecY protein transport family protein | | Phvul.011G16K10956 - protPhvul.011G16 |
| 8 | NDH-dependent cyclic electron flow 1 | | Phvul.001G11PTHR11122:SfPhvul.001G11 |
| 9 | rubredoxin family protein | | Phvul.002G03PTHR17130 - IPhvul.002G03 |
| 10 | Protein kinase superfamily protein | | Phvul.002G012.7.11.1 - NonPhvul.002G01 |
| 11 | Protein kinase superfamily protein | | Phvul.002G012.7.11.1 - NonPhvul.002G01 |
| 12 | ferredoxin 3 | | Phvul.007G02PTHR19370:SfPhvul.007G02 |
| 13 | transducin family protein / WD-40 repeat family protei | | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 14 | transducin family protein / WD-40 repeat family protei | | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 15 | REF4-related 1 | | Phvul.006G15PTHR33739:SfPhvul.006G15 |
| 16 | Alpha amylase family protein | | Phvul.006G04PTHR10357:SfPhvul.006G04 |
| 17 | cellulose synthase like G1 | | Phvul.005G00PTHR13301//IPhvul.005G00 |
| 18 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 19 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 20 | dihydrosphingosine phosphate lyase | | Phvul.008G014.1.2.27 - SphiPhvul.008G01 |
| 21 | dihydrosphingosine phosphate lyase | | Phvul.008G014.1.2.27 - SphiPhvul.008G01 |
| 22 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 23 | cytochrome P450, family 76, subfamily C, polypeptide 4 | | Phvul.007G101.14.13.152 - Phvul.007G10 |
| 24 | purine permease 1 | | Phvul.009G03PTHR31376:SfPhvul.009G03 |
| 25 | | 0 | 0 Phvul.L00244 |
| 26 | | 0 | 0 Phvul.L00244 |
| 27 | vacuolar iron transporter 1 | | Phvul.008G07KOG4473 - UnPhvul.008G07 |
| 28 | fatty acid desaturase 5 | | Phvul.010G15K00507 - steaiPhvul.010G15 |
| 29 | Protein of unknown function (DUF630 and DUF632) | | Phvul.009G21PF04782 - ProPhvul.009G21 |
| 30 | Integrase-type DNA-binding superfamily protein | | Phvul.008G04PF00847 - AP2Phvul.008G04 |
| 31 | | 0 | Phvul.009G07K17968 - TRIAPhvul.009G07 |
| 32 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 33 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 34 | Pentatricopeptide repeat (PPR) superfamily protein | | Phvul.003G15PF01535//PF1Phvul.003G15 |
| 35 | S-adenosyl-L-methionine-dependent methyltransferase | | Phvul.009G03PTHR10108//IPhvul.009G03 |
| 36 | thioredoxin-dependent peroxidase 1 | | Phvul.004G16PTHR10430 - IPhvul.004G16 |
| 37 | Protein prenyltransferase superfamily protein | | Phvul.009G16PF13414 - TPRPhvul.009G16 |
| 38 | Uncharacterised conserved protein UCP015417, vWA | | Phvul.002G11PTHR31373:SfPhvul.002G11 |
| 39 | alanine-2-oxoglutarate aminotransferase 2 | | Phvul.002G152.6.1.4 - GlyciPhvul.002G15 |
| 40 | chloroplastic NIFS-like cysteine desulfurase | | Phvul.002G274.4.1.16 - SelePhvul.002G27 |
| 41 | SecY protein transport family protein | | Phvul.011G16K10956 - protPhvul.011G16 |
| 42 | NDH-dependent cyclic electron flow 1 | | Phvul.001G11PTHR11122:SfPhvul.001G11 |
| 43 | rubredoxin family protein | | Phvul.002G03PTHR17130 - IPhvul.002G03 |
| 44 | Protein kinase superfamily protein | | Phvul.002G012.7.11.1 - NonPhvul.002G01 |
| 45 | Protein kinase superfamily protein | | Phvul.002G012.7.11.1 - NonPhvul.002G01 |
| 46 | ferredoxin 3 | | Phvul.007G02PTHR19370:SfPhvul.007G02 |
| 47 | transducin family protein / WD-40 repeat family protei | | Phvul.010G11PTHR13950 - IPhvul.010G11 |

| | | |
|----|---|---|
| 1 | transducin family protein / WD-40 repeat family protei | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 2 | REF4-related 1 | Phvul.006G15PTHR33739:SfPhvul.006G15 |
| 3 | Alpha amylase family protein | Phvul.006G04PTHR10357:SfPhvul.006G04 |
| 4 | cellulose synthase like G1 | Phvul.005G00PTHR13301//IPhvul.005G00 |
| 5 | negative regulator of systemic acquired resistance (SNI | 0 0 Phvul.003G05 |
| 6 | negative regulator of systemic acquired resistance (SNI | 0 0 Phvul.003G05 |
| 7 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - SphiPhvul.008G01 |
| 8 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - SphiPhvul.008G01 |
| 9 | negative regulator of systemic acquired resistance (SNI | 0 0 Phvul.003G05 |
| 10 | cytochrome P450, family 76, subfamily C, polypeptide 4 | Phvul.007G101.14.13.152 - IPhvul.007G10 |
| 11 | purine permease 1 | Phvul.009G03PTHR31376:SfPhvul.009G03 |
| 12 | | 0 0 Phvul.L00244 |
| 13 | | 0 0 Phvul.L00244 |
| 14 | vacuolar iron transporter 1 | Phvul.008G07KOG4473 - UnPhvul.008G07 |
| 15 | fatty acid desaturase 5 | Phvul.010G15K00507 - steaiPhvul.010G15 |
| 16 | Protein of unknown function (DUF630 and DUF632) | Phvul.009G21PF04782 - ProPhvul.009G21 |
| 17 | Integrase-type DNA-binding superfamily protein | Phvul.008G04PF00847 - AP2Phvul.008G04 |
| 18 | | 0 Phvul.009G07K17968 - TRIAPhvul.009G07 |
| 19 | embryo defective 2735 | 0 0 Phvul.001G19 |
| 20 | embryo defective 2735 | 0 0 Phvul.001G19 |
| 21 | Pentatricopeptide repeat (PPR) superfamily protein | Phvul.003G15PF01535//PF1Phvul.003G15 |
| 22 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.009G03PTHR10108//IPhvul.009G03 |
| 23 | thioredoxin-dependent peroxidase 1 | Phvul.004G16PTHR10430 - IPhvul.004G16 |
| 24 | Protein prenyltransferase superfamily protein | Phvul.009G16PF13414 - TPRPhvul.009G16 |
| 25 | Uncharacterised conserved protein UCP015417, vWA | Phvul.002G11PTHR31373:SfPhvul.002G11 |
| 26 | alanine-2-oxoglutarate aminotransferase 2 | Phvul.002G152.6.1.4 - GlyciPhvul.002G15 |
| 27 | chloroplastic NIFS-like cysteine desulfurase | Phvul.002G274.4.1.16 - SelePhvul.002G27 |
| 28 | SecY protein transport family protein | Phvul.011G16K10956 - protPhvul.011G16 |
| 29 | NDH-dependent cyclic electron flow 1 | Phvul.001G11PTHR11122:SfPhvul.001G11 |
| 30 | rubredoxin family protein | Phvul.002G03PTHR17130 - IPhvul.002G03 |
| 31 | Protein kinase superfamily protein | Phvul.002G012.7.11.1 - NonPhvul.002G01 |
| 32 | Protein kinase superfamily protein | Phvul.002G012.7.11.1 - NonPhvul.002G01 |
| 33 | ferredoxin 3 | Phvul.007G02PTHR19370:SfPhvul.007G02 |
| 34 | transducin family protein / WD-40 repeat family protei | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 35 | transducin family protein / WD-40 repeat family protei | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 36 | REF4-related 1 | Phvul.006G15PTHR33739:SfPhvul.006G15 |
| 37 | Alpha amylase family protein | Phvul.006G04PTHR10357:SfPhvul.006G04 |
| 38 | cellulose synthase like G1 | Phvul.005G00PTHR13301//IPhvul.005G00 |
| 39 | negative regulator of systemic acquired resistance (SNI | 0 0 Phvul.003G05 |
| 40 | negative regulator of systemic acquired resistance (SNI | 0 0 Phvul.003G05 |
| 41 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - SphiPhvul.008G01 |
| 42 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - SphiPhvul.008G01 |
| 43 | negative regulator of systemic acquired resistance (SNI | 0 0 Phvul.003G05 |
| 44 | cytochrome P450, family 76, subfamily C, polypeptide 4 | Phvul.007G101.14.13.152 - IPhvul.007G10 |
| 45 | purine permease 1 | Phvul.009G03PTHR31376:SfPhvul.009G03 |
| 46 | | 0 0 Phvul.L00244 |

| | | | |
|----|---|--|----------------|
| 1 | | | |
| 2 | | 0 | 0 |
| 3 | | | 0 Phvul.L00244 |
| 4 | vacuolar iron transporter 1 | Phvul.008G07KOG4473 - UnPhvul.008G07 | |
| 5 | fatty acid desaturase 5 | Phvul.010G15K00507 - steaPhvul.010G15 | |
| 6 | Protein of unknown function (DUF630 and DUF632) | Phvul.009G21PF04782 - ProPhvul.009G21 | |
| 7 | Integrase-type DNA-binding superfamily protein | Phvul.008G04PF00847 - AP ₂ Phvul.008G04 | |
| 8 | | 0 Phvul.009G07K17968 - TRIA | Phvul.009G07 |
| 9 | | | |
| 10 | embryo defective 2735 | | 0 Phvul.001G19 |
| 11 | embryo defective 2735 | | 0 Phvul.001G19 |
| 12 | Pentatricopeptide repeat (PPR) superfamily protein | Phvul.003G15PF01535//PF1 | Phvul.003G15 |
| 13 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.009G03PTHR10108//I | Phvul.009G03 |
| 14 | thioredoxin-dependent peroxidase 1 | Phvul.004G16PTHR10430 - I | Phvul.004G16 |
| 15 | Protein prenyltransferase superfamily protein | Phvul.009G16PF13414 - TPR | Phvul.009G16 |
| 16 | Uncharacterised conserved protein UCP015417, vWA | Phvul.002G11PTHR31373:Sf | Phvul.002G11 |
| 17 | alanine-2-oxoglutarate aminotransferase 2 | Phvul.002G152.6.1.4 - Glyci | Phvul.002G15 |
| 18 | chloroplastic NIFS-like cysteine desulfurase | Phvul.002G274.4.1.16 - Sele | Phvul.002G27 |
| 19 | SecY protein transport family protein | Phvul.011G16K10956 - prot | Phvul.011G16 |
| 20 | NDH-dependent cyclic electron flow 1 | Phvul.001G11PTHR11122:Sf | Phvul.001G11 |
| 21 | rubredoxin family protein | Phvul.002G03PTHR17130 - I | Phvul.002G03 |
| 22 | Protein kinase superfamily protein | Phvul.002G012.7.11.1 - Non | Phvul.002G01 |
| 23 | Protein kinase superfamily protein | Phvul.002G012.7.11.1 - Non | Phvul.002G01 |
| 24 | ferredoxin 3 | Phvul.007G02PTHR19370:Sf | Phvul.007G02 |
| 25 | transducin family protein / WD-40 repeat family protei | Phvul.010G11PTHR13950 - I | Phvul.010G11 |
| 26 | transducin family protein / WD-40 repeat family protei | Phvul.010G11PTHR13950 - I | Phvul.010G11 |
| 27 | REF4-related 1 | Phvul.006G15PTHR33739:Sf | Phvul.006G15 |
| 28 | Alpha amylase family protein | Phvul.006G04PTHR10357:Sf | Phvul.006G04 |
| 29 | cellulose synthase like G1 | Phvul.005G00PTHR13301//I | Phvul.005G00 |
| 30 | negative regulator of systemic acquired resistance (SNI | | 0 Phvul.003G05 |
| 31 | negative regulator of systemic acquired resistance (SNI | | 0 Phvul.003G05 |
| 32 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - Sphi | Phvul.008G01 |
| 33 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - Sphi | Phvul.008G01 |
| 34 | negative regulator of systemic acquired resistance (SNI | | 0 Phvul.003G05 |
| 35 | cytochrome P450, family 76, subfamily C, polypeptide | Phvul.007G101.14.13.152 - | Phvul.007G10 |
| 36 | purine permease 1 | Phvul.009G03PTHR31376:Sf | Phvul.009G03 |
| 37 | | 0 | 0 Phvul.L00244 |
| 38 | | 0 | 0 Phvul.L00244 |
| 39 | | | |
| 40 | vacuolar iron transporter 1 | Phvul.008G07KOG4473 - UnPhvul.008G07 | |
| 41 | fatty acid desaturase 5 | Phvul.010G15K00507 - steaPhvul.010G15 | |
| 42 | Protein of unknown function (DUF630 and DUF632) | Phvul.009G21PF04782 - ProPhvul.009G21 | |
| 43 | Integrase-type DNA-binding superfamily protein | Phvul.008G04PF00847 - AP ₂ Phvul.008G04 | |
| 44 | | 0 Phvul.009G07K17968 - TRIA | Phvul.009G07 |
| 45 | | | |
| 46 | embryo defective 2735 | | 0 Phvul.001G19 |
| 47 | embryo defective 2735 | | 0 Phvul.001G19 |
| 48 | Pentatricopeptide repeat (PPR) superfamily protein | Phvul.003G15PF01535//PF1 | Phvul.003G15 |
| 49 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.009G03PTHR10108//I | Phvul.009G03 |
| 50 | thioredoxin-dependent peroxidase 1 | Phvul.004G16PTHR10430 - I | Phvul.004G16 |
| 51 | Protein prenyltransferase superfamily protein | Phvul.009G16PF13414 - TPR | Phvul.009G16 |

| | | | | |
|----|---|-----------------------------|--------------|---------------------------|
| 1 | | | | |
| 2 | Uncharacterised conserved protein UCP015417, vWA | Phvul.002G11PTHR31373:SF | Phvul.002G11 | |
| 3 | alanine-2-oxoglutarate aminotransferase 2 | Phvul.002G152.6.1.4 - Glyci | Phvul.002G15 | |
| 4 | chloroplasmic NIFS-like cysteine desulfurase | Phvul.002G274.4.1.16 - Sele | Phvul.002G27 | |
| 5 | SecY protein transport family protein | Phvul.011G16K10956 - prot | Phvul.011G16 | |
| 6 | NDH-dependent cyclic electron flow 1 | Phvul.001G11PTHR11122:SF | Phvul.001G11 | |
| 7 | rubredoxin family protein | Phvul.002G03PTHR17130 - I | Phvul.002G03 | |
| 8 | Protein kinase superfamily protein | Phvul.002G012.7.11.1 - Non | Phvul.002G01 | |
| 9 | Protein kinase superfamily protein | Phvul.002G012.7.11.1 - Non | Phvul.002G01 | |
| 10 | ferredoxin 3 | Phvul.007G02PTHR19370:SF | Phvul.007G02 | |
| 11 | transducin family protein / WD-40 repeat family protei | Phvul.010G11PTHR13950 - I | Phvul.010G11 | |
| 12 | transducin family protein / WD-40 repeat family protei | Phvul.010G11PTHR13950 - I | Phvul.010G11 | |
| 13 | REF4-related 1 | Phvul.006G15PTHR33739:SF | Phvul.006G15 | |
| 14 | Alpha amylase family protein | Phvul.006G04PTHR10357:SF | Phvul.006G04 | |
| 15 | cellulose synthase like G1 | Phvul.005G00PTHR13301//I | Phvul.005G00 | |
| 16 | negative regulator of systemic acquired resistance (SNI | 0 | 0 | Phvul.003G05 |
| 17 | negative regulator of systemic acquired resistance (SNI | 0 | 0 | Phvul.003G05 |
| 18 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - Sph | Phvul.008G01 | |
| 19 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - Sph | Phvul.008G01 | |
| 20 | negative regulator of systemic acquired resistance (SNI | 0 | 0 | Phvul.003G05 |
| 21 | cytochrome P450, family 76, subfamily C, polypeptide 4 | Phvul.007G101.14.13.152 - | Phvul.007G10 | |
| 22 | purine permease 1 | Phvul.009G03PTHR31376:SF | Phvul.009G03 | |
| 23 | | 0 | 0 | Phvul.L00244 |
| 24 | | 0 | 0 | Phvul.L00244 |
| 25 | vacuolar iron transporter 1 | Phvul.008G07KOG4473 - Un | Phvul.008G07 | |
| 26 | fatty acid desaturase 5 | Phvul.010G15K00507 - stea | Phvul.010G15 | |
| 27 | Protein of unknown function (DUF630 and DUF632) | Phvul.009G21PF04782 - Pro | Phvul.009G21 | |
| 28 | Integrase-type DNA-binding superfamily protein | Phvul.008G04PF00847 - AP | Phvul.008G04 | |
| 29 | | 0 | 0 | Phvul.009G07K17968 - TRIA |
| 30 | embryo defective 2735 | 0 | 0 | Phvul.001G19 |
| 31 | embryo defective 2735 | 0 | 0 | Phvul.001G19 |
| 32 | Pentatricopeptide repeat (PPR) superfamily protein | Phvul.003G15PF01535//PF1 | Phvul.003G15 | |
| 33 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.009G03PTHR10108//I | Phvul.009G03 | |
| 34 | thioredoxin-dependent peroxidase 1 | Phvul.004G16PTHR10430 - I | Phvul.004G16 | |
| 35 | Protein prenyltransferase superfamily protein | Phvul.009G16PF13414 - TPR | Phvul.009G16 | |
| 36 | Uncharacterised conserved protein UCP015417, vWA | Phvul.002G11PTHR31373:SF | Phvul.002G11 | |
| 37 | alanine-2-oxoglutarate aminotransferase 2 | Phvul.002G152.6.1.4 - Glyci | Phvul.002G15 | |
| 38 | chloroplasmic NIFS-like cysteine desulfurase | Phvul.002G274.4.1.16 - Sele | Phvul.002G27 | |
| 39 | SecY protein transport family protein | Phvul.011G16K10956 - prot | Phvul.011G16 | |
| 40 | NDH-dependent cyclic electron flow 1 | Phvul.001G11PTHR11122:SF | Phvul.001G11 | |
| 41 | rubredoxin family protein | Phvul.002G03PTHR17130 - I | Phvul.002G03 | |
| 42 | Protein kinase superfamily protein | Phvul.002G012.7.11.1 - Non | Phvul.002G01 | |
| 43 | Protein kinase superfamily protein | Phvul.002G012.7.11.1 - Non | Phvul.002G01 | |
| 44 | ferredoxin 3 | Phvul.007G02PTHR19370:SF | Phvul.007G02 | |
| 45 | transducin family protein / WD-40 repeat family protei | Phvul.010G11PTHR13950 - I | Phvul.010G11 | |
| 46 | transducin family protein / WD-40 repeat family protei | Phvul.010G11PTHR13950 - I | Phvul.010G11 | |
| 47 | REF4-related 1 | Phvul.006G15PTHR33739:SF | Phvul.006G15 | |

| | | | |
|----|---|---|--|
| 1 | | | |
| 2 | Alpha amylase family protein | | Phvul.006G04PTHR10357:SFPhvul.006G04 |
| 3 | cellulose synthase like G1 | | Phvul.005G00PTHR13301//IPhvul.005G00 |
| 4 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 5 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 6 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 7 | dihydrosphingosine phosphate lyase | | Phvul.008G014.1.2.27 - SphiPhvul.008G01 |
| 8 | dihydrosphingosine phosphate lyase | | Phvul.008G014.1.2.27 - SphiPhvul.008G01 |
| 9 | dihydrosphingosine phosphate lyase | | Phvul.008G014.1.2.27 - SphiPhvul.008G01 |
| 10 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 11 | cytochrome P450, family 76, subfamily C, polypeptide 4 | | Phvul.007G101.14.13.152 - IPhvul.007G10 |
| 12 | cytochrome P450, family 76, subfamily C, polypeptide 4 | | Phvul.007G101.14.13.152 - IPhvul.007G10 |
| 13 | purine permease 1 | | Phvul.009G03PTHR31376:SFPhvul.009G03 |
| 14 | | 0 | 0 Phvul.L002444 |
| 15 | | 0 | 0 Phvul.L002444 |
| 16 | vacuolar iron transporter 1 | | Phvul.008G07KOG4473 - UnPhvul.008G07 |
| 17 | vacuolar iron transporter 1 | | Phvul.008G07KOG4473 - UnPhvul.008G07 |
| 18 | fatty acid desaturase 5 | | Phvul.010G15K00507 - steaIPhvul.010G15 |
| 19 | Protein of unknown function (DUF630 and DUF632) | | Phvul.009G21PF04782 - ProPhvul.009G21 |
| 20 | Integrase-type DNA-binding superfamily protein | | Phvul.008G04PF00847 - AP2Phvul.008G04 |
| 21 | Integrase-type DNA-binding superfamily protein | | Phvul.008G04PF00847 - AP2Phvul.008G04 |
| 22 | Integrase-type DNA-binding superfamily protein | 0 | Phvul.009G07K17968 - TRIAPhvul.009G07 |
| 23 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 24 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 25 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 26 | Pentatricopeptide repeat (PPR) superfamily protein | | Phvul.003G15PF01535//PF1Phvul.003G15 |
| 27 | S-adenosyl-L-methionine-dependent methyltransferase 6 | | Phvul.009G03PTHR10108//IPhvul.009G03 |
| 28 | thioredoxin-dependent peroxidase 1 | | Phvul.004G16PTHR10430 - IPhvul.004G16 |
| 29 | thioredoxin-dependent peroxidase 1 | | Phvul.004G16PTHR10430 - IPhvul.004G16 |
| 30 | Protein prenyltransferase superfamily protein | | Phvul.009G16PF13414 - TPRPhvul.009G16 |
| 31 | Uncharacterised conserved protein UCP015417, vWA | | Phvul.002G11PTHR31373:SFPhvul.002G11 |
| 32 | alanine-2-oxoglutarate aminotransferase 2 | | Phvul.002G152.6.1.4 - GlyciIPhvul.002G15 |
| 33 | alanine-2-oxoglutarate aminotransferase 2 | | Phvul.002G152.6.1.4 - GlyciIPhvul.002G15 |
| 34 | chloroplastic NIFS-like cysteine desulfurase | | Phvul.002G274.4.1.16 - SelePhvul.002G27 |
| 35 | SecY protein transport family protein | | Phvul.011G16K10956 - protIPhvul.011G16 |
| 36 | NDH-dependent cyclic electron flow 1 | | Phvul.001G11PTHR11122:SFPhvul.001G11 |
| 37 | rubredoxin family protein | | Phvul.002G03PTHR17130 - IPhvul.002G03 |
| 38 | rubredoxin family protein | | Phvul.002G03PTHR17130 - IPhvul.002G03 |
| 39 | Protein kinase superfamily protein | | Phvul.002G012.7.11.1 - NonPhvul.002G01 |
| 40 | Protein kinase superfamily protein | | Phvul.002G012.7.11.1 - NonPhvul.002G01 |
| 41 | Protein kinase superfamily protein | | Phvul.002G012.7.11.1 - NonPhvul.002G01 |
| 42 | ferredoxin 3 | | Phvul.007G02PTHR19370:SFPhvul.007G02 |
| 43 | transducin family protein / WD-40 repeat family protei | | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 44 | transducin family protein / WD-40 repeat family protei | | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 45 | transducin family protein / WD-40 repeat family protei | | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 46 | REF4-related 1 | | Phvul.006G15PTHR33739:SFPhvul.006G15 |
| 47 | Alpha amylase family protein | | Phvul.006G04PTHR10357:SFPhvul.006G04 |
| 48 | cellulose synthase like G1 | | Phvul.005G00PTHR13301//IPhvul.005G00 |
| 49 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 50 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 51 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 52 | dihydrosphingosine phosphate lyase | | Phvul.008G014.1.2.27 - SphiPhvul.008G01 |
| 53 | dihydrosphingosine phosphate lyase | | Phvul.008G014.1.2.27 - SphiPhvul.008G01 |
| 54 | dihydrosphingosine phosphate lyase | | Phvul.008G014.1.2.27 - SphiPhvul.008G01 |
| 55 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 56 | cytochrome P450, family 76, subfamily C, polypeptide 4 | | Phvul.007G101.14.13.152 - IPhvul.007G10 |
| 57 | cytochrome P450, family 76, subfamily C, polypeptide 4 | | Phvul.007G101.14.13.152 - IPhvul.007G10 |
| 58 | purine permease 1 | | Phvul.009G03PTHR31376:SFPhvul.009G03 |
| 59 | | 0 | 0 Phvul.L002444 |
| 60 | | 0 | 0 Phvul.L002444 |
| | vacuolar iron transporter 1 | | Phvul.008G07KOG4473 - UnPhvul.008G07 |

| | | | |
|----|---|-----------------------------|----------------|
| 1 | | | |
| 2 | fatty acid desaturase 5 | Phvul.010G15K00507 - stea | Phvul.010G15 |
| 3 | Protein of unknown function (DUF630 and DUF632) | Phvul.009G21PF04782 - Pro | Phvul.009G21 |
| 4 | Integrase-type DNA-binding superfamily protein | Phvul.008G04PF00847 - AP | Phvul.008G04 |
| 5 | | | |
| 6 | | 0 Phvul.009G07K17968 - TRIA | Phvul.009G07 |
| 7 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 8 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 9 | | | |
| 10 | Pentatricopeptide repeat (PPR) superfamily protein | Phvul.003G15PF01535//PF1 | Phvul.003G15 |
| 11 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.009G03PTHR10108//I | Phvul.009G03 |
| 12 | thioredoxin-dependent peroxidase 1 | Phvul.004G16PTHR10430 - I | Phvul.004G16 |
| 13 | Protein prenyltransferase superfamily protein | Phvul.009G16PF13414 - TP | Phvul.009G16 |
| 14 | Uncharacterised conserved protein UCP015417, vWA | Phvul.002G11PTHR31373:S | Phvul.002G11 |
| 15 | alanine-2-oxoglutarate aminotransferase 2 | Phvul.002G152.6.1.4 - Glyci | Phvul.002G15 |
| 16 | chloroplatic NIFS-like cysteine desulfurase | Phvul.002G274.4.1.16 - Sele | Phvul.002G27 |
| 17 | SecY protein transport family protein | Phvul.011G16K10956 - prot | Phvul.011G16 |
| 18 | NDH-dependent cyclic electron flow 1 | Phvul.001G11PTHR11122:S | Phvul.001G11 |
| 19 | rubredoxin family protein | Phvul.002G03PTHR17130 - I | Phvul.002G03 |
| 20 | Protein kinase superfamily protein | Phvul.002G012.7.11.1 - Non | Phvul.002G01 |
| 21 | Protein kinase superfamily protein | Phvul.002G012.7.11.1 - Non | Phvul.002G01 |
| 22 | ferredoxin 3 | Phvul.007G02PTHR19370:S | Phvul.007G02 |
| 23 | transducin family protein / WD-40 repeat family protei | Phvul.010G11PTHR13950 - I | Phvul.010G11 |
| 24 | transducin family protein / WD-40 repeat family protei | Phvul.010G11PTHR13950 - I | Phvul.010G11 |
| 25 | REF4-related 1 | Phvul.006G15PTHR33739:S | Phvul.006G15 |
| 26 | Alpha amylase family protein | Phvul.006G04PTHR10357:S | Phvul.006G04 |
| 27 | cellulose synthase like G1 | Phvul.005G00PTHR13301//I | Phvul.005G00 |
| 28 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 29 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 30 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - Sph | Phvul.008G01 |
| 31 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - Sph | Phvul.008G01 |
| 32 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 33 | cytochrome P450, family 76, subfamily C, polypeptide | Phvul.007G101.14.13.152 - | Phvul.007G10 |
| 34 | purine permease 1 | Phvul.009G03PTHR31376:S | Phvul.009G03 |
| 35 | | 0 | 0 Phvul.L00244 |
| 36 | | 0 | 0 Phvul.L00244 |
| 37 | vacuolar iron transporter 1 | Phvul.008G07KOG4473 - Un | Phvul.008G07 |
| 38 | fatty acid desaturase 5 | Phvul.010G15K00507 - stea | Phvul.010G15 |
| 39 | Protein of unknown function (DUF630 and DUF632) | Phvul.009G21PF04782 - Pro | Phvul.009G21 |
| 40 | Integrase-type DNA-binding superfamily protein | Phvul.008G04PF00847 - AP | Phvul.008G04 |
| 41 | | | |
| 42 | | 0 Phvul.009G07K17968 - TRIA | Phvul.009G07 |
| 43 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 44 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 45 | | | |
| 46 | Pentatricopeptide repeat (PPR) superfamily protein | Phvul.003G15PF01535//PF1 | Phvul.003G15 |
| 47 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.009G03PTHR10108//I | Phvul.009G03 |
| 48 | thioredoxin-dependent peroxidase 1 | Phvul.004G16PTHR10430 - I | Phvul.004G16 |
| 49 | Protein prenyltransferase superfamily protein | Phvul.009G16PF13414 - TP | Phvul.009G16 |
| 50 | Uncharacterised conserved protein UCP015417, vWA | Phvul.002G11PTHR31373:S | Phvul.002G11 |
| 51 | alanine-2-oxoglutarate aminotransferase 2 | Phvul.002G152.6.1.4 - Glyci | Phvul.002G15 |

| | | | | |
|----|---|---|---|---|
| 1 | | | | |
| 2 | chloroplastic NIFS-like cysteine desulfurase | | | Phvul.002G274.4.1.16 - SelePhvul.002G27 |
| 3 | SecY protein transport family protein | | | Phvul.011G16K10956 - protPhvul.011G16 |
| 4 | NDH-dependent cyclic electron flow 1 | | | Phvul.001G11PTHR11122:SFPhvul.001G11 |
| 5 | rubredoxin family protein | | | Phvul.002G03PTHR17130 - IPhvul.002G03 |
| 6 | Protein kinase superfamily protein | | | Phvul.002G012.7.11.1 - NonPhvul.002G01 |
| 7 | Protein kinase superfamily protein | | | Phvul.002G012.7.11.1 - NonPhvul.002G01 |
| 8 | ferredoxin 3 | | | Phvul.007G02PTHR19370:SFPhvul.007G02 |
| 9 | transducin family protein / WD-40 repeat family protei | | | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 10 | transducin family protein / WD-40 repeat family protei | | | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 11 | REF4-related 1 | | | Phvul.006G15PTHR33739:SFPhvul.006G15 |
| 12 | Alpha amylase family protein | | | Phvul.006G04PTHR10357:SFPhvul.006G04 |
| 13 | cellulose synthase like G1 | | | Phvul.005G00PTHR13301//IPhvul.005G00 |
| 14 | negative regulator of systemic acquired resistance (SNI | 0 | 0 | Phvul.003G05 |
| 15 | negative regulator of systemic acquired resistance (SNI | 0 | 0 | Phvul.003G05 |
| 16 | dihydrosphingosine phosphate lyase | | | Phvul.008G014.1.2.27 - SphiPhvul.008G01 |
| 17 | dihydrosphingosine phosphate lyase | | | Phvul.008G014.1.2.27 - SphiPhvul.008G01 |
| 18 | negative regulator of systemic acquired resistance (SNI | 0 | 0 | Phvul.003G05 |
| 19 | cytochrome P450, family 76, subfamily C, polypeptide 4 | | | Phvul.007G101.14.13.152 - Phvul.007G10 |
| 20 | purine permease 1 | | | Phvul.009G03PTHR31376:SFPhvul.009G03 |
| 21 | | 0 | 0 | Phvul.L00244 |
| 22 | | 0 | 0 | Phvul.L00244 |
| 23 | vacuolar iron transporter 1 | | | Phvul.008G07KOG4473 - UnPhvul.008G07 |
| 24 | fatty acid desaturase 5 | | | Phvul.010G15K00507 - steaiPhvul.010G15 |
| 25 | Protein of unknown function (DUF630 and DUF632) | | | Phvul.009G21PF04782 - ProPhvul.009G21 |
| 26 | Integrase-type DNA-binding superfamily protein | | | Phvul.008G04PF00847 - AP2Phvul.008G04 |
| 27 | | 0 | | Phvul.009G07K17968 - TRIAPhvul.009G07 |
| 28 | embryo defective 2735 | 0 | 0 | Phvul.001G19 |
| 29 | embryo defective 2735 | 0 | 0 | Phvul.001G19 |
| 30 | Pentatricopeptide repeat (PPR) superfamily protein | | | Phvul.003G15PF01535//PF1Phvul.003G15 |
| 31 | S-adenosyl-L-methionine-dependent methyltransferase | | | Phvul.009G03PTHR10108//IPhvul.009G03 |
| 32 | thioredoxin-dependent peroxidase 1 | | | Phvul.004G16PTHR10430 - IPhvul.004G16 |
| 33 | Protein prenyltransferase superfamily protein | | | Phvul.009G16PF13414 - TPRPhvul.009G16 |
| 34 | Uncharacterised conserved protein UCP015417, vWA | | | Phvul.002G11PTHR31373:SFPhvul.002G11 |
| 35 | alanine-2-oxoglutarate aminotransferase 2 | | | Phvul.002G152.6.1.4 - GlyciPhvul.002G15 |
| 36 | chloroplastic NIFS-like cysteine desulfurase | | | Phvul.002G274.4.1.16 - SelePhvul.002G27 |
| 37 | SecY protein transport family protein | | | Phvul.011G16K10956 - protPhvul.011G16 |
| 38 | NDH-dependent cyclic electron flow 1 | | | Phvul.001G11PTHR11122:SFPhvul.001G11 |
| 39 | rubredoxin family protein | | | Phvul.002G03PTHR17130 - IPhvul.002G03 |
| 40 | Protein kinase superfamily protein | | | Phvul.002G012.7.11.1 - NonPhvul.002G01 |
| 41 | Protein kinase superfamily protein | | | Phvul.002G012.7.11.1 - NonPhvul.002G01 |
| 42 | ferredoxin 3 | | | Phvul.007G02PTHR19370:SFPhvul.007G02 |
| 43 | transducin family protein / WD-40 repeat family protei | | | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 44 | transducin family protein / WD-40 repeat family protei | | | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 45 | REF4-related 1 | | | Phvul.006G15PTHR33739:SFPhvul.006G15 |
| 46 | Alpha amylase family protein | | | Phvul.006G04PTHR10357:SFPhvul.006G04 |
| 47 | cellulose synthase like G1 | | | Phvul.005G00PTHR13301//IPhvul.005G00 |

| | | | |
|----|---|---|-----------------|
| 1 | | | |
| 2 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 3 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 4 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - Sphi | Phvul.008G01 |
| 5 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - Sphi | Phvul.008G01 |
| 6 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - Sphi | Phvul.008G01 |
| 7 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 8 | cytochrome P450, family 76, subfamily C, polypeptide 4 | Phvul.007G101.14.13.152 - (Phvul.007G10 | |
| 9 | purine permease 1 | Phvul.009G03PTHR31376:SF | Phvul.009G03 |
| 10 | | | |
| 11 | | 0 | 0 Phvul.L002444 |
| 12 | | 0 | 0 Phvul.L002444 |
| 13 | | | |
| 14 | vacuolar iron transporter 1 | Phvul.008G07KOG4473 - Un | Phvul.008G07 |
| 15 | fatty acid desaturase 5 | Phvul.010G15K00507 - stea | Phvul.010G15 |
| 16 | Protein of unknown function (DUF630 and DUF632) | Phvul.009G21PF04782 - Pro | Phvul.009G21 |
| 17 | Integrase-type DNA-binding superfamily protein | Phvul.008G04PF00847 - AP2 | Phvul.008G04 |
| 18 | | 0 Phvul.009G07K17968 - TRIA | Phvul.009G07 |
| 19 | | | |
| 20 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 21 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 22 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 23 | Pentatricopeptide repeat (PPR) superfamily protein | Phvul.003G15PF01535//PF1 | Phvul.003G15 |
| 24 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.009G03PTHR10108//I | Phvul.009G03 |
| 25 | thioredoxin-dependent peroxidase 1 | Phvul.004G16PTHR10430 - I | Phvul.004G16 |
| 26 | Protein prenyltransferase superfamily protein | Phvul.009G16PF13414 - TPR | Phvul.009G16 |
| 27 | Protein prenyltransferase superfamily protein | Phvul.009G16PF13414 - TPR | Phvul.009G16 |
| 28 | Uncharacterised conserved protein UCP015417, vWA | Phvul.002G11PTHR31373:SF | Phvul.002G11 |
| 29 | alanine-2-oxoglutarate aminotransferase 2 | Phvul.002G152.6.1.4 - Glyci | Phvul.002G15 |
| 30 | chloroplastic NIFS-like cysteine desulfurase | Phvul.002G274.4.1.16 - Sele | Phvul.002G27 |
| 31 | SecY protein transport family protein | Phvul.011G16K10956 - prot | Phvul.011G16 |
| 32 | SecY protein transport family protein | Phvul.011G16K10956 - prot | Phvul.011G16 |
| 33 | NDH-dependent cyclic electron flow 1 | Phvul.001G11PTHR11122:SF | Phvul.001G11 |
| 34 | rubredoxin family protein | Phvul.002G03PTHR17130 - I | Phvul.002G03 |
| 35 | rubredoxin family protein | Phvul.002G03PTHR17130 - I | Phvul.002G03 |
| 36 | Protein kinase superfamily protein | Phvul.002G012.7.11.1 - Non | Phvul.002G01 |
| 37 | Protein kinase superfamily protein | Phvul.002G012.7.11.1 - Non | Phvul.002G01 |
| 38 | Protein kinase superfamily protein | Phvul.002G012.7.11.1 - Non | Phvul.002G01 |
| 39 | ferredoxin 3 | Phvul.007G02PTHR19370:SF | Phvul.007G02 |
| 40 | transducin family protein / WD-40 repeat family protei | Phvul.010G11PTHR13950 - I | Phvul.010G11 |
| 41 | transducin family protein / WD-40 repeat family protei | Phvul.010G11PTHR13950 - I | Phvul.010G11 |
| 42 | transducin family protein / WD-40 repeat family protei | Phvul.010G11PTHR13950 - I | Phvul.010G11 |
| 43 | REF4-related 1 | Phvul.006G15PTHR33739:SF | Phvul.006G15 |
| 44 | Alpha amylase family protein | Phvul.006G04PTHR10357:SF | Phvul.006G04 |
| 45 | cellulose synthase like G1 | Phvul.005G00PTHR13301//I | Phvul.005G00 |
| 46 | cellulose synthase like G1 | Phvul.005G00PTHR13301//I | Phvul.005G00 |
| 47 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 48 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 49 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 50 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - Sphi | Phvul.008G01 |
| 51 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - Sphi | Phvul.008G01 |
| 52 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - Sphi | Phvul.008G01 |
| 53 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 54 | cytochrome P450, family 76, subfamily C, polypeptide 4 | Phvul.007G101.14.13.152 - (Phvul.007G10 | |
| 55 | purine permease 1 | Phvul.009G03PTHR31376:SF | Phvul.009G03 |
| 56 | | 0 | 0 Phvul.L002444 |
| 57 | | 0 | 0 Phvul.L002444 |
| 58 | | | |
| 59 | vacuolar iron transporter 1 | Phvul.008G07KOG4473 - Un | Phvul.008G07 |
| 60 | fatty acid desaturase 5 | Phvul.010G15K00507 - stea | Phvul.010G15 |
| | Protein of unknown function (DUF630 and DUF632) | Phvul.009G21PF04782 - Pro | Phvul.009G21 |

| | | | |
|----|---|-----------------------------|----------------|
| 1 | | | |
| 2 | Integrase-type DNA-binding superfamily protein | Phvul.008G04PF00847 - AP2 | Phvul.008G04 |
| 3 | | 0 Phvul.009G07K17968 - TRIA | Phvul.009G07 |
| 4 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 5 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 6 | | | |
| 7 | Pentatricopeptide repeat (PPR) superfamily protein | Phvul.003G15PF01535//PF1 | Phvul.003G15 |
| 8 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.009G03PTHR10108//I | Phvul.009G03 |
| 9 | | | |
| 10 | thioredoxin-dependent peroxidase 1 | Phvul.004G16PTHR10430 - I | Phvul.004G16 |
| 11 | Protein prenyltransferase superfamily protein | Phvul.009G16PF13414 - TPR | Phvul.009G16 |
| 12 | Uncharacterised conserved protein UCP015417, vWA | Phvul.002G11PTHR31373:Sf | Phvul.002G11 |
| 13 | | | |
| 14 | alanine-2-oxoglutarate aminotransferase 2 | Phvul.002G152.6.1.4 - Glyci | Phvul.002G15 |
| 15 | chloroplastic NIFS-like cysteine desulfurase | Phvul.002G274.4.1.16 - Sele | Phvul.002G27 |
| 16 | SecY protein transport family protein | Phvul.011G16K10956 - prot | Phvul.011G16 |
| 17 | | | |
| 18 | NDH-dependent cyclic electron flow 1 | Phvul.001G11PTHR11122:Sf | Phvul.001G11 |
| 19 | rubredoxin family protein | Phvul.002G03PTHR17130 - I | Phvul.002G03 |
| 20 | Protein kinase superfamily protein | Phvul.002G012.7.11.1 - Non | Phvul.002G01 |
| 21 | Protein kinase superfamily protein | Phvul.002G012.7.11.1 - Non | Phvul.002G01 |
| 22 | | | |
| 23 | ferredoxin 3 | Phvul.007G02PTHR19370:Sf | Phvul.007G02 |
| 24 | transducin family protein / WD-40 repeat family protei | Phvul.010G11PTHR13950 - I | Phvul.010G11 |
| 25 | | | |
| 26 | transducin family protein / WD-40 repeat family protei | Phvul.010G11PTHR13950 - I | Phvul.010G11 |
| 27 | REF4-related 1 | Phvul.006G15PTHR33739:Sf | Phvul.006G15 |
| 28 | Alpha amylase family protein | Phvul.006G04PTHR10357:Sf | Phvul.006G04 |
| 29 | cellulose synthase like G1 | Phvul.005G00PTHR13301//I | Phvul.005G00 |
| 30 | | | |
| 31 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 32 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 33 | | | |
| 34 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - Sph | Phvul.008G01 |
| 35 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - Sph | Phvul.008G01 |
| 36 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 37 | | | |
| 38 | cytochrome P450, family 76, subfamily C, polypeptide 4 | Phvul.007G101.14.13.152 - (| Phvul.007G10 |
| 39 | purine permease 1 | Phvul.009G03PTHR31376:Sf | Phvul.009G03 |
| 40 | | 0 | 0 Phvul.L00244 |
| 41 | | 0 | 0 Phvul.L00244 |
| 42 | | | |
| 43 | vacuolar iron transporter 1 | Phvul.008G07KOG4473 - Un | Phvul.008G07 |
| 44 | fatty acid desaturase 5 | Phvul.010G15K00507 - stea | Phvul.010G15 |
| 45 | Protein of unknown function (DUF630 and DUF632) | Phvul.009G21PF04782 - Pro | Phvul.009G21 |
| 46 | | | |
| 47 | Integrase-type DNA-binding superfamily protein | Phvul.008G04PF00847 - AP2 | Phvul.008G04 |
| 48 | | 0 Phvul.009G07K17968 - TRIA | Phvul.009G07 |
| 49 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 50 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 51 | | | |
| 52 | Pentatricopeptide repeat (PPR) superfamily protein | Phvul.003G15PF01535//PF1 | Phvul.003G15 |
| 53 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.009G03PTHR10108//I | Phvul.009G03 |
| 54 | | | |
| 55 | thioredoxin-dependent peroxidase 1 | Phvul.004G16PTHR10430 - I | Phvul.004G16 |
| 56 | Protein prenyltransferase superfamily protein | Phvul.009G16PF13414 - TPR | Phvul.009G16 |
| 57 | Uncharacterised conserved protein UCP015417, vWA | Phvul.002G11PTHR31373:Sf | Phvul.002G11 |
| 58 | | | |
| 59 | alanine-2-oxoglutarate aminotransferase 2 | Phvul.002G152.6.1.4 - Glyci | Phvul.002G15 |
| 60 | chloroplastic NIFS-like cysteine desulfurase | Phvul.002G274.4.1.16 - Sele | Phvul.002G27 |
| | SecY protein transport family protein | Phvul.011G16K10956 - prot | Phvul.011G16 |

| | | | | |
|----|---|---|---|--|
| 1 | | | | |
| 2 | NDH-dependent cyclic electron flow 1 | | | Phvul.001G11PTHR11122:SfPhvul.001G11 |
| 3 | rubredoxin family protein | | | Phvul.002G03PTHR17130 - IPhvul.002G03 |
| 4 | Protein kinase superfamily protein | | | Phvul.002G012.7.11.1 - NonPhvul.002G01 |
| 5 | Protein kinase superfamily protein | | | Phvul.002G012.7.11.1 - NonPhvul.002G01 |
| 6 | ferredoxin 3 | | | Phvul.007G02PTHR19370:SfPhvul.007G02 |
| 7 | transducin family protein / WD-40 repeat family protei | | | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 8 | transducin family protein / WD-40 repeat family protei | | | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 9 | REF4-related 1 | | | Phvul.006G15PTHR33739:SfPhvul.006G15 |
| 10 | Alpha amylase family protein | | | Phvul.006G04PTHR10357:SfPhvul.006G04 |
| 11 | cellulose synthase like G1 | | | Phvul.005G00PTHR13301//IPhvul.005G00 |
| 12 | negative regulator of systemic acquired resistance (SNI | 0 | 0 | Phvul.003G05 |
| 13 | negative regulator of systemic acquired resistance (SNI | 0 | 0 | Phvul.003G05 |
| 14 | dihydrosphingosine phosphate lyase | | | Phvul.008G014.1.2.27 - SphiPhvul.008G01 |
| 15 | dihydrosphingosine phosphate lyase | | | Phvul.008G014.1.2.27 - SphiPhvul.008G01 |
| 16 | negative regulator of systemic acquired resistance (SNI | 0 | 0 | Phvul.003G05 |
| 17 | cytochrome P450, family 76, subfamily C, polypeptide 4 | | | Phvul.007G101.14.13.152 - IPhvul.007G10 |
| 18 | purine permease 1 | | | Phvul.009G03PTHR31376:SfPhvul.009G03 |
| 19 | | 0 | 0 | Phvul.L002444 |
| 20 | | 0 | 0 | Phvul.L002444 |
| 21 | vacuolar iron transporter 1 | | | Phvul.008G07KOG4473 - UnPhvul.008G07 |
| 22 | fatty acid desaturase 5 | | | Phvul.010G15K00507 - steaiPhvul.010G15 |
| 23 | Protein of unknown function (DUF630 and DUF632) | | | Phvul.009G21PF04782 - ProPhvul.009G21 |
| 24 | Integrase-type DNA-binding superfamily protein | | | Phvul.008G04PF00847 - AP2Phvul.008G04 |
| 25 | | | | 0 Phvul.009G07K17968 - TRIAPhvul.009G07 |
| 26 | embryo defective 2735 | 0 | 0 | Phvul.001G19 |
| 27 | embryo defective 2735 | 0 | 0 | Phvul.001G19 |
| 28 | Pentatricopeptide repeat (PPR) superfamily protein | | | Phvul.003G15PF01535//PF1Phvul.003G15 |
| 29 | S-adenosyl-L-methionine-dependent methyltransferase | | | Phvul.009G03PTHR10108//IPhvul.009G03 |
| 30 | thioredoxin-dependent peroxidase 1 | | | Phvul.004G16PTHR10430 - IPhvul.004G16 |
| 31 | Protein prenyltransferase superfamily protein | | | Phvul.009G16PF13414 - TPRPhvul.009G16 |
| 32 | Uncharacterised conserved protein UCP015417, vWA | | | Phvul.002G11PTHR31373:SfPhvul.002G11 |
| 33 | alanine-2-oxoglutarate aminotransferase 2 | | | Phvul.002G152.6.1.4 - GlyciiPhvul.002G15 |
| 34 | chloroplastic NIFS-like cysteine desulfurase | | | Phvul.002G274.4.1.16 - SelePhvul.002G27 |
| 35 | SecY protein transport family protein | | | Phvul.011G16K10956 - protiPhvul.011G16 |
| 36 | NDH-dependent cyclic electron flow 1 | | | Phvul.001G11PTHR11122:SfPhvul.001G11 |
| 37 | rubredoxin family protein | | | Phvul.002G03PTHR17130 - IPhvul.002G03 |
| 38 | Protein kinase superfamily protein | | | Phvul.002G012.7.11.1 - NonPhvul.002G01 |
| 39 | Protein kinase superfamily protein | | | Phvul.002G012.7.11.1 - NonPhvul.002G01 |
| 40 | ferredoxin 3 | | | Phvul.007G02PTHR19370:SfPhvul.007G02 |
| 41 | transducin family protein / WD-40 repeat family protei | | | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 42 | transducin family protein / WD-40 repeat family protei | | | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 43 | REF4-related 1 | | | Phvul.006G15PTHR33739:SfPhvul.006G15 |
| 44 | Alpha amylase family protein | | | Phvul.006G04PTHR10357:SfPhvul.006G04 |
| 45 | cellulose synthase like G1 | | | Phvul.005G00PTHR13301//IPhvul.005G00 |
| 46 | negative regulator of systemic acquired resistance (SNI | 0 | 0 | Phvul.003G05 |
| 47 | negative regulator of systemic acquired resistance (SNI | 0 | 0 | Phvul.003G05 |

| | | | |
|----|---|-----------------------------|---------------------------|
| 1 | | | |
| 2 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - Sphi | Phvul.008G01 |
| 3 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - Sphi | Phvul.008G01 |
| 4 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 5 | cytochrome P450, family 76, subfamily C, polypeptide 4 | Phvul.007G101.14.13.152 - | Phvul.007G10 |
| 6 | purine permease 1 | Phvul.009G03PTHR31376:Sf | Phvul.009G03 |
| 7 | | | |
| 8 | | 0 | 0 Phvul.L00244 |
| 9 | | | |
| 10 | | 0 | 0 Phvul.L00244 |
| 11 | vacuolar iron transporter 1 | Phvul.008G07KOG4473 - Un | Phvul.008G07 |
| 12 | fatty acid desaturase 5 | Phvul.010G15K00507 - stea | Phvul.010G15 |
| 13 | Protein of unknown function (DUF630 and DUF632) | Phvul.009G21PF04782 - Pro | Phvul.009G21 |
| 14 | Integrase-type DNA-binding superfamily protein | Phvul.008G04PF00847 - AP | Phvul.008G04 |
| 15 | | | |
| 16 | | 0 | Phvul.009G07K17968 - TRIA |
| 17 | | | Phvul.009G07 |
| 18 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 19 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 20 | Pentatricopeptide repeat (PPR) superfamily protein | Phvul.003G15PF01535//PF1 | Phvul.003G15 |
| 21 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.009G03PTHR10108//I | Phvul.009G03 |
| 22 | thioredoxin-dependent peroxidase 1 | Phvul.004G16PTHR10430 - I | Phvul.004G16 |
| 23 | Protein prenyltransferase superfamily protein | Phvul.009G16PF13414 - TPR | Phvul.009G16 |
| 24 | Uncharacterised conserved protein UCP015417, vWA | Phvul.002G11PTHR31373:Sf | Phvul.002G11 |
| 25 | alanine-2-oxoglutarate aminotransferase 2 | Phvul.002G152.6.1.4 - Glyci | Phvul.002G15 |
| 26 | chloroplatic NIFS-like cysteine desulfurase | Phvul.002G274.4.1.16 - Sele | Phvul.002G27 |
| 27 | SecY protein transport family protein | Phvul.011G16K10956 - prot | Phvul.011G16 |
| 28 | NDH-dependent cyclic electron flow 1 | Phvul.001G11PTHR11122:Sf | Phvul.001G11 |
| 29 | rubredoxin family protein | Phvul.002G03PTHR17130 - I | Phvul.002G03 |
| 30 | Protein kinase superfamily protein | Phvul.002G012.7.11.1 - Non | Phvul.002G01 |
| 31 | Protein kinase superfamily protein | Phvul.002G012.7.11.1 - Non | Phvul.002G01 |
| 32 | ferredoxin 3 | Phvul.007G02PTHR19370:Sf | Phvul.007G02 |
| 33 | transducin family protein / WD-40 repeat family protei | Phvul.010G11PTHR13950 - I | Phvul.010G11 |
| 34 | transducin family protein / WD-40 repeat family protei | Phvul.010G11PTHR13950 - I | Phvul.010G11 |
| 35 | REF4-related 1 | Phvul.006G15PTHR33739:Sf | Phvul.006G15 |
| 36 | Alpha amylase family protein | Phvul.006G04PTHR10357:Sf | Phvul.006G04 |
| 37 | cellulose synthase like G1 | Phvul.005G00PTHR13301//I | Phvul.005G00 |
| 38 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 39 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 40 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - Sphi | Phvul.008G01 |
| 41 | dihydrosphingosine phosphate lyase | Phvul.008G014.1.2.27 - Sphi | Phvul.008G01 |
| 42 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 43 | cytochrome P450, family 76, subfamily C, polypeptide 4 | Phvul.007G101.14.13.152 - | Phvul.007G10 |
| 44 | purine permease 1 | Phvul.009G03PTHR31376:Sf | Phvul.009G03 |
| 45 | | | |
| 46 | | 0 | 0 Phvul.L00244 |
| 47 | | | |
| 48 | | 0 | 0 Phvul.L00244 |
| 49 | vacuolar iron transporter 1 | Phvul.008G07KOG4473 - Un | Phvul.008G07 |
| 50 | fatty acid desaturase 5 | Phvul.010G15K00507 - stea | Phvul.010G15 |
| 51 | Protein of unknown function (DUF630 and DUF632) | Phvul.009G21PF04782 - Pro | Phvul.009G21 |
| 52 | Integrase-type DNA-binding superfamily protein | Phvul.008G04PF00847 - AP | Phvul.008G04 |
| 53 | | | |
| 54 | | 0 | Phvul.009G07K17968 - TRIA |
| 55 | | | Phvul.009G07 |

| | | | |
|----|---|------------------------------|----------------|
| 1 | | | |
| 2 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 3 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 4 | Pentatricopeptide repeat (PPR) superfamily protein | Phvul.003G15 PF01535//PF1 | Phvul.003G15 |
| 5 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.009G03 PTHR10108//I | Phvul.009G03 |
| 6 | thioredoxin-dependent peroxidase 1 | Phvul.004G16 PTHR10430 - I | Phvul.004G16 |
| 7 | Protein prenyltransferase superfamily protein | Phvul.009G16 PF13414 - TPR | Phvul.009G16 |
| 8 | Uncharacterised conserved protein UCP015417, vWA | Phvul.002G11 PTHR31373:SF | Phvul.002G11 |
| 9 | alanine-2-oxoglutarate aminotransferase 2 | Phvul.002G15 2.6.1.4 - Glyci | Phvul.002G15 |
| 10 | chloroplatic NIFS-like cysteine desulfurase | Phvul.002G27 4.4.1.16 - Sele | Phvul.002G27 |
| 11 | SecY protein transport family protein | Phvul.011G16 K10956 - prot | Phvul.011G16 |
| 12 | NDH-dependent cyclic electron flow 1 | Phvul.001G11 PTHR11122:SF | Phvul.001G11 |
| 13 | rubredoxin family protein | Phvul.002G03 PTHR17130 - I | Phvul.002G03 |
| 14 | Protein kinase superfamily protein | Phvul.002G01 2.7.11.1 - Non | Phvul.002G01 |
| 15 | Protein kinase superfamily protein | Phvul.002G01 2.7.11.1 - Non | Phvul.002G01 |
| 16 | ferredoxin 3 | Phvul.007G02 PTHR19370:SF | Phvul.007G02 |
| 17 | transducin family protein / WD-40 repeat family protei | Phvul.010G11 PTHR13950 - I | Phvul.010G11 |
| 18 | transducin family protein / WD-40 repeat family protei | Phvul.010G11 PTHR13950 - I | Phvul.010G11 |
| 19 | REF4-related 1 | Phvul.006G15 PTHR33739:SF | Phvul.006G15 |
| 20 | Alpha amylase family protein | Phvul.006G04 PTHR10357:SF | Phvul.006G04 |
| 21 | cellulose synthase like G1 | Phvul.005G00 PTHR13301//I | Phvul.005G00 |
| 22 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 23 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 24 | dihydrosphingosine phosphate lyase | Phvul.008G01 4.1.2.27 - Sph | Phvul.008G01 |
| 25 | dihydrosphingosine phosphate lyase | Phvul.008G01 4.1.2.27 - Sph | Phvul.008G01 |
| 26 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 27 | cytochrome P450, family 76, subfamily C, polypeptide 4 | Phvul.007G10 1.14.13.152 - | Phvul.007G10 |
| 28 | purine permease 1 | Phvul.009G03 PTHR31376:SF | Phvul.009G03 |
| 29 | | 0 | 0 Phvul.L00244 |
| 30 | | 0 | 0 Phvul.L00244 |
| 31 | vacuolar iron transporter 1 | Phvul.008G07 KOG4473 - Un | Phvul.008G07 |
| 32 | fatty acid desaturase 5 | Phvul.010G15 K00507 - stea | Phvul.010G15 |
| 33 | Protein of unknown function (DUF630 and DUF632) | Phvul.009G21 PF04782 - Pro | Phvul.009G21 |
| 34 | Integrase-type DNA-binding superfamily protein | Phvul.008G04 PF00847 - AP | Phvul.008G04 |
| 35 | | 0 Phvul.009G07 K17968 - TRIA | Phvul.009G07 |
| 36 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 37 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 38 | Pentatricopeptide repeat (PPR) superfamily protein | Phvul.003G15 PF01535//PF1 | Phvul.003G15 |
| 39 | S-adenosyl-L-methionine-dependent methyltransferase | Phvul.009G03 PTHR10108//I | Phvul.009G03 |
| 40 | thioredoxin-dependent peroxidase 1 | Phvul.004G16 PTHR10430 - I | Phvul.004G16 |
| 41 | Protein prenyltransferase superfamily protein | Phvul.009G16 PF13414 - TPR | Phvul.009G16 |
| 42 | Uncharacterised conserved protein UCP015417, vWA | Phvul.002G11 PTHR31373:SF | Phvul.002G11 |
| 43 | alanine-2-oxoglutarate aminotransferase 2 | Phvul.002G15 2.6.1.4 - Glyci | Phvul.002G15 |
| 44 | chloroplatic NIFS-like cysteine desulfurase | Phvul.002G27 4.4.1.16 - Sele | Phvul.002G27 |
| 45 | SecY protein transport family protein | Phvul.011G16 K10956 - prot | Phvul.011G16 |
| 46 | NDH-dependent cyclic electron flow 1 | Phvul.001G11 PTHR11122:SF | Phvul.001G11 |
| 47 | rubredoxin family protein | Phvul.002G03 PTHR17130 - I | Phvul.002G03 |

| | | | |
|----|---|---|---|
| 1 | | | |
| 2 | Protein kinase superfamily protein | | Phvul.002G012.7.11.1 - NonPhvul.002G01 |
| 3 | Protein kinase superfamily protein | | Phvul.002G012.7.11.1 - NonPhvul.002G01 |
| 4 | ferredoxin 3 | | Phvul.007G02PTHR19370:SfPhvul.007G02 |
| 5 | | | |
| 6 | transducin family protein / WD-40 repeat family protei | | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 7 | transducin family protein / WD-40 repeat family protei | | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 8 | REF4-related 1 | | Phvul.006G15PTHR33739:SfPhvul.006G15 |
| 9 | | | |
| 10 | Alpha amylase family protein | | Phvul.006G04PTHR10357:SfPhvul.006G04 |
| 11 | cellulose synthase like G1 | | Phvul.005G00PTHR13301//IPhvul.005G00 |
| 12 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 13 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 14 | dihydrosphingosine phosphate lyase | | Phvul.008G014.1.2.27 - SphiPhvul.008G01 |
| 15 | dihydrosphingosine phosphate lyase | | Phvul.008G014.1.2.27 - SphiPhvul.008G01 |
| 16 | | | |
| 17 | negative regulator of systemic acquired resistance (SNI | 0 | 0 Phvul.003G05 |
| 18 | cytochrome P450, family 76, subfamily C, polypeptide 4 | | Phvul.007G101.14.13.152 - Phvul.007G10 |
| 19 | purine permease 1 | | Phvul.009G03PTHR31376:SfPhvul.009G03 |
| 20 | | | |
| 21 | | | |
| 22 | | 0 | 0 Phvul.L00244 |
| 23 | | 0 | 0 Phvul.L00244 |
| 24 | vacuolar iron transporter 1 | | Phvul.008G07KOG4473 - UnPhvul.008G07 |
| 25 | fatty acid desaturase 5 | | Phvul.010G15K00507 - steaPhvul.010G15 |
| 26 | Protein prenyltransferase superfamily protein | | Phvul.009G16PF13414 - TPRPhvul.009G16 |
| 27 | Protein of unknown function (DUF630 and DUF632) | | Phvul.009G21PF04782 - ProPhvul.009G21 |
| 28 | ferredoxin 3 | | Phvul.007G02PTHR19370:SfPhvul.007G02 |
| 29 | | | |
| 30 | Integrase-type DNA-binding superfamily protein | | Phvul.008G04PF00847 - AP2Phvul.008G04 |
| 31 | | | 0 Phvul.009G07K17968 - TRIAPhvul.009G07 |
| 32 | | | |
| 33 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 34 | embryo defective 2735 | 0 | 0 Phvul.001G19 |
| 35 | | | |
| 36 | AMP-dependent synthetase and ligase family protein | | Phvul.009G16PTHR24096:SfPhvul.009G16 |
| 37 | Pentatricopeptide repeat (PPR) superfamily protein | | Phvul.003G15PF01535//PF1Phvul.003G15 |
| 38 | MAC/Perforin domain-containing protein | | Phvul.L00374(PF01823 - MAPhvul.L00374 |
| 39 | MAC/Perforin domain-containing protein | | Phvul.L00374(PF01823 - MAPhvul.L00374 |
| 40 | | | |
| 41 | S-adenosyl-L-methionine-dependent methyltransferas | | Phvul.009G03PTHR10108//IPhvul.009G03 |
| 42 | thioredoxin-dependent peroxidase 1 | | Phvul.004G16PTHR10430 - IPhvul.004G16 |
| 43 | Uncharacterised conserved protein UCP015417, vWA | | Phvul.002G11PTHR31373:SfPhvul.002G11 |
| 44 | alanine-2-oxoglutarate aminotransferase 2 | | Phvul.002G152.6.1.4 - GlyciPhvul.002G15 |
| 45 | chloroplastic NIFS-like cysteine desulfurase | | Phvul.002G274.4.1.16 - SelePhvul.002G27 |
| 46 | SecY protein transport family protein | | Phvul.011G16K10956 - protPhvul.011G16 |
| 47 | cation exchanger 1 | | Phvul.006G06K07300 - Ca2+Phvul.006G06 |
| 48 | | | |
| 49 | NDH-dependent cyclic electron flow 1 | | Phvul.001G11PTHR11122:SfPhvul.001G11 |
| 50 | rubredoxin family protein | | Phvul.002G03PTHR17130 - IPhvul.002G03 |
| 51 | | | |
| 52 | transducin family protein / WD-40 repeat family protei | | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 53 | transducin family protein / WD-40 repeat family protei | | Phvul.010G11PTHR13950 - IPhvul.010G11 |
| 54 | | | |
| 55 | C2 calcium/lipid-binding plant phosphoribosyltransfera | | Phvul.002G15PTHR10024:SfPhvul.002G15 |
| 56 | Plant invertase/pectin methylesterase inhibitor superf | | Phvul.009G22PTHR31707:SfPhvul.009G22 |
| 57 | Protein of unknown function (DUF630) ;Protein of unkr | | Phvul.002G10PF04782 - ProPhvul.002G10 |
| 58 | | | |
| 59 | FASCICLIN-like arabinogalactan 9 | | Phvul.005G09PTHR32077:SfPhvul.005G09 |
| 60 | basic helix-loop-helix (bHLH) DNA-binding superfamily | | Phvul.003G18PTHR12565:SfPhvul.003G18 |

| | | | |
|----|--|-----------------------------|--------------|
| 1 | | | |
| 2 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:Sf | Phvul.003G18 |
| 3 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132://I | Phvul.003G12 |
| 4 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132://I | Phvul.003G12 |
| 5 | Peroxidase superfamily protein | Phvul.006G071.11.1.7 - Perc | Phvul.006G07 |
| 6 | Peroxidase superfamily protein | Phvul.006G071.11.1.7 - Perc | Phvul.006G07 |
| 7 | Nucleoporin, Nup133/Nup155-like | Phvul.008G28K14300 - nucl | Phvul.008G28 |
| 8 | ubiquitin-protein ligase 4 | Phvul.007G16PTHR11254:Sf | Phvul.007G16 |
| 9 | ubiquitin-protein ligase 4 | Phvul.007G16PTHR11254:Sf | Phvul.007G16 |
| 10 | serine hydroxymethyltransferase 4 | Phvul.001G26PTHR11680://I | Phvul.001G26 |
| 11 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:Sf | Phvul.006G09 |
| 12 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:Sf | Phvul.006G09 |
| 13 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:Sf | Phvul.006G09 |
| 14 | Phosphatidylinositol 3- and 4-kinase family protein | Phvul.003G03PTHR15245:Sf | Phvul.003G03 |
| 15 | | 0 | 0 |
| 16 | | 0 | 0 |
| 17 | P-loop containing nucleoside triphosphate hydrolases | Phvul.003G10PTHR10799://I | Phvul.003G10 |
| 18 | P-loop containing nucleoside triphosphate hydrolases | Phvul.003G10PTHR10799://I | Phvul.003G10 |
| 19 | binding | Phvul.002G26PTHR23315:Sf | Phvul.002G26 |
| 20 | binding | Phvul.002G26PTHR23315:Sf | Phvul.002G26 |
| 21 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA | Phvul.002G29 |
| 22 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA | Phvul.002G29 |
| 23 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA | Phvul.002G29 |
| 24 | phytochrome interacting factor 3-like 5 | Phvul.007G15PTHR12565:Sf | Phvul.007G15 |
| 25 | phytochrome interacting factor 3-like 5 | Phvul.007G15PTHR12565:Sf | Phvul.007G15 |
| 26 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:Sf | Phvul.002G00 |
| 27 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:Sf | Phvul.002G00 |
| 28 | cellulose synthase like G1 | Phvul.005G00PTHR13301://I | Phvul.005G00 |
| 29 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:Sf | Phvul.002G00 |
| 30 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:Sf | Phvul.002G00 |
| 31 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.008G24PTHR21493://I | Phvul.008G24 |
| 32 | KNOTTED-like from Arabidopsis thaliana 2 | Phvul.007G20PTHR11850://I | Phvul.007G20 |
| 33 | KNOTTED-like from Arabidopsis thaliana 2 | Phvul.007G20PTHR11850://I | Phvul.007G20 |
| 34 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 35 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 36 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 37 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 38 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 39 | RING/U-box superfamily protein | Phvul.003G18PTHR22763:Sf | Phvul.003G18 |
| 40 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 41 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 42 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 43 | Protein of unknown function (DUF616) | Phvul.006G16PTHR12956://I | Phvul.006G16 |
| 44 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 45 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 46 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 47 | Peroxidase superfamily protein | Phvul.005G051.11.1.7 - Perc | Phvul.005G05 |
| 48 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 49 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 50 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 51 | Peroxidase superfamily protein | Phvul.005G051.11.1.7 - Perc | Phvul.005G05 |
| 52 | phosphatidylinositolglycan-related | Phvul.002G11K03858 - phos | Phvul.002G11 |
| 53 | myb-like HTH transcriptional regulator family protein | Phvul.008G10PF14379 - MY | Phvul.008G10 |
| 54 | myb-like HTH transcriptional regulator family protein | Phvul.008G10PF14379 - MY | Phvul.008G10 |
| 55 | protein binding | Phvul.008G07PTHR33601:Sf | Phvul.008G07 |
| 56 | SAUR-like auxin-responsive protein family | Phvul.003G26PTHR31374:Sf | Phvul.003G26 |
| 57 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155://I | Phvul.008G07 |
| 58 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155://I | Phvul.008G07 |
| 59 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155://I | Phvul.008G07 |
| 60 | gigantea protein (GI) | Phvul.004G08K12124 - GIG | Phvul.004G08 |
| | gigantea protein (GI) | Phvul.004G08K12124 - GIG | Phvul.004G08 |

| | | |
|----|---|---|
| 1 | | |
| 2 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 3 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20K01530 - phosPhvul.009G20 |
| 4 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SFPhvul.005G15 |
| 5 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SFPhvul.005G15 |
| 6 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SFPhvul.005G15 |
| 7 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20K01530 - phosPhvul.009G20 |
| 8 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 9 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 10 | Plant invertase/pectin methylesterase inhibitor superfamily | Phvul.009G22PTHR31707:SFPhvul.009G22 |
| 11 | Protein of unknown function (DUF630) ;Protein of unknown function | Phvul.002G10PF04782 - ProPhvul.002G10 |
| 12 | FASCICLIN-like arabinogalactan 9 | Phvul.005G09PTHR32077:SFPhvul.005G09 |
| 13 | FASCICLIN-like arabinogalactan 9 | Phvul.005G09PTHR32077:SFPhvul.005G09 |
| 14 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:SFPhvul.003G18 |
| 15 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:SFPhvul.003G18 |
| 16 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//IPhvul.003G12 |
| 17 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//IPhvul.003G12 |
| 18 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//IPhvul.003G12 |
| 19 | Peroxidase superfamily protein | Phvul.006G071.11.1.7 - PercPhvul.006G07 |
| 20 | Nucleoporin, Nup133/Nup155-like | Phvul.008G28K14300 - nucleoporinPhvul.008G28 |
| 21 | Nucleoporin, Nup133/Nup155-like | Phvul.008G28K14300 - nucleoporinPhvul.008G28 |
| 22 | ubiquitin-protein ligase 4 | Phvul.007G16PTHR11254:SFPhvul.007G16 |
| 23 | serine hydroxymethyltransferase 4 | Phvul.001G26PTHR11680//IPhvul.001G26 |
| 24 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SFPhvul.006G09 |
| 25 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SFPhvul.006G09 |
| 26 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SFPhvul.006G09 |
| 27 | Phosphatidylinositol 3- and 4-kinase family protein | Phvul.003G03PTHR15245:SFPhvul.003G03 |
| 28 | | 0 0 0 Phvul.009G00 |
| 29 | | 0 0 0 Phvul.009G00 |
| 30 | P-loop containing nucleoside triphosphate hydrolases superfamily | Phvul.003G10PTHR10799//IPhvul.003G10 |
| 31 | P-loop containing nucleoside triphosphate hydrolases superfamily | Phvul.003G10PTHR10799//IPhvul.003G10 |
| 32 | binding | Phvul.002G26PTHR23315:SFPhvul.002G26 |
| 33 | binding | Phvul.002G26PTHR23315:SFPhvul.002G26 |
| 34 | binding | Phvul.002G26PTHR23315:SFPhvul.002G26 |
| 35 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA cyclasePhvul.002G29 |
| 36 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA cyclasePhvul.002G29 |
| 37 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA cyclasePhvul.002G29 |
| 38 | phytochrome interacting factor 3-like 5 | Phvul.007G15PTHR12565:SFPhvul.007G15 |
| 39 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SFPhvul.002G00 |
| 40 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SFPhvul.002G00 |
| 41 | cellulose synthase like G1 | Phvul.005G00PTHR13301//IPhvul.005G00 |
| 42 | cellulose synthase like G1 | Phvul.005G00PTHR13301//IPhvul.005G00 |
| 43 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SFPhvul.002G00 |
| 44 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.008G24PTHR21493//IPhvul.008G24 |
| 45 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.008G24PTHR21493//IPhvul.008G24 |
| 46 | KNOTTED-like from Arabidopsis thaliana 2 | Phvul.007G20PTHR11850//IPhvul.007G20 |
| 47 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 48 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 49 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 50 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 51 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 52 | RING/U-box superfamily protein | Phvul.003G18PTHR22763:SFPhvul.003G18 |
| 53 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 54 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 55 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 56 | Protein of unknown function (DUF616) | Phvul.006G16PTHR12956//IPhvul.006G16 |
| 57 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 58 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 59 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 60 | Peroxidase superfamily protein | Phvul.005G051.11.1.7 - PeroxidasePhvul.005G05 |
| | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |

| | | |
|----|--|--|
| 1 | | |
| 2 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 3 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - PercPhvul.005G05 |
| 4 | phosphatidylinositolglycan-related | Phvul.002G11 K03858 - phosPhvul.002G11 |
| 5 | myb-like HTH transcriptional regulator family protein | Phvul.008G10 PF14379 - MY Phvul.008G10 |
| 6 | protein binding | Phvul.008G07 PTHR33601:SfPhvul.008G07 |
| 7 | SAUR-like auxin-responsive protein family | Phvul.003G26 PTHR31374:SfPhvul.003G26 |
| 8 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07 PTHR23155//IPhvul.008G07 |
| 9 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07 PTHR23155//IPhvul.008G07 |
| 10 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 11 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 12 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 13 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20 K01530 - phosPhvul.009G20 |
| 14 | Plant regulator RWP-RK family protein | Phvul.005G15 PTHR32002:SfPhvul.005G15 |
| 15 | Plant regulator RWP-RK family protein | Phvul.005G15 PTHR32002:SfPhvul.005G15 |
| 16 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20 K01530 - phosPhvul.009G20 |
| 17 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 18 | Plant invertase/pectin methylesterase inhibitor superfamily protein | Phvul.009G22 PTHR31707:SfPhvul.009G22 |
| 19 | Protein of unknown function (DUF630) ;Protein of unknown function (DUF630) | Phvul.002G10 PF04782 - ProPhvul.002G10 |
| 20 | FASCICLIN-like arabinogalactan 9 | Phvul.005G09 PTHR32077:SfPhvul.005G09 |
| 21 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | Phvul.003G18 PTHR12565:SfPhvul.003G18 |
| 22 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | Phvul.003G18 PTHR12565:SfPhvul.003G18 |
| 23 | Nucleotide-sugar transporter family protein | Phvul.003G12 PTHR11132//IPhvul.003G12 |
| 24 | Nucleotide-sugar transporter family protein | Phvul.003G12 PTHR11132//IPhvul.003G12 |
| 25 | Peroxidase superfamily protein | Phvul.006G07 1.11.1.7 - PercPhvul.006G07 |
| 26 | Nucleoporin, Nup133/Nup155-like | Phvul.008G28 K14300 - nucleoporinPhvul.008G28 |
| 27 | ubiquitin-protein ligase 4 | Phvul.007G16 PTHR11254:SfPhvul.007G16 |
| 28 | serine hydroxymethyltransferase 4 | Phvul.001G26 PTHR11680//IPhvul.001G26 |
| 29 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09 PTHR13780:SfPhvul.006G09 |
| 30 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09 PTHR13780:SfPhvul.006G09 |
| 31 | Phosphatidylinositol 3- and 4-kinase family protein | Phvul.003G03 PTHR15245:SfPhvul.003G03 |
| 32 | | 0 0 0 Phvul.009G00 |
| 33 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | Phvul.003G10 PTHR10799//IPhvul.003G10 |
| 34 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | Phvul.003G10 PTHR10799//IPhvul.003G10 |
| 35 | binding | Phvul.002G26 PTHR23315:SfPhvul.002G26 |
| 36 | binding | Phvul.002G26 PTHR23315:SfPhvul.002G26 |
| 37 | RNA cyclase family protein | Phvul.002G29 6.5.1.4 - RNA cyclasePhvul.002G29 |
| 38 | RNA cyclase family protein | Phvul.002G29 6.5.1.4 - RNA cyclasePhvul.002G29 |
| 39 | phytochrome interacting factor 3-like 5 | Phvul.007G15 PTHR12565:SfPhvul.007G15 |
| 40 | RING/U-box superfamily protein | Phvul.002G00 PTHR10044:SfPhvul.002G00 |
| 41 | RING/U-box superfamily protein | Phvul.002G00 PTHR10044:SfPhvul.002G00 |
| 42 | cellulose synthase like G1 | Phvul.005G00 PTHR13301//IPhvul.005G00 |
| 43 | RING/U-box superfamily protein | Phvul.002G00 PTHR10044:SfPhvul.002G00 |
| 44 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.008G24 PTHR21493//IPhvul.008G24 |
| 45 | KNOTTED-like from Arabidopsis thaliana 2 | Phvul.007G20 PTHR11850//IPhvul.007G20 |
| 46 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 47 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |

| | | |
|----|--|--|
| 1 | | |
| 2 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SFPhvul.007G15 |
| 3 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SFPhvul.007G15 |
| 4 | RING/U-box superfamily protein | Phvul.003G18 PTHR22763:SFPhvul.003G18 |
| 5 | | |
| 6 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SFPhvul.007G15 |
| 7 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SFPhvul.007G15 |
| 8 | Protein of unknown function (DUF616) | Phvul.006G16 PTHR12956//IPhvul.006G16 |
| 9 | | |
| 10 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SFPhvul.007G15 |
| 11 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SFPhvul.007G15 |
| 12 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - PercPhvul.005G05 |
| 13 | | |
| 14 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SFPhvul.007G15 |
| 15 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SFPhvul.007G15 |
| 16 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - PercPhvul.005G05 |
| 17 | | |
| 18 | phosphatidylinositolglycan-related | Phvul.002G11 K03858 - phosPhvul.002G11 |
| 19 | myb-like HTH transcriptional regulator family protein | Phvul.008G10 PF14379 - MY Phvul.008G10 |
| 20 | protein binding | Phvul.008G07 PTHR33601:SFPhvul.008G07 |
| 21 | | |
| 22 | SAUR-like auxin-responsive protein family | Phvul.003G26 PTHR31374:SFPhvul.003G26 |
| 23 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07 PTHR23155//IPhvul.008G07 |
| 24 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07 PTHR23155//IPhvul.008G07 |
| 25 | | |
| 26 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 27 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 28 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 29 | | |
| 30 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20 K01530 - phosPhvul.009G20 |
| 31 | Plant regulator RWP-RK family protein | Phvul.005G15 PTHR32002:SFPhvul.005G15 |
| 32 | Plant regulator RWP-RK family protein | Phvul.005G15 PTHR32002:SFPhvul.005G15 |
| 33 | | |
| 34 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20 K01530 - phosPhvul.009G20 |
| 35 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 36 | Plant invertase/pectin methylesterase inhibitor superfamily protein | Phvul.009G22 PTHR31707:SFPhvul.009G22 |
| 37 | Protein of unknown function (DUF630) ;Protein of unknown function (DUF630) | Phvul.002G10 PF04782 - ProPhvul.002G10 |
| 38 | | |
| 39 | FASCICLIN-like arabinogalactan 9 | Phvul.005G09 PTHR32077:SFPhvul.005G09 |
| 40 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | Phvul.003G18 PTHR12565:SFPhvul.003G18 |
| 41 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | Phvul.003G18 PTHR12565:SFPhvul.003G18 |
| 42 | | |
| 43 | Nucleotide-sugar transporter family protein | Phvul.003G12 PTHR11132//IPhvul.003G12 |
| 44 | Nucleotide-sugar transporter family protein | Phvul.003G12 PTHR11132//IPhvul.003G12 |
| 45 | Peroxidase superfamily protein | Phvul.006G07 1.11.1.7 - PercPhvul.006G07 |
| 46 | | |
| 47 | Nucleoporin, Nup133/Nup155-like | Phvul.008G28 K14300 - nuclPhvul.008G28 |
| 48 | ubiquitin-protein ligase 4 | Phvul.007G16 PTHR11254:SFPhvul.007G16 |
| 49 | serine hydroxymethyltransferase 4 | Phvul.001G26 PTHR11680//IPhvul.001G26 |
| 50 | | |
| 51 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09 PTHR13780:SFPhvul.006G09 |
| 52 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09 PTHR13780:SFPhvul.006G09 |
| 53 | Phosphatidylinositol 3- and 4-kinase family protein | Phvul.003G03 PTHR15245:SFPhvul.003G03 |
| 54 | | |
| 55 | | 0 0 0 Phvul.009G00 |
| 56 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | Phvul.003G10 PTHR10799//IPhvul.003G10 |
| 57 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | Phvul.003G10 PTHR10799//IPhvul.003G10 |
| 58 | | |
| 59 | binding | Phvul.002G26 PTHR23315:SFPhvul.002G26 |
| 60 | binding | Phvul.002G26 PTHR23315:SFPhvul.002G26 |
| | RNA cyclase family protein | Phvul.002G29 6.5.1.4 - RNA Phvul.002G29 |

| | | |
|----|--|--|
| 1 | | |
| 2 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA :Phvul.002G29 |
| 3 | phytochrome interacting factor 3-like 5 | Phvul.007G15 PTHR12565:SfPhvul.007G15 |
| 4 | RING/U-box superfamily protein | Phvul.002G00 PTHR10044:SfPhvul.002G00 |
| 5 | RING/U-box superfamily protein | Phvul.002G00 PTHR10044:SfPhvul.002G00 |
| 6 | cellulose synthase like G1 | Phvul.005G00 PTHR13301//IPhvul.005G00 |
| 7 | RING/U-box superfamily protein | Phvul.002G00 PTHR10044:SfPhvul.002G00 |
| 8 | | |
| 9 | | |
| 10 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.008G24 PTHR21493//IPhvul.008G24 |
| 11 | KNOTTED-like from Arabidopsis thaliana 2 | Phvul.007G20 PTHR11850//IPhvul.007G20 |
| 12 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 13 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 14 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 15 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 16 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 17 | RING/U-box superfamily protein | Phvul.003G18 PTHR22763:SfPhvul.003G18 |
| 18 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 19 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 20 | Protein of unknown function (DUF616) | Phvul.006G16 PTHR12956//IPhvul.006G16 |
| 21 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 22 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 23 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - PercPhvul.005G05 |
| 24 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 25 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 26 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - PercPhvul.005G05 |
| 27 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 28 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 29 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - PercPhvul.005G05 |
| 30 | phosphatidylinositolglycan-related | Phvul.002G11 K03858 - phosPhvul.002G11 |
| 31 | myb-like HTH transcriptional regulator family protein | Phvul.008G10 PF14379 - MY Phvul.008G10 |
| 32 | protein binding | Phvul.008G07 PTHR33601:SfPhvul.008G07 |
| 33 | SAUR-like auxin-responsive protein family | Phvul.003G26 PTHR31374:SfPhvul.003G26 |
| 34 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07 PTHR23155//IPhvul.008G07 |
| 35 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07 PTHR23155//IPhvul.008G07 |
| 36 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 37 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 38 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 39 | ATPase E1-E2 type family protein / haloacid dehalogen | Phvul.009G20 K01530 - phosPhvul.009G20 |
| 40 | Plant regulator RWP-RK family protein | Phvul.005G15 PTHR32002:SfPhvul.005G15 |
| 41 | Plant regulator RWP-RK family protein | Phvul.005G15 PTHR32002:SfPhvul.005G15 |
| 42 | ATPase E1-E2 type family protein / haloacid dehalogen | Phvul.009G20 K01530 - phosPhvul.009G20 |
| 43 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 44 | Plant invertase/pectin methylesterase inhibitor superf | Phvul.009G22 PTHR31707:SfPhvul.009G22 |
| 45 | Protein of unknown function (DUF630) ;Protein of unkr | Phvul.002G10 PF04782 - Pro Phvul.002G10 |
| 46 | FASCICLIN-like arabinoogalactan 9 | Phvul.005G09 PTHR32077:SfPhvul.005G09 |
| 47 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18 PTHR12565:SfPhvul.003G18 |
| 48 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18 PTHR12565:SfPhvul.003G18 |
| 49 | Nucleotide-sugar transporter family protein | Phvul.003G12 PTHR11132//IPhvul.003G12 |
| 50 | Nucleotide-sugar transporter family protein | Phvul.003G12 PTHR11132//IPhvul.003G12 |
| 51 | Peroxidase superfamily protein | Phvul.006G07 1.11.1.7 - PercPhvul.006G07 |
| 52 | Nucleoporin, Nup133/Nup155-like | Phvul.008G28 K14300 - nuclPhvul.008G28 |
| 53 | ubiquitin-protein ligase 4 | Phvul.007G16 PTHR11254:SfPhvul.007G16 |

| | | |
|----|--|---|
| 1 | | |
| 2 | serine hydroxymethyltransferase 4 | Phvul.001G26PTHR11680//IPhvul.001G26 |
| 3 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SfPhvul.006G09 |
| 4 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SfPhvul.006G09 |
| 5 | Phosphatidylinositol 3- and 4-kinase family protein | Phvul.003G03PTHR15245:SfPhvul.003G03 |
| 6 | | 0 0 0 Phvul.009G00 |
| 7 | | |
| 8 | P-loop containing nucleoside triphosphate hydrolases | sPhvul.003G10PTHR10799//IPhvul.003G10 |
| 9 | P-loop containing nucleoside triphosphate hydrolases | sPhvul.003G10PTHR10799//IPhvul.003G10 |
| 10 | binding | Phvul.002G26PTHR23315:SfPhvul.002G26 |
| 11 | binding | Phvul.002G26PTHR23315:SfPhvul.002G26 |
| 12 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA :Phvul.002G29 |
| 13 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA :Phvul.002G29 |
| 14 | phytochrome interacting factor 3-like 5 | Phvul.007G15PTHR12565:SfPhvul.007G15 |
| 15 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SfPhvul.002G00 |
| 16 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SfPhvul.002G00 |
| 17 | cellulose synthase like G1 | Phvul.005G00PTHR13301//IPhvul.005G00 |
| 18 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SfPhvul.002G00 |
| 19 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.008G24PTHR21493//IPhvul.008G24 |
| 20 | KNOTTED-like from Arabidopsis thaliana 2 | Phvul.007G20PTHR11850//IPhvul.007G20 |
| 21 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 22 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 23 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 24 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 25 | RING/U-box superfamily protein | Phvul.003G18PTHR22763:SfPhvul.003G18 |
| 26 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 27 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 28 | Protein of unknown function (DUF616) | Phvul.006G16PTHR12956//IPhvul.006G16 |
| 29 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 30 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 31 | Peroxidase superfamily protein | Phvul.005G051.11.1.7 - PercPhvul.005G05 |
| 32 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 33 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 34 | Peroxidase superfamily protein | Phvul.005G051.11.1.7 - PercPhvul.005G05 |
| 35 | phosphatidylinositolglycan-related | Phvul.002G11K03858 - phosPhvul.002G11 |
| 36 | myb-like HTH transcriptional regulator family protein | Phvul.008G10PF14379 - MYPhvul.008G10 |
| 37 | protein binding | Phvul.008G07PTHR33601:SfPhvul.008G07 |
| 38 | SAUR-like auxin-responsive protein family | Phvul.003G26PTHR31374:SfPhvul.003G26 |
| 39 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//IPhvul.008G07 |
| 40 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//IPhvul.008G07 |
| 41 | gigantea protein (GI) | Phvul.004G08K12124 - GIG#Phvul.004G08 |
| 42 | gigantea protein (GI) | Phvul.004G08K12124 - GIG#Phvul.004G08 |
| 43 | gigantea protein (GI) | Phvul.004G08K12124 - GIG#Phvul.004G08 |
| 44 | ATPase E1-E2 type family protein / haloacid dehalogen | Phvul.009G20K01530 - phosPhvul.009G20 |
| 45 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SfPhvul.005G15 |
| 46 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SfPhvul.005G15 |
| 47 | ATPase E1-E2 type family protein / haloacid dehalogen | Phvul.009G20K01530 - phosPhvul.009G20 |
| 48 | gigantea protein (GI) | Phvul.004G08K12124 - GIG#Phvul.004G08 |

| | | | |
|----|---|------------------------------|--------------|
| 1 | Plant invertase/pectin methylesterase inhibitor superfamily | Phvul.009G22 PTHR31707:SF | Phvul.009G22 |
| 2 | Protein of unknown function (DUF630) ;Protein of unknown function | Phvul.002G10 PF04782 - Pro | Phvul.002G10 |
| 3 | FASCICLIN-like arabinogalactan 9 | Phvul.005G09 PTHR32077:SF | Phvul.005G09 |
| 4 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18 PTHR12565:SF | Phvul.003G18 |
| 5 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18 PTHR12565:SF | Phvul.003G18 |
| 6 | Nucleotide-sugar transporter family protein | Phvul.003G12 PTHR11132://I | Phvul.003G12 |
| 7 | Nucleotide-sugar transporter family protein | Phvul.003G12 PTHR11132://I | Phvul.003G12 |
| 8 | Peroxidase superfamily protein | Phvul.006G07 1.11.1.7 - Perc | Phvul.006G07 |
| 9 | Nucleoporin, Nup133/Nup155-like | Phvul.008G28 K14300 - nucle | Phvul.008G28 |
| 10 | ubiquitin-protein ligase 4 | Phvul.007G16 PTHR11254:SF | Phvul.007G16 |
| 11 | serine hydroxymethyltransferase 4 | Phvul.001G26 PTHR11680://I | Phvul.001G26 |
| 12 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09 PTHR13780:SF | Phvul.006G09 |
| 13 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09 PTHR13780:SF | Phvul.006G09 |
| 14 | Phosphatidylinositol 3- and 4-kinase family protein | Phvul.003G03 PTHR15245:SF | Phvul.003G03 |
| 15 | | 0 | 0 |
| 16 | | 0 | 0 |
| 17 | P-loop containing nucleoside triphosphate hydrolases superfamily | Phvul.003G10 PTHR10799://I | Phvul.003G10 |
| 18 | P-loop containing nucleoside triphosphate hydrolases superfamily | Phvul.003G10 PTHR10799://I | Phvul.003G10 |
| 19 | binding | Phvul.002G26 PTHR23315:SF | Phvul.002G26 |
| 20 | binding | Phvul.002G26 PTHR23315:SF | Phvul.002G26 |
| 21 | RNA cyclase family protein | Phvul.002G29 6.5.1.4 - RNA | Phvul.002G29 |
| 22 | RNA cyclase family protein | Phvul.002G29 6.5.1.4 - RNA | Phvul.002G29 |
| 23 | phytochrome interacting factor 3-like 5 | Phvul.007G15 PTHR12565:SF | Phvul.007G15 |
| 24 | RING/U-box superfamily protein | Phvul.002G00 PTHR10044:SF | Phvul.002G00 |
| 25 | RING/U-box superfamily protein | Phvul.002G00 PTHR10044:SF | Phvul.002G00 |
| 26 | cellulose synthase like G1 | Phvul.005G00 PTHR13301://I | Phvul.005G00 |
| 27 | RING/U-box superfamily protein | Phvul.002G00 PTHR10044:SF | Phvul.002G00 |
| 28 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.008G24 PTHR21493://I | Phvul.008G24 |
| 29 | KNOTTED-like from Arabidopsis thaliana 2 | Phvul.007G20 PTHR11850://I | Phvul.007G20 |
| 30 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 31 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 32 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 33 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 34 | RING/U-box superfamily protein | Phvul.003G18 PTHR22763:SF | Phvul.003G18 |
| 35 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 36 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 37 | Protein of unknown function (DUF616) | Phvul.006G16 PTHR12956://I | Phvul.006G16 |
| 38 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 39 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 40 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - Perc | Phvul.005G05 |
| 41 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 42 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 43 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - Perc | Phvul.005G05 |
| 44 | phosphatidylinositolglycan-related | Phvul.002G11 K03858 - phos | Phvul.002G11 |
| 45 | myb-like HTH transcriptional regulator family protein | Phvul.008G10 PF14379 - MY | Phvul.008G10 |
| 46 | protein binding | Phvul.008G07 PTHR33601:SF | Phvul.008G07 |
| 47 | SAUR-like auxin-responsive protein family | Phvul.003G26 PTHR31374:SF | Phvul.003G26 |

| | | |
|----|--|---|
| 1 | | |
| 2 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//IPhvul.008G07 |
| 3 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//IPhvul.008G07 |
| 4 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 5 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 6 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 7 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 8 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20K01530 - phosPhvul.009G20 |
| 9 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20K01530 - phosPhvul.009G20 |
| 10 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SFPhvul.005G15 |
| 11 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SFPhvul.005G15 |
| 12 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20K01530 - phosPhvul.009G20 |
| 13 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20K01530 - phosPhvul.009G20 |
| 14 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 15 | Plant invertase/pectin methylesterase inhibitor superfamily | Phvul.009G22PTHR31707:SFPhvul.009G22 |
| 16 | Protein of unknown function (DUF630) ;Protein of unknown function (DUF630) | Phvul.002G10PF04782 - ProPhvul.002G10 |
| 17 | Protein of unknown function (DUF630) ;Protein of unknown function (DUF630) | Phvul.002G10PF04782 - ProPhvul.002G10 |
| 18 | FASCICLIN-like arabinogalactan 9 | Phvul.005G09PTHR32077:SFPhvul.005G09 |
| 19 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:SFPhvul.003G18 |
| 20 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:SFPhvul.003G18 |
| 21 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:SFPhvul.003G18 |
| 22 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//IPhvul.003G12 |
| 23 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//IPhvul.003G12 |
| 24 | Peroxidase superfamily protein | Phvul.006G071.11.1.7 - PercPhvul.006G07 |
| 25 | Peroxidase superfamily protein | Phvul.006G071.11.1.7 - PercPhvul.006G07 |
| 26 | Nucleoporin, Nup133/Nup155-like | Phvul.008G28K14300 - nuclPhvul.008G28 |
| 27 | ubiquitin-protein ligase 4 | Phvul.007G16PTHR11254:SFPhvul.007G16 |
| 28 | serine hydroxymethyltransferase 4 | Phvul.001G26PTHR11680//IPhvul.001G26 |
| 29 | serine hydroxymethyltransferase 4 | Phvul.001G26PTHR11680//IPhvul.001G26 |
| 30 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SFPhvul.006G09 |
| 31 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SFPhvul.006G09 |
| 32 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SFPhvul.006G09 |
| 33 | Phosphatidylinositol 3- and 4-kinase family protein | Phvul.003G03PTHR15245:SFPhvul.003G03 |
| 34 | Phosphatidylinositol 3- and 4-kinase family protein | Phvul.003G03PTHR15245:SFPhvul.003G03 |
| 35 | P-loop containing nucleoside triphosphate hydrolases superfamily | Phvul.003G10PTHR10799//IPhvul.003G10 |
| 36 | P-loop containing nucleoside triphosphate hydrolases superfamily | Phvul.003G10PTHR10799//IPhvul.003G10 |
| 37 | P-loop containing nucleoside triphosphate hydrolases superfamily | Phvul.003G10PTHR10799//IPhvul.003G10 |
| 38 | binding | Phvul.002G26PTHR23315:SFPhvul.002G26 |
| 39 | binding | Phvul.002G26PTHR23315:SFPhvul.002G26 |
| 40 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA Phvul.002G29 |
| 41 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA Phvul.002G29 |
| 42 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA Phvul.002G29 |
| 43 | phytochrome interacting factor 3-like 5 | Phvul.007G15PTHR12565:SFPhvul.007G15 |
| 44 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SFPhvul.002G00 |
| 45 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SFPhvul.002G00 |
| 46 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SFPhvul.002G00 |
| 47 | cellulose synthase like G1 | Phvul.005G00PTHR13301//IPhvul.005G00 |
| 48 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SFPhvul.002G00 |
| 49 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.008G24PTHR21493//IPhvul.008G24 |
| 50 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.008G24PTHR21493//IPhvul.008G24 |
| 51 | KNOTTED-like from Arabidopsis thaliana 2 | Phvul.007G20PTHR11850//IPhvul.007G20 |
| 52 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 53 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 54 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 55 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 56 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 57 | RING/U-box superfamily protein | Phvul.003G18PTHR22763:SFPhvul.003G18 |
| 58 | RING/U-box superfamily protein | Phvul.003G18PTHR22763:SFPhvul.003G18 |
| 59 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 60 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| | Protein of unknown function (DUF616) | Phvul.006G16PTHR12956//IPhvul.006G16 |

| | | | |
|----|---|-----------------------------|--------------|
| 1 | | | |
| 2 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SF | Phvul.007G15 |
| 3 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SF | Phvul.007G15 |
| 4 | Peroxidase superfamily protein | Phvul.005G051.11.1.7 - Perc | Phvul.005G05 |
| 5 | | | |
| 6 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SF | Phvul.007G15 |
| 7 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SF | Phvul.007G15 |
| 8 | Peroxidase superfamily protein | Phvul.005G051.11.1.7 - Perc | Phvul.005G05 |
| 9 | | | |
| 10 | phosphatidylinositolglycan-related | Phvul.002G11K03858 - phos | Phvul.002G11 |
| 11 | myb-like HTH transcriptional regulator family protein | Phvul.008G10PF14379 - MY | Phvul.008G10 |
| 12 | protein binding | Phvul.008G07PTHR33601:SF | Phvul.008G07 |
| 13 | | | |
| 14 | SAUR-like auxin-responsive protein family | Phvul.003G26PTHR31374:SF | Phvul.003G26 |
| 15 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//I | Phvul.008G07 |
| 16 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//I | Phvul.008G07 |
| 17 | | | |
| 18 | gigantea protein (GI) | Phvul.004G08K12124 - GIG | Phvul.004G08 |
| 19 | gigantea protein (GI) | Phvul.004G08K12124 - GIG | Phvul.004G08 |
| 20 | gigantea protein (GI) | Phvul.004G08K12124 - GIG | Phvul.004G08 |
| 21 | | | |
| 22 | ATPase E1-E2 type family protein / haloacid dehalogen | Phvul.009G20K01530 - phos | Phvul.009G20 |
| 23 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SF | Phvul.005G15 |
| 24 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SF | Phvul.005G15 |
| 25 | | | |
| 26 | ATPase E1-E2 type family protein / haloacid dehalogen | Phvul.009G20K01530 - phos | Phvul.009G20 |
| 27 | gigantea protein (GI) | Phvul.004G08K12124 - GIG | Phvul.004G08 |
| 28 | Plant invertase/pectin methylesterase inhibitor superfa | Phvul.009G22PTHR31707:SF | Phvul.009G22 |
| 29 | Protein of unknown function (DUF630) ;Protein of unkr | Phvul.002G10PF04782 - Pro | Phvul.002G10 |
| 30 | | | |
| 31 | FASCICLIN-like arabinoogalactan 9 | Phvul.005G09PTHR32077:SF | Phvul.005G09 |
| 32 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:SF | Phvul.003G18 |
| 33 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:SF | Phvul.003G18 |
| 34 | | | |
| 35 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//I | Phvul.003G12 |
| 36 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//I | Phvul.003G12 |
| 37 | | | |
| 38 | Peroxidase superfamily protein | Phvul.006G071.11.1.7 - Perc | Phvul.006G07 |
| 39 | Nucleoporin, Nup133/Nup155-like | Phvul.008G28K14300 - nucl | Phvul.008G28 |
| 40 | ubiquitin-protein ligase 4 | Phvul.007G16PTHR11254:SF | Phvul.007G16 |
| 41 | serine hydroxymethyltransferase 4 | Phvul.001G26PTHR11680//I | Phvul.001G26 |
| 42 | | | |
| 43 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SF | Phvul.006G09 |
| 44 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SF | Phvul.006G09 |
| 45 | Phosphatidylinositol 3- and 4-kinase family protein | Phvul.003G03PTHR15245:SF | Phvul.003G03 |
| 46 | | | |
| 47 | | 0 0 0 | Phvul.009G00 |
| 48 | P-loop containing nucleoside triphosphate hydrolases s | Phvul.003G10PTHR10799//I | Phvul.003G10 |
| 49 | P-loop containing nucleoside triphosphate hydrolases s | Phvul.003G10PTHR10799//I | Phvul.003G10 |
| 50 | | | |
| 51 | binding | Phvul.002G26PTHR23315:SF | Phvul.002G26 |
| 52 | binding | Phvul.002G26PTHR23315:SF | Phvul.002G26 |
| 53 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA | Phvul.002G29 |
| 54 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA | Phvul.002G29 |
| 55 | | | |
| 56 | phytochrome interacting factor 3-like 5 | Phvul.007G15PTHR12565:SF | Phvul.007G15 |
| 57 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SF | Phvul.002G00 |
| 58 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SF | Phvul.002G00 |
| 59 | cellulose synthase like G1 | Phvul.005G00PTHR13301//I | Phvul.005G00 |
| 60 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SF | Phvul.002G00 |

| | | | |
|----|--|------------------------------|--------------|
| 1 | | | |
| 2 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.008G24PTHR21493//I | Phvul.008G24 |
| 3 | KNOTTED-like from Arabidopsis thaliana 2 | Phvul.007G20PTHR11850//I | Phvul.007G20 |
| 4 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 5 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 6 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 7 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 8 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 9 | RING/U-box superfamily protein | Phvul.003G18PTHR22763:Sf | Phvul.003G18 |
| 10 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 11 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 12 | Protein of unknown function (DUF616) | Phvul.006G16PTHR12956//I | Phvul.006G16 |
| 13 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 14 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 15 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - Perc | Phvul.005G05 |
| 16 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 17 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 18 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - Perc | Phvul.005G05 |
| 19 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 20 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:Sf | Phvul.007G15 |
| 21 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - Perc | Phvul.005G05 |
| 22 | phosphatidylinositolglycan-related | Phvul.002G11K03858 - phos | Phvul.002G11 |
| 23 | myb-like HTH transcriptional regulator family protein | Phvul.008G10PF14379 - MY | Phvul.008G10 |
| 24 | protein binding | Phvul.008G07PTHR33601:Sf | Phvul.008G07 |
| 25 | SAUR-like auxin-responsive protein family | Phvul.003G26PTHR31374:Sf | Phvul.003G26 |
| 26 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//I | Phvul.008G07 |
| 27 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//I | Phvul.008G07 |
| 28 | gigantea protein (GI) | Phvul.004G08K12124 - GIG | Phvul.004G08 |
| 29 | gigantea protein (GI) | Phvul.004G08K12124 - GIG | Phvul.004G08 |
| 30 | gigantea protein (GI) | Phvul.004G08K12124 - GIG | Phvul.004G08 |
| 31 | ATPase E1-E2 type family protein / haloacid dehalogen | Phvul.009G20K01530 - phos | Phvul.009G20 |
| 32 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:Sf | Phvul.005G15 |
| 33 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:Sf | Phvul.005G15 |
| 34 | ATPase E1-E2 type family protein / haloacid dehalogen | Phvul.009G20K01530 - phos | Phvul.009G20 |
| 35 | gigantea protein (GI) | Phvul.004G08K12124 - GIG | Phvul.004G08 |
| 36 | Plant invertase/pectin methylesterase inhibitor superfa | Phvul.009G22PTHR31707:Sf | Phvul.009G22 |
| 37 | Protein of unknown function (DUF630) ;Protein of unkn | Phvul.002G10PF04782 - Pro | Phvul.002G10 |
| 38 | FASCICLIN-like arabinoogalactan 9 | Phvul.005G09PTHR32077:Sf | Phvul.005G09 |
| 39 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:Sf | Phvul.003G18 |
| 40 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:Sf | Phvul.003G18 |
| 41 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//I | Phvul.003G12 |
| 42 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//I | Phvul.003G12 |
| 43 | Peroxidase superfamily protein | Phvul.006G07 1.11.1.7 - Perc | Phvul.006G07 |
| 44 | Nucleoporin, Nup133/Nup155-like | Phvul.008G28K14300 - nucl | Phvul.008G28 |
| 45 | ubiquitin-protein ligase 4 | Phvul.007G16PTHR11254:Sf | Phvul.007G16 |
| 46 | serine hydroxymethyltransferase 4 | Phvul.001G26PTHR11680//I | Phvul.001G26 |
| 47 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:Sf | Phvul.006G09 |
| 48 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:Sf | Phvul.006G09 |
| 49 | Phosphatidylinositol 3- and 4-kinase family protein | Phvul.003G03PTHR15245:Sf | Phvul.003G03 |
| 50 | | 0 | 0 |
| 51 | | 0 | 0 |
| 52 | P-loop containing nucleoside triphosphate hydrolases s | Phvul.003G10PTHR10799//I | Phvul.003G10 |

| | | |
|----|--|---|
| 1 | | |
| 2 | P-loop containing nucleoside triphosphate hydrolases | sPhvul.003G10PTHR10799//IPhvul.003G10 |
| 3 | binding | Phvul.002G26PTHR23315:SfPhvul.002G26 |
| 4 | binding | Phvul.002G26PTHR23315:SfPhvul.002G26 |
| 5 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA :Phvul.002G29 |
| 6 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA :Phvul.002G29 |
| 7 | phytochrome interacting factor 3-like 5 | Phvul.007G15PTHR12565:SfPhvul.007G15 |
| 8 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SfPhvul.002G00 |
| 9 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SfPhvul.002G00 |
| 10 | cellulose synthase like G1 | Phvul.005G00PTHR13301//IPhvul.005G00 |
| 11 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SfPhvul.002G00 |
| 12 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.008G24PTHR21493//IPhvul.008G24 |
| 13 | KNOTTED-like from Arabidopsis thaliana 2 | Phvul.007G20PTHR11850//IPhvul.007G20 |
| 14 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 15 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 16 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 17 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 18 | RING/U-box superfamily protein | Phvul.003G18PTHR22763:SfPhvul.003G18 |
| 19 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 20 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 21 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 22 | RING/U-box superfamily protein | Phvul.003G18PTHR22763:SfPhvul.003G18 |
| 23 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 24 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 25 | Protein of unknown function (DUF616) | Phvul.006G16PTHR12956//IPhvul.006G16 |
| 26 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 27 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 28 | Peroxidase superfamily protein | Phvul.005G051.11.1.7 - PercPhvul.005G05 |
| 29 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 30 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 31 | Peroxidase superfamily protein | Phvul.005G051.11.1.7 - PercPhvul.005G05 |
| 32 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 33 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 34 | Peroxidase superfamily protein | Phvul.005G051.11.1.7 - PercPhvul.005G05 |
| 35 | phosphatidylinositolglycan-related | Phvul.002G11K03858 - phosPhvul.002G11 |
| 36 | myb-like HTH transcriptional regulator family protein | Phvul.008G10PF14379 - MY Phvul.008G10 |
| 37 | protein binding | Phvul.008G07PTHR33601:SfPhvul.008G07 |
| 38 | SAUR-like auxin-responsive protein family | Phvul.003G26PTHR31374:SfPhvul.003G26 |
| 39 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//IPhvul.008G07 |
| 40 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//IPhvul.008G07 |
| 41 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 42 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 43 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 44 | ATPase E1-E2 type family protein / haloacid dehalogen | Phvul.009G20K01530 - phosPhvul.009G20 |
| 45 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SfPhvul.005G15 |
| 46 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SfPhvul.005G15 |
| 47 | ATPase E1-E2 type family protein / haloacid dehalogen | Phvul.009G20K01530 - phosPhvul.009G20 |
| 48 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 49 | Plant invertase/pectin methylesterase inhibitor superfa | Phvul.009G22PTHR31707:SfPhvul.009G22 |
| 50 | Protein of unknown function (DUF630) ;Protein of unkr | Phvul.002G10PF04782 - ProPhvul.002G10 |
| 51 | FASCICLIN-like arabinogalactan 9 | Phvul.005G09PTHR32077:SfPhvul.005G09 |
| 52 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:SfPhvul.003G18 |
| 53 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:SfPhvul.003G18 |
| 54 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//IPhvul.003G12 |

| | | |
|----|--|--|
| 1 | | |
| 2 | Nucleotide-sugar transporter family protein | Phvul.003G12 PTHR11132//IPhvul.003G12 |
| 3 | Peroxidase superfamily protein | Phvul.006G07 1.11.1.7 - PercPhvul.006G07 |
| 4 | Nucleoporin, Nup133/Nup155-like | Phvul.008G28 K14300 - nuclIPhvul.008G28 |
| 5 | ubiquitin-protein ligase 4 | Phvul.007G16 PTHR11254:SFPhvul.007G16 |
| 6 | serine hydroxymethyltransferase 4 | Phvul.001G26 PTHR11680//IPhvul.001G26 |
| 7 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09 PTHR13780:SFPhvul.006G09 |
| 8 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09 PTHR13780:SFPhvul.006G09 |
| 9 | Phosphatidylinositol 3- and 4-kinase family protein | Phvul.003G03 PTHR15245:SFPhvul.003G03 |
| 10 | | 0 0 0 Phvul.009G00 |
| 11 | | |
| 12 | | |
| 13 | | |
| 14 | P-loop containing nucleoside triphosphate hydrolases s | Phvul.003G10 PTHR10799//IPhvul.003G10 |
| 15 | P-loop containing nucleoside triphosphate hydrolases s | Phvul.003G10 PTHR10799//IPhvul.003G10 |
| 16 | binding | Phvul.002G26 PTHR23315:SFPhvul.002G26 |
| 17 | binding | Phvul.002G26 PTHR23315:SFPhvul.002G26 |
| 18 | RNA cyclase family protein | Phvul.002G29 6.5.1.4 - RNA :Phvul.002G29 |
| 19 | RNA cyclase family protein | Phvul.002G29 6.5.1.4 - RNA :Phvul.002G29 |
| 20 | phytochrome interacting factor 3-like 5 | Phvul.007G15 PTHR12565:SFPhvul.007G15 |
| 21 | RING/U-box superfamily protein | Phvul.002G00 PTHR10044:SFPhvul.002G00 |
| 22 | RING/U-box superfamily protein | Phvul.002G00 PTHR10044:SFPhvul.002G00 |
| 23 | cellulose synthase like G1 | Phvul.005G00 PTHR13301//IPhvul.005G00 |
| 24 | RING/U-box superfamily protein | Phvul.002G00 PTHR10044:SFPhvul.002G00 |
| 25 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.008G24 PTHR21493//IPhvul.008G24 |
| 26 | KNOTTED-like from Arabidopsis thaliana 2 | Phvul.007G20 PTHR11850//IPhvul.007G20 |
| 27 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SFPhvul.007G15 |
| 28 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SFPhvul.007G15 |
| 29 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SFPhvul.007G15 |
| 30 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SFPhvul.007G15 |
| 31 | RING/U-box superfamily protein | Phvul.003G18 PTHR22763:SFPhvul.003G18 |
| 32 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SFPhvul.007G15 |
| 33 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SFPhvul.007G15 |
| 34 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SFPhvul.007G15 |
| 35 | Protein of unknown function (DUF616) | Phvul.006G16 PTHR12956//IPhvul.006G16 |
| 36 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SFPhvul.007G15 |
| 37 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SFPhvul.007G15 |
| 38 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - PercPhvul.005G05 |
| 39 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SFPhvul.007G15 |
| 40 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SFPhvul.007G15 |
| 41 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - PercPhvul.005G05 |
| 42 | phosphatidylinositolglycan-related | Phvul.002G11 K03858 - phosPhvul.002G11 |
| 43 | myb-like HTH transcriptional regulator family protein | Phvul.008G10 PF14379 - MY Phvul.008G10 |
| 44 | protein binding | Phvul.008G07 PTHR33601:SFPhvul.008G07 |
| 45 | SAUR-like auxin-responsive protein family | Phvul.003G26 PTHR31374:SFPhvul.003G26 |
| 46 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07 PTHR23155//IPhvul.008G07 |
| 47 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07 PTHR23155//IPhvul.008G07 |
| 48 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 49 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 50 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 51 | ATPase E1-E2 type family protein / haloacid dehalogen | Phvul.009G20 K01530 - phosPhvul.009G20 |

| | | | |
|----|---|------------------------------|--------------|
| 1 | Plant regulator RWP-RK family protein | Phvul.005G15 PTHR32002:SF | Phvul.005G15 |
| 2 | Plant regulator RWP-RK family protein | Phvul.005G15 PTHR32002:SF | Phvul.005G15 |
| 3 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20 K01530 - phos | Phvul.009G20 |
| 4 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG | Phvul.004G08 |
| 5 | Plant invertase/pectin methylesterase inhibitor superfamily | Phvul.009G22 PTHR31707:SF | Phvul.009G22 |
| 6 | Protein of unknown function (DUF630) ;Protein of unknown function | Phvul.002G10 PF04782 - Pro | Phvul.002G10 |
| 7 | FASCICLIN-like arabinogalactan 9 | Phvul.005G09 PTHR32077:SF | Phvul.005G09 |
| 8 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18 PTHR12565:SF | Phvul.003G18 |
| 9 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18 PTHR12565:SF | Phvul.003G18 |
| 10 | Nucleotide-sugar transporter family protein | Phvul.003G12 PTHR11132://I | Phvul.003G12 |
| 11 | Nucleotide-sugar transporter family protein | Phvul.003G12 PTHR11132://I | Phvul.003G12 |
| 12 | Peroxidase superfamily protein | Phvul.006G07 1.11.1.7 - Perc | Phvul.006G07 |
| 13 | Nucleoporin, Nup133/Nup155-like | Phvul.008G28 K14300 - nucl | Phvul.008G28 |
| 14 | ubiquitin-protein ligase 4 | Phvul.007G16 PTHR11254:SF | Phvul.007G16 |
| 15 | serine hydroxymethyltransferase 4 | Phvul.001G26 PTHR11680://I | Phvul.001G26 |
| 16 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09 PTHR13780:SF | Phvul.006G09 |
| 17 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09 PTHR13780:SF | Phvul.006G09 |
| 18 | Phosphatidylinositol 3- and 4-kinase family protein | Phvul.003G03 PTHR15245:SF | Phvul.003G03 |
| 19 | | 0 | 0 |
| 20 | | 0 | 0 |
| 21 | P-loop containing nucleoside triphosphate hydrolases | Phvul.003G10 PTHR10799://I | Phvul.003G10 |
| 22 | P-loop containing nucleoside triphosphate hydrolases | Phvul.003G10 PTHR10799://I | Phvul.003G10 |
| 23 | binding | Phvul.002G26 PTHR23315:SF | Phvul.002G26 |
| 24 | binding | Phvul.002G26 PTHR23315:SF | Phvul.002G26 |
| 25 | RNA cyclase family protein | Phvul.002G29 6.5.1.4 - RNA | Phvul.002G29 |
| 26 | RNA cyclase family protein | Phvul.002G29 6.5.1.4 - RNA | Phvul.002G29 |
| 27 | phytochrome interacting factor 3-like 5 | Phvul.007G15 PTHR12565:SF | Phvul.007G15 |
| 28 | RING/U-box superfamily protein | Phvul.002G00 PTHR10044:SF | Phvul.002G00 |
| 29 | RING/U-box superfamily protein | Phvul.002G00 PTHR10044:SF | Phvul.002G00 |
| 30 | cellulose synthase like G1 | Phvul.005G00 PTHR13301://I | Phvul.005G00 |
| 31 | RING/U-box superfamily protein | Phvul.002G00 PTHR10044:SF | Phvul.002G00 |
| 32 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.008G24 PTHR21493://I | Phvul.008G24 |
| 33 | KNOTTED-like from Arabidopsis thaliana 2 | Phvul.007G20 PTHR11850://I | Phvul.007G20 |
| 34 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 35 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 36 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 37 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 38 | RING/U-box superfamily protein | Phvul.003G18 PTHR22763:SF | Phvul.003G18 |
| 39 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 40 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 41 | Protein of unknown function (DUF616) | Phvul.006G16 PTHR12956://I | Phvul.006G16 |
| 42 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 43 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 44 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - Perc | Phvul.005G05 |
| 45 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 46 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SF | Phvul.007G15 |
| 47 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - Perc | Phvul.005G05 |

| | | |
|----|--|---|
| 1 | | |
| 2 | phosphatidylinositolglycan-related | Phvul.002G11K03858 - phosPhvul.002G11 |
| 3 | myb-like HTH transcriptional regulator family protein | Phvul.008G10PF14379 - MY Phvul.008G10 |
| 4 | protein binding | Phvul.008G07PTHR33601:SfPhvul.008G07 |
| 5 | SAUR-like auxin-responsive protein family | Phvul.003G26PTHR31374:SfPhvul.003G26 |
| 6 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//IPhvul.008G07 |
| 7 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//IPhvul.008G07 |
| 8 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 9 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 10 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 11 | ATPase E1-E2 type family protein / haloacid dehalogen | Phvul.009G20K01530 - phosPhvul.009G20 |
| 12 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SfPhvul.005G15 |
| 13 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SfPhvul.005G15 |
| 14 | ATPase E1-E2 type family protein / haloacid dehalogen | Phvul.009G20K01530 - phosPhvul.009G20 |
| 15 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 16 | Plant invertase/pectin methylesterase inhibitor superfam | Phvul.009G22PTHR31707:SfPhvul.009G22 |
| 17 | Protein of unknown function (DUF630) ;Protein of unkn | Phvul.002G10PF04782 - Pro Phvul.002G10 |
| 18 | FASCICLIN-like arabinogalactan 9 | Phvul.005G09PTHR32077:SfPhvul.005G09 |
| 19 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:SfPhvul.003G18 |
| 20 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:SfPhvul.003G18 |
| 21 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//IPhvul.003G12 |
| 22 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//IPhvul.003G12 |
| 23 | Peroxidase superfamily protein | Phvul.006G071.11.1.7 - PercPhvul.006G07 |
| 24 | Nucleoporin, Nup133/Nup155-like | Phvul.008G28K14300 - nuclPhvul.008G28 |
| 25 | ubiquitin-protein ligase 4 | Phvul.007G16PTHR11254:SfPhvul.007G16 |
| 26 | serine hydroxymethyltransferase 4 | Phvul.001G26PTHR11680//IPhvul.001G26 |
| 27 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SfPhvul.006G09 |
| 28 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SfPhvul.006G09 |
| 29 | Phosphatidylinositol 3- and 4-kinase family protein | Phvul.003G03PTHR15245:SfPhvul.003G03 |
| 30 | | 0 0 0 Phvul.009G00 |
| 31 | P-loop containing nucleoside triphosphate hydrolases s | Phvul.003G10PTHR10799//IPhvul.003G10 |
| 32 | P-loop containing nucleoside triphosphate hydrolases s | Phvul.003G10PTHR10799//IPhvul.003G10 |
| 33 | binding | Phvul.002G26PTHR23315:SfPhvul.002G26 |
| 34 | binding | Phvul.002G26PTHR23315:SfPhvul.002G26 |
| 35 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA Phvul.002G29 |
| 36 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA Phvul.002G29 |
| 37 | phytochrome interacting factor 3-like 5 | Phvul.007G15PTHR12565:SfPhvul.007G15 |
| 38 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SfPhvul.002G00 |
| 39 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SfPhvul.002G00 |
| 40 | cellulose synthase like G1 | Phvul.005G00PTHR13301//IPhvul.005G00 |
| 41 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SfPhvul.002G00 |
| 42 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.008G24PTHR21493//IPhvul.008G24 |
| 43 | KNOTTED-like from Arabidopsis thaliana 2 | Phvul.007G20PTHR11850//IPhvul.007G20 |
| 44 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 45 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 46 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 47 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 48 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |

| | | |
|----|--|--|
| 1 | | |
| 2 | RING/U-box superfamily protein | Phvul.003G18PTHR22763:SfPhvul.003G18 |
| 3 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 4 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 5 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 6 | Protein of unknown function (DUF616) | Phvul.006G16PTHR12956//IPhvul.006G16 |
| 7 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 8 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 9 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 10 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - PercPhvul.005G05 |
| 11 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 12 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 13 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 14 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - PercPhvul.005G05 |
| 15 | phosphatidylinositolglycan-related | Phvul.002G11K03858 - phosPhvul.002G11 |
| 16 | myb-like HTH transcriptional regulator family protein | Phvul.008G10PF14379 - MY Phvul.008G10 |
| 17 | protein binding | Phvul.008G07PTHR33601:SfPhvul.008G07 |
| 18 | protein binding | Phvul.008G07PTHR33601:SfPhvul.008G07 |
| 19 | SAUR-like auxin-responsive protein family | Phvul.003G26PTHR31374:SfPhvul.003G26 |
| 20 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//IPhvul.008G07 |
| 21 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//IPhvul.008G07 |
| 22 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//IPhvul.008G07 |
| 23 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 24 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 25 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 26 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 27 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20K01530 - phosPhvul.009G20 |
| 28 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SfPhvul.005G15 |
| 29 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SfPhvul.005G15 |
| 30 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SfPhvul.005G15 |
| 31 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20K01530 - phosPhvul.009G20 |
| 32 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20K01530 - phosPhvul.009G20 |
| 33 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 34 | Plant invertase/pectin methylesterase inhibitor superfamily protein | Phvul.009G22PTHR31707:SfPhvul.009G22 |
| 35 | Protein of unknown function (DUF630) ;Protein of unknown function (DUF630) | Phvul.002G10PF04782 - ProPhvul.002G10 |
| 36 | FASCICLIN-like arabinogalactan 9 | Phvul.005G09PTHR32077:SfPhvul.005G09 |
| 37 | FASCICLIN-like arabinogalactan 9 | Phvul.005G09PTHR32077:SfPhvul.005G09 |
| 38 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | Phvul.003G18PTHR12565:SfPhvul.003G18 |
| 39 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | Phvul.003G18PTHR12565:SfPhvul.003G18 |
| 40 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//IPhvul.003G12 |
| 41 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//IPhvul.003G12 |
| 42 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//IPhvul.003G12 |
| 43 | Peroxidase superfamily protein | Phvul.006G07 1.11.1.7 - PercPhvul.006G07 |
| 44 | Nucleoporin, Nup133/Nup155-like | Phvul.008G28K14300 - nuclPhvul.008G28 |
| 45 | ubiquitin-protein ligase 4 | Phvul.007G16PTHR11254:SfPhvul.007G16 |
| 46 | ubiquitin-protein ligase 4 | Phvul.007G16PTHR11254:SfPhvul.007G16 |
| 47 | serine hydroxymethyltransferase 4 | Phvul.001G26PTHR11680//IPhvul.001G26 |
| 48 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SfPhvul.006G09 |
| 49 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SfPhvul.006G09 |
| 50 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SfPhvul.006G09 |
| 51 | Phosphatidylinositol 3- and 4-kinase family protein | Phvul.003G03PTHR15245:SfPhvul.003G03 |
| 52 | | 0 0 0 Phvul.009G00 |
| 53 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | Phvul.003G10PTHR10799//IPhvul.003G10 |
| 54 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | Phvul.003G10PTHR10799//IPhvul.003G10 |
| 55 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | Phvul.003G10PTHR10799//IPhvul.003G10 |
| 56 | binding | Phvul.002G26PTHR23315:SfPhvul.002G26 |
| 57 | binding | Phvul.002G26PTHR23315:SfPhvul.002G26 |
| 58 | RNA cyclase family protein | Phvul.002G29 6.5.1.4 - RNA Phvul.002G29 |
| 59 | RNA cyclase family protein | Phvul.002G29 6.5.1.4 - RNA Phvul.002G29 |
| 60 | RNA cyclase family protein | Phvul.002G29 6.5.1.4 - RNA Phvul.002G29 |
| | phytochrome interacting factor 3-like 5 | Phvul.007G15PTHR12565:SfPhvul.007G15 |

| | | |
|----|--|--|
| 1 | | |
| 2 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SFPhvul.002G00 |
| 3 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SFPhvul.002G00 |
| 4 | cellulose synthase like G1 | Phvul.005G00PTHR13301//IPhvul.005G00 |
| 5 | | |
| 6 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SFPhvul.002G00 |
| 7 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.008G24PTHR21493//IPhvul.008G24 |
| 8 | KNOTTED-like from Arabidopsis thaliana 2 | Phvul.007G20PTHR11850//IPhvul.007G20 |
| 9 | | |
| 10 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 11 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 12 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 13 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 14 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 15 | RING/U-box superfamily protein | Phvul.003G18PTHR22763:SFPhvul.003G18 |
| 16 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 17 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 18 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 19 | Protein of unknown function (DUF616) | Phvul.006G16PTHR12956//IPhvul.006G16 |
| 20 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 21 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 22 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 23 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - PercPhvul.005G05 |
| 24 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 25 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 26 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 27 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - PercPhvul.005G05 |
| 28 | phosphatidylinositolglycan-related | Phvul.002G11K03858 - phosPhvul.002G11 |
| 29 | myb-like HTH transcriptional regulator family protein | Phvul.008G10PF14379 - MY Phvul.008G10 |
| 30 | protein binding | Phvul.008G07PTHR33601:SFPhvul.008G07 |
| 31 | SAUR-like auxin-responsive protein family | Phvul.003G26PTHR31374:SFPhvul.003G26 |
| 32 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//IPhvul.008G07 |
| 33 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//IPhvul.008G07 |
| 34 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//IPhvul.008G07 |
| 35 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//IPhvul.008G07 |
| 36 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 37 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 38 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 39 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 40 | ATPase E1-E2 type family protein / haloacid dehalogen | Phvul.009G20K01530 - phosPhvul.009G20 |
| 41 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SFPhvul.005G15 |
| 42 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SFPhvul.005G15 |
| 43 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SFPhvul.005G15 |
| 44 | ATPase E1-E2 type family protein / haloacid dehalogen | Phvul.009G20K01530 - phosPhvul.009G20 |
| 45 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 46 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 47 | Plant invertase/pectin methylesterase inhibitor superfa | Phvul.009G22PTHR31707:SFPhvul.009G22 |
| 48 | Protein of unknown function (DUF630) ;Protein of unkr | Phvul.002G10PF04782 - ProPhvul.002G10 |
| 49 | FASCICLIN-like arabinogalactan 9 | Phvul.005G09PTHR32077:SFPhvul.005G09 |
| 50 | | |
| 51 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:SFPhvul.003G18 |
| 52 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:SFPhvul.003G18 |
| 53 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//IPhvul.003G12 |
| 54 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//IPhvul.003G12 |
| 55 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//IPhvul.003G12 |
| 56 | Peroxidase superfamily protein | Phvul.006G07 1.11.1.7 - PercPhvul.006G07 |
| 57 | Nucleoporin, Nup133/Nup155-like | Phvul.008G28K14300 - nuclPhvul.008G28 |
| 58 | ubiquitin-protein ligase 4 | Phvul.007G16PTHR11254:SFPhvul.007G16 |
| 59 | serine hydroxymethyltransferase 4 | Phvul.001G26PTHR11680//IPhvul.001G26 |
| 60 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SFPhvul.006G09 |

| | | |
|----|--|---|
| 1 | | |
| 2 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SfPhvul.006G09 |
| 3 | Phosphatidylinositol 3- and 4-kinase family protein | Phvul.003G03PTHR15245:SfPhvul.003G03 |
| 4 | | 0 0 0 Phvul.009G00 |
| 5 | | |
| 6 | P-loop containing nucleoside triphosphate hydrolases s | Phvul.003G10PTHR10799//IPhvul.003G10 |
| 7 | P-loop containing nucleoside triphosphate hydrolases s | Phvul.003G10PTHR10799//IPhvul.003G10 |
| 8 | binding | Phvul.002G26PTHR23315:SfPhvul.002G26 |
| 9 | binding | Phvul.002G26PTHR23315:SfPhvul.002G26 |
| 10 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA :Phvul.002G29 |
| 11 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA :Phvul.002G29 |
| 12 | phytochrome interacting factor 3-like 5 | Phvul.007G15PTHR12565:SfPhvul.007G15 |
| 13 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SfPhvul.002G00 |
| 14 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SfPhvul.002G00 |
| 15 | cellulose synthase like G1 | Phvul.005G00PTHR13301//IPhvul.005G00 |
| 16 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SfPhvul.002G00 |
| 17 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.008G24PTHR21493//IPhvul.008G24 |
| 18 | KNOTTED-like from Arabidopsis thaliana 2 | Phvul.007G20PTHR11850//IPhvul.007G20 |
| 19 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 20 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 21 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 22 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 23 | RING/U-box superfamily protein | Phvul.003G18PTHR22763:SfPhvul.003G18 |
| 24 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 25 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 26 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 27 | Peroxidase superfamily protein | Phvul.005G051.11.1.7 - PercPhvul.005G05 |
| 28 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 29 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 30 | Peroxidase superfamily protein | Phvul.005G051.11.1.7 - PercPhvul.005G05 |
| 31 | phosphatidylinositolglycan-related | Phvul.002G11K03858 - phosPhvul.002G11 |
| 32 | myb-like HTH transcriptional regulator family protein | Phvul.008G10PF14379 - MY Phvul.008G10 |
| 33 | protein binding | Phvul.008G07PTHR33601:SfPhvul.008G07 |
| 34 | SAUR-like auxin-responsive protein family | Phvul.003G26PTHR31374:SfPhvul.003G26 |
| 35 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//IPhvul.008G07 |
| 36 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155//IPhvul.008G07 |
| 37 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 38 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 39 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 40 | ATPase E1-E2 type family protein / haloacid dehalogen | Phvul.009G20K01530 - phosPhvul.009G20 |
| 41 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SfPhvul.005G15 |
| 42 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SfPhvul.005G15 |
| 43 | ATPase E1-E2 type family protein / haloacid dehalogen | Phvul.009G20K01530 - phosPhvul.009G20 |
| 44 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 45 | Plant invertase/pectin methylesterase inhibitor superf | Phvul.009G22PTHR31707:SfPhvul.009G22 |
| 46 | Protein of unknown function (DUF630) ;Protein of unkr | Phvul.002G10PF04782 - ProPhvul.002G10 |

| | | |
|----|--|---|
| 1 | | |
| 2 | FASCICLIN-like arabinogalactan 9 | Phvul.005G09PTHR32077:SFPhvul.005G09 |
| 3 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:SFPhvul.003G18 |
| 4 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:SFPhvul.003G18 |
| 5 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132://IPhvul.003G12 |
| 6 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132://IPhvul.003G12 |
| 7 | Peroxidase superfamily protein | Phvul.006G071.11.1.7 - PercPhvul.006G07 |
| 8 | Nucleoporin, Nup133/Nup155-like | Phvul.008G28K14300 - nuclPhvul.008G28 |
| 9 | ubiquitin-protein ligase 4 | Phvul.007G16PTHR11254:SFPhvul.007G16 |
| 10 | serine hydroxymethyltransferase 4 | Phvul.001G26PTHR11680://IPhvul.001G26 |
| 11 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SFPhvul.006G09 |
| 12 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SFPhvul.006G09 |
| 13 | Phosphatidylinositol 3- and 4-kinase family protein | Phvul.003G03PTHR15245:SFPhvul.003G03 |
| 14 | | 0 0 0 Phvul.009G00 |
| 15 | P-loop containing nucleoside triphosphate hydrolases | Phvul.003G10PTHR10799://IPhvul.003G10 |
| 16 | P-loop containing nucleoside triphosphate hydrolases | Phvul.003G10PTHR10799://IPhvul.003G10 |
| 17 | binding | Phvul.002G26PTHR23315:SFPhvul.002G26 |
| 18 | binding | Phvul.002G26PTHR23315:SFPhvul.002G26 |
| 19 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA Phvul.002G29 |
| 20 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA Phvul.002G29 |
| 21 | phytochrome interacting factor 3-like 5 | Phvul.007G15PTHR12565:SFPhvul.007G15 |
| 22 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SFPhvul.002G00 |
| 23 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SFPhvul.002G00 |
| 24 | cellulose synthase like G1 | Phvul.005G00PTHR13301://IPhvul.005G00 |
| 25 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SFPhvul.002G00 |
| 26 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.008G24PTHR21493://IPhvul.008G24 |
| 27 | KNOTTED-like from Arabidopsis thaliana 2 | Phvul.007G20PTHR11850://IPhvul.007G20 |
| 28 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 29 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 30 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 31 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 32 | RING/U-box superfamily protein | Phvul.003G18PTHR22763:SFPhvul.003G18 |
| 33 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 34 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 35 | Protein of unknown function (DUF616) | Phvul.006G16PTHR12956://IPhvul.006G16 |
| 36 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 37 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 38 | Peroxidase superfamily protein | Phvul.005G051.11.1.7 - PercPhvul.005G05 |
| 39 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 40 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SFPhvul.007G15 |
| 41 | Peroxidase superfamily protein | Phvul.005G051.11.1.7 - PercPhvul.005G05 |
| 42 | phosphatidylinositolglycan-related | Phvul.002G11K03858 - phosPhvul.002G11 |
| 43 | myb-like HTH transcriptional regulator family protein | Phvul.008G10PF14379 - MY Phvul.008G10 |
| 44 | protein binding | Phvul.008G07PTHR33601:SFPhvul.008G07 |
| 45 | SAUR-like auxin-responsive protein family | Phvul.003G26PTHR31374:SFPhvul.003G26 |
| 46 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155://IPhvul.008G07 |
| 47 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07PTHR23155://IPhvul.008G07 |

| | | |
|----|--|---|
| 1 | | |
| 2 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 3 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 4 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 5 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 6 | ATPase E1-E2 type family protein / haloacid dehalogen | Phvul.009G20K01530 - phosPhvul.009G20 |
| 7 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SfPhvul.005G15 |
| 8 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SfPhvul.005G15 |
| 9 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SfPhvul.005G15 |
| 10 | ATPase E1-E2 type family protein / haloacid dehalogen | Phvul.009G20K01530 - phosPhvul.009G20 |
| 11 | gigantea protein (GI) | Phvul.004G08K12124 - GIG/Phvul.004G08 |
| 12 | Plant invertase/pectin methylesterase inhibitor superfam | Phvul.009G22PTHR31707:SfPhvul.009G22 |
| 13 | Plant invertase/pectin methylesterase inhibitor superfam | Phvul.009G22PTHR31707:SfPhvul.009G22 |
| 14 | Protein of unknown function (DUF630) ;Protein of unkn | Phvul.002G10PF04782 - ProPhvul.002G10 |
| 15 | FASCICLIN-like arabinogalactan 9 | Phvul.005G09PTHR32077:SfPhvul.005G09 |
| 16 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:SfPhvul.003G18 |
| 17 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:SfPhvul.003G18 |
| 18 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18PTHR12565:SfPhvul.003G18 |
| 19 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//IPhvul.003G12 |
| 20 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//IPhvul.003G12 |
| 21 | Nucleotide-sugar transporter family protein | Phvul.003G12PTHR11132//IPhvul.003G12 |
| 22 | Peroxidase superfamily protein | Phvul.006G071.11.1.7 - PercPhvul.006G07 |
| 23 | Nucleoporin, Nup133/Nup155-like | Phvul.008G28K14300 - nuclPhvul.008G28 |
| 24 | ubiquitin-protein ligase 4 | Phvul.007G16PTHR11254:SfPhvul.007G16 |
| 25 | ubiquitin-protein ligase 4 | Phvul.007G16PTHR11254:SfPhvul.007G16 |
| 26 | serine hydroxymethyltransferase 4 | Phvul.001G26PTHR11680//IPhvul.001G26 |
| 27 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SfPhvul.006G09 |
| 28 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SfPhvul.006G09 |
| 29 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09PTHR13780:SfPhvul.006G09 |
| 30 | Phosphatidylinositol 3- and 4-kinase family protein | Phvul.003G03PTHR15245:SfPhvul.003G03 |
| 31 | | 0 0 0 Phvul.009G00 |
| 32 | P-loop containing nucleoside triphosphate hydrolases s | Phvul.003G10PTHR10799//IPhvul.003G10 |
| 33 | P-loop containing nucleoside triphosphate hydrolases s | Phvul.003G10PTHR10799//IPhvul.003G10 |
| 34 | P-loop containing nucleoside triphosphate hydrolases s | Phvul.003G10PTHR10799//IPhvul.003G10 |
| 35 | binding | Phvul.002G26PTHR23315:SfPhvul.002G26 |
| 36 | binding | Phvul.002G26PTHR23315:SfPhvul.002G26 |
| 37 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA :Phvul.002G29 |
| 38 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA :Phvul.002G29 |
| 39 | RNA cyclase family protein | Phvul.002G296.5.1.4 - RNA :Phvul.002G29 |
| 40 | phytochrome interacting factor 3-like 5 | Phvul.007G15PTHR12565:SfPhvul.007G15 |
| 41 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SfPhvul.002G00 |
| 42 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SfPhvul.002G00 |
| 43 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SfPhvul.002G00 |
| 44 | cellulose synthase like G1 | Phvul.005G00PTHR13301//IPhvul.005G00 |
| 45 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SfPhvul.002G00 |
| 46 | RING/U-box superfamily protein | Phvul.002G00PTHR10044:SfPhvul.002G00 |
| 47 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.008G24PTHR21493//IPhvul.008G24 |
| 48 | KNOTTED-like from Arabidopsis thaliana 2 | Phvul.007G20PTHR11850//IPhvul.007G20 |
| 49 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 50 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 51 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 52 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 53 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 54 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 55 | RING/U-box superfamily protein | Phvul.003G18PTHR22763:SfPhvul.003G18 |
| 56 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 57 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 58 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| 59 | Protein of unknown function (DUF616) | Phvul.006G16PTHR12956//IPhvul.006G16 |
| 60 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |
| | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15PTHR24320:SfPhvul.007G15 |

| | | |
|----|--|--|
| 1 | | |
| 2 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - PercPhvul.005G05 |
| 3 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 4 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 5 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 6 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - PercPhvul.005G05 |
| 7 | phosphatidylinositolglycan-related | Phvul.002G11 K03858 - phosPhvul.002G11 |
| 8 | myb-like HTH transcriptional regulator family protein | Phvul.008G10 PF14379 - MY Phvul.008G10 |
| 9 | protein binding | Phvul.008G07 PTHR33601:SfPhvul.008G07 |
| 10 | SAUR-like auxin-responsive protein family | Phvul.003G26 PTHR31374:SfPhvul.003G26 |
| 11 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07 PTHR23155//IPhvul.008G07 |
| 12 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07 PTHR23155//IPhvul.008G07 |
| 13 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07 PTHR23155//IPhvul.008G07 |
| 14 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07 PTHR23155//IPhvul.008G07 |
| 15 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 16 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 17 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 18 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 19 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20 K01530 - phosPhvul.009G20 |
| 20 | Plant regulator RWP-RK family protein | Phvul.005G15 PTHR32002:SfPhvul.005G15 |
| 21 | Plant regulator RWP-RK family protein | Phvul.005G15 PTHR32002:SfPhvul.005G15 |
| 22 | Plant regulator RWP-RK family protein | Phvul.005G15 PTHR32002:SfPhvul.005G15 |
| 23 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20 K01530 - phosPhvul.009G20 |
| 24 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20 K01530 - phosPhvul.009G20 |
| 25 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 26 | Plant invertase/pectin methylesterase inhibitor superfamily protein | Phvul.009G22 PTHR31707:SfPhvul.009G22 |
| 27 | Protein of unknown function (DUF630) ;Protein of unknown function (DUF630) | Phvul.002G10 PF04782 - ProPhvul.002G10 |
| 28 | FASCICLIN-like arabinogalactan 9 | Phvul.005G09 PTHR32077:SfPhvul.005G09 |
| 29 | FASCICLIN-like arabinogalactan 9 | Phvul.005G09 PTHR32077:SfPhvul.005G09 |
| 30 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | Phvul.003G18 PTHR12565:SfPhvul.003G18 |
| 31 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | Phvul.003G18 PTHR12565:SfPhvul.003G18 |
| 32 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | Phvul.003G18 PTHR12565:SfPhvul.003G18 |
| 33 | Nucleotide-sugar transporter family protein | Phvul.003G12 PTHR11132//IPhvul.003G12 |
| 34 | Nucleotide-sugar transporter family protein | Phvul.003G12 PTHR11132//IPhvul.003G12 |
| 35 | Peroxidase superfamily protein | Phvul.006G07 1.11.1.7 - PercPhvul.006G07 |
| 36 | Nucleoporin, Nup133/Nup155-like | Phvul.008G28 K14300 - nuclPhvul.008G28 |
| 37 | ubiquitin-protein ligase 4 | Phvul.007G16 PTHR11254:SfPhvul.007G16 |
| 38 | ubiquitin-protein ligase 4 | Phvul.007G16 PTHR11254:SfPhvul.007G16 |
| 39 | serine hydroxymethyltransferase 4 | Phvul.001G26 PTHR11680//IPhvul.001G26 |
| 40 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09 PTHR13780:SfPhvul.006G09 |
| 41 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09 PTHR13780:SfPhvul.006G09 |
| 42 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09 PTHR13780:SfPhvul.006G09 |
| 43 | Phosphatidylinositol 3- and 4-kinase family protein | Phvul.003G03 PTHR15245:SfPhvul.003G03 |
| 44 | | 0 0 0 Phvul.009G00 |
| 45 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | Phvul.003G10 PTHR10799//IPhvul.003G10 |
| 46 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | Phvul.003G10 PTHR10799//IPhvul.003G10 |
| 47 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | Phvul.003G10 PTHR10799//IPhvul.003G10 |
| 48 | binding | Phvul.002G26 PTHR23315:SfPhvul.002G26 |
| 49 | binding | Phvul.002G26 PTHR23315:SfPhvul.002G26 |
| 50 | binding | Phvul.002G26 PTHR23315:SfPhvul.002G26 |
| 51 | RNA cyclase family protein | Phvul.002G29 6.5.1.4 - RNA Phvul.002G29 |
| 52 | RNA cyclase family protein | Phvul.002G29 6.5.1.4 - RNA Phvul.002G29 |
| 53 | RNA cyclase family protein | Phvul.002G29 6.5.1.4 - RNA Phvul.002G29 |
| 54 | phytochrome interacting factor 3-like 5 | Phvul.007G15 PTHR12565:SfPhvul.007G15 |
| 55 | RING/U-box superfamily protein | Phvul.002G00 PTHR10044:SfPhvul.002G00 |
| 56 | RING/U-box superfamily protein | Phvul.002G00 PTHR10044:SfPhvul.002G00 |
| 57 | cellulose synthase like G1 | Phvul.005G00 PTHR13301//IPhvul.005G00 |
| 58 | cellulose synthase like G1 | Phvul.005G00 PTHR13301//IPhvul.005G00 |
| 59 | RING/U-box superfamily protein | Phvul.002G00 PTHR10044:SfPhvul.002G00 |
| 60 | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | Phvul.008G24 PTHR21493//IPhvul.008G24 |
| | KNOTTED-like from Arabidopsis thaliana 2 | Phvul.007G20 PTHR11850//IPhvul.007G20 |

| | | |
|----|--|--|
| 1 | | |
| 2 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 3 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 4 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 5 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 6 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 7 | RING/U-box superfamily protein | Phvul.003G18 PTHR22763:SfPhvul.003G18 |
| 8 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 9 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 10 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 11 | Protein of unknown function (DUF616) | Phvul.006G16 PTHR12956//IPhvul.006G16 |
| 12 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 13 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 14 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 15 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - PercPhvul.005G05 |
| 16 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 17 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 18 | NAD(P)-binding Rossmann-fold superfamily protein | Phvul.007G15 PTHR24320:SfPhvul.007G15 |
| 19 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - PercPhvul.005G05 |
| 20 | phosphatidylinositolglycan-related | Phvul.002G11 K03858 - phosPhvul.002G11 |
| 21 | myb-like HTH transcriptional regulator family protein | Phvul.008G10 PF14379 - MY Phvul.008G10 |
| 22 | protein binding | Phvul.008G07 PTHR33601:SfPhvul.008G07 |
| 23 | SAUR-like auxin-responsive protein family | Phvul.003G26 PTHR31374:SfPhvul.003G26 |
| 24 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07 PTHR23155//IPhvul.008G07 |
| 25 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07 PTHR23155//IPhvul.008G07 |
| 26 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 27 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 28 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 29 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20 K01530 - phosPhvul.009G20 |
| 30 | Plant regulator RWP-RK family protein | Phvul.005G15 PTHR32002:SfPhvul.005G15 |
| 31 | Plant regulator RWP-RK family protein | Phvul.005G15 PTHR32002:SfPhvul.005G15 |
| 32 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20 K01530 - phosPhvul.009G20 |
| 33 | gigantea protein (GI) | Phvul.004G08 K12124 - GIG/Phvul.004G08 |
| 34 | Peroxidase superfamily protein | Phvul.006G07 1.11.1.7 - PercPhvul.006G07 |
| 35 | Nucleoporin, Nup133/Nup155-like | Phvul.008G28 K14300 - nuclPhvul.008G28 |
| 36 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09 PTHR13780:SfPhvul.006G09 |
| 37 | Plant invertase/pectin methylesterase inhibitor superfamily | Phvul.009G22 PTHR31707:SfPhvul.009G22 |
| 38 | homolog of yeast sucrose nonfermenting 4 | Phvul.006G09 PTHR13780:SfPhvul.006G09 |
| 39 | Protein of unknown function (DUF630) ;Protein of unknown function (DUF630) | Phvul.002G10 PF04782 - ProPhvul.002G10 |
| 40 | FASCICLIN-like arabinogalactan 9 | Phvul.005G09 PTHR32077:SfPhvul.005G09 |
| 41 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18 PTHR12565:SfPhvul.003G18 |
| 42 | basic helix-loop-helix (bHLH) DNA-binding superfamily | Phvul.003G18 PTHR12565:SfPhvul.003G18 |
| 43 | Nucleotide-sugar transporter family protein | Phvul.003G12 PTHR11132//IPhvul.003G12 |
| 44 | Nucleotide-sugar transporter family protein | Phvul.003G12 PTHR11132//IPhvul.003G12 |
| 45 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - PercPhvul.005G05 |
| 46 | Peroxidase superfamily protein | Phvul.005G05 1.11.1.7 - PercPhvul.005G05 |
| 47 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07 PTHR23155//IPhvul.008G07 |
| 48 | Disease resistance protein (CC-NBS-LRR class) family | Phvul.008G07 PTHR23155//IPhvul.008G07 |
| 49 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20 K01530 - phosPhvul.009G20 |
| 50 | Plant regulator RWP-RK family protein | Phvul.005G15 PTHR32002:SfPhvul.005G15 |
| 51 | Plant regulator RWP-RK family protein | Phvul.005G15 PTHR32002:SfPhvul.005G15 |

| | | |
|----|--|---|
| 1 | | |
| 2 | ATPase E1-E2 type family protein / haloacid dehalogenase | Phvul.009G20K01530 - phosPhvul.009G20 |
| 3 | Plant regulator RWP-RK family protein | Phvul.005G15PTHR32002:SFPhvul.005G15 |
| 4 | Leucine-rich repeat transmembrane protein kinase family | Phvul.009G112.7.11.1 - NonPhvul.009G11 |
| 5 | heavy metal atpase 1 | Phvul.003G24PTHR24093:SFPhvul.003G24 |
| 6 | Polynucleotide adenyltransferase family protein | Phvul.002G28PTHR13734:SFPhvul.002G28 |
| 7 | Polynucleotide adenyltransferase family protein | Phvul.002G28PTHR13734:SFPhvul.002G28 |
| 8 | Polynucleotide adenyltransferase family protein | Phvul.002G28PTHR13734:SFPhvul.002G28 |
| 9 | Polynucleotide adenyltransferase family protein | Phvul.002G28PTHR13734:SFPhvul.002G28 |
| 10 | sucrose phosphate synthase 1F | Phvul.003G17PTHR12526//IPhvul.003G17 |
| 11 | Tetratricopeptide repeat (TPR)-like superfamily protein | Phvul.011G17PF01535//PF1Phvul.011G17 |
| 12 | dolichol phosphate-mannose biosynthesis regulatory p | Phvul.003G28K09658 - dolichPhvul.003G28 |
| 13 | ubiquitin-protein ligase 4 | Phvul.007G16PTHR11254:SFPhvul.007G16 |
| 14 | Phosphatidylinositol 3- and 4-kinase family protein | Phvul.003G03PTHR15245:SFPhvul.003G03 |
| 15 | serine hydroxymethyltransferase 4 | Phvul.001G26PTHR11680//IPhvul.001G26 |
| 16 | CRINKLY4 related 3 | Phvul.001G24PTHR27003:SFPhvul.001G24 |
| 17 | cation exchanger 1 | Phvul.006G06K07300 - Ca2+Phvul.006G06 |
| 18 | UDP-Glycosyltransferase superfamily protein | Phvul.008G14PTHR11926:SFPhvul.008G14 |
| 19 | | |
| 20 | | |
| 21 | | |
| 22 | | |
| 23 | | |
| 24 | | |
| 25 | | |
| 26 | | |
| 27 | | |
| 28 | | |
| 29 | | |
| 30 | | |
| 31 | | |
| 32 | | |
| 33 | | |
| 34 | | |
| 35 | | |
| 36 | | |
| 37 | | |
| 38 | | |
| 39 | | |
| 40 | | |
| 41 | | |
| 42 | | |
| 43 | | |
| 44 | | |
| 45 | | |
| 46 | | |
| 47 | | |
| 48 | | |
| 49 | | |
| 50 | | |
| 51 | | |
| 52 | | |
| 53 | | |
| 54 | | |
| 55 | | |
| 56 | | |
| 57 | | |
| 58 | | |
| 59 | | |
| 60 | | |

Do not distribute

1 Carbohydrate UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip
2 Carbohydrate UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip
3 Carbohydrate UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip
4 Cell wall organo caffeoyl-CoA 3-O-methyltransferase (CCoA-OMT) (original description: pacid=371629
5 not assigned.ε (original description: pacid=37171837 transcript=Phvul.006G169300.1 locus=Phvul.C
6 not assigned.r no hits & (original description: pacid=37164135 transcript=Phvul.007G164800.1 locu
7 Carbohydrate UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip
8 Carbohydrate UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip
9 Carbohydrate UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip
10 Carbohydrate UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip
11 Carbohydrate UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip
12 Cell wall organo caffeoyl-CoA 3-O-methyltransferase (CCoA-OMT) (original description: pacid=371629
13 not assigned.ε (original description: pacid=37171837 transcript=Phvul.006G169300.1 locus=Phvul.C
14 not assigned.r no hits & (original description: pacid=37164135 transcript=Phvul.007G164800.1 locu
15 Carbohydrate UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip
16 Carbohydrate UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip
17 Carbohydrate UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip
18 Cell wall organo caffeoyl-CoA 3-O-methyltransferase (CCoA-OMT) (original description: pacid=371629
19 RNA biosynthetranscription factor (TCP) (original description: pacid=37143823 transcript=Phvul.01C
20 not assigned.r no hits & (original description: pacid=37176752 transcript=Phvul.002G325300.2 locu
21 Cell cycle organoPARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971
22 not assigned.ε (original description: pacid=37154217 transcript=Phvul.005G001200.1 locus=Phvul.C
23 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
24 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
25 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
26 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
27 not assigned.r no hits & (original description: pacid=37173262 transcript=Phvul.006G086200.1 locu
28 Solute transport:calcium cation exchanger (CCX) (original description: pacid=37143954 transcri
29 RNA biosynthetranscription factor (TCP) (original description: pacid=37143823 transcript=Phvul.01C
30 not assigned.r no hits & (original description: pacid=37176752 transcript=Phvul.002G325300.2 locu
31 Cell cycle organoPARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971
32 not assigned.ε (original description: pacid=37154217 transcript=Phvul.005G001200.1 locus=Phvul.C
33 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
34 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
35 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
36 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
37 not assigned.r no hits & (original description: pacid=37173262 transcript=Phvul.006G086200.1 locu
38 Solute transport:calcium cation exchanger (CCX) (original description: pacid=37143954 transcri
39 RNA biosynthetranscription factor (TCP) (original description: pacid=37143823 transcript=Phvul.01C
40 not assigned.r no hits & (original description: pacid=37176752 transcript=Phvul.002G325300.2 locu
41 Cell cycle organoPARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971
42 not assigned.ε (original description: pacid=37154217 transcript=Phvul.005G001200.1 locus=Phvul.C
43 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
44 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
45 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
46 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
47 not assigned.r no hits & (original description: pacid=37173262 transcript=Phvul.006G086200.1 locu
48 Solute transport:calcium cation exchanger (CCX) (original description: pacid=37143954 transcri
49 RNA biosynthetranscription factor (TCP) (original description: pacid=37143823 transcript=Phvul.01C
50 not assigned.r no hits & (original description: pacid=37176752 transcript=Phvul.002G325300.2 locu
51 Cell cycle organoPARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971
52 not assigned.ε (original description: pacid=37154217 transcript=Phvul.005G001200.1 locus=Phvul.C
53 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
54 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
55 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
56 not assigned.r no hits & (original description: pacid=37173262 transcript=Phvul.006G086200.1 locu
57 Solute transport:calcium cation exchanger (CCX) (original description: pacid=37143954 transcri
58 RNA biosynthetranscription factor (TCP) (original description: pacid=37143823 transcript=Phvul.01C
59 not assigned.r no hits & (original description: pacid=37176752 transcript=Phvul.002G325300.2 locu
60 Cell cycle organoPARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971
not assigned.ε (original description: pacid=37154217 transcript=Phvul.005G001200.1 locus=Phvul.C

1 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
2 not assigned.r no hits & (original description: pacid=37173262 transcript=Phvul.006G086200.1 locu
3 Solute transp cation:calcium cation exchanger (CCX) (original description: pacid=37143954 transcri
4 RNA biosynth ranscription factor (TCP) (original description: pacid=37143823 transcript=Phvul.01C
5 not assigned.r no hits & (original description: pacid=37176752 transcript=Phvul.002G325300.2 locu
6 Cell cycle orga PARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971
7 not assigned.ε (original description: pacid=37154217 transcript=Phvul.005G001200.1 locus=Phvul.C
8 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
9 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
10 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
11 not assigned.r no hits & (original description: pacid=37173262 transcript=Phvul.006G086200.1 locu
12 Solute transp cation:calcium cation exchanger (CCX) (original description: pacid=37143954 transcri
13 RNA biosynth ranscription factor (TCP) (original description: pacid=37143823 transcript=Phvul.01C
14 not assigned.r no hits & (original description: pacid=37176752 transcript=Phvul.002G325300.2 locu
15 Cell cycle orga PARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971
16 not assigned.ε (original description: pacid=37154217 transcript=Phvul.005G001200.1 locus=Phvul.C
17 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
18 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
19 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
20 not assigned.r no hits & (original description: pacid=37173262 transcript=Phvul.006G086200.1 locu
21 Solute transp cation:calcium cation exchanger (CCX) (original description: pacid=37143954 transcri
22 RNA biosynth ranscription factor (TCP) (original description: pacid=37143823 transcript=Phvul.01C
23 not assigned.r no hits & (original description: pacid=37176752 transcript=Phvul.002G325300.2 locu
24 Cell cycle orga PARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971
25 not assigned.ε (original description: pacid=37154217 transcript=Phvul.005G001200.1 locus=Phvul.C
26 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
27 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
28 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
29 not assigned.r no hits & (original description: pacid=37173262 transcript=Phvul.006G086200.1 locu
30 Solute transp cation:calcium cation exchanger (CCX) (original description: pacid=37143954 transcri
31 RNA biosynth ranscription factor (TCP) (original description: pacid=37143823 transcript=Phvul.01C
32 not assigned.r no hits & (original description: pacid=37176752 transcript=Phvul.002G325300.2 locu
33 Cell cycle orga PARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971
34 not assigned.ε (original description: pacid=37154217 transcript=Phvul.005G001200.1 locus=Phvul.C
35 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
36 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
37 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
38 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
39 not assigned.r no hits & (original description: pacid=37173262 transcript=Phvul.006G086200.1 locu
40 Solute transp cation:calcium cation exchanger (CCX) (original description: pacid=37143954 transcri
41 RNA biosynth ranscription factor (TCP) (original description: pacid=37143823 transcript=Phvul.01C
42 not assigned.r no hits & (original description: pacid=37176752 transcript=Phvul.002G325300.2 locu
43 Cell cycle orga PARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971
44 not assigned.ε (original description: pacid=37154217 transcript=Phvul.005G001200.1 locus=Phvul.C
45 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
46 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
47 not assigned.r no hits & (original description: pacid=37157814 transcript=Phvul.008G147100.4 locu
48 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
49 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
50 RNA biosynth ranscription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
51 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
52 not assigned.ε (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
53 not assigned.ε (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
54 Solute transp anion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
55 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
56 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu

1 Solute transpc
2 solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00
3 Chromatin or ξ chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
4 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
5 not assigned. ϵ (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C
6 not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
7 RNA biosynth ξ transcription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
8 not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu
9 not assigned. ϵ (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
10 External stim ξ GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
11 External stim ξ GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
12 RNA biosynth ξ transcription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
13 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
14 not assigned. ϵ (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
15 not assigned. ϵ (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
16 Solute transpc
17 anion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
18 Amino acid m
19 serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
20 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
21 Solute transpc
22 solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00
23 Chromatin or ξ chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
24 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
25 not assigned. ϵ (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C
26 not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
27 RNA biosynth ξ transcription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
28 not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu
29 not assigned. ϵ (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
30 External stim ξ GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
31 External stim ξ GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
32 RNA biosynth ξ transcription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
33 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
34 not assigned. ϵ (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
35 not assigned. ϵ (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
36 Solute transpc
37 anion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
38 Amino acid m
39 serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
40 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
41 Solute transpc
42 solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00
43 Chromatin or ξ chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
44 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
45 not assigned. ϵ (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C
46 not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
47 RNA biosynth ξ transcription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
48 not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu
49 not assigned. ϵ (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
50 External stim ξ GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
51 External stim ξ GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
52 RNA biosynth ξ transcription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
53 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07

1 not assigned.ε (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
2 not assigned.ε (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
3 Solute transp anion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
4 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
5 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
6 Solute transp solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00
7 Chromatin orç chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
8 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
9 not assigned.ε (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C
10 not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
11 RNA biosynth r transcription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
12 not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu
13 not assigned.ε (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
14 External stim u GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
15 External stim u GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
16 RNA biosynth r transcription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
17 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
18 not assigned.ε (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
19 not assigned.ε (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
20 Solute transp anion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
21 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
22 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
23 Solute transp solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00
24 Chromatin orç chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
25 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
26 not assigned.ε (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C
27 not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
28 RNA biosynth r transcription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
29 not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu
30 not assigned.ε (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
31 External stim u GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
32 External stim u GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
33 RNA biosynth r transcription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
34 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
35 not assigned.ε (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
36 not assigned.ε (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
37 Solute transp anion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
38 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
39 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
40 Solute transp solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00
41 Chromatin orç chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
42 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
43 not assigned.ε (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C
44 not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
45 RNA biosynth r transcription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
46 not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu
47 not assigned.ε (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
48 External stim u GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
49 External stim u GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
50 RNA biosynth r transcription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
51 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
52 not assigned.ε (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
53 not assigned.ε (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
54 Solute transp anion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
55 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
56 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
57 Solute transp solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00
58 Chromatin orç chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
59 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
60 not assigned.ε (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C
not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
RNA biosynth r transcription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu

1 not assigned.ε (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
2 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
3 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
4 RNA biosynthetranscription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
5 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
6 not assigned.ε (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
7 not assigned.ε (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
8 Solute transpc anion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
9 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
10 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
11 Solute transpc solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00
12 Chromatin orę chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
13 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
14 not assigned.ε (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C
15 not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
16 RNA biosynthetranscription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
17 not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu
18 not assigned.ε (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
19 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
20 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
21 RNA biosynthetranscription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
22 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
23 not assigned.ε (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
24 not assigned.ε (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
25 Solute transpc anion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
26 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
27 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
28 Solute transpc solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00
29 Chromatin orę chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
30 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
31 not assigned.ε (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C
32 not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
33 RNA biosynthetranscription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
34 not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu
35 not assigned.ε (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
36 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
37 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
38 RNA biosynthetranscription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
39 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
40 not assigned.ε (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
41 not assigned.ε (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
42 Solute transpc anion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
43 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
44 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
45 Solute transpc solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00
46 Chromatin orę chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
47 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
48 not assigned.ε (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C
49 not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
50 RNA biosynthetranscription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
51 not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu
52 not assigned.ε (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
53 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
54 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
55 RNA biosynthetranscription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
56 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
57 not assigned.ε (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
58 not assigned.ε (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
59 Solute transpc anion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
60 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
Solute transpc solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00
Chromatin orę chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=

1 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
2 not assigned.ε (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C
3 not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
4 RNA biosynthtranscription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
5 not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu
6 not assigned.ε (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
7 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
8 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
9 RNA biosynthtranscription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
10 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
11 not assigned.ε (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
12 not assigned.ε (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
13 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
14 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
15 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
16 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
17 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
18 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
19 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
20 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
21 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
22 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
23 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
24 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
25 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
26 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
27 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
28 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
29 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
30 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
31 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
32 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
33 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
34 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
35 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
36 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
37 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
38 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
39 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
40 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
41 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
42 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
43 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
44 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
45 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
46 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
47 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
48 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
49 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
50 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
51 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
52 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
53 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
54 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
55 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
56 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
57 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
58 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
59 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
60 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu

1 Solute transpncanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
2 Amino acid m:serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
3 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
4 Solute transpncanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
5 Solute transpncanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
6 Solute transpncanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
7 Chromatin orç chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
8 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
9 not assigned.ç (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C
10 not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
11 RNA biosynthç transcription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
12 not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu
13 not assigned.ç (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
14 External stimç GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
15 External stimç GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
16 RNA biosynthç transcription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
17 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
18 not assigned.ç (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
19 not assigned.ç (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
20 Solute transpncanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
21 Amino acid m:serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
22 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
23 Solute transpncanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
24 Solute transpncanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
25 Chromatin orç chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
26 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
27 not assigned.ç (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C
28 not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
29 RNA biosynthç transcription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
30 not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu
31 not assigned.ç (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
32 External stimç GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
33 External stimç GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
34 RNA biosynthç transcription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
35 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
36 not assigned.ç (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
37 not assigned.ç (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
38 Solute transpncanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
39 Amino acid m:serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
40 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
41 Solute transpncanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
42 Solute transpncanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
43 Chromatin orç chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
44 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
45 not assigned.ç (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C
46 not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
47 RNA biosynthç transcription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
48 not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu
49 not assigned.ç (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
50 External stimç GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
51 External stimç GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
52 RNA biosynthç transcription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
53 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
54 not assigned.ç (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
55 not assigned.ç (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
56 Solute transpncanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
57 Amino acid m:serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
58 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
59 Solute transpncanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
60 Solute transpncanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
Chromatin orç chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
not assigned.ç (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C
not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
RNA biosynthç transcription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu
not assigned.ç (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
External stimç GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio

1 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptor
2 RNA biosynth transcription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
3 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
4 not assigned.ε (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
5 not assigned.ε (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
6 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
7 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
8 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
9 Solute transpc solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00
10 Chromatin orç chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
11 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
12 not assigned.ε (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C
13 not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
14 RNA biosynth transcription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
15 not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu
16 not assigned.ε (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
17 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptor
18 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptor
19 RNA biosynth transcription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
20 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
21 not assigned.ε (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
22 not assigned.ε (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
23 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
24 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
25 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
26 Solute transpc solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00
27 Chromatin orç chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
28 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
29 not assigned.ε (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C
30 not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
31 RNA biosynth transcription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
32 not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu
33 not assigned.ε (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
34 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptor
35 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptor
36 RNA biosynth transcription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
37 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
38 not assigned.ε (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
39 not assigned.ε (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
40 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
41 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
42 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
43 Solute transpc solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00
44 Chromatin orç chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
45 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
46 not assigned.ε (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C
47 not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
48 RNA biosynth transcription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
49 not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu
50 not assigned.ε (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
51 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptor
52 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptor
53 RNA biosynth transcription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
54 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
55 not assigned.ε (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
56 not assigned.ε (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
57 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
58 Amino acid m serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
59 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
60 Solute transpc solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00
Chromatin orç chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
not assigned.ε (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C

1 not assigned.r no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
2 RNA biosynthtranscription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
3 not assigned.r no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu
4 not assigned.ε (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
5 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
6 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
7 RNA biosynthtranscription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
8 not assigned.ε (original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.C
9 Protein modif protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
10 not assigned.ε (original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.C
11 not assigned.ε (original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.C
12 Solute transpcanion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
13 Solute transpcsolute transporter (UmamiT) (original description: pacid=37178271 transcript=Phvul.
14 Solute transpcsolute transporter (UmamiT) (original description: pacid=37174567 transcript=Phvul.
15 Solute transpcsolute transporter (UmamiT) (original description: pacid=37174567 transcript=Phvul.
16 Amino acid mserine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
17 not assigned.r no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
18 Solute transpcsolute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00
19 Chromatin orgchromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
20 Protein modif protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
21 not assigned.ε (original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.C
22 not assigned.ε (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C
23 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C
24 Cell wall orgarxylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
25 Solute transpcpolyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran:
26 not assigned.ε (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C
27 Protein homepepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09
28 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
29 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
30 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
31 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
32 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
33 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
34 RNA biosynthtranscription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
35 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C
36 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C
37 RNA biosynthcomponent GRF of GRF-GIF transcriptional complex (original description: pacid=3716
38 RNA processirtRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
39 RNA processirtRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
40 Solute transpcNodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
41 Solute transpctransport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009
42 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
43 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
44 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
45 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
46 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu

1 not assigned.ε (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C
2 Protein home pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G1C
3 RNA biosynthtranscriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
4 Protein modif protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009Gε
5 not assigned.ε (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C
6 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C
7 Cell wall orgar xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
8 Solute transpc polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran:
9 not assigned.ε (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C
10 Protein home pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G0ε
11 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
12 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
13 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
14 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
15 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
16 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
17 RNA biosynthtranscription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
18 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C
19 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C
20 RNA biosynthcomponent GRF of GRF-GIF transcriptional complex (original description: pacid=3716
21 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
22 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
23 Solute transpc Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
24 Solute transpc transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.00ε
25 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
26 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
27 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
28 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
29 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
30 not assigned.ε (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C
31 Protein home pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G1C
32 RNA biosynthtranscriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
33 Protein modif protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009Gε
34 not assigned.ε (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C
35 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C
36 Cell wall orgar xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
37 Solute transpc polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran:
38 not assigned.ε (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C
39 Protein home pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G0ε
40 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
41 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
42 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
43 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
44 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
45 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
46 RNA biosynthtranscription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C
2 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C
3 RNA biosynthcomponent GRF of GRF-GIF transcriptional complex (original description: pacid=3716
4 RNA processirtRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
5 RNA processirtRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
6 Solute transpNodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
7 Solute transptransport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009
8 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
9 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
10 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
11 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
12 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
13 not assigned.ε (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C
14 Protein homepepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10
15 RNA biosynthtranscriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
16 Protein modif protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G2
17 not assigned.ε (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C
18 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C
19 Cell wall orgaxylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
20 Solute transp polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran
21 not assigned.ε (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C
22 Protein homepepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09
23 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
24 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
25 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
26 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
27 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
28 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
29 RNA biosynthtranscription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
30 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C
31 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C
32 RNA biosynthcomponent GRF of GRF-GIF transcriptional complex (original description: pacid=3716
33 RNA processirtRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
34 RNA processirtRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
35 Solute transpNodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
36 Solute transptransport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009
37 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
38 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
39 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
40 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
41 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
42 not assigned.ε (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C
43 Protein homepepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10
44 RNA biosynthtranscriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
45 Protein modif protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G2
46 not assigned.ε (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C

1 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C
2 Cell wall orgar xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
3 Solute transpc polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran:
4 not assigned.ε (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C
5 Protein home pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09
6 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
7 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
8 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
9 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
10 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
11 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
12 RNA biosynthtranscription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
13 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C
14 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C
15 RNA biosynthcomponent GRF of GRF-GIF transcriptional complex (original description: pacid=3716
16 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
17 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
18 Solute transpc Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
19 Solute transpc transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009
20 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
21 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
22 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
23 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
24 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
25 not assigned.ε (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C
26 Protein home pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G1C
27 RNA biosynthtranscriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
28 Protein modif protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G
29 not assigned.ε (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C
30 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C
31 Cell wall orgar xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
32 Solute transpc polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran:
33 not assigned.ε (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C
34 Protein home pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09
35 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
36 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
37 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
38 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
39 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
40 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
41 RNA biosynthtranscription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
42 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C
43 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C
44 RNA biosynthcomponent GRF of GRF-GIF transcriptional complex (original description: pacid=3716
45 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
46 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra

1 Solute transp
2 Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
3 Solute transp
4 transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009
5 Cytoskeleton
6 microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
7 Cytoskeleton
8 microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
9 RNA biosynth
10 transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
11 RNA biosynth
12 transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
13 not assigned.r
14 no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
15 not assigned.ε
16 (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C
17 Protein home
18 pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10
19 RNA biosynth
20 transcriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
21 Protein modif
22 protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G
23 not assigned.ε
24 (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C
25 not assigned.ε
26 (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C
27 Cell wall orga
28 rxylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
29 Solute transp
30 polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran
31 not assigned.ε
32 (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C
33 Protein home
34 pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09
35 Multi-process
36 circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
37 Protein biosyr
38 component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
39 Protein modif
40 protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
41 Protein modif
42 protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
43 not assigned.r
44 no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
45 not assigned.r
46 no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
47 RNA biosynth
48 transcription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
49 not assigned.ε
50 (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C
51 not assigned.ε
52 (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C
53 RNA biosynth
54 component GRF of GRF-GIF transcriptional complex (original description: pacid=3716
55 RNA processir
56 tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
57 RNA processir
58 tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
59 Solute transp
60 Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
Solute transp
transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009
Cytoskeleton
microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
Cytoskeleton
microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
RNA biosynth
transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
RNA biosynth
transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
not assigned.r
no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
not assigned.ε
(original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C
Protein home
pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10
RNA biosynth
transcriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
Protein modif
protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G
not assigned.ε
(original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C
not assigned.ε
(original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C
Cell wall orga
rxylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
Solute transp
polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran
not assigned.ε
(original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C
Protein home
pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09

1 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
2 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
3 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
4 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
5 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
6 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
7 RNA biosynthtranscription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
8 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C
9 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C
10 RNA biosynthcomponent GRF of GRF-GIF transcriptional complex (original description: pacid=3716
11 RNA processirtRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
12 RNA processirtRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
13 Solute transpcNodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
14 Solute transpctransport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009
15 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
16 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
17 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
18 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
19 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
20 not assigned.ε (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C
21 Protein homepepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10
22 RNA biosynthtranscriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
23 Protein modif protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G
24 not assigned.ε (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C
25 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C
26 Cell wall orgaxylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
27 Solute transpcpolyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran
28 not assigned.ε (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C
29 Protein homepepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09
30 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
31 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
32 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
33 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
34 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
35 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
36 RNA biosynthtranscription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
37 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C
38 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C
39 RNA biosynthcomponent GRF of GRF-GIF transcriptional complex (original description: pacid=3716
40 RNA processirtRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
41 RNA processirtRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
42 Solute transpcNodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
43 Solute transpctransport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009
44 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
45 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
46 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C

1 RNA biosynthetranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
2 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
3 not assigned.ε (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C
4 Protein homepepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G1C
5 RNA biosynthetranscriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
6 Protein modif protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G
7 not assigned.ε (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C
8 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C
9 Cell wall orgar xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
10 Solute transpc polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran
11 not assigned.ε (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C
12 Protein homepepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G0C
13 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
14 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
15 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
16 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
17 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
18 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
19 RNA biosynthetranscription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
20 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C
21 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C
22 RNA biosynthecomponent GRF of GRF-GIF transcriptional complex (original description: pacid=371C
23 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
24 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
25 Solute transpc Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
26 Solute transpc transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.00C
27 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
28 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
29 RNA biosynthetranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
30 RNA biosynthetranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
31 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
32 not assigned.ε (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C
33 Protein homepepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G1C
34 RNA biosynthetranscriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
35 Protein modif protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G
36 not assigned.ε (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C
37 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C
38 Cell wall orgar xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
39 Solute transpc polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran
40 not assigned.ε (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C
41 Protein homepepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G0C
42 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
43 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
44 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
45 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
46 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu

1 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
2 RNA biosynthtranscription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
3 not assigned.a (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C
4 not assigned.a (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C
5 RNA biosynthcomponent GRF of GRF-GIF transcriptional complex (original description: pacid=3716
6 RNA processirtRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
7 RNA processirtRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
8 Solute transpcNodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
9 Solute transpctransport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009
10 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
11 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
12 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
13 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
14 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
15 not assigned.a (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C
16 Protein homepepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10
17 RNA biosynthtranscriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
18 Protein modif protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G
19 not assigned.a (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C
20 not assigned.a (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C
21 Cell wall orgaxylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
22 Solute transpcpolyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran
23 not assigned.a (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C
24 Protein homepepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09
25 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
26 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
27 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
28 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
29 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
30 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
31 RNA biosynthtranscription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
32 not assigned.a (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C
33 not assigned.a (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C
34 RNA biosynthcomponent GRF of GRF-GIF transcriptional complex (original description: pacid=3716
35 RNA processirtRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
36 RNA processirtRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
37 Solute transpcNodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
38 Solute transpctransport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009
39 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
40 Cytoskeleton imicrotubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
41 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
42 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
43 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
44 not assigned.a (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C
45 Protein homepepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10
46 RNA biosynthtranscriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans

1 Protein modif protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G2
2 not assigned.ε (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C
3 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C
4 Cell wall organ xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
5 Solute transp polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran
6 not assigned.ε (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C
7 Protein home pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09
8 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
9 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
10 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
11 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
12 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
13 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
14 RNA biosynth transcription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
15 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C
16 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C
17 RNA biosynth component GRF of GRF-GIF transcriptional complex (original description: pacid=3716
18 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
19 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
20 Solute transp Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
21 Solute transp transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009
22 Cytoskeleton microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
23 Cytoskeleton microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
24 RNA biosynth transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
25 RNA biosynth transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
26 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
27 not assigned.ε (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C
28 Protein home pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G1C
29 RNA biosynth transcriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
30 Protein modif protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G2
31 not assigned.ε (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C
32 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C
33 Cell wall organ xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
34 Solute transp polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran
35 not assigned.ε (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C
36 Protein home pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09
37 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
38 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
39 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
40 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
41 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
42 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
43 RNA biosynth transcription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
44 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C
45 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C
46 RNA biosynth component GRF of GRF-GIF transcriptional complex (original description: pacid=3716

1 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
2 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
3 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
4 Solute transp; Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
5 Solute transp; transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009
6 Cytoskeleton ;microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
7 Cytoskeleton ;microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
8 RNA biosynth; transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
9 RNA biosynth; transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
10 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
11 not assigned.ε (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C
12 Protein home; pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10
13 RNA biosynth; transcriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
14 Protein modif; protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G2
15 not assigned.ε (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C
16 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C
17 Cell wall orga; xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
18 Solute transp; polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran
19 not assigned.ε (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C
20 Protein home; pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09
21 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
22 Protein biosyr; component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
23 Protein modif; protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
24 Protein modif; protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
25 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
26 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
27 RNA biosynth; transcription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
28 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C
29 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C
30 RNA biosynth; component GRF of GRF-GIF transcriptional complex (original description: pacid=3716
31 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
32 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
33 Solute transp; Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
34 Solute transp; transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009
35 Cytoskeleton ;microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
36 Cytoskeleton ;microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
37 RNA biosynth; transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
38 RNA biosynth; transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
39 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
40 not assigned.ε (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C
41 Protein home; pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10
42 RNA biosynth; transcriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
43 Protein modif; protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G2
44 not assigned.ε (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C
45 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C
46 Cell wall orga; xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
47 Solute transp; polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran

1 not assigned.ε (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C
2 Protein home pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09
3 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
4 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
5 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
6 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
7 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
8 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
9 RNA biosynthtranscription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
10 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C
11 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C
12 RNA biosynthcomponent GRF of GRF-GIF transcriptional complex (original description: pacid=3716
13 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
14 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
15 Solute transpNodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
16 Solute transptransport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009
17 Cytoskeleton microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
18 Cytoskeleton microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
19 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
20 RNA biosynthtranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
21 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
22 not assigned.ε (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C
23 Protein home pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10
24 RNA biosynthtranscriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
25 Protein modif protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G2
26 not assigned.ε (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C
27 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C
28 Cell wall orgar xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
29 Solute transp polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran
30 not assigned.ε (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C
31 Protein home pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09
32 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
33 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
34 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
35 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
36 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
37 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
38 RNA biosynthtranscription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
39 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C
40 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C
41 RNA biosynthcomponent GRF of GRF-GIF transcriptional complex (original description: pacid=3716
42 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
43 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
44 Solute transpNodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
45 Solute transptransport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009
46 Cytoskeleton microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript

1 Cytoskeleton (microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
2 RNA biosynthetranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
3 RNA biosynthetranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
4 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
5 not assigned.ε (original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.C
6 Protein home pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G1C
7 RNA biosynthetranscriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
8 Protein modif protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G
9 RNA biosynthetranscription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
10 Solute transpc polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran
11 Cytoskeleton (microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
12 Cytoskeleton (microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
13 not assigned.ε (original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.C
14 not assigned.ε (original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.C
15 not assigned.ε (original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.C
16 Cell wall orgar xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
17 Protein home pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09
18 Multi-process circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
19 Protein modif protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G
20 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37151
21 Multi-process phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37151
22 not assigned.r no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
23 not assigned.r no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
24 not assigned.ε (original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.C
25 Protein biosyr component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
26 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
27 Protein modif protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
28 not assigned.ε (original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.C
29 RNA biosynthecomponent GRF of GRF-GIF transcriptional complex (original description: pacid=3716
30 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
31 RNA processir tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
32 Protein home pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G1C
33 Solute transpc Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
34 Solute transpc transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009
35 RNA biosynthetranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
36 RNA biosynthetranscription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.C
37 not assigned.r no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
38 Protein modif protein kinase (LRR-III) (original description: pacid=37166830 transcript=Phvul.007G
39 Lipid metabolidelta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
40 not assigned.ε (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C
41 External stimu RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 t
42 Lipid metabolicomponent Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
43 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
44 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
45 not assigned.ε (original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.C
46 not assigned.ε (original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.C

1 Redox homeo type-2 peroxiredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
2 not assigned.r no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
3 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
4 Photosynthesi glutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
5 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
6 Protein transl subunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
7 Photosynthesi component PnsB2/NDF2 of NDH subcomplex B (original description: pacid=3716998
8 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
9 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
10 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
11 Photosynthesiferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.0C
12 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
13 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
14 RNA biosynthi component MED5/MED24/MED33 of tail module of MEDIATOR transcription co-activ
15 Carbohydrate starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
16 not assigned.a (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
17 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
18 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
19 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
20 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
21 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
22 Enzyme classii Geraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vwz7|c76b6_catro : 434.0) &
23 Solute transpc organic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
24 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
25 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
26 Nutrient uptal iron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G0
27 Lipid metabolidelta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
28 not assigned.a (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C
29 External stimu RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 i
30 Lipid metabolicomponent Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
31 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
32 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
33 not assigned.a (original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.C
34 not assigned.a (original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.C
35 Redox homeo type-2 peroxiredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
36 not assigned.r no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
37 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
38 Photosynthesi glutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
39 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
40 Protein transl subunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
41 Photosynthesi component PnsB2/NDF2 of NDH subcomplex B (original description: pacid=3716998
42 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
43 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
44 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
45 Photosynthesiferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.0C
46 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu

1 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
2 RNA biosynthcomponent MED5/MED24/MED33 of tail module of MEDIATOR transcription co-activ
3 Carbohydrate starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
4 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
5 External stimuSNI1 systemic acquired resistance regulator protein (original description: pacid=3714
6 External stimuSNI1 systemic acquired resistance regulator protein (original description: pacid=3714
7 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
8 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
9 External stimuSNI1 systemic acquired resistance regulator protein (original description: pacid=3714
10 Enzyme classiiGeraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vzw7|c76b6_catro : 434.0) &
11 Solute transporganic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
12 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
13 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
14 Nutrient uptaliron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G07
15 Lipid metabolidelta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
16 not assigned.ε (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C
17 External stimuRAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 t
18 Lipid metabolicomponent Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
19 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
20 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
21 not assigned.ε (original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.C
22 not assigned.ε (original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.C
23 Redox homeo type-2 peroxidoredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
24 not assigned.r no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
25 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
26 Photosynthesiglutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
27 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
28 Protein translsunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
29 Photosynthesicomponent PnsB2/NDF2 of NDH subcomplex B (original description: pacid=3716998ε
30 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
31 Enzyme classiiProbable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|qε
32 Enzyme classiiProbable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|qε
33 Photosynthesiferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.0C
34 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
35 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
36 RNA biosynthcomponent MED5/MED24/MED33 of tail module of MEDIATOR transcription co-activ
37 Carbohydrate starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
38 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
39 External stimuSNI1 systemic acquired resistance regulator protein (original description: pacid=3714
40 External stimuSNI1 systemic acquired resistance regulator protein (original description: pacid=3714
41 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
42 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
43 External stimuSNI1 systemic acquired resistance regulator protein (original description: pacid=3714
44 Enzyme classiiGeraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vzw7|c76b6_catro : 434.0) &
45 Solute transporganic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
46 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl

1 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
2 Nutrient uptaliron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G07
3 Lipid metabolidelta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
4 not assigned.ε (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C
5 External stimu RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 1
6 Lipid metabolicomponent Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
7 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
8 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
9 not assigned.ε (original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.C
10 not assigned.ε (original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.C
11 Redox homeo type-2 peroxiredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
12 not assigned.r no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
13 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
14 Photosynthesiglutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
15 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
16 Protein translsubunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
17 Photosynthesicomponent PnsB2/NDF2 of NDH subcomplex B (original description: pacid=37169988
18 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
19 Enzyme classiiProbable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|qε
20 Enzyme classiiProbable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|qε
21 Photosynthesiferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.0C
22 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
23 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
24 RNA biosyntheicomponent MED5/MED24/MED33 of tail module of MEDIATOR transcription co-activ
25 Carbohydrate starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
26 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
27 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
28 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
29 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
30 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
31 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
32 Enzyme classiiGeraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vwz7|c76b6_catro : 434.0) &
33 Solute transpcorganic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
34 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
35 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
36 Nutrient uptaliron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G07
37 Lipid metabolidelta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
38 not assigned.ε (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C
39 External stimu RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 1
40 Lipid metabolicomponent Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
41 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
42 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
43 not assigned.ε (original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.C
44 not assigned.ε (original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.C
45 Redox homeo type-2 peroxiredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
46 not assigned.r no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu

1 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
2 Photosynthesi glutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
3 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
4 Protein transl subunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
5 Photosynthesi component PnsB2/NDF2 of NDH subcomplex B (original description: pacid=37169988
6 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
7 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
8 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
9 Photosynthesi ferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.00
10 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
11 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
12 RNA biosynthesi component MED5/MED24/MED33 of tail module of MEDIATOR transcription co-acti
13 Carbohydrate starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
14 not assigned.r (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
15 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
16 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
17 Lipid metabolis sphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
18 Lipid metabolis sphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
19 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
20 Enzyme classii Geraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vwz7|c76b6_catro : 434.0) &
21 Solute transp organic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
22 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
23 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
24 Nutrient uptal iron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G07
25 Lipid metabolis delta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
26 not assigned.r (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C
27 External stimu RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 t
28 Lipid metabolis component Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
29 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
30 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
31 not assigned.r (original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.C
32 not assigned.r (original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.C
33 Redox homeo type-2 peroxiredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
34 not assigned.r no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
35 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
36 Photosynthesi glutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
37 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
38 Protein transl subunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
39 Photosynthesi component PnsB2/NDF2 of NDH subcomplex B (original description: pacid=37169988
40 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
41 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
42 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
43 Photosynthesi ferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.00
44 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
45 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
46 RNA biosynthesi component MED5/MED24/MED33 of tail module of MEDIATOR transcription co-acti

1 Carbohydrate starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
2 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
3 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
4 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
5 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
6 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
7 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
8 Enzyme classii Geraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vwz7|c76b6_catro : 434.0) &
9 Solute transpc organic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
10 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
11 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
12 Nutrient uptal iron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G07
13 Lipid metaboli delta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
14 not assigned.ε (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C
15 External stimu RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 1
16 Lipid metaboli component Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
17 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
18 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
19 not assigned.ε (original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.C
20 not assigned.ε (original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.C
21 Redox homeo type-2 peroxiredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
22 not assigned.r no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
23 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
24 Photosynthesi glutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
25 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
26 Protein transi subunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
27 Photosynthesi component PnsB2/NDF2 of NDH subcomplex B (original description: pacid=3716998ε
28 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
29 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|qε
30 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|qε
31 Photosynthesi ferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.0C
32 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
33 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
34 RNA biosynthi component MED5/MED24/MED33 of tail module of MEDIATOR transcription co-acti
35 Carbohydrate starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
36 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
37 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
38 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
39 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
40 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
41 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
42 Enzyme classii Geraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vwz7|c76b6_catro : 434.0) &
43 Solute transpc organic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
44 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
45 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
46 Nutrient uptal iron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G07

1 Lipid metabolidelta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
2 not assigned.ε (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C
3 External stimu RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 t
4 Lipid metabolicomponent Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
5 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
6 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
7 not assigned.ε (original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.C
8 not assigned.ε (original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.C
9 Redox homeo type-2 peroxiredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
10 not assigned.r no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
11 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
12 Photosynthesiglutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
13 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
14 Protein transksubunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
15 Photosynthesicomponent PnsB2/NDF2 of NDH subcomplex B (original description: pacid=3716998ε
16 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
17 Enzyme classiiProbable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|qε
18 Enzyme classiiProbable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|qε
19 Photosynthesiferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.0C
20 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
21 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
22 RNA biosynthicomponent MED5/MED24/MED33 of tail module of MEDIATOR transcription co-activ
23 Carbohydrate starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
24 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
25 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
26 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
27 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
28 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
29 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
30 Enzyme classiiGeraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vwz7|c76b6_catro : 434.0) &
31 Solute transporganic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
32 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
33 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
34 Nutrient uptaliron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G07
35 Lipid metabolidelta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
36 not assigned.ε (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C
37 External stimu RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 t
38 Lipid metabolicomponent Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
39 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
40 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
41 not assigned.ε (original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.C
42 not assigned.ε (original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.C
43 Redox homeo type-2 peroxiredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
44 not assigned.r no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
45 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
46 Photosynthesiglutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=

1 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
2 Protein transls subunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
3 Photosynthesi component PnsB2/NDF2 of NDH subcomplex B (original description: pacid=3716998
4 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
5 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
6 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
7 Photosynthesi ferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.0C
8 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
9 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
10 RNA biosynth component MED5/MED24/MED33 of tail module of MEDIATOR transcription co-activ
11 Carbohydrate starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
12 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
13 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
14 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
15 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
16 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
17 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
18 Enzyme classii Geraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vwz7|c76b6_catro : 434.0) &
19 Solute transp organic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
20 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
21 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
22 Nutrient uptal iron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G07
23 Lipid metabolidelta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
24 not assigned.ε (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C
25 External stimu RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 t
26 Lipid metabolis component Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
27 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
28 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
29 not assigned.ε (original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.C
30 not assigned.ε (original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.C
31 Redox homeo type-2 peroxiredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
32 not assigned.r no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
33 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
34 Photosynthesi glutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
35 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
36 Protein transls subunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
37 Photosynthesi component PnsB2/NDF2 of NDH subcomplex B (original description: pacid=3716998
38 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
39 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
40 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
41 Photosynthesi ferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.0C
42 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
43 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
44 RNA biosynth component MED5/MED24/MED33 of tail module of MEDIATOR transcription co-activ
45 Carbohydrate starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
46 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C

1 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
2 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
3 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
4 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
5 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
6 Enzyme classiiGeraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vzw7|c76b6_catro : 434.0) &
7 Solute transporganic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
8 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
9 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
10 Nutrient uptaliron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G07
11 Lipid metabolidelta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
12 not assigned.ε (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C
13 External stimu RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 t
14 Lipid metabolicomponent Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
15 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
16 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
17 not assigned.ε (original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.C
18 not assigned.ε (original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.C
19 Redox homeo type-2 peroxidoredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
20 not assigned.r no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
21 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
22 Photosynthesiglutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
23 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
24 Protein translsubunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
25 Photosynthesicomponent PnsB2/NDF2 of NDH subcomplex B (original description: pacid=3716998
26 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
27 Enzyme classiiProbable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
28 Enzyme classiiProbable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
29 Photosynthesiferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.0C
30 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
31 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
32 RNA biosynthecomponent MED5/MED24/MED33 of tail module of MEDIATOR transcription co-acti
33 Carbohydrate starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
34 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
35 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
36 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
37 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
38 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
39 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
40 Enzyme classiiGeraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vzw7|c76b6_catro : 434.0) &
41 Solute transporganic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
42 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
43 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
44 Nutrient uptaliron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G07
45 Lipid metabolidelta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
46 not assigned.ε (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C

1 External stimu RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 1
2 Lipid metabol component Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
3 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
4 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
5 not assigned.a (original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.C
6 not assigned.a (original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.C
7 Redox homeo type-2 peroxiredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
8 not assigned.r no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
9 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
10 Photosynthesi glutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
11 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
12 Protein transi subunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
13 Photosynthesi component PnsB2/NDF2 of NDH subcomplex B (original description: pacid=3716998
14 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
15 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
16 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
17 Photosynthesiferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.0C
18 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
19 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
20 RNA biosynthi component MED5/MED24/MED33 of tail module of MEDIATOR transcription co-acti
21 Carbohydrate starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
22 not assigned.a (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
23 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
24 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
25 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
26 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
27 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
28 Enzyme classii Geraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vzw7|c76b6_catro : 434.0) &
29 Solute transporganic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
30 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
31 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
32 Nutrient uptaliron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G0
33 Lipid metabolidelta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
34 not assigned.a (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C
35 External stimu RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 1
36 Lipid metabol component Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
37 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
38 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
39 not assigned.a (original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.C
40 not assigned.a (original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.C
41 Redox homeo type-2 peroxiredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
42 not assigned.r no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
43 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
44 Photosynthesi glutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
45 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
46 Protein transi subunit alpha of co-translational insertion system Sec61 subcomplex (original descrip

1
2 Photosynthesis component PnsB2/NDF2 of NDH subcomplex B (original description: pacid=37169988
3 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
4 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
5 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
6 Photosynthesis ferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.0C
7 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
8 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
9
10 RNA biosynthesis component MED5/MED24/MED33 of tail module of MEDIATOR transcription co-activ
11 Carbohydrate starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
12 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
13 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
14 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
15 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
16 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
17 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
18 Enzyme classii Geraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vwz7|c76b6_catro : 434.0) &
19 Solute transporganic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
20 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
21 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
22 Nutrient uptaliron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G07
23 Lipid metabolidelta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
24 not assigned.ε (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C
25 External stimu RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 1
26 Lipid metabolicomponent Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
27 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
28 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
29 not assigned.ε (original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.C
30 not assigned.ε (original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.C
31 Redox homeo type-2 peroxidoredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
32 not assigned.r no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
33 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
34 Photosynthesis glutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
35 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
36 Protein transls subunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
37 Photosynthesis component PnsB2/NDF2 of NDH subcomplex B (original description: pacid=37169988
38 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
39 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
40 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
41 Photosynthesis ferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.0C
42 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
43 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
44 RNA biosynthesis component MED5/MED24/MED33 of tail module of MEDIATOR transcription co-activ
45 Carbohydrate starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
46 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
47 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
48 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714

1 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
2 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
3 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
4 Enzyme classii Geraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vwz7|c76b6_catro : 434.0) &
5 Solute transp organic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
6 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
7 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
8 Nutrient uptal iron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G07
9 Lipid metabolidelta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
10 not assigned.ε (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C
11 External stimu RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 t
12 Lipid metabolicomponent Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
13 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
14 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
15 not assigned.ε (original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.C
16 not assigned.ε (original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.C
17 Redox homeo type-2 peroxidoredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
18 not assigned.r no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
19 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
20 Photosynthesi glutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
21 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
22 Protein transi subunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
23 Photosynthesicomponent PnsB2/NDF2 of NDH subcomplex B (original description: pacid=3716998ε
24 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
25 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|qε
26 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|qε
27 Photosynthesiferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.0C
28 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
29 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
30 RNA biosynthicomponent MED5/MED24/MED33 of tail module of MEDIATOR transcription co-activ
31 Carbohydrate starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
32 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
33 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
34 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
35 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
36 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
37 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
38 Enzyme classii Geraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vwz7|c76b6_catro : 434.0) &
39 Solute transp organic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
40 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
41 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
42 Nutrient uptal iron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G07
43 Lipid metabolidelta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
44 not assigned.ε (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C
45 External stimu RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 t
46 Lipid metabolicomponent Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip

1 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
2 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
3 not assigned.a (original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.C
4 not assigned.a (original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.C
5 Redox homeo type-2 peroxiredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
6 not assigned.r no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
7 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
8 Photosynthesiglutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
9 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
10 Protein translsubunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
11 Photosynthesicomponent PnsB2/NDF2 of NDH subcomplex B (original description: pacid=3716998
12 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
13 Enzyme classiiProbable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
14 Enzyme classiiProbable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q
15 Photosynthesiferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.0C
16 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
17 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
18 RNA biosynthesicomponent MED5/MED24/MED33 of tail module of MEDIATOR transcription co-acti
19 Carbohydrate starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
20 not assigned.a (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
21 External stimuSNI1 systemic acquired resistance regulator protein (original description: pacid=3714
22 External stimuSNI1 systemic acquired resistance regulator protein (original description: pacid=3714
23 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
24 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
25 External stimuSNI1 systemic acquired resistance regulator protein (original description: pacid=3714
26 Enzyme classiiGeraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vwz7|c76b6_catro : 434.0) &
27 Solute transporganic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
28 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
29 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
30 Nutrient uptaliron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G0
31 Lipid metabolidelta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
32 not assigned.a (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C
33 External stimuRAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 t
34 Lipid metabolicomponent Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
35 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
36 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
37 not assigned.a (original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.C
38 not assigned.a (original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.C
39 Redox homeo type-2 peroxiredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
40 not assigned.r no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
41 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
42 Photosynthesiglutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
43 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
44 Protein translsubunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
45 Photosynthesicomponent PnsB2/NDF2 of NDH subcomplex B (original description: pacid=3716998
46 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu

1 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q̄
2 Enzyme classii Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q̄
3 Photosynthesisferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.0C
4 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
5 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
6 RNA biosynthi component MED5/MED24/MED33 of tail module of MEDIATOR transcription co-acti
7 Carbohydrate starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
8 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
9 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
10 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
11 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
12 Lipid metabolisphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
13 External stimu SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
14 Enzyme classii Geraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vwz7|c76b6_catro : 434.0) &
15 Solute transpc organic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
16 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
17 not assigned.r no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
18 Nutrient uptal iron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G0
19 Lipid metabolidelta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
20 not assigned.r no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
21 not assigned.ε (original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.C
22 Photosynthesisferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.0C
23 External stimu RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 1
24 Lipid metabolicomponent Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
25 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
26 not assigned.r no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
27 not assigned.ε (original description: pacid=37151389 transcript=Phvul.009G167700.2 locus=Phvul.C
28 not assigned.ε (original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.C
29 not assigned.ε (original description: pacid=37174307 transcript=Phvul.L003746.2 locus=Phvul.L003
30 not assigned.ε (original description: pacid=37174307 transcript=Phvul.L003746.2 locus=Phvul.L003
31 not assigned.ε (original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.C
32 Redox homeo type-2 peroxidoredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
33 not assigned.r no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
34 Photosynthesisglutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
35 not assigned.r no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
36 Protein transk subunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
37 Solute transpc cation antiporter (CAX) (original description: pacid=37171893 transcript=Phvul.006G
38 Photosynthesisi component PnsB2/NDF2 of NDH subcomplex B (original description: pacid=3716998ε
39 not assigned.r no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
40 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
41 not assigned.r no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
42 not assigned.ε (original description: pacid=37177587 transcript=Phvul.002G157000.1 locus=Phvul.C
43 Cell wall orgar pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
44 not assigned.ε (original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.C
45 Cell wall orgar fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcrip
46 RNA biosynthi transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.0C

1 RNA biosynthetranscription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
2 Solute transp nucleotide sugar transporter (UAFT) (original description: pacid=37144593 transcript:
3 Solute transp nucleotide sugar transporter (UAFT) (original description: pacid=37144593 transcript:
4 not assigned.ε (original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.C
5 Protein transk NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
6 Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcrip
7 Amino acid m serine hydroxymethyltransferase (original description: pacid=37167850 transcript=Pl
8 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
9 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
10 Multi-process phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
11 Solute transp outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Phv
12 Chromatin org chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
13 Chromatin org chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
14 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
15 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
16 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
17 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
18 External stimu PIF red/far-red light perception transcriptional regulator (original description: pacid=
19 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
20 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
21 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
22 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
23 not assigned.r no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 locu
24 RNA biosynthetranscription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
25 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
26 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
27 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
28 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
29 not assigned.ε (original description: pacid=37147019 transcript=Phvul.003G181600.1 locus=Phvul.C
30 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
31 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
32 not assigned.r no hits & (original description: pacid=37174067 transcript=Phvul.006G164800.1 locu
33 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
34 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
35 not assigned.ε (original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.C
36 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
37 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
38 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
39 not assigned.ε (original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.C
40 Protein modif component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
41 RNA biosynthG2-like GARP transcription factor (original description: pacid=37159020 transcript=Pl
42 not assigned.r no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu
43 not assigned.ε (original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.C
44 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
45 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
46 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
47 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio

1 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
2 Solute transp P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
3 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
4 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
5 Solute transp P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
6 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
7 Cell wall orgar pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
8 not assigned.ε (original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.C
9 Cell wall orgar fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcrip
10 RNA biosynth transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
11 RNA biosynth transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
12 Solute transp nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
13 Solute transp nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
14 not assigned.ε (original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.C
15 Protein transl NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
16 Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcrip
17 Amino acid m serine hydroxymethyltransferase (original description: pacid=37167850 transcript=Pl
18 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
19 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
20 Multi-process phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
21 Solute transp outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Ph
22 Chromatin org chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
23 Chromatin org chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
24 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
25 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
26 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
27 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
28 External stimu PIF red/far-red light perception transcriptional regulator (original description: pacid=
29 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
30 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
31 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
32 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
33 not assigned.r no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 locu
34 RNA biosynth transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
35 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
36 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
37 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
38 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
39 not assigned.ε (original description: pacid=37147019 transcript=Phvul.003G181600.1 locus=Phvul.C
40 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
41 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
42 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
43 not assigned.r no hits & (original description: pacid=37174067 transcript=Phvul.006G164800.1 locu
44 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
45 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
46 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
47 not assigned.ε (original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.C
48 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

1 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
2 not assigned.ε (original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.C
3 Protein modif component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
4 RNA biosynthG2-like GARP transcription factor (original description: pacid=37159020 transcript=Pl
5 not assigned.r no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu
6 not assigned.ε (original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.C
7 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
8 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
9 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
10 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
11 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
12 Solute transpcP4-type ATPase component ALA of phospholipid flippase complex (original descriptio
13 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
14 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
15 Solute transpcP4-type ATPase component ALA of phospholipid flippase complex (original descriptio
16 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
17 Cell wall orgar pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
18 not assigned.ε (original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.C
19 Cell wall orgar fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcrip
20 RNA biosynthtranscription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
21 RNA biosynthtranscription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
22 Solute transpcnucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
23 Solute transpcnucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
24 not assigned.ε (original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.C
25 Protein transkNUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
26 Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcrip
27 Amino acid mserine hydroxymethyltransferase (original description: pacid=37167850 transcript=Pl
28 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
29 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
30 Multi-process phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
31 Solute transpcouter membrane porin (OEP21) (original description: pacid=37152022 transcript=Ph
32 Chromatin orgchromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
33 Chromatin orgchromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
34 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
35 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
36 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
37 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
38 External stimu PIF red/far-red light perception transcriptional regulator (original description: pacid=
39 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
40 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
41 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
42 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
43 not assigned.r no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 locu
44 RNA biosynthtranscription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
45 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
46 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

1 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
2 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
3 not assigned.ε (original description: pacid=37147019 transcript=Phvul.003G181600.1 locus=Phvul.C
4 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
5 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
6 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
7 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
8 not assigned.r no hits & (original description: pacid=37174067 transcript=Phvul.006G164800.1 locu
9 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
10 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
11 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
12 not assigned.ε (original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.C
13 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
14 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
15 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
16 not assigned.ε (original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.C
17 Protein modif component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
18 RNA biosynthεG2-like GARP transcription factor (original description: pacid=37159020 transcript=Pl
19 not assigned.r no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu
20 not assigned.ε (original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.C
21 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
22 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
23 External stimε GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
24 External stimε GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
25 External stimε GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
26 Solute transpε P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
27 External stimε transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
28 External stimε transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
29 Solute transpε P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
30 External stimε GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
31 Cell wall orgar pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
32 not assigned.ε (original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.C
33 Cell wall orgar fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri
34 RNA biosynthε transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
35 RNA biosynthε transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
36 Solute transpε nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
37 Solute transpε nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
38 not assigned.ε (original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.C
39 Protein translε NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
40 Protein homeε monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri
41 Amino acid mε serine hydroxymethyltransferase (original description: pacid=37167850 transcript=Pl
42 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
43 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
44 Multi-process phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
45 Solute transpε outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Ph
46 Chromatin orgε chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
47 Chromatin orgε chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
48 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
49 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
50 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C

1 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
2 External stimu PIF red/far-red light perception transcriptional regulator (original description: pacid=
3 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
4 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
5 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
6 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
7 not assigned.ε (original description: pacid=37166363 transcript=Phvul.007G157500.5 locus=Phvul.C
8 not assigned.ε (original description: pacid=37166363 transcript=Phvul.007G157500.5 locus=Phvul.C
9 not assigned.r no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 locu
10 RNA biosynthtranscription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
11 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
12 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
13 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
14 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
15 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
16 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
17 not assigned.ε (original description: pacid=37147019 transcript=Phvul.003G181600.1 locus=Phvul.C
18 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
19 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
20 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
21 not assigned.r no hits & (original description: pacid=37174067 transcript=Phvul.006G164800.1 locu
22 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
23 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
24 not assigned.ε (original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.C
25 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
26 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
27 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
28 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
29 not assigned.ε (original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.C
30 Protein modif component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
31 RNA biosynthG2-like GARP transcription factor (original description: pacid=37159020 transcript=Pl
32 not assigned.r no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu
33 not assigned.ε (original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.C
34 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
35 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
36 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
37 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
38 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
39 Solute transpcP4-type ATPase component ALA of phospholipid flippase complex (original descriptic
40 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
41 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
42 Solute transpcP4-type ATPase component ALA of phospholipid flippase complex (original descriptic
43 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
44 Cell wall orgar pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
45 not assigned.ε (original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.C
46 Cell wall orgar fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri
47 RNA biosynthtranscription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
48 RNA biosynthtranscription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
49 Solute transpcnucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
50 Solute transpcnucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
51 not assigned.ε (original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.C
52 Protein transkNUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
53 Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri

1 Amino acid m serine hydroxymethyltransferase (original description: pacid=37167850 transcript=Pl
2 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
3 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
4 Multi-process phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
5 Solute transp outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Phv
6 Chromatin org chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
7 Chromatin org chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
8 Cell wall org ar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
9 Cell wall org ar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
10 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
11 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
12 External stimu PIF red/far-red light perception transcriptional regulator (original description: pacid=
13 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
14 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
15 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
16 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
17 not assigned.r no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 locu
18 RNA biosynth transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
19 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
20 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
21 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
22 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
23 not assigned.ε (original description: pacid=37147019 transcript=Phvul.003G181600.1 locus=Phvul.C
24 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
25 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
26 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
27 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
28 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
29 not assigned.ε (original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.C
30 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
31 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
32 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
33 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
34 not assigned.r no hits & (original description: pacid=37174067 transcript=Phvul.006G164800.1 locu
35 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
36 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
37 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
38 not assigned.ε (original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.C
39 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
40 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
41 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
42 not assigned.ε (original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.C
43 Protein modif component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
44 RNA biosynth G2-like GARP transcription factor (original description: pacid=37159020 transcript=Pl
45 not assigned.r no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu
46 not assigned.ε (original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.C
47 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
48 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
49 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
50 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
51 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
52 Solute transp P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
53 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
54 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
55 Solute transp P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
56 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio

1 Cell wall organ pectin methyltransferase (original description: pacid=37148958 transcript=Phvul.009G2
2 not assigned.ε (original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.C
3 Cell wall organ fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcrip
4 RNA biosynthesis transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
5 RNA biosynthesis transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
6 Solute transport nucleotide sugar transporter (UAF1) (original description: pacid=37144593 transcript:
7 Solute transport nucleotide sugar transporter (UAF1) (original description: pacid=37144593 transcript:
8 not assigned.ε (original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.C
9 Protein transmembrane NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
10 Protein homeodomain monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcrip
11 Amino acid methylserine hydroxymethyltransferase (original description: pacid=37167850 transcript=PI
12 Multi-process regulatory subunit beta gamma of SnRK1 kinase complex (original description: pacid=
13 Multi-process regulatory subunit beta gamma of SnRK1 kinase complex (original description: pacid=
14 Multi-process phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
15 Solute transport outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Ph
16 Chromatin organization chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
17 Chromatin organization chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
18 Cell wall organ CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
19 Cell wall organ CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
20 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
21 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
22 External stimulus PIF red/far-red light perception transcriptional regulator (original description: pacid=
23 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
24 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
25 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
26 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
27 not assigned.r no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 locu
28 RNA biosynthesis transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
29 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
30 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
31 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
32 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
33 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
34 not assigned.ε (original description: pacid=37147019 transcript=Phvul.003G181600.1 locus=Phvul.C
35 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
36 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
37 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
38 not assigned.r no hits & (original description: pacid=37174067 transcript=Phvul.006G164800.1 locu
39 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
40 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
41 not assigned.ε (original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.C
42 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
43 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
44 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
45 not assigned.ε (original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.C
46 Protein modification component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
47 RNA biosynthesis G2-like GARP transcription factor (original description: pacid=37159020 transcript=PI
48 not assigned.r no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu
49 not assigned.ε (original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.C

1 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
2 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
3 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
4 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
5 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
6 Solute transp P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
7 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
8 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
9 Solute transp P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
10 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
11 Cell wall orgar pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
12 not assigned.ε (original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.C
13 Cell wall orgar fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri
14 RNA biosynth transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
15 RNA biosynth transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
16 Solute transp nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
17 Solute transp nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
18 not assigned.ε (original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.C
19 Protein transk NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
20 Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri
21 Amino acid m serine hydroxymethyltransferase (original description: pacid=37167850 transcript=Pl
22 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
23 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
24 Multi-process phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
25 Solute transp outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Phv
26 Chromatin org chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
27 Chromatin org chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
28 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
29 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
30 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
31 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
32 External stimu PIF red/far-red light perception transcriptional regulator (original description: pacid=
33 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
34 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
35 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
36 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
37 not assigned.r no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 loc
38 RNA biosynth transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
39 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
40 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
41 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
42 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
43 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
44 not assigned.ε (original description: pacid=37147019 transcript=Phvul.003G181600.1 locus=Phvul.C
45 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
46 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
47 not assigned.r no hits & (original description: pacid=37174067 transcript=Phvul.006G164800.1 loc

1 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
2 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
3 not assigned.ε (original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.C
4 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
5 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
6 not assigned.ε (original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.C
7 Protein modif component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
8 RNA biosynthεG2-like GARP transcription factor (original description: pacid=37159020 transcript=Pl
9 not assigned.r no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu
10 not assigned.ε (original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.C
11 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
12 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
13 External stimεGIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
14 External stimεGIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
15 External stimεGIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
16 Solute transpεP4-type ATPase component ALA of phospholipid flippase complex (original descriptio
17 External stimεtranscription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
18 External stimεtranscription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
19 Solute transpεP4-type ATPase component ALA of phospholipid flippase complex (original descriptio
20 External stimεGIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
21 Cell wall orgar pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
22 not assigned.ε (original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.C
23 Cell wall orgar fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri
24 RNA biosynthεtranscription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
25 RNA biosynthεtranscription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
26 Solute transpεnucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
27 Solute transpεnucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
28 not assigned.ε (original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.C
29 Protein translnUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
30 Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri
31 Amino acid mεserine hydroxymethyltransferase (original description: pacid=37167850 transcript=Pl
32 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
33 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
34 Multi-process phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
35 Solute transpεouter membrane porin (OEP21) (original description: pacid=37152022 transcript=Ph
36 Chromatin orgεchromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
37 Chromatin orgεchromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
38 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
39 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
40 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
41 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
42 External stimεPIF red/far-red light perception transcriptional regulator (original description: pacid=
43 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
44 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
45 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
46 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C

1 not assigned.r no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 locu
2 RNA biosynthtranscription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
3 not assigned.a (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
4 not assigned.a (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
5 not assigned.a (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
6 not assigned.a (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
7 not assigned.a (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
8 not assigned.a (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
9 not assigned.a (original description: pacid=37147019 transcript=Phvul.003G181600.1 locus=Phvul.C
10 not assigned.a (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
11 not assigned.a (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
12 not assigned.a (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
13 not assigned.r no hits & (original description: pacid=37174067 transcript=Phvul.006G164800.1 locu
14 not assigned.a (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
15 not assigned.a (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
16 not assigned.a (original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.C
17 not assigned.a (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
18 not assigned.a (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
19 not assigned.a (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
20 not assigned.a (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
21 not assigned.a (original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.C
22 Protein modif component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
23 RNA biosynthG2-like GARP transcription factor (original description: pacid=37159020 transcript=Pl
24 not assigned.r no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu
25 not assigned.a (original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.C
26 not assigned.a (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
27 not assigned.a (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
28 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
29 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
30 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
31 Solute transpcP4-type ATPase component ALA of phospholipid flippase complex (original descriptic
32 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
33 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
34 Solute transpcP4-type ATPase component ALA of phospholipid flippase complex (original descriptic
35 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
36 Cell wall orgar pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
37 not assigned.a (original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.C
38 Cell wall orgar fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri
39 RNA biosynthtranscription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
40 RNA biosynthtranscription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
41 Solute transpcnucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
42 Solute transpcnucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
43 not assigned.a (original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.C
44 Protein transkNUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
45 Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri
46 Amino acid mserine hydroxymethyltransferase (original description: pacid=37167850 transcript=Pl
47 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
48 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
49 Multi-process phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
50 Solute transpcouter membrane porin (OEP21) (original description: pacid=37152022 transcript=Phv
51 Chromatin orgchromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=

1 Chromatin org chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=

2 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176

3 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176

4 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C

5 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C

6 External stimu PIF red/far-red light perception transcriptional regulator (original description: pacid=

7 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C

8 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C

9 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C

10 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C

11 not assigned.r no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 locu

12 RNA biosynth transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0

13 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

14 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

15 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

16 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

17 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

18 not assigned.ε (original description: pacid=37147019 transcript=Phvul.003G181600.1 locus=Phvul.C

19 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

20 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

21 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

22 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

23 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

24 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

25 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

26 not assigned.r no hits & (original description: pacid=37174067 transcript=Phvul.006G164800.1 locu

27 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

28 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

29 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

30 not assigned.ε (original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.C

31 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

32 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

33 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

34 not assigned.ε (original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.C

35 Protein modif component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti

36 RNA biosynth G2-like GARP transcription factor (original description: pacid=37159020 transcript=Pl

37 not assigned.r no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu

38 not assigned.ε (original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.C

39 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C

40 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C

41 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio

42 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio

43 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio

44 Solute transp P4-type ATPase component ALA of phospholipid flippase complex (original descriptio

45 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005

46 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005

47 Solute transp P4-type ATPase component ALA of phospholipid flippase complex (original descriptio

48 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio

49 Cell wall orgar pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2

50 not assigned.ε (original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.C

51 Cell wall orgar fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri

52 RNA biosynth transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.0(

53 RNA biosynth transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.0(

54 Solute transp nucleotide sugar transporter (UAFT) (original description: pacid=37144593 transcript=

1 Solute transp nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
2 not assigned.ε (original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.C
3 Protein transk NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
4 Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcrip
5 Amino acid m serine hydroxymethyltransferase (original description: pacid=37167850 transcript=Pl
6 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
7 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
8 Multi-process phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
9 Solute transp outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Phv
10 Chromatin orε chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
11 Chromatin orε chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
12 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
13 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
14 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
15 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
16 External stimu PIF red/far-red light perception transcriptional regulator (original description: pacid=
17 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
18 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
19 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
20 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
21 not assigned.r no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 locu
22 RNA biosynth transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
23 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
24 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
25 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
26 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
27 not assigned.ε (original description: pacid=37147019 transcript=Phvul.003G181600.1 locus=Phvul.C
28 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
29 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
30 not assigned.r no hits & (original description: pacid=37174067 transcript=Phvul.006G164800.1 locu
31 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
32 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
33 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
34 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
35 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
36 not assigned.ε (original description: pacid=37147019 transcript=Phvul.003G181600.1 locus=Phvul.C
37 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
38 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
39 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
40 not assigned.r no hits & (original description: pacid=37174067 transcript=Phvul.006G164800.1 locu
41 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
42 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
43 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
44 not assigned.ε (original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.C
45 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
46 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
47 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
48 not assigned.ε (original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.C
49 Protein modif component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
50 RNA biosynth G2-like GARP transcription factor (original description: pacid=37159020 transcript=Pl
51 not assigned.r no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu
52 not assigned.ε (original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.C
53 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
54 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
55 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
56 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
57 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
58 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
59 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
60 Solute transp P4-type ATPase component ALA of phospholipid flippase complex (original descriptio

1 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
2 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
3 Solute transp P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
4 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
5 Cell wall orgar pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
6 not assigned.ã (original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.C
7 Cell wall orgar fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri
8 RNA biosynth transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
9 RNA biosynth transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
10 Solute transp nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
11 Solute transp nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
12 not assigned.ã (original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.C
13 Protein transl NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
14 Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri
15 Amino acid m serine hydroxymethyltransferase (original description: pacid=37167850 transcript=Pl
16 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
17 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
18 Multi-process phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
19 Solute transp outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Ph
20 Chromatin org chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
21 Chromatin org chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
22 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
23 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
24 not assigned.ã (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
25 not assigned.ã (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
26 External stimu PIF red/far-red light perception transcriptional regulator (original description: pacid=
27 not assigned.ã (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
28 not assigned.ã (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
29 not assigned.ã (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
30 not assigned.ã (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
31 not assigned.ã (original description: pacid=37160747 transcript=Phvul.008G243700.1 locu
32 RNA biosynth transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
33 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
34 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
35 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
36 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
37 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
38 not assigned.ã (original description: pacid=37147019 transcript=Phvul.003G181600.1 locus=Phvul.C
39 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
40 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
41 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
42 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
43 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
44 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
45 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
46 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
47 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
48 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
49 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
50 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
51 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
52 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
53 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
54 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
55 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
56 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
57 not assigned.ã (original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.C
58 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
59 not assigned.ã (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
60 not assigned.ã (original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.C

1 Protein modification component PIG-H of GPI N-acetylglucosamine transferase complex (original description: not assigned.
2 RNA biosynthesis G2-like GARP transcription factor (original description: pacid=37159020 transcript=Phvul.008G075300.1 locus=Phvul.C
3 not assigned.
4 not assigned.
5 not assigned.
6 not assigned.
7 External stimulus GIGANTEA zeitlupe-mediated photoperception regulator protein (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
8 External stimulus GIGANTEA zeitlupe-mediated photoperception regulator protein (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
9 External stimulus GIGANTEA zeitlupe-mediated photoperception regulator protein (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
10 External stimulus GIGANTEA zeitlupe-mediated photoperception regulator protein (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
11 External stimulus GIGANTEA zeitlupe-mediated photoperception regulator protein (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
12 External stimulus GIGANTEA zeitlupe-mediated photoperception regulator protein (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
13 Solute transport P4-type ATPase component ALA of phospholipid flippase complex (original description: pacid=37153734 transcript=Phvul.005G075300.1 locus=Phvul.C
14 External stimulus transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005G075300.1 locus=Phvul.C
15 External stimulus transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005G075300.1 locus=Phvul.C
16 Solute transport P4-type ATPase component ALA of phospholipid flippase complex (original description: pacid=37153734 transcript=Phvul.005G075300.1 locus=Phvul.C
17 External stimulus GIGANTEA zeitlupe-mediated photoperception regulator protein (original description: pacid=37153734 transcript=Phvul.005G075300.1 locus=Phvul.C
18 Cell wall organization pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G075300.1 locus=Phvul.C
19 not assigned.
20 not assigned.
21 Cell wall organization fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcript=Phvul.009G075300.1 locus=Phvul.C
22 RNA biosynthesis transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.009G075300.1 locus=Phvul.C
23 RNA biosynthesis transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.009G075300.1 locus=Phvul.C
24 Solute transport nucleotide sugar transporter (UAFT) (original description: pacid=37144593 transcript=Phvul.009G075300.1 locus=Phvul.C
25 Solute transport nucleotide sugar transporter (UAFT) (original description: pacid=37144593 transcript=Phvul.009G075300.1 locus=Phvul.C
26 not assigned.
27 not assigned.
28 Protein transport NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37144593 transcript=Phvul.009G075300.1 locus=Phvul.C
29 Protein homeostasis monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcript=Phvul.009G075300.1 locus=Phvul.C
30 Amino acid metabolism serine hydroxymethyltransferase (original description: pacid=37167850 transcript=Phvul.009G075300.1 locus=Phvul.C
31 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=37167850 transcript=Phvul.009G075300.1 locus=Phvul.C
32 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=37167850 transcript=Phvul.009G075300.1 locus=Phvul.C
33 Multi-process phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 transcript=Phvul.009G075300.1 locus=Phvul.C
34 Solute transport outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Phvul.009G075300.1 locus=Phvul.C
35 Chromatin organization chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=Phvul.009G075300.1 locus=Phvul.C
36 Chromatin organization chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=Phvul.009G075300.1 locus=Phvul.C
37 Cell wall organization CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717691 transcript=Phvul.002G299004.3 locus=Phvul.C
38 Cell wall organization CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717691 transcript=Phvul.002G299004.3 locus=Phvul.C
39 not assigned.
40 not assigned.
41 External stimulus PIF red/far-red light perception transcriptional regulator (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
42 not assigned.
43 not assigned.
44 not assigned.
45 not assigned.
46 not assigned.
47 not assigned.
48 not assigned.
49 not assigned.
50 not assigned.
51 not assigned.
52 not assigned.
53 not assigned.
54 not assigned.
55 not assigned.
56 RNA biosynthesis transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.007G157500.5 locus=Phvul.C
57 not assigned.
58 not assigned.
59 not assigned.
60 not assigned.

1 not assigned.ε (original description: pacid=37147019 transcript=Phvul.003G181600.1 locus=Phvul.C
2 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
3 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
4 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
5 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
6 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
7 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
8 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
9 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
10 not assigned.ε (original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.C
11 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
12 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
13 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
14 not assigned.ε (original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.C
15 Protein modif component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
16 RNA biosynthG2-like GARP transcription factor (original description: pacid=37159020 transcript=Pl
17 not assigned.r no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu
18 not assigned.ε (original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.C
19 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
20 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
21 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
22 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
23 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
24 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
25 Solute transpc P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
26 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
27 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
28 Solute transpc P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
29 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
30 Cell wall orgar pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
31 not assigned.ε (original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.C
32 Cell wall orgar fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri
33 RNA biosynthtranscription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
34 RNA biosynthtranscription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
35 Solute transpc nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
36 Solute transpc nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
37 not assigned.ε (original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.C
38 Protein transkNUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
39 Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri
40 Amino acid m serine hydroxymethyltransferase (original description: pacid=37167850 transcript=Pl
41 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
42 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
43 Multi-process phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
44 Solute transpc outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Phv
45 Chromatin org chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
46 Chromatin org chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
47 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
48 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
49 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
50 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
51 External stimu PIF red/far-red light perception transcriptional regulator (original description: pacid=

1 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
2 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
3 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
4 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
5 not assigned.r no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 locu
6 RNA biosynthtranscription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
7 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
8 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
9 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
10 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
11 not assigned.ε (original description: pacid=37147019 transcript=Phvul.003G181600.1 locus=Phvul.C
12 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
13 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
14 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
15 not assigned.r no hits & (original description: pacid=37174067 transcript=Phvul.006G164800.1 locu
16 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
17 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
18 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
19 not assigned.r no hits & (original description: pacid=37174067 transcript=Phvul.006G164800.1 locu
20 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
21 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
22 not assigned.ε (original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.C
23 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
24 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
25 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
26 not assigned.ε (original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.C
27 Protein modif component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
28 RNA biosynthG2-like GARP transcription factor (original description: pacid=37159020 transcript=Pl
29 not assigned.r no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu
30 not assigned.ε (original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.C
31 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
32 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
33 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
34 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
35 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
36 Solute transpcP4-type ATPase component ALA of phospholipid flippase complex (original descriptio
37 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
38 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
39 Solute transpcP4-type ATPase component ALA of phospholipid flippase complex (original descriptio
40 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
41 Cell wall orgar pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
42 not assigned.ε (original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.C
43 Cell wall orgar fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri
44 RNA biosynthtranscription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
45 RNA biosynthtranscription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
46 Solute transpcnucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
47 Solute transpcnucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
48 not assigned.ε (original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.C
49 Protein translNUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
50 Protein homeimeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri
51 Amino acid mserine hydroxymethyltransferase (original description: pacid=37167850 transcript=Pl
52 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=

1 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
2 Multi-process phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
3 Solute transpouter membrane porin (OEP21) (original description: pacid=37152022 transcript=Phv
4 Chromatin or chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
5 Chromatin or chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
6 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
7 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
8 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
9 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
10 External stimu PIF red/far-red light perception transcriptional regulator (original description: pacid=
11 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
12 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
13 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
14 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
15 not assigned.r no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 locu
16 RNA biosynthtranscription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
17 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
18 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
19 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
20 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
21 not assigned.ε (original description: pacid=37147019 transcript=Phvul.003G181600.1 locus=Phvul.C
22 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
23 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
24 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
25 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
26 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
27 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
28 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
29 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
30 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
31 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
32 not assigned.r no hits & (original description: pacid=37174067 transcript=Phvul.006G164800.1 locu
33 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
34 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
35 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
36 not assigned.ε (original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.C
37 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
38 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
39 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
40 not assigned.ε (original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.C
41 Protein modif component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
42 RNA biosynthG2-like GARP transcription factor (original description: pacid=37159020 transcript=Pl
43 not assigned.r no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu
44 not assigned.ε (original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.C
45 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
46 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
47 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
48 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
49 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
50 Solute transpP4-type ATPase component ALA of phospholipid flippase complex (original descriptio
51 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
52 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
53 Solute transpP4-type ATPase component ALA of phospholipid flippase complex (original descriptio
54 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
55 Cell wall orgar pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
56 not assigned.ε (original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.C

1 Cell wall organ fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcript=Phvul.006G075600.1 locus=Phvul.C
2 RNA biosynthesis transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.006G075600.1 locus=Phvul.C
3 RNA biosynthesis transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.006G075600.1 locus=Phvul.C
4 Solute transport nucleotide sugar transporter (UAFT) (original description: pacid=37144593 transcript=Phvul.006G075600.1 locus=Phvul.C
5 Solute transport nucleotide sugar transporter (UAFT) (original description: pacid=37144593 transcript=Phvul.006G075600.1 locus=Phvul.C
6 not assigned.ε (original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.C
7 Protein transport NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37165600 transcript=Phvul.006G075600.1 locus=Phvul.C
8 Protein homeostasis monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcript=Phvul.006G075600.1 locus=Phvul.C
9 Amino acid metabolism serine hydroxymethyltransferase (original description: pacid=37167850 transcript=Phvul.006G075600.1 locus=Phvul.C
10 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=37167850 transcript=Phvul.006G075600.1 locus=Phvul.C
11 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=37167850 transcript=Phvul.006G075600.1 locus=Phvul.C
12 Multi-process phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 transcript=Phvul.006G075600.1 locus=Phvul.C
13 Solute transport outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Phvul.006G075600.1 locus=Phvul.C
14 Chromatin organization chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=Phvul.006G075600.1 locus=Phvul.C
15 Chromatin organization chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=Phvul.006G075600.1 locus=Phvul.C
16 Cell wall organ CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717691 transcript=Phvul.002G299004.3 locus=Phvul.C
17 Cell wall organ CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717691 transcript=Phvul.002G299004.3 locus=Phvul.C
18 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
19 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
20 External stimulus PIF red/far-red light perception transcriptional regulator (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
21 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
22 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
23 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
24 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
25 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
26 not assigned.ε (original description: pacid=37160747 transcript=Phvul.008G243700.1 locus=Phvul.C
27 RNA biosynthesis transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.007G157500.5 locus=Phvul.C
28 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
29 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
30 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
31 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
32 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
33 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
34 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
35 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
36 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
37 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
38 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
39 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
40 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
41 not assigned.ε (original description: pacid=37147019 transcript=Phvul.003G181600.1 locus=Phvul.C
42 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
43 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
44 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
45 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
46 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
47 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
48 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
49 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
50 not assigned.ε (original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.C
51 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
52 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
53 not assigned.ε (original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.C
54 Protein modification component PIG-H of GPI N-acetylglucosamine transferase complex (original description: pacid=37159020 transcript=Phvul.008G075300.1 locus=Phvul.C
55 RNA biosynthesis G2-like GARP transcription factor (original description: pacid=37159020 transcript=Phvul.008G075300.1 locus=Phvul.C
56 not assigned.ε (original description: pacid=37159999 transcript=Phvul.008G075300.1 locus=Phvul.C
57 not assigned.ε (original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.C
58 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
59 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
60 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C

1 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptor
2 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptor
3 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptor
4 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptor
5 Solute transp cP4-type ATPase component ALA of phospholipid flippase complex (original descriptio
6 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
7 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
8 Solute transp cP4-type ATPase component ALA of phospholipid flippase complex (original descriptio
9 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptor
10 Cell wall orgar pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
11 not assigned.ε (original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.C
12 Cell wall orgar fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcrip
13 RNA biosynth transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
14 RNA biosynth transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
15 Solute transp c nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
16 Solute transp c nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
17 not assigned.ε (original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.C
18 Protein transk NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
19 Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcrip
20 Amino acid m serine hydroxymethyltransferase (original description: pacid=37167850 transcript=PI
21 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
22 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
23 Multi-process phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
24 Solute transp c outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Phv
25 Chromatin org chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
26 Chromatin org chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
27 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
28 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
29 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
30 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
31 External stimu PIF red/far-red light perception transcriptional regulator (original description: pacid=
32 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
33 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
34 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
35 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
36 not assigned.r no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 locu
37 RNA biosynth transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
38 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
39 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
40 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
41 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
42 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
43 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
44 not assigned.ε (original description: pacid=37147019 transcript=Phvul.003G181600.1 locus=Phvul.C
45 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
46 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
47 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
48 not assigned.r no hits & (original description: pacid=37174067 transcript=Phvul.006G164800.1 locu
49 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
50 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C

1 not assigned.ε (original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.C
 2 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
 3 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
 4 not assigned.ε (original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.C
 5 Protein modif component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
 6 RNA biosynthG2-like GARP transcription factor (original description: pacid=37159020 transcript=Pl
 7 not assigned.r no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu
 8 not assigned.ε (original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.C
 9 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
 10 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
 11 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
 12 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
 13 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
 14 Solute transpP4-type ATPase component ALA of phospholipid flippase complex (original descriptio
 15 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
 16 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
 17 Solute transpP4-type ATPase component ALA of phospholipid flippase complex (original descriptio
 18 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
 19 Cell wall orgar pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
 20 not assigned.ε (original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.C
 21 Cell wall orgar fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri
 22 RNA biosynthtranscription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
 23 RNA biosynthtranscription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
 24 Solute transpnucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
 25 Solute transpnucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
 26 not assigned.ε (original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.C
 27 Protein translNUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
 28 Protein home monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri
 29 Amino acid mserine hydroxymethyltransferase (original description: pacid=37167850 transcript=Pl
 30 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
 31 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
 32 Multi-process phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
 33 Solute transpouter membrane porin (OEP21) (original description: pacid=37152022 transcript=Phv
 34 Chromatin orgchromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
 35 Chromatin orgchromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
 36 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
 37 Cell wall orgar CSI-type cellulose synthase CSC-interactive protein (original description: pacid=37176
 38 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
 39 not assigned.ε (original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.C
 40 External stimu PIF red/far-red light perception transcriptional regulator (original description: pacid=
 41 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
 42 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
 43 not assigned.ε (original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.C
 44 not assigned.ε (original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.C
 45 not assigned.r no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 locu
 46 RNA biosynthtranscription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0

1 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
2 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
3 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
4 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
5 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
6 not assigned.ε (original description: pacid=37147019 transcript=Phvul.003G181600.1 locus=Phvul.C
7 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
8 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
9 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
10 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
11 not assigned.r no hits & (original description: pacid=37174067 transcript=Phvul.006G164800.1 locu
12 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
13 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
14 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
15 not assigned.ε (original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.C
16 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
17 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
18 not assigned.ε (original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.C
19 not assigned.ε (original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.C
20 Protein modif component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
21 RNA biosynthG2-like GARP transcription factor (original description: pacid=37159020 transcript=Pl
22 not assigned.r no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu
23 not assigned.ε (original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.C
24 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
25 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
26 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
27 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
28 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
29 Solute transpcP4-type ATPase component ALA of phospholipid flippase complex (original descriptic
30 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
31 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
32 Solute transpcP4-type ATPase component ALA of phospholipid flippase complex (original descriptic
33 External stimu GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
34 not assigned.ε (original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.C
35 Protein translnUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
36 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
37 Cell wall orgar pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
38 Multi-process regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
39 not assigned.ε (original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.C
40 Cell wall orgar fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri
41 RNA biosynthtranscription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.0(
42 RNA biosynthtranscription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.0(
43 Solute transpcnucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
44 Solute transpcnucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript:
45 not assigned.ε (original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.C
46 not assigned.ε (original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.C
47 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
48 not assigned.ε (original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.C
49 Solute transpcP4-type ATPase component ALA of phospholipid flippase complex (original descriptic
50 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
51 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005

1
2 Solute transpP4-type ATPase component ALA of phospholipid flippase complex (original descriptio
3 External stimu transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
4 Nutrient uptalCEPR systemic nitrogen signalling CEP-receptor kinase (original description: pacid=37
5 Solute transpP1B-type heavy metal cation-transporting ATPase (HMA) (original description: pacid=
6 not assigned.r no hits & (original description: pacid=37176152 transcript=Phvul.002G283000.4 locu
7 not assigned.r no hits & (original description: pacid=37176152 transcript=Phvul.002G283000.4 locu
8 not assigned.r no hits & (original description: pacid=37176152 transcript=Phvul.002G283000.4 locu
9 Carbohydrate sucrose-phosphate synthase (original description: pacid=37147754 transcript=Phvul.
10 not assigned.ã (original description: pacid=37156011 transcript=Phvul.011G173600.1 locus=Phvul.C
11 Protein modif membrane-anchor component DPMS2 of DPMS dolichol-phosphate-mannose syntha
12 Protein homeimeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcrip
13 Multi-process phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
14 Amino acid mserine hydroxymethyltransferase (original description: pacid=37167850 transcript=PI
15 Enzyme classiiPutative serine/threonine-protein kinase-like protein CCR3 OS=Arabidopsis thaliana (
16 Solute transpcation antiporter (CAX) (original description: pacid=37171893 transcript=Phvul.006G
17 Enzyme classiiHydroquinone glucosyltransferase OS=Rauvolfia serpentina (sp|q9ar73|hqgt_rause :
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1 pt=Phvul.011G065700.3 locus=Phvul.011G065700 ID=Phvul.011G065700.3.v2.1 annot-version=v2.1
2 pt=Phvul.011G065700.3 locus=Phvul.011G065700 ID=Phvul.011G065700.3.v2.1 annot-version=v2.1
3 pt=Phvul.011G065700.3 locus=Phvul.011G065700 ID=Phvul.011G065700.3.v2.1 annot-version=v2.1
4 089 transcript=Phvul.004G172600.2 locus=Phvul.004G172600 ID=Phvul.004G172600.2.v2.1 annot-v
5 006G169300 ID=Phvul.006G169300.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g29670 (C
6 us=Phvul.007G164800 ID=Phvul.007G164800.1.v2.1 annot-version=v2.1)
7 pt=Phvul.011G065700.3 locus=Phvul.011G065700 ID=Phvul.011G065700.3.v2.1 annot-version=v2.1
8 pt=Phvul.011G065700.3 locus=Phvul.011G065700 ID=Phvul.011G065700.3.v2.1 annot-version=v2.1
9 pt=Phvul.011G065700.3 locus=Phvul.011G065700 ID=Phvul.011G065700.3.v2.1 annot-version=v2.1
10 pt=Phvul.011G065700.3 locus=Phvul.011G065700 ID=Phvul.011G065700.3.v2.1 annot-version=v2.1
11 089 transcript=Phvul.004G172600.2 locus=Phvul.004G172600 ID=Phvul.004G172600.2.v2.1 annot-v
12 006G169300 ID=Phvul.006G169300.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g29670 (C
13 us=Phvul.007G164800 ID=Phvul.007G164800.1.v2.1 annot-version=v2.1)
14 pt=Phvul.011G065700.3 locus=Phvul.011G065700 ID=Phvul.011G065700.3.v2.1 annot-version=v2.1
15 pt=Phvul.011G065700.3 locus=Phvul.011G065700 ID=Phvul.011G065700.3.v2.1 annot-version=v2.1
16 pt=Phvul.011G065700.3 locus=Phvul.011G065700 ID=Phvul.011G065700.3.v2.1 annot-version=v2.1
17 089 transcript=Phvul.004G172600.2 locus=Phvul.004G172600 ID=Phvul.004G172600.2.v2.1 annot-v
18 0089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
19 us=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
20 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
21 005G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C
22 us=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
23 us=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
24 us=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
25 us=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
26 ipt=Phvul.010G128500.1 locus=Phvul.010G128500 ID=Phvul.010G128500.1.v2.1 annot-version=v2.1
27 0089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
28 us=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
29 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
30 005G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C
31 us=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
32 us=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
33 us=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
34 us=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
35 ipt=Phvul.010G128500.1 locus=Phvul.010G128500 ID=Phvul.010G128500.1.v2.1 annot-version=v2.1
36 0089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
37 us=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
38 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
39 005G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C
40 us=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
41 us=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
42 us=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
43 us=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
44 ipt=Phvul.010G128500.1 locus=Phvul.010G128500 ID=Phvul.010G128500.1.v2.1 annot-version=v2.1
45 0089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
46 us=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
47 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
48 005G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C
49 us=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
50 us=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
51 us=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
52 us=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
53 ipt=Phvul.010G128500.1 locus=Phvul.010G128500 ID=Phvul.010G128500.1.v2.1 annot-version=v2.1
54 0089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
55 us=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
56 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
57 005G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C

1
2 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
3 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
4 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
5 js=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
6
7 ipt=Phvul.010G128500.1 locus=Phvul.010G128500 ID=Phvul.010G128500.1.v2.1 annot-version=v2.1
8)G089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
9
10 js=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
11
12 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
13)05G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C
14
15 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
16 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
17 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
18 js=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
19
20 ipt=Phvul.010G128500.1 locus=Phvul.010G128500 ID=Phvul.010G128500.1.v2.1 annot-version=v2.1
21)G089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
22
23 js=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
24
25 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
26)05G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C
27
28 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
29 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
30 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
31 js=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
32
33 ipt=Phvul.010G128500.1 locus=Phvul.010G128500 ID=Phvul.010G128500.1.v2.1 annot-version=v2.1
34)G089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
35
36 js=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
37
38 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
39)05G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C
40
41 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
42 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
43 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
44 js=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
45
46 ipt=Phvul.010G128500.1 locus=Phvul.010G128500 ID=Phvul.010G128500.1.v2.1 annot-version=v2.1
47)G089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
48
49 js=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
50
51 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
52)05G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C
53
54 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
55 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
56 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
57 js=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
58
59 ipt=Phvul.010G128500.1 locus=Phvul.010G128500 ID=Phvul.010G128500.1.v2.1 annot-version=v2.1
60)G089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
61
62 js=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
63
64 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
65)05G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C
66
67 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)

1
2 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
3 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
4 js=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
5
6 ipt=Phvul.010G128500.1 locus=Phvul.010G128500 ID=Phvul.010G128500.1.v2.1 annot-version=v2.1)
7 JG089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
8 js=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
9
10 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
11 J05G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C
12 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
13 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
14 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
15 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
16 js=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
17
18 ipt=Phvul.010G128500.1 locus=Phvul.010G128500 ID=Phvul.010G128500.1.v2.1 annot-version=v2.1)
19 JG089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
20 js=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
21
22 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
23 J05G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C
24 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
25 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
26 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
27 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
28 js=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
29
30 ipt=Phvul.010G128500.1 locus=Phvul.010G128500 ID=Phvul.010G128500.1.v2.1 annot-version=v2.1)
31 JG089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
32 js=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
33
34 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
35 J05G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C
36 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
37 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
38 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
39 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
40 js=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
41
42 ipt=Phvul.010G128500.1 locus=Phvul.010G128500 ID=Phvul.010G128500.1.v2.1 annot-version=v2.1)
43 JG089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
44 js=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
45
46 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
47 J05G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C
48 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
49 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
50 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
51 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
52 js=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
53
54 ipt=Phvul.010G128500.1 locus=Phvul.010G128500 ID=Phvul.010G128500.1.v2.1 annot-version=v2.1)
55 JG089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
56 js=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
57
58 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
59 J05G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C
60 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)

1 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
2 js=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
3 ipt=Phvul.010G128500.1 locus=Phvul.010G128500 ID=Phvul.010G128500.1.v2.1 annot-version=v2.1)
4 G089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
5 js=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
6 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
7 005G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C
8 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
9 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
10 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
11 js=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
12 ipt=Phvul.010G128500.1 locus=Phvul.010G128500 ID=Phvul.010G128500.1.v2.1 annot-version=v2.1)
13 G089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
14 js=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
15 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
16 005G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C
17 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
18 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
19 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
20 js=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
21 ipt=Phvul.010G128500.1 locus=Phvul.010G128500 ID=Phvul.010G128500.1.v2.1 annot-version=v2.1)
22 G089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
23 js=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
24 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
25 005G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C
26 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
27 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
28 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
29 js=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
30 ipt=Phvul.010G128500.1 locus=Phvul.010G128500 ID=Phvul.010G128500.1.v2.1 annot-version=v2.1)
31 G089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
32 js=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
33 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
34 005G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C
35 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
36 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
37 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
38 js=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
39 ipt=Phvul.010G128500.1 locus=Phvul.010G128500 ID=Phvul.010G128500.1.v2.1 annot-version=v2.1)
40 G089100.2 locus=Phvul.010G089100 ID=Phvul.010G089100.2.v2.1 annot-version=v2.1) &
41 js=Phvul.002G325300 ID=Phvul.002G325300.2.v2.1 annot-version=v2.1)
42 l transcript=Phvul.004G139200.1 locus=Phvul.004G139200 ID=Phvul.004G139200.1.v2.1 annot-vers
43 005G001200 ID=Phvul.005G001200.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g33811 (C
44 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
45 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
46 js=Phvul.008G147100 ID=Phvul.008G147100.4.v2.1 annot-version=v2.1)
47 js=Phvul.006G086200 ID=Phvul.006G086200.1.v2.1 annot-version=v2.1)
48 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
49 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
50 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
51 77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
52 011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro
53 008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
54 transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
55 ivul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
56 js=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)

1)1G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
2 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
3 :246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
4 :09G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
5 :rs=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
6 :vul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
7 :rs=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
8 :011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
9 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
10 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
11 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
12 :77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
13 :011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pr
14 :08G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like proteir
15 transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
16 :vul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
17 :rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
18 :1G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
19 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
20 :246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
21 :09G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
22 :rs=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
23 :vul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
24 :rs=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
25 :011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
26 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
27 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
28 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
29 :77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
30 :011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pr
31 :08G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like proteir
32 transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
33 :vul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
34 :rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
35 :1G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
36 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
37 :246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
38 :09G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
39 :rs=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
40 :vul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
41 :rs=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
42 :011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
43 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
44 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
45 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
46 :77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
47 :011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pr
48 :08G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like proteir
49 transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
50 :vul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
51 :rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
52 :1G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
53 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
54 :246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
55 :09G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
56 :rs=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
57 :vul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
58 :rs=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
59 :011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
60 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &

1
2 011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro
3 008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
4 transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
5 ivul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
6 rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
7 01G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
8 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
9 246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
10 009G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
11 rs=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
12 rlvul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
13 rs=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
14 011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
15 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
16 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
17 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
18 077800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
19 011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro
20 008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
21 transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
22 ivul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
23 rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
24 01G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
25 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
26 246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
27 009G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
28 rs=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
29 rlvul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
30 rs=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
31 011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
32 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
33 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
34 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
35 077800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
36 011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro
37 008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
38 transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
39 ivul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
40 rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
41 01G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
42 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
43 246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
44 009G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
45 rs=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
46 rlvul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
47 rs=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
48 011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
49 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
50 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
51 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
52 077800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
53 011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro
54 008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
55 transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
56 ivul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
57 rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
58 01G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
59 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
60 246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
009G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
rs=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
rlvul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
rs=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)

1
2 011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
3 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
4 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
5 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
6 77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
7 011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro
8 008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
9 n transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
10 ivul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
11 rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
12 01G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
13 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
14 246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
15 009G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
16 rs=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
17 rnvul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
18 rs=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
19 011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
20 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
21 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
22 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
23 77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
24 011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro
25 008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
26 n transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
27 ivul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
28 rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
29 01G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
30 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
31 246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
32 009G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
33 rs=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
34 rnvul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
35 rs=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
36 011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
37 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
38 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
39 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
40 77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
41 011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro
42 008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
43 n transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
44 ivul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
45 rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
46 01G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
47 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
48 246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
49 009G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
50 rs=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
51 rnvul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
52 rs=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
53 011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
54 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
55 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
56 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
57 77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
58 011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro
59 008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
60 n transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
ivul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
01G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
=Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {

1
2 :246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
3 :09G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
4 rs=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
5 :vul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
6 rs=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
7 :11G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contain
8 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
9 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
10 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
11 :77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
12 :11G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro
13 :08G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
14 n transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
15 ion=Phvul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
16 rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
17 :1G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
18 :=Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) &
19 :246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
20 :09G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
21 rs=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
22 :vul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
23 rs=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
24 :11G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contain
25 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
26 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
27 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
28 :77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
29 :11G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro
30 :08G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
31 n transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
32 ion=Phvul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
33 rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
34 :1G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
35 :=Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) &
36 :246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
37 :09G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
38 rs=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
39 :vul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
40 rs=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
41 :11G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contain
42 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
43 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
44 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
45 :77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
46 :11G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro
47 :08G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
48 n transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
49 ion=Phvul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
50 rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
51 :1G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
52 :=Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) &
53 :246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
54 :09G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
55 rs=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
56 :vul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
57 rs=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
58 :11G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contain
59 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
60 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
:77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
:11G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro
:08G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei

1 transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
2 v.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
3 s=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
4)1G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
5 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
6 246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
7 09G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
8 s=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
9 v.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
10 s=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
11 011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
12 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
13 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
14 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
15 077800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
16 011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pr
17 008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
18 n transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
19 v.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
20 s=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
21)1G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
22 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
23 246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
24 09G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
25 s=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
26 v.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
27 s=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
28 011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
29 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
30 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
31 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
32 077800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
33 011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pr
34 008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
35 n transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
36 v.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
37 s=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
38)1G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
39 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
40 246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
41 09G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
42 s=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
43 v.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
44 s=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
45 011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
46 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
47 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
48 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
49 077800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
50 011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pr
51 008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
52 n transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
53 v.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
54 s=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
55)1G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
56 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
57 246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
58 09G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
59 s=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
60 v.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
s=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500

1 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
2 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
3 77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
4 011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro
5 008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
6 r transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
7 ivul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
8 rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
9 01G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
10 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
11 246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
12 009G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
13 rs=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
14 rlvul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
15 rs=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
16 011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
17 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
18 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
19 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
20 77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
21 011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro
22 008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
23 r transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
24 ivul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
25 rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
26 01G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
27 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
28 246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
29 009G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
30 rs=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
31 rlvul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
32 rs=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
33 011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
34 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
35 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
36 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
37 77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
38 011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro
39 008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
40 r transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
41 ivul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
42 rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
43 01G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
44 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
45 246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
46 009G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
47 rs=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
48 rlvul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
49 rs=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
50 011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
51 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
52 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
53 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
54 77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
55 011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro
56 008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
57 r transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
58 ivul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
59 rs=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
60 01G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
=Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
009G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2

1
2 js=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
3 vul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
4 js=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
5 011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
6 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
7 n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G083500
8 ul.011G079800.1 locus=Phvul.011G079800 ID=Phvul.011G079800.1.v2.1 annot-version=v2.1) &
9 011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
10 011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pro
11 008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like proteir
12 transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
13 .002G073200.1 locus=Phvul.002G073200 ID=Phvul.002G073200.1.v2.1 annot-version=v2.1) &
14 .002G073100.2 locus=Phvul.002G073100 ID=Phvul.002G073100.2.v2.1 annot-version=v2.1) &
15 .002G073100.2 locus=Phvul.002G073100 ID=Phvul.002G073100.2.v2.1 annot-version=v2.1) &
16 ivul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
17 js=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
18 01G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
19 =Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1) {
20 0246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
21 009G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
22 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
23 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
24 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
25 script=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=
26 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (
27 093600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
28 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
29 :Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
30 0037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
31 0037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
32 js=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)
33 js=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
34 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &
35 008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
36 005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
37 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno
38 ranscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
39 ranscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
40 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1
41 09G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
42 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
43 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
44 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
45 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
46 js=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)

1 001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliana
2 005200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
3 transcript=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v
4 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
5 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
6 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
7 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
8 transcript=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=v
9 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (C
10 093600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
11 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
12 :Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
13 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
14 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
15 us=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)
16 us=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
17 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &
18 008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v3C
19 005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
20 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno
21 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
22 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
23 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1
24 09G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
25 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
26 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
27 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
28 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
29 us=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)
30 001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliana
31 005200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
32 transcript=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v
33 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
34 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
35 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
36 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
37 transcript=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=v
38 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (C
39 093600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
40 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
41 :Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
42 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
43 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
44 us=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)
45 us=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
46 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &

1 008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
2 005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
3 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno
4 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
5 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
6 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1
7 9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
8 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1) &
9 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
10 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
11 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
12 s=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)
13 001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliar
14 05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
15 nscript=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v
16 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
17 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
18 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
19 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
20 nscript=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=
21 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (C
22 93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
23 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
24 :Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
25 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
26 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
27 s=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)
28 s=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
29 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &
30 008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
31 005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
32 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno
33 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
34 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
35 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1
36 9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
37 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1) &
38 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
39 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
40 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
41 s=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)
42 001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliar
43 05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
44 nscript=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v
45 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
46 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol

1 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
2 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
3 script=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=
4 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (
5 93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
6 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
7 :Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
8 ;037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
9 ;037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
10 :s=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)
11 :s=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
12 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &
13 008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
14 005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
15 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno
16 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
17 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
18 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1
19 9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
20 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
21 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
22 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
23 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
24 :s=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)
25 001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliar
26 05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
27 :script=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v
28 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
29 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
30 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
31 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
32 script=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=
33 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (
34 93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
35 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
36 :Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
37 ;037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
38 ;037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
39 :s=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)
40 :s=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
41 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &
42 008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
43 005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
44 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno
45 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
46 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version

1 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1
2 9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
3 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
4 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
5 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
6 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
7 js=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)
8 001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliar
9 05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
10 script=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v
11 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
12 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
13 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
14 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
15 script=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=
16 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (
17 93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
18 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
19 :Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
20 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
21 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
22 js=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)
23 js=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
24 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &
25 008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
26 005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
27 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno
28 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
29 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
30 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1
31 9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
32 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
33 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
34 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
35 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
36 js=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)
37 001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliar
38 05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
39 script=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v
40 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
41 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
42 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
43 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
44 script=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=
45 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (
46 93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &

1 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
2 :Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
3 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
4 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
5 js=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)
6 js=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
7 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &
8 J08G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
9 J05G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
10 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno
11 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
12 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
13 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1
14 9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
15 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
16 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
17 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
18 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
19 js=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)
20 J01G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliar
21 J05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
22 script=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v
23 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
24 J04G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
25 J02G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
26 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
27 script=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=
28 J06G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (C
29 93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
30 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
31 :Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
32 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
33 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
34 js=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)
35 js=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
36 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &
37 J08G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
38 J05G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
39 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno
40 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
41 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
42 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1
43 9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
44 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
45 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
46 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &

1 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
2 js=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)
3 001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliana
4 05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
5 script=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v
6 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
7 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
8 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
9 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
10 script=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=v
11 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (C
12 93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
13 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
14 :Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
15 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
16 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
17 js=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)
18 js=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
19 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &
20 008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
21 005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
22 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno
23 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
24 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
25 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1
26 9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
27 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
28 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
29 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
30 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
31 js=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)
32 001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliana
33 05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
34 script=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v
35 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
36 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
37 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
38 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
39 script=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=v
40 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (C
41 93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
42 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
43 :Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
44 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
45 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
46 js=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)

1
2 js=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
3 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &
4 008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
5 005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
6 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno
7 rnscrip=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
8 rnscrip=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
9 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1
10 9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
11 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
12 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
13 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
14 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
15 js=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)
16 001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliar
17 05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
18 scrip=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v
19 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
20 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
21 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
22 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
23 scrip=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=
24 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (C
25 93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
26 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
27 :Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
28 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
29 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
30 js=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)
31 js=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
32 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &
33 008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
34 005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
35 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno
36 rnscrip=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
37 rnscrip=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
38 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1
39 9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
40 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
41 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
42 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
43 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
44 js=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)
45 001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliar
46 05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
47 scrip=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v

244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
script=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=
006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (C
093600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
0037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
0037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
ms=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)
ms=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
.007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &
008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno
transcript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
transcript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1
09G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
ms=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)
001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliana
05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
script=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v
244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
script=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=
006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (C
093600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
0037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
0037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
ms=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)
ms=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
.007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &
008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno

1
2 transcript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
3 transcript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
4 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1
5 9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
6 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
7 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
8 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
9 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
10 us=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)
11 001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliana
12 05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
13 transcript=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v
14 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
15 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
16 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
17 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
18 script=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=
19 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (C
20 93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
21 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
22 :Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
23 0037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
24 0037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
25 us=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)
26 us=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
27 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &
28 008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
29 005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
30 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno
31 transcript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
32 transcript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
33 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1
34 9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
35 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
36 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
37 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
38 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
39 us=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)
40 001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliana
41 05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
42 transcript=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v
43 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
44 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
45 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
46 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
47 script=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=
48
49
50
51
52
53
54
55
56
57
58
59
60

1 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (C
2 93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
3 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
4 :Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
5 :037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
6 :037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
7 :s=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)
8 :s=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
9 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &
10 008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
11 005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
12 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno
13 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
14 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
15 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1
16 9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
17 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
18 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
19 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
20 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
21 :s=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)
22 001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliana
23 05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
24 ript=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v
25 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
26 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
27 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
28 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
29 ript=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=
30 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (C
31 93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
32 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
33 :Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
34 :037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
35 :037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
36 :s=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)
37 :s=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
38 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &
39 008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
40 005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
41 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno
42 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
43 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
44 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1
45 9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
46 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)

1 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
2 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
3 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
4 us=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)
5 001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliana
6 05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
7 script=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v
8 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
9 .007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &
10 script=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=
11 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
12 t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
13 006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (C
14 004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
15 002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
16 G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
17 93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
18 il.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
19 244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
20 1870 transcript=Phvul.009G121200.2 locus=Phvul.009G121200 ID=Phvul.009G121200.2.v2.1 annot-
21 1870 transcript=Phvul.009G121200.2 locus=Phvul.009G121200 ID=Phvul.009G121200.2.v2.1 annot-
22 us=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)
23 us=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
24 008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
25 :Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
26 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
27 i037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
28 005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
29 59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno
30 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
31 nscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
32 05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
33 pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1
34 9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
35 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
36 010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
37 us=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)
38 029900.1 locus=Phvul.007G029900 ID=Phvul.007G029900.1.v2.1 annot-version=v2.1) &
39 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
40 009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C
41 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
42 on: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079
43 us=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
44 us=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
45 003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
46 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas

1 004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
2 s=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
3 s=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
4 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &
5 s=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
6 tion: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166200.1.v2.1
7 & transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
8 s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
9 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
10 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
11 007G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
12 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
13 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
14 vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0
15 06G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &
16 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
17 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
18 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
19 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
20 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
21 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
22 t Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with in
23 vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
24 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
25 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
26 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &
27 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
28 009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C
29 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
30 tion: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079
31 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
32 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
33 003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
34 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas
35 004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
36 s=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
37 s=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
38 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &
39 s=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
40 tion: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166200.1.v2.1
41 & transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
42 s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
43 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
44 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
45 007G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
46 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)

1 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
2
3 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &
4 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
5 009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (
6 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
7 on: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079
8 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
9 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
10 003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
11 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferase
12 004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
13 s=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
14 s=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
15 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &
16 s=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
17 on: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166
18 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
19 s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
20 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
21 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
22 007G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
23 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
24 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
25 vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0
26 05G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &
27 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
28 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
29 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
30 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
31 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
32 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
33 t, Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i
34 vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
35 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
36 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
37 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &
38 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
39 009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (
40 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
41 on: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079
42 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
43 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
44 003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
45 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferase
46 004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
47 s=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)

1
2 js=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
3 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &
4 js=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
5
6 otion: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166
7 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
8
9 js=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
10
11 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
12 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
13 07G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
14 js=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
15 js=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
16 vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0
17 5G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &
18 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
19 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
20 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
21
22 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
23 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
24 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
25
26 t Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i
27 rvl.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
28
29 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
30 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
31
32 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &
33 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
34 009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C
35 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
36
37 otion: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079
38
39 js=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
40 js=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
41 003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
42 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas
43 004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
44 js=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
45
46 js=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
47 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &
48
49 js=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
50
51 otion: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166
52 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
53
54 js=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
55
56 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
57 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
58 07G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
59
60 js=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
js=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0

1
2 5G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &
3 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
4 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
5 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
6 vul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
7 vul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
8 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
9 t Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i
10 vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
11 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
12 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
13 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &
14 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
15 009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C
16 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
17 tion: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079
18 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
19 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
20 003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
21 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas
22 004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
23 s=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
24 s=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
25 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &
26 s=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
27 tion: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166
28 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
29 s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
30 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
31 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
32 007G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
33 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
34 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
35 vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0
36 5G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &
37 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
38 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
39 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
40 vul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
41 vul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
42 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
43 t Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i
44 vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
45 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
46 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
47 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &

1 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
2 009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (
3 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
4 on: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079
5 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
6 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
7 003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
8 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas
9 004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
10 s=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
11 s=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
12 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &
13 s=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
14 on: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166
15 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
16 s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
17 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
18 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
19 007G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
20 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
21 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
22 vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0
23 006G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &
24 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
25 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
26 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
27 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
28 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
29 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
30 t Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i
31 vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
32 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
33 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
34 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &
35 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
36 009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (
37 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
38 on: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079
39 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
40 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
41 003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
42 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas
43 004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
44 s=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
45 s=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
46 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &

1
2 js=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
3 otion: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166200.1.v2.1
4 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
5 js=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
6
7 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
8 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
9
10 07G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
11 js=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
12 js=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
13
14 vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0
15 5G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &
16 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
17 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
18 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
19 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
20 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
21 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
22 t, Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i
23 vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
24 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
25 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
26 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &
27 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
28 009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C
29 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
30 otion: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079
31 js=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
32 js=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
33 003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
34 009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas
35 004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
36 js=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
37 js=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
38 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &
39 js=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
40 otion: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166200.1.v2.1
41 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
42 js=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
43 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
44 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
45 07G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
46 js=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
47 js=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
48 vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0
49 5G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &
50 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1

transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
tion: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
1009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas
1004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
1009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
1002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
1002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &
1002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
1011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166200 ID=Phvul.011G166200.1.v2.1
1001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
1002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
1007G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
1010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
1010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0
1006G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &
1005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
1003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
1003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
1008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
1008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
1003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with in
1009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
1008G070000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &
1010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
1009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (
transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
tion: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
3 s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
4 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
5 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
6 J7G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
7 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
8 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
9
10 vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0
11 5G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &
12 J05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
13 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
14 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
15 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
16 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
17 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
18 t, Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with in
19 vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
20 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
21 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
22 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &
23 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
24 J09G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C
25 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
26 on: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079
27 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
28 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
29 J03G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
30 J09G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferase
31 J04G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
32 s=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
33 s=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
34 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &
35 s=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
36 on: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166
37 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
38 s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
39 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
40 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
41 J7G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
42 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
43 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
44 vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0
45 5G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &
46 J05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
47 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
48 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno

1
2 Phvul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
3 Phvul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
4 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
5
6 t; Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i
7 Phvul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
8 Phvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
9 Phvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
10
11 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &
12 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
13 Phvul.009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (
14 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
15 on: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079
16
17 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
18 s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
19 Phvul.003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
20 Phvul.009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferase
21 Phvul.004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
22 s=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
23 s=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
24 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &
25 s=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
26
27 on: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166
28
29 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
30
31 s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
32
33 3edl4 |y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
34 3edl4 |y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
35 Phvul.007G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
36 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
37 s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
38
39 vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0
40
41 Phvul.006G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &
42 Phvul.005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
43 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
44 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
45
46 Phvul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
47 Phvul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
48 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
49
50 t; Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i
51 Phvul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
52 Phvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
53 Phvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
54
55 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &
56 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
57 Phvul.009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (
58 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
59 on: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079
60

1
2 js=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
3 js=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
4 J03G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
5 J09G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas
6 J04G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
7 js=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
8
9 js=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
10
11 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &
12 js=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
13
14 otion: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166
15 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
16 js=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
17
18 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
19 3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
20 J07G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
21 js=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
22 js=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
23
24 vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0
25 5G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &
26 J05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
27 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
28 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
29
30 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
31 ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
32 46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
33
34 t, Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i
35 vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
36 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
37 hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
38
39 70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &
40 t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
41 J09G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C
42 transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
43
44 otion: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079
45 js=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
46 js=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
47 J03G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
48 J09G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas
49 J04G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
50 js=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
51 js=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
52 =Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &
53 js=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
54
55 otion: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166
56 8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
57 js=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
58
59
60

3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
J7G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
js=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
js=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0
5G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &
J05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
t Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i
vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &
t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
js=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
J09G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (
J7G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
tion: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G079
js=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
js=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
J09G167700 ID=Phvul.009G167700.2.v2.1 annot-version=v2.1) & 4-coumarate--CoA ligase-like 9 OS
J03G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
746 ID=Phvul.L003746.2.v2.1 annot-version=v2.1) & MACPF domain-containing protein At1g14780
746 ID=Phvul.L003746.2.v2.1 annot-version=v2.1) & MACPF domain-containing protein At1g14780
J09G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas
J04G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
js=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
=Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &
js=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
otion: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G166
067900.1 locus=Phvul.006G067900 ID=Phvul.006G067900.1.v2.1 annot-version=v2.1) &
8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
js=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
js=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
js=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
J02G157000 ID=Phvul.002G157000.1.v2.1 annot-version=v2.1) & no description available(sp|q9m2
J22600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
J02G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (
pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &

03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
 006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
 7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
 pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
 hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
 transcript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
 vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
 =37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1 ;
 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
 us=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)
 007G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 us=Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)
 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 005G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
 ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G1168
 hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
 us=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
 003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300

1 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
2 on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
3 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
4 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
5 on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
6 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
7 222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
8 002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C
9 pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
10 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
11 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
12 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
13 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
14 006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
15 7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
16 pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
17 hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
18 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
19 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
20 ranscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
21 vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
22 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
23 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
24 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
25 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
26 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosphatase
27 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosphatase
28 =37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1 ;
29 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=Arabidopsis
30 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=Arabidopsis
31 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
32 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=Arabidopsis
33 us=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)
34 007G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
35 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
36 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
37 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
38 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
39 003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
40 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
41 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
42 us=Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)
43 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
44 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
45 005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabidopsis
46 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

1 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
2 005G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
3 ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G1168
4 hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
5 js=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
6 003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
7 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
8 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
9 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
10 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
11 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
12 on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G20160
13 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
14 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
15 on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G20160
16 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
17 22600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
18 002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C
19 pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
20 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
21 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
22 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
23 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
24 006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
25 7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
26 pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
27 hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
28 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
29 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
30 ranscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
31 nul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
32 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
33 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
34 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
35 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
36 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosphat
37 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosphat
38 =37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1 ;
39 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
40 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
41 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
42 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
43 js=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)
44 007G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
45 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
46 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

1 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
2 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
3 003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
4 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
5 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
6 μs=Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)
7 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
8 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
9 005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
10 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
11 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
12 005G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
13 ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G1168
14 hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
15 μs=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
16 003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
17 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
18 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
19 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
20 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
21 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
22 on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
23 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
24 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
25 on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
26 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
27 222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
28 002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C
29 pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
30 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
31 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
32 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
33 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
34 006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
35 7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
36 pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
37 hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
38 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
39 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
40 ranscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
41 vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
42 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
43 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
44 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
45 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
46 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosphatase

1
2 J02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosphatase
3 :37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1 ;
4 J02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=Arabidopsis
5 J02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=Arabidopsis
6 J05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
7 J02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=Arabidopsis
8
9
10
11
12 J07G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
13 J07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
14 J07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
15 J07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
16 J07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
17
18 J03G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
19 J07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
20 J07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
21
22
23
24
25
26 J05G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabidopsis
27 J07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
28 J07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
29
30 J05G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabidopsis
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G116800.1.v2.1
hvu.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
ns=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
J03G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
J08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
J08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300.4.v2.1
n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300.4.v2.1
n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300.4.v2.1
n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600.2.v2.1
5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600.2.v2.1
n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300.4.v2.1
222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
J02G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (NRC2)
pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1) &
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
J06G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis hypogaea
7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1

1 hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
2 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
3 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
4 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
5 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
6 =37173827 transcript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
7 v2.1) &
8 =Phvul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
9 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
10 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
11 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
12 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
13 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
14 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
15 =37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1 ;
16 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
17 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
18 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
19 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
20 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
21 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
22 008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)
23 007G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
24 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
25 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
26 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
27 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
28 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
29 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
30 003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
31 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
32 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
33 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
34 006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)
35 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
36 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
37 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
38 005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
39 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
40 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
41 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
42 005G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
43 ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G1168
44 hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
45 008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
46 003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
47 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
48 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
49 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
50 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
51 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
52 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
53 n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
54 n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
55 n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
56 005G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
57 005G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
58 009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600 ID=Phvul.009G201600
59 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
60 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300

1 222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
2 002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (c
3 pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
4 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
5 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
6 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
7 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
8 006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
9 7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
10 pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
11 hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
12 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
13 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
14 =37173827 transcript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
15 vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
16 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
17 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
18 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
19 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
20 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
21 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
22 =37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1 ;
23 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
24 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
25 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
26 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
27 =37164783 transcript=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)
28 007G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
29 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
30 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
31 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
32 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
33 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
34 003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
35 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
36 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
37 =37164783 transcript=Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)
38 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
39 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
40 005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
41 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
42 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
43 005G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
44 ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G1168
45 hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
46 =37164783 transcript=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
47 003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50

1 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
2 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
3 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
4 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
5 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
6 n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
7 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
8 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
9 n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
10 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
11 222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
12 002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (
13 pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
14 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
15 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
16 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
17 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
18 006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
19 7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
20 pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
21 hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
22 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
23 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
24 ranscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
25 vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
26 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
27 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
28 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
29 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
30 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
31 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
32 =37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1 ;
33 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
34 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
35 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
36 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
37 s=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)
38 007G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
39 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
40 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
41 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
42 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
43 003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
44 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
45 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
46 s=Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)

1
2 J07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
3 J07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
4 J05G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
5 J07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
6 J07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
7 J05G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
8 ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G1168
9 hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
10 us=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
11 J03G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
12 J08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
13 J08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
14 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
15 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
16 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
17 on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
18 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
19 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
20 on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
21 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
22 22600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
23 J02G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C
24 pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
25 03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
26 03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
27 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
28 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
29 J06G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
30 7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
31 pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
32 hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
33 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
34 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
35 ranscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
36 vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
37 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
38 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
39 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
40 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
41 J02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosphatase
42 J02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosphatase
43 =37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1 ;
44 J02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=Arabid
45 J02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=Arabid
46 J05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
47 J02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=Arabid

1
 2 js=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)
 3 07G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
 4 07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 5 07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 6 07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 7 07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 8 07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 9 03G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
 10 07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 11 07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 12 07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 13 js=Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)
 14 07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 15 07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 16 07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 17 05G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
 18 07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 19 07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 20 07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 21 05G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
 22 ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G1168
 23 hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
 24 js=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
 25 03G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
 26 08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
 27 08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
 28 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
 29 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
 30 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
 31 on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G20160
 32 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
 33 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
 34 on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G20160
 35 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
 36 22600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
 37 02G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C
 38 pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1)
 39 03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
 40 03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
 41 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
 42 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
 43 06G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
 44 7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
 45 pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1)
 46 hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
 47 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
 48 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
 49 ranscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
 50 vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
 51 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) &

1 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
2 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
3 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
4 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
5 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
6 :37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1 ;
7 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
8 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
9 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
10 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
11 us=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)
12 007G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
13 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
14 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
15 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
16 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
17 003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
18 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
19 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
20 us=Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)
21 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
22 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
23 005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
24 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
25 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
26 005G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
27 ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G1168
28 hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
29 us=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
30 003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
31 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
32 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
33 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
34 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
35 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
36 n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
37 005G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
38 005G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
39 n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
40 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
41 002G222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
42 002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C
43 pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
44 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
45 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
46 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) ,

1 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
 2 006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
 3 7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
 4 pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
 5 hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
 6 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
 7 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
 8 ranscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
 9 v.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
 10 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
 11 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
 12 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
 13 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
 14 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
 15 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
 16 =37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1 ;
 17 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
 18 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
 19 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
 20 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
 21 s=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)
 22 007G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
 23 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 24 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 25 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 26 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 27 003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
 28 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 29 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 30 s=Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)
 31 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 32 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 33 005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
 34 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 35 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 36 005G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
 37 ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G1168
 38 hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
 39 s=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
 40 003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
 41 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
 42 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
 43 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
 44 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
 45 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
 46 on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600

1 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
2 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
3 on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
4 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
5 ?22600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
6 ?02G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (
7 pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
8 03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
9 03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
10 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
11 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
12 ?06G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
13 7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
14 pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
15 hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
16 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
17 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
18 ranscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
19 vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
20 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
21 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
22 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
23 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
24 ?02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosphatase
25 ?02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosphatase
26 =37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1 ;
27 ?02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=Arabidopsis
28 ?02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=Arabidopsis
29 ?05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
30 ?02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=Arabidopsis
31 =Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)
32 ?07G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
33 ?07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
34 ?07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
35 ?07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
36 ?07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
37 ?03G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
38 ?07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
39 ?07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
40 =Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)
41 ?07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
42 ?07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
43 ?05G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabidopsis
44 ?07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
45 ?07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
46 ?05G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabidopsis

ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G116800.1.v2.1 annot-version=v2.1) &
 hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
 us=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)

003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote

n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300.4.v2.1 annot-version=v2.1) &
 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300.4.v2.1 annot-version=v2.1) &
 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300.4.v2.1 annot-version=v2.1) &
 on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600.2.v2.1 annot-version=v2.1) &
 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &

on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600.2.v2.1 annot-version=v2.1) &
 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300.4.v2.1 annot-version=v2.1) &
 222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
 002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (
 pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1) &
 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &

006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
 7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
 pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1) &
 hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
 ranscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
 vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
 =37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1 ;
 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
 us=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)

007G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

1 003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
 2 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 3 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 4 006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)
 5 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 6 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 7 005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
 8 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 9 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
 10 005G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
 11 ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G1168
 12 hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
 13 008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
 14 003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
 15 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
 16 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
 17 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
 18 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
 19 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
 20 on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G20160
 21 05G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
 22 05G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
 23 on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G20160
 24 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
 25 222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
 26 002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C
 27 pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
 28 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
 29 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
 30 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
 31 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
 32 006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
 33 7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
 34 pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
 35 hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
 36 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
 37 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
 38 ranscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
 39 vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
 40 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
 41 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
 42 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
 43 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
 44 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosphatase
 45 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosphatase
 46 :37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1 ;

1 J02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
2 J02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
3 J05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
4 J02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

us=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)
07G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
03G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
us=Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
05G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
05G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G1168
hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
us=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
03G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
02G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (C
pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
06G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
=37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;

1 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
2
3 transcript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
4 vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
5 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
6 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
7 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
8 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
9 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
10 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
11 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
12 =37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1 ;
13 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
14 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
15 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
16 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
17 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
18 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
19 008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)
20 007G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
21 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
22 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
23 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
24 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
25 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
26 003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
27 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
28 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
29 008G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)
30 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
31 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
32 005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
33 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
34 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
35 005G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
36 ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G1168
37 hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
38 008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
39 003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
40 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
41 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
42 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
43 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
44 n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
45 005G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
46 005G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
47 n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
48 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
49 002G222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
50 002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (

1 pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
2 03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
3 03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
4 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
5 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
6 006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
7 7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
8 pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
9 hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
10 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
11 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
12 ranscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
13 vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
14 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
15 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
16 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
17 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
18 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
19 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
20 =37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1 ;
21 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
22 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
23 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
24 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
25 us=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)
26 007G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
27 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
28 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
29 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
30 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
31 003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
32 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
33 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
34 us=Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)
35 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
36 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
37 005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
38 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
39 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
40 005G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
41 ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G1168
42 hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
43 us=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
44 003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
45 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
46 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote

1 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
2 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
3 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
4 n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
5 n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
6 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
7 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
8 n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
9 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
10 222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
11 002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (
12 pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
13 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
14 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
15 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
16 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
17 006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
18 7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
19 pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
20 hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
21 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
22 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
23 ranscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
24 vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
25 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
26 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
27 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
28 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
29 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
30 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospho
31 =37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1 ;
32 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
33 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
34 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
35 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
36 s=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)
37 007G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
38 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
39 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
40 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
41 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
42 003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
43 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
44 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
45 s=Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)
46 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
47 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

1 005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
2 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
3 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
4 005G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
5 ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G1168
6 hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
7 js=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
8 003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
9 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
10 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
11 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
12 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
13 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
14 on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
15 005G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
16 005G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
17 on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
18 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
19 022600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
20 002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (
21 pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
22 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
23 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
24 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
25 =Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) &
26 006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
27 7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
28 pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
29 hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
30 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
31 =37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
32 ranscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
33 vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
34 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
35 =Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) {
36 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
37 6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
38 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosphatase
39 002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosphatase
40 =37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1 ;
41 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
42 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
43 005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
44 002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
45 js=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)
46 007G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &

1 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
2 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
3 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
4 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
5 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
6 003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
7 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
8 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
9 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
10 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
11 006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)
12 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
13 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
14 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
15 005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
16 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
17 007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
18 005G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
19 ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G1168
20 hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
21 008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
22 003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
23 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
24 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
25 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
26 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
27 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
28 n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
29 005G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
30 005G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
31 n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
32 n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G088300
33 006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
34 008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
35 n: pacid=37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
36 009G222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
37 n: pacid=37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1 ;
38 002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (c
39 pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1)
40 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
41 003G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
42 003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) ;
43 003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1) ;
44 005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
45 005G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
46 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
47 008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
48 n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
49 005G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
50 005G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &

1
2 on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G201600
3 5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
4 7150436 transcript=Phvul.009G114400.1 locus=Phvul.009G114400 ID=Phvul.009G114400.1.v2.1 and
5 =37145343 transcript=Phvul.003G240100.1 locus=Phvul.003G240100 ID=Phvul.003G240100.1.v2.1
6 rs=Phvul.002G283000 ID=Phvul.002G283000.4.v2.1 annot-version=v2.1)
7 rs=Phvul.002G283000 ID=Phvul.002G283000.4.v2.1 annot-version=v2.1)
8 rs=Phvul.002G283000 ID=Phvul.002G283000.4.v2.1 annot-version=v2.1)
9 .003G170100.1 locus=Phvul.003G170100 ID=Phvul.003G170100.1.v2.1 annot-version=v2.1) &
10 011G173600 ID=Phvul.011G173600.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containi
11 ase complex (original description: pacid=37146956 transcript=Phvul.003G283500.1 locus=Phvul.003
12 pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
13 ranscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
14 hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
15 (sp|q9ly50|accr3_arath : 328.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase trans
16 067900.1 locus=Phvul.006G067900 ID=Phvul.006G067900.1.v2.1 annot-version=v2.1) &
17 : 481.0) & Enzyme classification.EC_2 transferases.EC_2.4 glycosyltransferase(50.2.4 : 410.0) (origin
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3 .) &
4 .) &
5 .) &
6 .) &
7 /ersion=v2.1) &
8 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 282.0)
9
10
11 .) &
12 .) &
13 .) &
14 .) &
15 /ersion=v2.1) &
16 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 282.0)
17
18
19 .) &
20 .) &
21 .) &
22 .) &
23 /ersion=v2.1) &
24 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 282.0)
25
26
27 .) &
28 .) &
29 .) &
30 .) &
31 /ersion=v2.1) &
32 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 282.0)
33
34
35 .) &
36 .) &
37 .) &
38 .) &
39 /ersion=v2.1) &
40 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 282.0)
41
42
43 .) &
44 .) &
45 .) &
46 .) &
47 /ersion=v2.1) &
48 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 282.0)
49
50
51 .) &
52 .) &
53 .) &
54 .) &
55 /ersion=v2.1) &
56 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 282.0)
57
58
59 .) &
60 .) &
61 .) &

1
2 /ersion=v2.1) &
3 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 282.0)
4
5
6 .) &
7 .) &
8 .) &
9
10 /ersion=v2.1) &
11 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 282.0)
12
13
14 .) &
15 .) &
16 .) &
17
18 /ersion=v2.1) &
19 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 282.0)
20
21
22 .) &
23 .) &
24 .) &
25
26 /ersion=v2.1) &
27 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 282.0)
28
29
30 .) &
31 .) &
32 .) &
33
34 /ersion=v2.1) &
35 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 282.0)
36
37
38 .) &
39 .) &
40 .) &
41
42 /ersion=v2.1) &
43 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 282.0)
44
45
46 .) &
47 .) &
48 .) &
49
50 /ersion=v2.1) &
51 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 282.0)
52
53
54 .) &
55 .) &
56 .) &
57
58 /ersion=v2.1) &
59 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 282.0)
60
61 .) &

1
2 .) &
3 .) &
4 /ersion=v2.1) &
5 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 282.0)

6
7
8 .) &
9 .) &
10 .) &
11 .) &
12 /ersion=v2.1) &
13 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 282.0)

14
15
16 .) &
17 .) &
18 .) &
19 .) &
20 /ersion=v2.1) &

21
22
23
24 sion=v2.1) &
25 OS=Arabidopsis thaliana (sp|q8l5z1|gdl17_arath : 502.0)

26
27
28
29
30
31
32 1) &

33
34
35
36 sion=v2.1) &
37 OS=Arabidopsis thaliana (sp|q8l5z1|gdl17_arath : 502.0)

38
39
40
41
42
43
44 1) &

45
46
47
48 sion=v2.1) &
49 OS=Arabidopsis thaliana (sp|q8l5z1|gdl17_arath : 502.0)

50
51
52
53
54
55
56 1) &

57
58
59
60 sion=v2.1) &
OS=Arabidopsis thaliana (sp|q8l5z1|gdl17_arath : 502.0)

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1) &

sion=v2.1) &
OS=Arabidopsis thaliana (sp|q8l5z1|gdl17_arath : 502.0)

1) &

sion=v2.1) &
OS=Arabidopsis thaliana (sp|q8l5z1|gdl17_arath : 502.0)

1) &

sion=v2.1) &
OS=Arabidopsis thaliana (sp|q8l5z1|gdl17_arath : 502.0)

1) &

sion=v2.1) &
OS=Arabidopsis thaliana (sp|q8l5z1|gdl17_arath : 502.0)

1) &

sion=v2.1) &
OS=Arabidopsis thaliana (sp|q8l5z1|gdl17_arath : 502.0)

Do not distribute

1
2
3
4
5
6 1) &
7
8
9

10 sion=v2.1) &
11 OS=Arabidopsis thaliana (sp|q8l5z1|gdl17_arath : 502.0)
12
13
14
15
16

17
18 1) &
19
20

21 sion=v2.1) &
22 OS=Arabidopsis thaliana (sp|q8l5z1|gdl17_arath : 502.0)
23
24
25
26
27
28

29
30 1) &
31
32

33 sion=v2.1) &
34 OS=Arabidopsis thaliana (sp|q8l5z1|gdl17_arath : 502.0)
35
36
37
38
39
40

41
42 1) &
43
44

45 sion=v2.1) &
46 OS=Arabidopsis thaliana (sp|q8l5z1|gdl17_arath : 502.0)
47
48
49
50
51

52
53 1) &
54
55
56

57 sion=v2.1) &
58 OS=Arabidopsis thaliana (sp|q8l5z1|gdl17_arath : 502.0)
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

1) &

sion=v2.1) &

OS=Arabidopsis thaliana (sp|q8l5z1|gdl17_arath : 502.0)

1) &

sion=v2.1) &

OS=Arabidopsis thaliana (sp|q8l5z1|gdl17_arath : 502.0)

1) &

sion=v2.1) &

OS=Arabidopsis thaliana (sp|q8l5z1|gdl17_arath : 502.0)

1) &

sion=v2.1) &

OS=Arabidopsis thaliana (sp|q8l5z1|gdl17_arath : 502.0)

0.2.v2.1 annot-version=v2.1) &

0.2.v2.1 annot-version=v2.1) &

otein At4g28100 OS=Arabidopsis thaliana (sp|q9suc9|ugpi7_arath : 356.0)

n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25_arath : 146.0)

ision=v2.1) &

Do not distribute

1
2
3 &
4
5

6 26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq_arath : 910.0)
7
8
9

10
11 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591_arath : 1384.0)
12 0.2.v2.1 annot-version=v2.1) &
13 0.2.v2.1 annot-version=v2.1) &
14
15
16

17
18 otein At4g28100 OS=Arabidopsis thaliana (sp|q9suc9|ugpi7_arath : 356.0)
19 n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25_arath : 146.0)
20 ion=v2.1) &
21
22
23
24

25 &
26
27

28 26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq_arath : 910.0)
29
30
31
32

33 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591_arath : 1384.0)
34 0.2.v2.1 annot-version=v2.1) &
35 0.2.v2.1 annot-version=v2.1) &
36
37
38
39

40 otein At4g28100 OS=Arabidopsis thaliana (sp|q9suc9|ugpi7_arath : 356.0)
41 n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25_arath : 146.0)
42 ion=v2.1) &
43
44
45
46
47

48 &
49
50

51 26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq_arath : 910.0)
52
53
54
55

56 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591_arath : 1384.0)
57 0.2.v2.1 annot-version=v2.1) &
58 0.2.v2.1 annot-version=v2.1) &
59
60

1
2 otein At4g28100 OS=Arabidopsis thaliana (sp|q9suc9|ugpi7_arath : 356.0)
3 n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25_arath : 146.0)
4 ion=v2.1) &

5
6
7
8
9
10 &

11
12 26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq_arath : 910.0)
13
14
15
16

17
18 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591_arath : 1384.0)
19 0.2.v2.1 annot-version=v2.1) &
20 0.2.v2.1 annot-version=v2.1) &
21
22
23

24 otein At4g28100 OS=Arabidopsis thaliana (sp|q9suc9|ugpi7_arath : 356.0)
25 n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25_arath : 146.0)
26 ion=v2.1) &
27
28
29
30
31

32 &
33
34

35 26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq_arath : 910.0)
36
37
38
39

40 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591_arath : 1384.0)
41 0.2.v2.1 annot-version=v2.1) &
42 0.2.v2.1 annot-version=v2.1) &
43
44
45

46 otein At4g28100 OS=Arabidopsis thaliana (sp|q9suc9|ugpi7_arath : 356.0)
47 n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25_arath : 146.0)
48 ion=v2.1) &
49
50
51
52
53

54 &
55
56

57 26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq_arath : 910.0)
58
59
60

1
2 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591_arath : 1384.0)
3 0.2.v2.1 annot-version=v2.1) &
4 0.2.v2.1 annot-version=v2.1) &
5

6
7
8 otein At4g28100 OS=Arabidopsis thaliana (sp|q9suc9|ugpi7_arath : 356.0)
9 n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25_arath : 146.0)
10
11 ion=v2.1) &
12

13
14
15
16 &
17

18
19 26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq_arath : 910.0)
20
21

22
23
24 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591_arath : 1384.0)
25 0.2.v2.1 annot-version=v2.1) &
26 0.2.v2.1 annot-version=v2.1) &
27
28

29
30
31 otein At4g28100 OS=Arabidopsis thaliana (sp|q9suc9|ugpi7_arath : 356.0)
32 n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25_arath : 146.0)
33 ion=v2.1) &
34

35
36
37
38 &
39

40
41 26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq_arath : 910.0)
42
43

44
45
46 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591_arath : 1384.0)
47 0.2.v2.1 annot-version=v2.1) &
48 0.2.v2.1 annot-version=v2.1) &
49
50

51
52
53 otein At4g28100 OS=Arabidopsis thaliana (sp|q9suc9|ugpi7_arath : 356.0)
54 n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25_arath : 146.0)
55 ion=v2.1) &
56
57

58
59
60 &

1
2
3 26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq_arath : 910.0)
4
5
6
7

8 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591_arath : 1384.0)
9 0.2.v2.1 annot-version=v2.1) &
10 0.2.v2.1 annot-version=v2.1) &
11
12
13
14

15 otein At4g28100 OS=Arabidopsis thaliana (sp|q9suc9|ugpi7_arath : 356.0)
16 n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25_arath : 146.0)
17 ion=v2.1) &
18
19
20
21
22

23 &
24
25

26 26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq_arath : 910.0)
27
28
29
30

31 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591_arath : 1384.0)
32 0.2.v2.1 annot-version=v2.1) &
33 0.2.v2.1 annot-version=v2.1) &
34
35
36

37 otein At4g28100 OS=Arabidopsis thaliana (sp|q9suc9|ugpi7_arath : 356.0)
38 n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25_arath : 146.0)
39 ion=v2.1) &
40
41
42
43
44

45 &
46
47

48 26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq_arath : 910.0)
49
50
51
52

53 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591_arath : 1384.0)
54 0.2.v2.1 annot-version=v2.1) &
55 0.2.v2.1 annot-version=v2.1) &
56
57
58
59

60 otein At4g28100 OS=Arabidopsis thaliana (sp|q9suc9|ugpi7_arath : 356.0)
n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25_arath : 146.0)

1
2 iion=v2.1) &
3
4
5
6

7 &
8
9

10 26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq_arath : 910.0)
11
12
13
14

15 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591_arath : 1384.0)

16 0.2.v2.1 annot-version=v2.1) &
17

18 0.2.v2.1 annot-version=v2.1) &
19
20
21

22 otein At4g28100 OS=Arabidopsis thaliana (sp|q9suc9|ugpi7_arath : 356.0)

23 n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25_arath : 146.0)

24 iion=v2.1) &
25
26
27
28
29

30 &
31
32

32 26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq_arath : 910.0)
33
34
35
36
37

37 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591_arath : 1384.0)

38 0.2.v2.1 annot-version=v2.1) &
39

40 0.2.v2.1 annot-version=v2.1) &
41
42
43

44 otein At4g28100 OS=Arabidopsis thaliana (sp|q9suc9|ugpi7_arath : 356.0)

45 n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25_arath : 146.0)

46 iion=v2.1) &
47
48
49
50
51

52 &
53
54

54 26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq_arath : 910.0)
55
56
57
58
59

59 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591_arath : 1384.0)

60 0.2.v2.1 annot-version=v2.1) &

1
2 0.2.v2.1 annot-version=v2.1) &
3
4

5
6 otein At4g28100 OS=Arabidopsis thaliana (sp|q9suc9|ugpi7_arath : 356.0)
7 n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25_arath : 146.0)
8 ion=v2.1) &
9

10
11
12
13
14 &
15

16 26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq_arath : 910.0)
17
18
19

20
21
22 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591_arath : 1384.0)
23 0.2.v2.1 annot-version=v2.1) &
24 0.2.v2.1 annot-version=v2.1) &
25

26
27
28 otein At4g28100 OS=Arabidopsis thaliana (sp|q9suc9|ugpi7_arath : 356.0)
29 n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25_arath : 146.0)
30 ion=v2.1) &
31
32

33
34
35
36 &
37
38

39 26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq_arath : 910.0)
40
41
42

43
44 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591_arath : 1384.0)
45 0.2.v2.1 annot-version=v2.1) &
46 0.2.v2.1 annot-version=v2.1) &
47
48

49
50
51 otein At4g28100 OS=Arabidopsis thaliana (sp|q9suc9|ugpi7_arath : 356.0)
52 n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25_arath : 146.0)
53 ion=v2.1) &
54
55

56
57
58 &
59
60

26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq_arath : 910.0)

1
2
3
4
5
6 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591_arath : 1384.0)
7 0.2.v2.1 annot-version=v2.1) &
8 0.2.v2.1 annot-version=v2.1) &
9

10
11 ining protein At1g05910 OS=Arabidopsis thaliana (sp|f4iae9|y1591_arath : 1384.0)
12

13
14 otein At4g28100 OS=Arabidopsis thaliana (sp|q9suc9|ugpi7_arath : 356.0)
15 n kinase 25 OS=Arabidopsis thaliana (sp|q9m0x5|crk25_arath : 146.0)
16 iion=v2.1) &
17

18
19
20
21
22
23
24
25 &
26

27
28 26 OS=Arabidopsis thaliana (sp|q8l7v3|pmtq_arath : 910.0)
29 lanum lycopersicum (sp|q6jn46|eix2_sollc : 491.0)
30 rprotein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5_arath : 201.0)
31
32 v2.1) &
33 OS=Arabidopsis thaliana (sp|q67zi9|gdl48_arath : 413.0)
34
35
36
37
38

39 &
40
41
42
43
44
45
46

47 98|rrt1_arath : 178.0)
48 =Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)
49 rt-version=v2.1) &
50 r=v2.1) &
51 r=v2.1) &
52 l) &
53
54

55 &
56
57 &
58
59
60

1 na (sp|q0wpu1|myo15_arath : 357.0)

2 /v2.1) &

3 lanum lycopersicum (sp|q6jn46|eix2_sollc : 491.0)

4 protein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5_arath : 201.0)

5 v2.1) &

6 OS=Arabidopsis thaliana (sp|q67zi9|gdl48_arath : 413.0)

7

8 |rrt1_arath : 178.0)

9 =Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)

10 it-version=v2.1) &

11 r=v2.1) &

12 r=v2.1) &

13 l) &

14 &

15 &

16 na (sp|q0wpu1|myo15_arath : 357.0)

17 /v2.1) &

18 lanum lycopersicum (sp|q6jn46|eix2_sollc : 491.0)

19 protein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5_arath : 201.0)

20 v2.1) &

21 OS=Arabidopsis thaliana (sp|q67zi9|gdl48_arath : 413.0)

22

1
2 98|rrt1_arath : 178.0)
3 =Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)
4 it-version=v2.1) &
5 r=v2.1) &
6 r=v2.1) &
7 l) &
8
9
10
11 &
12 &
13
14
15
16
17 na (sp|q0wpu1|myo15_arath : 357.0)
18
19
20 /2.1) &
21
22
23 lanum lycopersicum (sp|q6jn46|eix2_sollc : 491.0)
24 rotein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5_arath : 201.0)
25
26
27 v2.1) &
28 OS=Arabidopsis thaliana (sp|q67zi9|gdl48_arath : 413.0)
29
30
31
32
33
34
35
36
37
38
39
40 98|rrt1_arath : 178.0)
41 =Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)
42 it-version=v2.1) &
43 r=v2.1) &
44 r=v2.1) &
45 l) &
46
47
48
49 &
50 &
51
52
53
54
55
56 na (sp|q0wpu1|myo15_arath : 357.0)
57
58
59 /2.1) &
60
lanum lycopersicum (sp|q6jn46|eix2_sollc : 491.0)

1 protein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5_arath : 201.0)

2 v2.1) &

3 OS=Arabidopsis thaliana (sp|q67zi9|gdl48_arath : 413.0)

4 &

5 &|rrt1_arath : 178.0)

6 =Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)

7 it-version=v2.1) &

8 r=v2.1) &

9 r=v2.1) &

10 l) &

11 &

12 &

13 na (sp|q0wpu1|myo15_arath : 357.0)

14 /2.1) &

15 lanum lycopersicum (sp|q6jn46|eix2_sollc : 491.0)

16 protein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5_arath : 201.0)

17 v2.1) &

18 OS=Arabidopsis thaliana (sp|q67zi9|gdl48_arath : 413.0)

19 &

20 &|rrt1_arath : 178.0)

21 =Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)

22 it-version=v2.1) &

23 r=v2.1) &

24 r=v2.1) &

1
2 l) &

3
4 &

5
6 &

7
8
9
10
11 na (sp|q0wpu1|myo15_arath : 357.0)

12
13
14 /v2.1) &

15
16 lanum lycopersicum (sp|q6jn46|eix2_sollc : 491.0)

17
18 protein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5_arath : 201.0)

19
20 v2.1) &

21
22 OS=Arabidopsis thaliana (sp|q67zi9|gdl48_arath : 413.0)

23
24
25
26 k

27
28
29
30
31
32
33 8|rrt1_arath : 178.0)

34
35 =Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)

36
37 it-version=v2.1) &

38
39 r=v2.1) &

40
41 l) &

42
43 &

44
45 &

46
47
48
49 na (sp|q0wpu1|myo15_arath : 357.0)

50
51
52 /v2.1) &

53
54 lanum lycopersicum (sp|q6jn46|eix2_sollc : 491.0)

55
56 protein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5_arath : 201.0)

57
58 v2.1) &

59
60 OS=Arabidopsis thaliana (sp|q67zi9|gdl48_arath : 413.0)

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

8|rrt1_arath : 178.0)
=Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)
it-version=v2.1) &

r=v2.1) &
r=v2.1) &
l) &

&
&

na (sp|q0wpu1|myo15_arath : 357.0)

/2.1) &

lanum lycopersicum (sp|q6jn46|eix2_sollc : 491.0)
rotein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5_arath : 201.0)

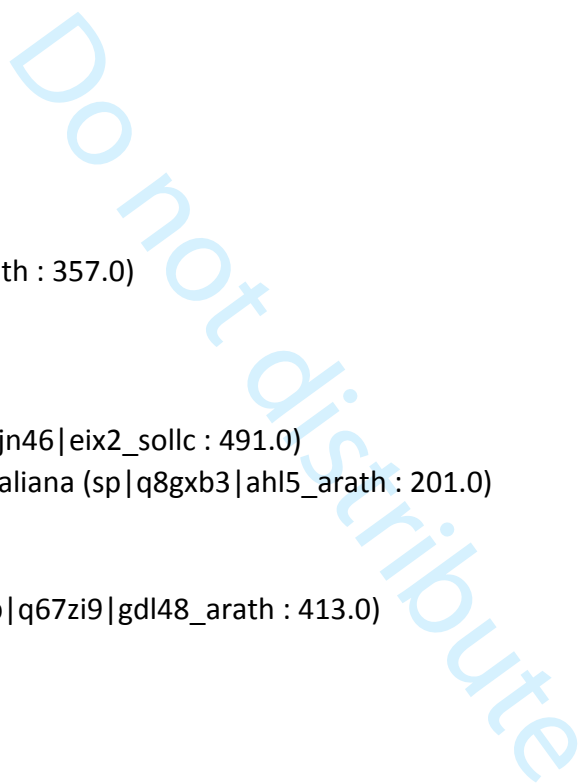
v2.1) &
OS=Arabidopsis thaliana (sp|q67zi9|gdl48_arath : 413.0)

8|rrt1_arath : 178.0)

8|rrt1_arath : 178.0)
=Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)
it-version=v2.1) &

r=v2.1) &
r=v2.1) &
l) &

&
&



1
2
3
4 na (sp|q0wpu1|myo15_arath : 357.0)

5
6
7 /v2.1) &

8
9
10 lanum lycopersicum (sp|q6jn46|eix2_sollc : 491.0)
11 protein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5_arath : 201.0)

12
13
14 v2.1) &
15 OS=Arabidopsis thaliana (sp|q67zi9|gdl48_arath : 413.0)

16
17
18
19 &

20
21
22
23
24
25
26
27 8|rrt1_arath : 178.0)
28 -Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)
29 it-version=v2.1) &

30
31 r=v2.1) &
32 r=v2.1) &
33 l) &

34
35
36 &
37 &

38
39
40
41
42 na (sp|q0wpu1|myo15_arath : 357.0)

43
44
45 /v2.1) &

46
47
48 lanum lycopersicum (sp|q6jn46|eix2_sollc : 491.0)
49 protein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5_arath : 201.0)

50
51
52 v2.1) &
53 OS=Arabidopsis thaliana (sp|q67zi9|gdl48_arath : 413.0)

54
55
56
57 &

58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

98|rrt1_arath : 178.0)
-Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)
it-version=v2.1) &
r=v2.1) &
r=v2.1) &
) &
&
&
na (sp|q0wpu1|myo15_arath : 357.0)
/2.1) &
lanum lycopersicum (sp|q6jn46|eix2_sollc : 491.0)
rotein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5_arath : 201.0)
v2.1) &
OS=Arabidopsis thaliana (sp|q67zi9|gdl48_arath : 413.0)
k
98|rrt1_arath : 178.0)
-Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)
it-version=v2.1) &
r=v2.1) &
r=v2.1) &
) &
&
&
na (sp|q0wpu1|myo15_arath : 357.0)
/2.1) &

lanum lycopersicum (sp|q6jn46|eix2_sollc : 491.0)
protein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5_arath : 201.0)

v2.1) &
OS=Arabidopsis thaliana (sp|q67zi9|gdl48_arath : 413.0)

↓

8|rrt1_arath : 178.0)
=Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)
it-version=v2.1) &
v2.1) &
v2.1) &
) &

&
&

na (sp|q0wpu1|myo15_arath : 357.0)

v2.1) &

lanum lycopersicum (sp|q6jn46|eix2_sollc : 491.0)
protein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5_arath : 201.0)

v2.1) &
OS=Arabidopsis thaliana (sp|q67zi9|gdl48_arath : 413.0)

↓

8|rrt1_arath : 178.0)
=Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)
it-version=v2.1) &

1
 2 v2.1) &
 3 v2.1) &
 4 l) &
 5
 6
 7 &
 8 &
 9
 10
 11
 12
 13
 14 na (sp|q0wpu1|myo15_arath : 357.0)
 15
 16 v2.1) &
 17
 18
 19 lanum lycopersicum (sp|q6jn46|eix2_sollc : 491.0)
 20 rotein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5_arath : 201.0)
 21
 22
 23 v2.1) &
 24 OS=Arabidopsis thaliana (sp|q67zi9|gdl48_arath : 413.0)
 25
 26
 27
 28 &
 29
 30
 31
 32
 33
 34
 35
 36 8|rrt1_arath : 178.0)
 37 =Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)
 38 t-version=v2.1) &
 39 v2.1) &
 40 v2.1) &
 41 v2.1) &
 42 l) &
 43
 44
 45 &
 46 &
 47
 48
 49
 50
 51
 52 na (sp|q0wpu1|myo15_arath : 357.0)
 53
 54 v2.1) &
 55
 56
 57 lanum lycopersicum (sp|q6jn46|eix2_sollc : 491.0)
 58 rotein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5_arath : 201.0)
 59
 60
 v2.1) &

1 OS=Arabidopsis thaliana (sp|q67zi9|gdl48_arath : 413.0)

2
3
4
5
6 k

7
8
9
10
11
12
13
14 98|rrt1_arath : 178.0)

15 =Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)

16 it-version=v2.1) &

17 r=v2.1) &

18 r=v2.1) &

19 l) &

20
21
22
23 &

24 &

25
26
27
28
29 na (sp|q0wpu1|myo15_arath : 357.0)

30
31
32 /2.1) &

33
34 lanum lycopersicum (sp|q6jn46|eix2_sollc : 491.0)

35 protein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5_arath : 201.0)

36
37
38
39 v2.1) &

40 OS=Arabidopsis thaliana (sp|q67zi9|gdl48_arath : 413.0)

41
42
43
44 k

45
46
47
48
49
50
51
52 98|rrt1_arath : 178.0)

53 =Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)

54 it-version=v2.1) &

55 r=v2.1) &

56 r=v2.1) &

57 l) &

58
59
60 &

1
2 &
3
4
5
6
7 na (sp|q0wpu1|myo15_arath : 357.0)
8
9
10 /v2.1) &
11
12
13
14 v2.1) &
15 &
16 &
17 OS=Arabidopsis thaliana (sp|q67zi9|gdl48_arath : 413.0)
18 lanum lycopersicum (sp|q6jn46|eix2_sollc : 491.0)
19 protein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5_arath : 201.0)
20
21
22
23
24
25
26
27 -version=v2.1) &
28 -version=v2.1) &
29
30
31
32 8|rrt1_arath : 178.0)
33
34
35
36
37 =Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)
38 t-version=v2.1) &
39 r=v2.1) &
40 r=v2.1) &
41
42
43
44 l) &
45
46
47
48
49
50
51
52) &
53 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)
54 ion=v2.1) &
55 400.3.v2.1 annot-version=v2.1) &
56
57
58
59
60 ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)
se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)

1
2
3
4
5
6 &
7
8 6200.1.v2.1 annot-version=v2.1) &
9 version=v2.1) &
10
11
12 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
13 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
14
15
16
17
18
19 006G154900 ID=Phvul.006G154900.1.v2.1 annot-version=v2.1) &
20
21 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
22 t-version=v2.1) &
23 t-version=v2.1) &
24
25
26
27
28 t-version=v2.1) &
29 ncorporation or reduction of molecular oxygen(50.1.13 : 325.4) (original description: pacid=371646
30
31
32
33
34
35
36) &
37 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)
38 ion=v2.1) &
39 0400.3.v2.1 annot-version=v2.1) &
40
41
42
43
44 ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)
45 se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)
46
47
48
49
50
51 &
52
53 6200.1.v2.1 annot-version=v2.1) &
54 version=v2.1) &
55
56
57 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
58 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
59
60

1
2
3 006G154900 ID=Phvul.006G154900.1.v2.1 annot-version=v2.1) &

4
5
6 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)

7 it-version=v2.1) &

8 it-version=v2.1) &

9
10
11
12 it-version=v2.1) &

13 ncorporation or reduction of molecular oxygen(50.1.13 : 325.4) (original description: pacid=371646

14
15
16
17
18
19
20) &

21 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)

22 ion=v2.1) &

23 00400.3.v2.1 annot-version=v2.1) &

24
25
26
27
28 ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)

29 se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)

30
31
32
33
34
35 &

36
37 006200.1.v2.1 annot-version=v2.1) &

38 sion=v2.1) &

39
40
41 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph

42 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph

43
44
45
46
47
48 006G154900 ID=Phvul.006G154900.1.v2.1 annot-version=v2.1) &

49
50
51 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)

52 it-version=v2.1) &

53 it-version=v2.1) &

54
55
56
57 it-version=v2.1) &

58 ncorporation or reduction of molecular oxygen(50.1.13 : 325.4) (original description: pacid=371646

59
60

1
2
3
4) &

5 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)

6 ion=v2.1) &

7 400.3.v2.1 annot-version=v2.1) &

8
9
10
11
12 ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)

13 se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)

14
15
16
17
18
19 &

20
21 6200.1.v2.1 annot-version=v2.1) &

22 version=v2.1) &

23
24
25 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph

26 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph

27
28
29
30
31
32 J06G154900 ID=Phvul.006G154900.1.v2.1 annot-version=v2.1) &

33
34
35 L OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)

36 it-version=v2.1) &

37 it-version=v2.1) &

38
39
40
41 it-version=v2.1) &

42 ncorporation or reduction of molecular oxygen(50.1.13 : 325.4) (original description: pacid=371646

43
44
45
46
47
48
49) &

50 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)

51 ion=v2.1) &

52 400.3.v2.1 annot-version=v2.1) &

53
54
55
56
57 ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)

58 se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)

59
60

1
2
3 &
4
5
6 6200.1.v2.1 annot-version=v2.1) &
7 rsion=v2.1) &
8
9
10 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
11 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
12
13
14
15
16 J06G154900 ID=Phvul.006G154900.1.v2.1 annot-version=v2.1) &
17
18
19 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
20 it-version=v2.1) &
21 it-version=v2.1) &
22
23
24
25
26 it-version=v2.1) &
27 ncorporation or reduction of molecular oxygen(50.1.13 : 325.4) (original description: pacid=371646
28
29
30
31
32
33) &
34 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)
35 ion=v2.1) &
36 3400.3.v2.1 annot-version=v2.1) &
37
38
39
40
41 ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)
42 se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)
43
44
45
46
47
48 &
49
50
51 6200.1.v2.1 annot-version=v2.1) &
52 rsion=v2.1) &
53
54
55 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
56 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
57
58
59
60
J06G154900 ID=Phvul.006G154900.1.v2.1 annot-version=v2.1) &

1
2
3 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)

4 it-version=v2.1) &

5 it-version=v2.1) &

6
7
8
9 it-version=v2.1) &

10 incorporation or reduction of molecular oxygen(50.1.13 : 325.4) (original description: pacid=371646

11
12
13
14
15
16
17) &

18 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)

19 ion=v2.1) &

20 3400.3.v2.1 annot-version=v2.1) &

21
22
23
24
25 ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)

26 se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)

27
28
29
30
31
32 &

33
34 6200.1.v2.1 annot-version=v2.1) &

35 sion=v2.1) &

36
37
38 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph

39 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph

40
41
42
43
44
45 006G154900 ID=Phvul.006G154900.1.v2.1 annot-version=v2.1) &

46
47
48 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)

49 it-version=v2.1) &

50 it-version=v2.1) &

51
52
53
54 it-version=v2.1) &

55 incorporation or reduction of molecular oxygen(50.1.13 : 325.4) (original description: pacid=371646

56
57
58
59
60

1) &
2 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)
3 ion=v2.1) &
4 400.3.v2.1 annot-version=v2.1) &
5
6
7
8
9
10 ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)
11 se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)
12
13
14
15
16 &
17
18
19 6200.1.v2.1 annot-version=v2.1) &
20 sion=v2.1) &
21
22
23 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
24 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
25
26
27
28
29 I06G154900 ID=Phvul.006G154900.1.v2.1 annot-version=v2.1) &
30
31
32 L OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
33 rt-version=v2.1) &
34 rt-version=v2.1) &
35
36
37
38
39 rt-version=v2.1) &
40 ncorporation or reduction of molecular oxygen(50.1.13 : 325.4) (original description: pacid=371646
41
42
43
44
45
46
47) &
48 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)
49 ion=v2.1) &
50 400.3.v2.1 annot-version=v2.1) &
51
52
53
54
55 ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)
56 se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)
57
58
59
60 &

1
2
3 6200.1.v2.1 annot-version=v2.1) &
4 version=v2.1) &

5
6
7 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
8 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
9

10
11
12
13
14 J06G154900 ID=Phvul.006G154900.1.v2.1 annot-version=v2.1) &

15
16 L OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
17 it-version=v2.1) &
18 it-version=v2.1) &

19
20
21
22
23 it-version=v2.1) &
24 ncorporation or reduction of molecular oxygen(50.1.13 : 325.4) (original description: pacid=371646
25
26
27
28
29

30
31) &
32 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)
33 ion=v2.1) &
34 J400.3.v2.1 annot-version=v2.1) &
35
36
37
38

39 ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)
40 se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)
41
42
43
44

45 &
46
47

48 6200.1.v2.1 annot-version=v2.1) &
49 version=v2.1) &
50

51
52 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
53 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
54
55
56
57

58 J06G154900 ID=Phvul.006G154900.1.v2.1 annot-version=v2.1) &
59
60

L OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)

1
2 it-version=v2.1) &

3 it-version=v2.1) &

6
7 it-version=v2.1) &

8 ncorporation or reduction of molecular oxygen(50.1.13 : 325.4) (original description: pacid=371646

14
15) &

16 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)

17 ion=v2.1) &

18 400.3.v2.1 annot-version=v2.1) &

22
23 ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)

24 se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)

28
29 &

31
32 6200.1.v2.1 annot-version=v2.1) &

33 sion=v2.1) &

34
35
36 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph

37 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph

39
40
41
42
43 I06G154900 ID=Phvul.006G154900.1.v2.1 annot-version=v2.1) &

44
45 L OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)

46 it-version=v2.1) &

47 it-version=v2.1) &

49
50
51
52 it-version=v2.1) &

53 ncorporation or reduction of molecular oxygen(50.1.13 : 325.4) (original description: pacid=371646

56
57
58
59) &

60 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)

ion=v2.1) &

400.3.v2.1 annot-version=v2.1) &

ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)

se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)

&

6200.1.v2.1 annot-version=v2.1) &

ersion=v2.1) &

ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph

ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph

06G154900 ID=Phvul.006G154900.1.v2.1 annot-version=v2.1) &

l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)

rt-version=v2.1) &

rt-version=v2.1) &

rt-version=v2.1) &

ncorporation or reduction of molecular oxygen(50.1.13 : 325.4) (original description: pacid=371646

) &

OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)

ion=v2.1) &

400.3.v2.1 annot-version=v2.1) &

ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)

se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)

&

6200.1.v2.1 annot-version=v2.1) &

1
2 'sion=v2.1) &

3
4 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
5 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
6
7
8
9

10
11)06G154900 ID=Phvul.006G154900.1.v2.1 annot-version=v2.1) &

12
13
14 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)

15 it-version=v2.1) &

16 it-version=v2.1) &

17
18
19
20 it-version=v2.1) &

21 ncorporation or reduction of molecular oxygen(50.1.13 : 325.4) (original description: pacid=371646
22
23
24
25
26
27

28) &

29 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)

30 ion=v2.1) &

31)400.3.v2.1 annot-version=v2.1) &

32
33
34
35
36 ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)

37 se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)
38
39
40
41
42

43 &

44
45 6200.1.v2.1 annot-version=v2.1) &

46 'sion=v2.1) &

47
48
49 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
50 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
51
52
53
54
55

56)06G154900 ID=Phvul.006G154900.1.v2.1 annot-version=v2.1) &

57
58 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)

59 it-version=v2.1) &

60 it-version=v2.1) &

1
2
3
4 it-version=v2.1) &
5 incorporation or reduction of molecular oxygen(50.1.13 : 325.4) (original description: pacid=371646
6
7
8
9
10
11

12) &
13 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)
14 ion=v2.1) &
15 400.3.v2.1 annot-version=v2.1) &
16
17
18
19

20 ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)
21 se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)
22
23
24
25
26

27 &
28
29 6200.1.v2.1 annot-version=v2.1) &
30 sion=v2.1) &
31
32

33 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
34 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
35
36
37
38
39

40 06G154900 ID=Phvul.006G154900.1.v2.1 annot-version=v2.1) &
41
42

43 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
44 it-version=v2.1) &
45 it-version=v2.1) &
46
47
48

49 it-version=v2.1) &
50 incorporation or reduction of molecular oxygen(50.1.13 : 325.4) (original description: pacid=371646
51
52
53
54
55
56

57) &
58 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)
59 ion=v2.1) &
60 400.3.v2.1 annot-version=v2.1) &

1
2
3
4 ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)
5 se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)
6
7
8
9

10
11 &
12
13 6200.1.v2.1 annot-version=v2.1) &
14 rsion=v2.1) &
15
16
17 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
18 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
19
20
21
22
23

24 J06G154900 ID=Phvul.006G154900.1.v2.1 annot-version=v2.1) &
25
26

27 L OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
28 it-version=v2.1) &
29 it-version=v2.1) &
30
31
32

33 it-version=v2.1) &
34 ncorporation or reduction of molecular oxygen(50.1.13 : 325.4) (original description: pacid=371646
35
36
37
38
39
40

41) &
42 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)
43 ion=v2.1) &
44 3400.3.v2.1 annot-version=v2.1) &
45
46
47
48

49 ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)
50 se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)
51
52
53
54
55

56 &
57
58 6200.1.v2.1 annot-version=v2.1) &
59 rsion=v2.1) &
60

1
2 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
3 ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
4
5
6
7
8)06G154900 ID=Phvul.006G154900.1.v2.1 annot-version=v2.1) &
9
10
11 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
12 it-version=v2.1) &
13 it-version=v2.1) &
14
15
16
17
18 it-version=v2.1) &
19 ncorporation or reduction of molecular oxygen(50.1.13 : 325.4) (original description: pacid=371646
20
21
22
23
24
25) &
26
27
28 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)
29
30
31 ion=v2.1) &
32)400.3.v2.1 annot-version=v2.1) &
33
34
35
36 s=Arabidopsis thaliana (sp|q84p23|4cll9_arath : 619.0)
37 ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)
38 OS=Arabidopsis thaliana (sp|q8l612|macp1_arath : 346.0)
39 OS=Arabidopsis thaliana (sp|q8l612|macp1_arath : 346.0)
40 se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)
41
42
43
44
45 &
46
47
48 6200.1.v2.1 annot-version=v2.1) &
49
50
51 rsion=v2.1) &
52
53
54
55
56 !r0|ftip3_arath : 1142.0)
57
58 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 254.0)
59 1) &
60

1
2
3 &
4 &
5
6 hypogaea (sp|p22195|per1_arahy : 381.0)
7 not-version=v2.1) &
8 l) &
9
10
11 annot-version=v2.1) &
12 annot-version=v2.1) &
13 in=v2.1) &
14
15
16 &
17 &
18 :-version=v2.1) &
19 :-version=v2.1) &
20
21 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
22 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
23 annot-version=v2.1) &
24
25 rabadopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
26 rabadopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
27 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
28 rabadopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
29
30
31
32
33 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
34 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
35 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
36 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
37 OS=Gossypium hirsutum (sp|p0ch30|ring1_goshi : 103.0)
38 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
39 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
40
41 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
42 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
43
44 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
45 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
46 lopsis thaliana (sp|o81755|per48_arath : 290.0)
47 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
48 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
49 lopsis thaliana (sp|o81755|per48_arath : 272.0)
50
51 300.1.v2.1 annot-version=v2.1) &
52
53
54
55
56 l OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
57 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
58 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
59 0.4.v2.1 annot-version=v2.1) &
60 0.4.v2.1 annot-version=v2.1) &

1
 2 0.4.v2.1 annot-version=v2.1) &
 3 J0.2.v2.1 annot-version=v2.1) &
 4
 5
 6
 7 J0.2.v2.1 annot-version=v2.1) &
 8 0.4.v2.1 annot-version=v2.1) &
 9
 10
 11 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 254.0)
 12 1) &
 13
 14
 15
 16 &
 17 &
 18 &
 19 hypogaea (sp|p22195|per1_arahy : 381.0)
 20 not-version=v2.1) &
 21 l) &
 22
 23
 24 annot-version=v2.1) &
 25 annot-version=v2.1) &
 26 in=v2.1) &
 27
 28
 29 &
 30 &
 31 &
 32 :-version=v2.1) &
 33 :-version=v2.1) &
 34
 35 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 36 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 37 annot-version=v2.1) &
 38
 39 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 40 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 41 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
 42 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 43
 44
 45
 46 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 47 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 48 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 49 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 50 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 51 OS=Gossypium hirsutum (sp|p0ch30|ring1_goshi : 103.0)
 52 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 53 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 54
 55
 56
 57 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 58 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 59 Arabidopsis thaliana (sp|o81755|per48_arath : 290.0)
 60 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)

2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 lopsis thaliana (sp|o81755|per48_arath : 272.0)
 300.1.v2.1 annot-version=v2.1) &

 OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 0.4.v2.1 annot-version=v2.1) &
 0.4.v2.1 annot-version=v2.1) &
 0.4.v2.1 annot-version=v2.1) &
 0.2.v2.1 annot-version=v2.1) &

 0.2.v2.1 annot-version=v2.1) &
 0.4.v2.1 annot-version=v2.1) &

 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 254.0)
 1) &

 &
 &
 hypogaea (sp|p22195|per1_arahy : 381.0)
 not-version=v2.1) &
 l) &

 annot-version=v2.1) &
 annot-version=v2.1) &
 in=v2.1) &

 &
 &
 :-version=v2.1) &
 :-version=v2.1) &
 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 annot-version=v2.1) &
 rabadopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 rabadopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
 rabadopsis thaliana (sp|q8rx22|mip1_arath : 389.0)

 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)

1
 2 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 3 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 4 OS=Gossypium hirsutum (sp|p0ch30|ring1_goshi : 103.0)
 5
 6 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 7 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 8
 9
 10 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 11 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 12 lopsis thaliana (sp|o81755|per48_arath : 290.0)
 13
 14 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 15 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 16 lopsis thaliana (sp|o81755|per48_arath : 272.0)
 17
 18 300.1.v2.1 annot-version=v2.1) &
 19
 20
 21
 22 l OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
 23 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 24 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 25
 26 0.4.v2.1 annot-version=v2.1) &
 27 0.4.v2.1 annot-version=v2.1) &
 28 0.4.v2.1 annot-version=v2.1) &
 29
 30 00.2.v2.1 annot-version=v2.1) &
 31
 32
 33
 34 00.2.v2.1 annot-version=v2.1) &
 35 0.4.v2.1 annot-version=v2.1) &
 36
 37
 38 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 254.0)
 39 l) &
 40
 41
 42
 43 &
 44 &
 45 hypogaea (sp|p22195|per1_arahy : 381.0)
 46 not-version=v2.1) &
 47 l) &
 48
 49
 50
 51 annot-version=v2.1) &
 52 annot-version=v2.1) &
 53 in=v2.1) &
 54
 55
 56 &
 57 &
 58 :-version=v2.1) &
 59 :-version=v2.1) &
 60 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)

1
2 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
3 annot-version=v2.1) &
4 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
5 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
6 L OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
7 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
8
9
10
11
12 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
13 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
14 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
15 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
16 OS=Gossypium hirsutum (sp|p0ch30|ring1_goshi : 103.0)
17 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
18 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
19
20 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
21
22
23 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
24 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
25 Arabidopsis thaliana (sp|o81755|per48_arath : 290.0)
26 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
27 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
28 Arabidopsis thaliana (sp|o81755|per48_arath : 272.0)
29 300.1.v2.1 annot-version=v2.1) &
30
31
32
33
34
35 L OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
36 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
37 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
38 0.4.v2.1 annot-version=v2.1) &
39 0.4.v2.1 annot-version=v2.1) &
40 0.4.v2.1 annot-version=v2.1) &
41 0.2.v2.1 annot-version=v2.1) &
42
43
44
45
46 0.2.v2.1 annot-version=v2.1) &
47 0.4.v2.1 annot-version=v2.1) &
48
49
50
51 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 254.0)
52 1) &
53
54
55
56 &
57 &
58 hypogaea (sp|p22195|per1_arahy : 381.0)
59 not-version=v2.1) &
60 L) &

1
 2
 3 annot-version=v2.1) &
 4 annot-version=v2.1) &
 5 in=v2.1) &
 6
 7
 8 &
 9 &
 10
 11 :-version=v2.1) &
 12 :-version=v2.1) &
 13
 14 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 15 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 16 annot-version=v2.1) &
 17
 18 arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 19 arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 20 L OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
 21 arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 22
 23
 24
 25
 26 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 27 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 28 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 29 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 30 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 31 OS=Gossypium hirsutum (sp|p0ch30|ring1_goshi : 103.0)
 32 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 33 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 34
 35
 36 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 37 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 38
 39 lopsis thaliana (sp|o81755|per48_arath : 290.0)
 40 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 41 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 42 lopsis thaliana (sp|o81755|per48_arath : 272.0)
 43 300.1.v2.1 annot-version=v2.1) &
 44
 45
 46
 47
 48 l OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
 49 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 50 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 51 0.4.v2.1 annot-version=v2.1) &
 52 0.4.v2.1 annot-version=v2.1) &
 53 0.4.v2.1 annot-version=v2.1) &
 54 00.2.v2.1 annot-version=v2.1) &
 55
 56
 57
 58
 59 00.2.v2.1 annot-version=v2.1) &
 60 0.4.v2.1 annot-version=v2.1) &

1
 2
 3 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 254.0)
 4 1) &
 5
 6
 7
 8 &
 9 &
 10
 11 hypogaea (sp|p22195|per1_arahy : 381.0)
 12 not-version=v2.1) &
 13 l) &
 14
 15
 16 annot-version=v2.1) &
 17 annot-version=v2.1) &
 18 in=v2.1) &
 19
 20
 21 &
 22 &
 23
 24 :-version=v2.1) &
 25 :-version=v2.1) &
 26
 27 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 28 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 29 annot-version=v2.1) &
 30
 31 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 32 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 33 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
 34 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 35
 36
 37
 38
 39 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 40 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 41 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 42 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 43 OS=Gossypium hirsutum (sp|p0ch30|ring1_goshi : 103.0)
 44 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 45 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 46
 47
 48
 49 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 50 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 51 Arabidopsis thaliana (sp|o81755|per48_arath : 290.0)
 52 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 53 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 54 Arabidopsis thaliana (sp|o81755|per48_arath : 272.0)
 55 300.1.v2.1 annot-version=v2.1) &
 56
 57
 58
 59
 60
 61 OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)

1
 2 :in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 3 :in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 4 0.4.v2.1 annot-version=v2.1) &
 5 0.4.v2.1 annot-version=v2.1) &
 6 0.4.v2.1 annot-version=v2.1) &
 7 0.4.v2.1 annot-version=v2.1) &
 8 0.2.v2.1 annot-version=v2.1) &
 9
 10
 11
 12 0.2.v2.1 annot-version=v2.1) &
 13 0.4.v2.1 annot-version=v2.1) &
 14
 15
 16 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 254.0)
 17 1) &
 18
 19
 20
 21 &
 22 &
 23 hypogaea (sp|p22195|per1_arahy : 381.0)
 24 not-version=v2.1) &
 25 l) &
 26
 27
 28
 29 annot-version=v2.1) &
 30 annot-version=v2.1) &
 31 in=v2.1) &
 32
 33
 34
 35 &
 36 &
 37 :-version=v2.1) &
 38 :-version=v2.1) &
 39
 40 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 41 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 42 annot-version=v2.1) &
 43 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 44 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 45 L OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
 46 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 47
 48
 49
 50
 51
 52 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 53 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 54 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 55 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 56 OS=Gossypium hirsutum (sp|p0ch30|ring1_goshi : 103.0)
 57 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 58 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 59
 60

1
 2 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 3 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 4 lopsis thaliana (sp|o81755|per48_arath : 290.0)
 5
 6 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 7 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 8 lopsis thaliana (sp|o81755|per48_arath : 272.0)
 9
 10 300.1.v2.1 annot-version=v2.1) &
 11
 12
 13
 14 l OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
 15 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 16 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 17
 18 0.4.v2.1 annot-version=v2.1) &
 19 0.4.v2.1 annot-version=v2.1) &
 20 0.4.v2.1 annot-version=v2.1) &
 21 00.2.v2.1 annot-version=v2.1) &
 22
 23
 24
 25 00.2.v2.1 annot-version=v2.1) &
 26 0.4.v2.1 annot-version=v2.1) &
 27
 28
 29 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 254.0)
 30 l) &
 31
 32
 33
 34
 35 &
 36 &
 37 hypogaea (sp|p22195|per1_arahy : 381.0)
 38 not-version=v2.1) &
 39 l) &
 40
 41
 42 annot-version=v2.1) &
 43 annot-version=v2.1) &
 44 in=v2.1) &
 45
 46
 47
 48 &
 49 &
 50 :-version=v2.1) &
 51 :-version=v2.1) &
 52
 53 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 54 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 55 annot-version=v2.1) &
 56 rabadopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 57 rabadopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 58 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
 59 rabadopsis thaliana (sp|q8rx22|mip1_arath : 389.0)

1
 2
 3
 4 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 5 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 6 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 7 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 8 OS=Gossypium hirsutum (sp|p0ch30|ring1_goshi : 103.0)
 9 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 10 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 11
 12 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 13 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 14
 15 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 16 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 17 lopsis thaliana (sp|o81755|per48_arath : 290.0)
 18 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 19 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 20 lopsis thaliana (sp|o81755|per48_arath : 272.0)
 21 300.1.v2.1 annot-version=v2.1) &
 22
 23
 24
 25
 26
 27 OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
 28 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 29 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 30 0.4.v2.1 annot-version=v2.1) &
 31 0.4.v2.1 annot-version=v2.1) &
 32 0.4.v2.1 annot-version=v2.1) &
 33 0.2.v2.1 annot-version=v2.1) &
 34
 35
 36
 37
 38
 39 0.2.v2.1 annot-version=v2.1) &
 40 0.4.v2.1 annot-version=v2.1) &
 41
 42
 43 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 254.0)
 44 1) &
 45
 46
 47
 48 &
 49 &
 50 hypogaea (sp|p22195|per1_arahy : 381.0)
 51 not-version=v2.1) &
 52 l) &
 53
 54
 55
 56 annot-version=v2.1) &
 57 annot-version=v2.1) &
 58 in=v2.1) &
 59
 60 &

1
 2 &
 3 :-version=v2.1) &
 4 :-version=v2.1) &
 5
 6 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 7 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 8 annot-version=v2.1) &
 9
 10 rabadopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 11 rabadopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 12 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
 13 rabadopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 14
 15
 16
 17
 18 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 19 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 20 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 21 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 22 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 23 OS=Gossypium hirsutum (sp|p0ch30|ring1_goshi : 103.0)
 24 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 25 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 26
 27
 28 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 29 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 30
 31 lopsis thaliana (sp|o81755|per48_arath : 290.0)
 32 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 33 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 34 lopsis thaliana (sp|o81755|per48_arath : 272.0)
 35 300.1.v2.1 annot-version=v2.1) &
 36
 37
 38
 39
 40 l OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
 41 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 42 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 43 0.4.v2.1 annot-version=v2.1) &
 44 0.4.v2.1 annot-version=v2.1) &
 45 0.4.v2.1 annot-version=v2.1) &
 46 0.4.v2.1 annot-version=v2.1) &
 47 0.2.v2.1 annot-version=v2.1) &
 48
 49
 50
 51
 52 0.2.v2.1 annot-version=v2.1) &
 53 0.4.v2.1 annot-version=v2.1) &
 54
 55
 56 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 254.0)
 57 1) &
 58
 59
 60
 &

1 &
 2 &
 3 hypogaea (sp|p22195|per1_arahy : 381.0)
 4 not-version=v2.1) &
 5 l) &
 6
 7
 8 annot-version=v2.1) &
 9 annot-version=v2.1) &
 10 in=v2.1) &
 11
 12
 13 &
 14 &
 15 :-version=v2.1) &
 16 :-version=v2.1) &
 17
 18
 19 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 20 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 21 annot-version=v2.1) &
 22
 23 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 24 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 25 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
 26 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 27
 28
 29
 30
 31 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 32 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 33 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 34 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 35 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 36 OS=Gossypium hirsutum (sp|p0ch30|ring1_goshi : 103.0)
 37 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 38 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 39
 40
 41 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 42 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 43 Arabidopsis thaliana (sp|o81755|per48_arath : 290.0)
 44 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 45 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 46 Arabidopsis thaliana (sp|o81755|per48_arath : 272.0)
 47
 48
 49 300.1.v2.1 annot-version=v2.1) &
 50
 51
 52
 53 l OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
 54 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 55 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 56 0.4.v2.1 annot-version=v2.1) &
 57 0.4.v2.1 annot-version=v2.1) &
 58 0.4.v2.1 annot-version=v2.1) &
 59 0.4.v2.1 annot-version=v2.1) &
 60 0.4.v2.1 annot-version=v2.1) &

1
 2
 3
 4 J0.2.v2.1 annot-version=v2.1) &
 5 0.4.v2.1 annot-version=v2.1) &
 6
 7
 8 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 254.0)
 9 1) &
 10
 11
 12
 13 &
 14 &
 15 hypogaea (sp|p22195|per1_arahy : 381.0)
 16 not-version=v2.1) &
 17 l) &
 18
 19
 20
 21 annot-version=v2.1) &
 22 annot-version=v2.1) &
 23 in=v2.1) &
 24
 25
 26
 27 &
 28 &
 29 :-version=v2.1) &
 30 :-version=v2.1) &
 31
 32 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 33 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 34 annot-version=v2.1) &
 35 arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 36 arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 37 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
 38 arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 39
 40
 41
 42
 43
 44 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 45 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 46 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 47 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 48 OS=Gossypium hirsutum (sp|p0ch30|ring1_goshi : 103.0)
 49 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 50 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 51
 52
 53
 54 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 55 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 56 Arabidopsis thaliana (sp|o81755|per48_arath : 290.0)
 57 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 58 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 59 Arabidopsis thaliana (sp|o81755|per48_arath : 272.0)
 60

1 300.1.v2.1 annot-version=v2.1) &
 2
 3
 4
 5
 6 | OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
 7 |in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 8 |in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 9
 10 0.4.v2.1 annot-version=v2.1) &
 11 0.4.v2.1 annot-version=v2.1) &
 12 0.4.v2.1 annot-version=v2.1) &
 13 00.2.v2.1 annot-version=v2.1) &
 14
 15
 16
 17 00.2.v2.1 annot-version=v2.1) &
 18 0.4.v2.1 annot-version=v2.1) &
 19
 20
 21 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 254.0)
 22 1) &
 23
 24
 25
 26
 27 &
 28 &
 29 hypogaea (sp|p22195|per1_arahy : 381.0)
 30 not-version=v2.1) &
 31 l) &
 32
 33
 34
 35 annot-version=v2.1) &
 36 annot-version=v2.1) &
 37 in=v2.1) &
 38
 39
 40 &
 41 &
 42 :-version=v2.1) &
 43 :-version=v2.1) &
 44
 45 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 46 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 47 annot-version=v2.1) &
 48 rabadopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 49 rabadopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 50 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
 51 rabadopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 52
 53
 54
 55
 56
 57 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 58 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 59 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 60 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)

1 OS=Gossypium hirsutum (sp|p0ch30|ring1_goshi : 103.0)
 2 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 3 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 4
 5
 6
 7 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 8 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 9
 10 lopsis thaliana (sp|o81755|per48_arath : 290.0)
 11 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 12 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 13 lopsis thaliana (sp|o81755|per48_arath : 272.0)
 14 300.1.v2.1 annot-version=v2.1) &
 15
 16
 17
 18
 19 OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
 20 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 21 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 22 0.4.v2.1 annot-version=v2.1) &
 23 0.4.v2.1 annot-version=v2.1) &
 24 0.4.v2.1 annot-version=v2.1) &
 25 00.2.v2.1 annot-version=v2.1) &
 26
 27
 28
 29
 30
 31 00.2.v2.1 annot-version=v2.1) &
 32 0.4.v2.1 annot-version=v2.1) &
 33
 34
 35 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 254.0)
 36 1) &
 37
 38
 39
 40 &
 41 &
 42
 43 hypogaea (sp|p22195|per1_arahy : 381.0)
 44 not-version=v2.1) &
 45 l) &
 46
 47
 48 annot-version=v2.1) &
 49 annot-version=v2.1) &
 50 in=v2.1) &
 51
 52
 53 &
 54 &
 55
 56 :-version=v2.1) &
 57 :-version=v2.1) &
 58 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 59 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 60 annot-version=v2.1) &

1
2 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
3 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
4 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
5 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
6
7
8
9
10 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
11 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
12 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
13 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
14 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
15 OS=Gossypium hirsutum (sp|p0ch30|ring1_goshi : 103.0)
16 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
17 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
18
19
20 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
21 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
22 Arabidopsis thaliana (sp|o81755|per48_arath : 290.0)
23 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
24 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
25 Arabidopsis thaliana (sp|o81755|per48_arath : 272.0)
26 300.1.v2.1 annot-version=v2.1) &
27
28
29
30
31
32 l OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
33 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
34 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
35 0.4.v2.1 annot-version=v2.1) &
36 0.4.v2.1 annot-version=v2.1) &
37 0.4.v2.1 annot-version=v2.1) &
38 0.4.v2.1 annot-version=v2.1) &
39 0.4.v2.1 annot-version=v2.1) &
40 0.4.v2.1 annot-version=v2.1) &
41
42
43
44 0.4.v2.1 annot-version=v2.1) &
45 0.4.v2.1 annot-version=v2.1) &
46
47
48 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 254.0)
49 1) &
50
51
52
53 &
54 &
55
56 hypogaea (sp|p22195|per1_arahy : 381.0)
57 not-version=v2.1) &
58 l) &
59
60
annot-version=v2.1) &

1
 2 annot-version=v2.1) &
 3 in=v2.1) &
 4
 5
 6 &
 7 &
 8 :-version=v2.1) &
 9 :-version=v2.1) &
 10
 11 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 12 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 13
 14 annot-version=v2.1) &
 15 rabadopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 16 rabadopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 17
 18 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
 19 rabadopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 20
 21
 22
 23 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 24 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 25 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 26 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 27 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 28 OS=Gossypium hirsutum (sp|p0ch30|ring1_goshi : 103.0)
 29 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 30 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 31
 32
 33 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 34 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 35
 36 lopsis thaliana (sp|o81755|per48_arath : 290.0)
 37 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 38 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 39
 40 lopsis thaliana (sp|o81755|per48_arath : 272.0)
 41
 42 300.1.v2.1 annot-version=v2.1) &
 43
 44
 45
 46 l OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
 47 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 48 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 49 0.4.v2.1 annot-version=v2.1) &
 50 0.4.v2.1 annot-version=v2.1) &
 51 0.4.v2.1 annot-version=v2.1) &
 52 0.4.v2.1 annot-version=v2.1) &
 53 00.2.v2.1 annot-version=v2.1) &
 54
 55
 56
 57 00.2.v2.1 annot-version=v2.1) &
 58 0.4.v2.1 annot-version=v2.1) &
 59
 60 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 254.0)

1
2 1) &
3
4
5
6 &
7 &
8 hypogaea (sp|p22195|per1_arahy : 381.0)
9 not-version=v2.1) &
10 l) &
11
12
13 annot-version=v2.1) &
14 annot-version=v2.1) &
15 in=v2.1) &
16
17
18
19 &
20 &
21 :-version=v2.1) &
22 :-version=v2.1) &
23 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
24 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
25
26 annot-version=v2.1) &
27 arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
28 arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
29 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
30 arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
31
32
33
34
35
36 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
37 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
38 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
39 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
40 OS=Gossypium hirsutum (sp|p0ch30|ring1_goshi : 103.0)
41 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
42 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
43
44 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
45
46 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
47 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
48 Arabidopsis thaliana (sp|o81755|per48_arath : 290.0)
49 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
50 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
51 Arabidopsis thaliana (sp|o81755|per48_arath : 272.0)
52 300.1.v2.1 annot-version=v2.1) &
53
54
55
56
57
58 l OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
59 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
60 in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)

1
 2 0.4.v2.1 annot-version=v2.1) &
 3 0.4.v2.1 annot-version=v2.1) &
 4 0.4.v2.1 annot-version=v2.1) &
 5
 6 J0.2.v2.1 annot-version=v2.1) &
 7
 8
 9
 10 J0.2.v2.1 annot-version=v2.1) &
 11 0.4.v2.1 annot-version=v2.1) &
 12
 13
 14 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 254.0)
 15 1) &
 16
 17
 18
 19 &
 20 &
 21 hypogaea (sp|p22195|per1_arahy : 381.0)
 22 not-version=v2.1) &
 23 l) &
 24
 25
 26
 27 annot-version=v2.1) &
 28 annot-version=v2.1) &
 29 in=v2.1) &
 30
 31
 32 &
 33 &
 34
 35 :-version=v2.1) &
 36 :-version=v2.1) &
 37 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 38 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 39 annot-version=v2.1) &
 40 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 41 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 42 Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
 43 Arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 44
 45
 46
 47
 48
 49 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 50 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 51 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 52 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 53 OS=Gossypium hirsutum (sp|p0ch30|ring1_goshi : 103.0)
 54 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 55 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 56
 57
 58
 59
 60 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)

1
 2 lopsis thaliana (sp|o81755|per48_arath : 290.0)
 3 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 4 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
 5
 6 lopsis thaliana (sp|o81755|per48_arath : 272.0)
 7 300.1.v2.1 annot-version=v2.1) &
 8
 9
 10
 11 OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
 12 :in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 13 :in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)
 14
 15 0.4.v2.1 annot-version=v2.1) &
 16 0.4.v2.1 annot-version=v2.1) &
 17 0.4.v2.1 annot-version=v2.1) &
 18 00.2.v2.1 annot-version=v2.1) &
 19
 20
 21
 22
 23 00.2.v2.1 annot-version=v2.1) &
 24 0.4.v2.1 annot-version=v2.1) &
 25
 26
 27 OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 254.0)
 28 1) &
 29
 30
 31
 32 &
 33 &
 34 hypogaea (sp|p22195|per1_arahy : 381.0)
 35 not-version=v2.1) &
 36 l) &
 37
 38
 39
 40 annot-version=v2.1) &
 41 annot-version=v2.1) &
 42 in=v2.1) &
 43
 44
 45 &
 46 &
 47 :-version=v2.1) &
 48 :-version=v2.1) &
 49
 50 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 51 ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
 52
 53 annot-version=v2.1) &
 54
 55 arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 56 arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 57 l OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
 58 arabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
 59
 60

1
2 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
3 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
4 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
5 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
6 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
7 OS=Gossypium hirsutum (sp|p0ch30|ring1_goshi : 103.0)
8 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
9 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
10
11
12 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
13 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
14 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
15 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
16 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
17 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
18 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
19 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
20 2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
21 300.1.v2.1 annot-version=v2.1) &
22
23
24 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
25 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
26 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
27 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
28 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
29 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
30 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
31 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
32 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
33 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
34 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
35 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
36 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
37 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
38 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
39 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
40 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
41 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
42 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
43 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
44 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
45 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
46 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
47 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
48 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
49 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
50 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
51 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
52 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
53 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
54 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
55 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
56 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
57 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
58 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
59 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
60 2, chloroplastic OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)

1
2 0.2.v2.1 annot-version=v2.1) &

3
4 not-version=v2.1) &
5
6 annot-version=v2.1) &
7
8
9
10
11

12 ing protein At3g09040, mitochondrial OS=Arabidopsis thaliana (sp|q9ss83|pp220_arath : 397.0)
13 3G283500 ID=Phvul.003G283500.1.v2.1 annot-version=v2.1) &

14 l) &
15
16 in=v2.1) &
17
18

19 sferring phosphorus-containing group(50.2.7 : 89.3) (original description: pacid=37170327 transcrip

20
21
22 ial description: pacid=37159307 transcript=Phvul.008G140600.1 locus=Phvul.008G140600 ID=Phvul
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &

i60 transcript=Phvul.007G106300.1 locus=Phvul.007G106300 ID=Phvul.007G106300.1.v2.1 annot-v

Do not distribute

vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

60 transcript=Phvul.007G106300.1 locus=Phvul.007G106300 ID=Phvul.007G106300.1.v2.1 annot-v

vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &

60 transcript=Phvul.007G106300.1 locus=Phvul.007G106300 ID=Phvul.007G106300.1.v2.1 annot-v

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &

60 transcript=Phvul.007G106300.1 locus=Phvul.007G106300 ID=Phvul.007G106300.1.v2.1 annot-v

1
2
3
4
5
6
7
8
9
10 vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
11 vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26

27 i60 transcript=Phvul.007G106300.1 locus=Phvul.007G106300 ID=Phvul.007G106300.1.v2.1 annot-v
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55 vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
56 vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

i60 transcript=Phvul.007G106300.1 locus=Phvul.007G106300 ID=Phvul.007G106300.1.v2.1 annot-v

vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &

i60 transcript=Phvul.007G106300.1 locus=Phvul.007G106300 ID=Phvul.007G106300.1.v2.1 annot-v

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &

i60 transcript=Phvul.007G106300.1 locus=Phvul.007G106300 ID=Phvul.007G106300.1.v2.1 annot-v

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &

i60 transcript=Phvul.007G106300.1 locus=Phvul.007G106300 ID=Phvul.007G106300.1.v2.1 annot-v

Do not distribute

1
2
3
4
5
6
7
8 i60 transcript=Phvul.007G106300.1 locus=Phvul.007G106300 ID=Phvul.007G106300.1.v2.1 annot-v
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36 vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
37 vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53 i60 transcript=Phvul.007G106300.1 locus=Phvul.007G106300 ID=Phvul.007G106300.1.v2.1 annot-v
54
55
56
57
58
59
60

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &

i60 transcript=Phvul.007G106300.1 locus=Phvul.007G106300 ID=Phvul.007G106300.1.v2.1 annot-v

Do not distribute

1
2
3
4 vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
5 vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49 vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
50 vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
51
52
53
54
55
56
57
58
59
60

60 transcript=Phvul.007G106300.1 locus=Phvul.007G106300 ID=Phvul.007G106300.1.v2.1 annot-v

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

i60 transcript=Phvul.007G106300.1 locus=Phvul.007G106300 ID=Phvul.007G106300.1.v2.1 annot-v

vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &

i60 transcript=Phvul.007G106300.1 locus=Phvul.007G106300 ID=Phvul.007G106300.1.v2.1 annot-v

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &

i60 transcript=Phvul.007G106300.1 locus=Phvul.007G106300 ID=Phvul.007G106300.1.v2.1 annot-v

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &
vul.002G017700.2 locus=Phvul.002G017700 ID=Phvul.002G017700.2.v2.1 annot-version=v2.1) &

i60 transcript=Phvul.007G106300.1 locus=Phvul.007G106300 ID=Phvul.007G106300.1.v2.1 annot-v

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

it=Phvul.001G243500.2 locus=Phvul.001G243500 ID=Phvul.001G243500.2.v2.1 annot-version=v2.1)
l.008G140600.1.v2.1 annot-version=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

ersion=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

ersion=v2.1) &

ersion=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

ersion=v2.1) &

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

ersion=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

ersion=v2.1) &

Do not distribute

ersion=v2.1) &

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

ersion=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

ersion=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

ersion=v2.1) &

ersion=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

ersion=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

ersion=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

ersion=v2.1) &

ersion=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

ersion=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

ersion=v2.1) &

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28
- 29
- 30
- 31
- 32
- 33
- 34
- 35
- 36
- 37
- 38
- 39
- 40
- 41
- 42
- 43
- 44
- 45
- 46
- 47
- 48
- 49
- 50
- 51
- 52
- 53
- 54
- 55
- 56
- 57
- 58
- 59
- 60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

Do not distribute

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60

) &

Do not distribute

Supplementary Table 4: Primers used for qPCR experiments

| cDNA | Gene reference no. | Function | Primer sequence |
|---------------|---------------------------|------------------------------|--|
| UBI | CV543388 | Ubiquitin | GAGGATGGTCGCACCCTGGCT CCCTCCTTGTCTGAATCTTA |
| EF1- α | GI151368189 | Elongation factor 1 α | CAAGGATCTCAAGCGTGGTTTCG TGGGAGGTGTGGCAATCAAGC |
| WRK72 | Phvul.003G068700 | WRKY72 TF | CCATTCCTGGGGCATCTTTG TGATTGCTTTGGTTGCAGCT |